


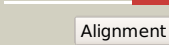
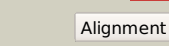



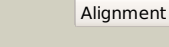



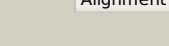



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2797c_(-)_3105629_3107317
Date	Wed Aug 7 12:50:45 BST 2019
Unique Job ID	80a47e58f1a9bb00

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4cgkA_	 Alignment		98.2	14	PDB header: cell cycle Chain: A: PDB Molecule: secreted 45 kda protein; PDBTitle: crystal structure of the essential protein pcsb from streptococcus2 pneumoniae
2	d1tcaa_	 Alignment		98.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
3	c3icvA_	 Alignment		97.9	20	PDB header: hydrolase Chain: A: PDB Molecule: lipase b; PDBTitle: structural consequences of a circular permutation on lipase b from2 candida antartica
4	d1cexa_	 Alignment		97.7	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
5	c4psdA_	 Alignment		97.6	21	PDB header: hydrolase Chain: A: PDB Molecule: carbohydrate esterase family 5; PDBTitle: structure of trichoderma reesei cutinase native form.
6	c3dd5F_	 Alignment		97.6	13	PDB header: hydrolase Chain: F: PDB Molecule: cutinase; PDBTitle: glomerella cingulata e600-cutinase complex
7	c3gbsA_	 Alignment		97.6	15	PDB header: hydrolase Chain: A: PDB Molecule: cutinase 1; PDBTitle: crystal structure of aspergillus oryzae cutinase
8	c5x88A_	 Alignment		97.6	14	PDB header: hydrolase Chain: A: PDB Molecule: cutinase; PDBTitle: a crystal structure of cutinases from malbranchea cinnamomea
9	d1tiaa_	 Alignment		97.5	24	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
10	d1g66a_	 Alignment		97.4	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
11	c3vkgA_	 Alignment		97.4	12	PDB header: motor protein Chain: A: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of an mtbd truncation mutant of dynein motor domain

12	c3uuuA_	Alignment		97.4	13	PDB header: hydrolase Chain: A; PDB Molecule: lip1, secretory lipase (family 3); PDBTitle: crystal structure of mono- and diacylglycerol lipase from malassezia2 globosa
13	c5gw8A_	Alignment		97.3	14	PDB header: hydrolase Chain: A; PDB Molecule: hypothetical secretory lipase (family 3); PDBTitle: crystal structure of a putative dag-like lipase (mgmdl2) from2 malassezia globosa
14	c3g7nA_	Alignment		97.3	12	PDB header: hydrolase Chain: A; PDB Molecule: lipase; PDBTitle: crystal structure of a triacylglycerol lipase from penicillium2 expansum at 1.3
15	d1uwca_	Alignment		97.3	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
16	c5ew5C_	Alignment		97.3	10	PDB header: hydrolase Chain: C; PDB Molecule: colicin-e9; PDBTitle: crystal structure of colicin e9 in complex with its immunity protein2 im9
17	c3lp5A_	Alignment		97.2	17	PDB header: hydrolase Chain: A; PDB Molecule: putative cell surface hydrolase; PDBTitle: the crystal structure of the putative cell surface hydrolase from2 lactobacillus plantarum wcfs1
18	c3wolB_	Alignment		97.2	10	PDB header: hydrolase Chain: B; PDB Molecule: dipeptidyl aminopeptidase bii; PDBTitle: crystal structure of the dap bii dipeptide complex i
19	d1tiba_	Alignment		97.2	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
20	d1qoza_	Alignment		97.1	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
21	c4oylC_	Alignment	not modelled	97.1	15	PDB header: hydrolase Chain: C; PDB Molecule: cutinase; PDBTitle: humicola insolens cutinase in complex with mono-ethylphosphate
22	c5xk2A_	Alignment	not modelled	97.0	20	PDB header: hydrolase Chain: A; PDB Molecule: diacylglycerol lipase; PDBTitle: crystal structure of mono- and diacylglycerol lipase from aspergillus2 oryzae
23	d1ex9a_	Alignment	not modelled	97.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
24	c3bdvB_	Alignment	not modelled	97.0	18	PDB header: hydrolase Chain: B; PDB Molecule: uncharacterized protein duf1234; PDBTitle: crystal structure of a putative yden-like hydrolase (eca3091) from2 pectobacterium atrosepticum scri1043 at 1.66 a resolution
25	c3ajaA_	Alignment	not modelled	97.0	17	PDB header: hydrolase Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of msmeg_6394
26	c4nfuB_	Alignment	not modelled	97.0	16	PDB header: signaling protein Chain: B; PDB Molecule: senescence-associated carboxylesterase 101; PDBTitle: structure of the central plant immunity signaling node eds1 in complex2 with its interaction partner sag101
27	d1ispa_	Alignment	not modelled	97.0	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
28	c3ngmB_	Alignment	not modelled	97.0	23	PDB header: hydrolase Chain: B; PDB Molecule: extracellular lipase; PDBTitle: crystal structure of lipase from gibberella zeae

29	c3o0dF_	Alignment	not modelled	96.9	23	PDB header: hydrolase Chain: F; PDB Molecule: triacylglycerol lipase; PDBTitle: crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution
30	c6o7xa_	Alignment	not modelled	96.9	12	PDB header: membrane protein Chain: A; PDB Molecule: vacuolar atp synthase catalytic subunit a; PDBTitle: saccharomyces cerevisiae v-atpase stv1-v1vo state 3
31	c1mo2A_	Alignment	not modelled	96.8	23	PDB header: transferase Chain: A; PDB Molecule: erythronolide synthase, modules 5 and 6; PDBTitle: thioesterase domain from 6-deoxyerythronolide synthase (debs te), ph2 8.5
32	d1mo2a_	Alignment	not modelled	96.8	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
33	d1ei9a_	Alignment	not modelled	96.8	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases
34	c2i1kA_	Alignment	not modelled	96.7	10	PDB header: cell adhesion, membrane protein Chain: A; PDB Molecule: moesin; PDBTitle: moesin from spodoptera frugiperda reveals the coiled-coil domain at2 3.0 angstrom resolution
35	c5gasN_	Alignment	not modelled	96.7	16	PDB header: hydrolase Chain: N; PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2
36	c3vkgB_	Alignment	not modelled	96.7	13	PDB header: motor protein Chain: B; PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of an mtd truncation mutant of dynein motor domain
37	c6qppA_	Alignment	not modelled	96.7	21	PDB header: hydrolase Chain: A; PDB Molecule: lipase; PDBTitle: rhizomucor miehei lipase propeptide complex, native
38	c3ilsA_	Alignment	not modelled	96.7	21	PDB header: hydrolase Chain: A; PDB Molecule: afatoxin biosynthesis polyketide synthase; PDBTitle: the thioesterase domain from pksa
39	c6cl4A_	Alignment	not modelled	96.7	16	PDB header: hydrolase Chain: A; PDB Molecule: lipase c12; PDBTitle: lipc12 - lipase from metagenomics
40	c4gw3A_	Alignment	not modelled	96.6	18	PDB header: hydrolase Chain: A; PDB Molecule: putative lipase; PDBTitle: crystal structure of the lipase from proteus mirabilis
41	c2czqB_	Alignment	not modelled	96.6	25	PDB header: hydrolase Chain: B; PDB Molecule: cutinase-like protein; PDBTitle: a novel cutinase-like protein from cryptococcus sp.
42	c2yiiA_	Alignment	not modelled	96.5	20	PDB header: hydrolase Chain: A; PDB Molecule: phospholipase a1-iigamma; PDBTitle: crystal structure of phospholipase a1
43	c1y4cA_	Alignment	not modelled	96.5	9	PDB header: de novo protein Chain: A; PDB Molecule: maltose binding protein fused with designed PDBTitle: designed helical protein fusion mbp
44	d3tgla_	Alignment	not modelled	96.5	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
45	c3ds8A_	Alignment	not modelled	96.4	21	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: lin2722 protein; PDBTitle: the crysatl structure of the gene lin2722 products from listeria2 innocua
46	c5h6bA_	Alignment	not modelled	96.4	16	PDB header: hydrolase Chain: A; PDB Molecule: putative secreted lipase; PDBTitle: crystal structure of a thermostable lipase from marine streptomyces
47	c5f2hA_	Alignment	not modelled	96.2	21	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
48	c6gapB_	Alignment	not modelled	96.2	10	PDB header: viral protein Chain: B; PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t3d reovirus sigma1 coiled coil tail and body
49	d1cvla_	Alignment	not modelled	96.2	29	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
50	c2qjwA_	Alignment	not modelled	96.2	20	PDB header: hydrolase Chain: A; PDB Molecule: uncharacterized protein xcc1541; PDBTitle: crystal structure of a putative hydrolase of the alpha/beta2 superfamily (xcc1541) from xanthomonas campestris pv. campestris at3 1.35 a resolution
51	c2rauA_	Alignment	not modelled	96.1	16	PDB header: hydrolase Chain: A; PDB Molecule: putative esterase; PDBTitle: crystal structure of a putative lipase (np_343859.1) from sulfolobus2 solfataricus at 1.85 a resolution
52	c2vs0B_	Alignment	not modelled	96.1	10	PDB header: cell invasion Chain: B; PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
53	c3lcrA_	Alignment	not modelled	96.1	22	PDB header: hydrolase Chain: A; PDB Molecule: tautomycin biosynthetic pks; PDBTitle: thioesterase from tautomycin biosynthetic pathway
54	c2qmqA_	Alignment	not modelled	96.1	16	PDB header: signaling protein Chain: A; PDB Molecule: protein ndrg2; PDBTitle: crystal structure of a n-myc downstream regulated 2 protein (ndrg2,2 syld, ndr2, ai182517, au040374) from mus musculus at 1.70 a3 resolution

55	c2q0xA	Alignment	not modelled	96.1	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: alpha/beta hydrolase fold protein of unknown function
56	c3I80A	Alignment	not modelled	96.0	18	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1393c; PDBTitle: crystal structure of smu.1393c from streptococcus mutans ua159
57	c1qgeD	Alignment	not modelled	96.0	27	PDB header: hydrolase Chain: D: PDB Molecule: protein (triacylglycerol hydrolase); PDBTitle: new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
58	d1lgya	Alignment	not modelled	96.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
59	c6ogdB	Alignment	not modelled	96.0	9	PDB header: toxin Chain: B: PDB Molecule: toxin subunit yena2; PDBTitle: cryo-em structure of yentca in its prepore state
60	d2h7xa1	Alignment	not modelled	96.0	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
61	c3ojaB	Alignment	not modelled	95.9	10	PDB header: protein binding Chain: B: PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of lrim1/apl1c complex
62	c4iogD	Alignment	not modelled	95.9	9	PDB header: unknown function Chain: D: PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. sterne
63	c5hdfB	Alignment	not modelled	95.9	14	PDB header: hydrolase Chain: B: PDB Molecule: hydrolase; PDBTitle: hydrolase semet-stna
64	d1jmkc	Alignment	not modelled	95.9	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
65	c3gvmA	Alignment	not modelled	95.8	13	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
66	d4lipd	Alignment	not modelled	95.7	25	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
67	c6e6uA	Alignment	not modelled	95.6	18	PDB header: biosynthetic protein Chain: A: PDB Molecule: dieckmann cyclase, ncmc; PDBTitle: variant c89s of dieckmann cyclase, ncmc
68	c2h7xA	Alignment	not modelled	95.5	22	PDB header: hydrolase Chain: A: PDB Molecule: type i polyketide synthase pikaiv; PDBTitle: pikromycin thioesterase adduct with reduced triketide2 affinity label
69	c3zbhC	Alignment	not modelled	95.5	14	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
70	c3qmwD	Alignment	not modelled	95.5	21	PDB header: hydrolase Chain: D: PDB Molecule: thioesterase; PDBTitle: redj with peg molecule bound in the active site
71	c6gajA	Alignment	not modelled	95.4	15	PDB header: viral protein Chain: A: PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t1l reovirus sigma1 coiled coil tail (iodide)
72	c6o7ua	Alignment	not modelled	95.4	12	PDB header: membrane protein Chain: A: PDB Molecule: PDBTitle: saccharomyces cerevisiae v-atpase stv1-vo
73	c5t6oA	Alignment	not modelled	95.3	22	PDB header: biosynthetic protein Chain: A: PDB Molecule: poly-beta-hydroxybuterate polymerase; PDBTitle: structure of the catalytic domain of the class i polyhydroxybutyrate2 synthase from cupriavidus necator
74	c2y6vB	Alignment	not modelled	95.3	13	PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal membrane protein lpx1; PDBTitle: peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from saccharomyces2 cerevisiae (crystal form i)
75	c3fleB	Alignment	not modelled	95.3	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: se_1780 protein; PDBTitle: se_1780 protein of unknown function from staphylococcus epidermidis.
76	c5cwsj	Alignment	not modelled	95.3	10	PDB header: protein transport Chain: J: PDB Molecule: nucleoporin nup49; PDBTitle: crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
77	c2oryA	Alignment	not modelled	95.2	15	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of m37 lipase
78	c2zyiB	Alignment	not modelled	95.2	16	PDB header: hydrolase Chain: B: PDB Molecule: lipase, putative; PDBTitle: a. fulgidus lipase with fatty acid fragment and calcium
79	c2vtvA	Alignment	not modelled	95.2	13	PDB header: hydrolase Chain: A: PDB Molecule: phb depolymerase phaz7; PDBTitle: phaz7 depolymerase from paucimonas lemoignei
80	c4rh7A	Alignment	not modelled	95.2	14	PDB header: motor protein Chain: A: PDB Molecule: green fluorescent protein/cytoplasmic dynein 2 heavy chain PDBTitle: crystal structure of human cytoplasmic dynein 2 motor domain in2 complex with adp.vi

81	c5xavB	Alignment	not modelled	95.2	15	PDB header: biosynthetic protein Chain: B: PDB Molecule: intracellular polyhydroxyalkanoate synthase; PDBTitle: structure of phac from chromobacterium sp. usm2
82	c2vavL	Alignment	not modelled	95.1	13	PDB header: transferase Chain: L: PDB Molecule: acetyl-coa--deacetylcephalosporin c acetyltransferase; PDBTitle: crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)
83	c4x96B	Alignment	not modelled	95.0	18	PDB header: transferase Chain: B: PDB Molecule: phosphatidylcholine-sterol acyltransferase; PDBTitle: low resolution crystal structure of lecithin:cholesterol2 acyltransferase (lcat; residues 21-397)
84	c2cbgA	Alignment	not modelled	95.0	21	PDB header: hydrolase Chain: A: PDB Molecule: fengycin synthetase; PDBTitle: crystal structure of the pmsf-inhibited thioesterase domain of the2 fengycin biosynthesis cluster
85	c5uohA	Alignment	not modelled	95.0	28	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase a; PDBTitle: crystal structure of hip1 (rv2224c) t466a mutant
86	c3i28A	Alignment	not modelled	94.9	12	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
87	c4x91C	Alignment	not modelled	94.8	20	PDB header: transferase Chain: C: PDB Molecule: group xv phospholipase a2; PDBTitle: crystal structure of lysosomal phospholipase a2 in complex with2 isopropyl dodec-11-enylfluorophosphonate (idfp)
88	d1bu8a2	Alignment	not modelled	94.8	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
89	d1etha2	Alignment	not modelled	94.7	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
90	c6ewyA	Alignment	not modelled	94.7	14	PDB header: structural protein Chain: A: PDB Molecule: peptidoglycan endopeptidase ripa; PDBTitle: ripa peptidoglycan hydrolase (rv1477, mycobacterium tuberculosis) n-2 terminal domain
91	c3e0xB	Alignment	not modelled	94.7	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: lipase-esterase related protein; PDBTitle: the crystal structure of a lipase-esterase related protein2 from clostridium acetobutylicum atcc 824
92	c4lwsA	Alignment	not modelled	94.6	10	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
93	d1xkta	Alignment	not modelled	94.6	26	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
94	c5yalA	Alignment	not modelled	94.6	19	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: ferulic acid esterase from streptomyces cinnamoneus at 1.5 a2 resolution
95	c6gaoC	Alignment	not modelled	94.5	10	PDB header: viral protein Chain: C: PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t11 reovirus sigma1 coiled coil tail and body
96	c1cr6A	Alignment	not modelled	94.5	11	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
97	d1lppb2	Alignment	not modelled	94.5	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
98	c3u59C	Alignment	not modelled	94.4	7	PDB header: contractile protein Chain: C: PDB Molecule: tropomyosin beta chain; PDBTitle: n-terminal 98-aa fragment of smooth muscle tropomyosin beta
99	c5w8pA	Alignment	not modelled	94.3	17	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: homoserine transacetylase meta from mycobacterium abscessus
100	c3v48B	Alignment	not modelled	94.3	19	PDB header: hydrolase Chain: B: PDB Molecule: putative aminoacrylate hydrolase rtd; PDBTitle: crystal structure of the putative alpha/beta hydrolase rtd from2 e.coli
101	c5voxb	Alignment	not modelled	94.0	9	PDB header: hydrolase Chain: B: PDB Molecule: v-type proton atpase subunit b; PDBTitle: yeast v-atpase in complex with legionella pneumophila effector sidk2 (rotational state 1)
102	c1gplA	Alignment	not modelled	93.9	15	PDB header: serine esterase Chain: A: PDB Molecule: rp2 lipase; PDBTitle: rp2 lipase
103	d2h1ia1	Alignment	not modelled	93.8	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
104	c1c1gA	Alignment	not modelled	93.8	10	PDB header: contractile protein Chain: A: PDB Molecule: tropomyosin; PDBTitle: crystal structure of tropomyosin at 7 angstroms resolution in the2 spermine-induced crystal form
105	d1gpla2	Alignment	not modelled	93.7	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
106	c4a7fB	Alignment	not modelled	93.7	15	PDB header: structural protein/hydrolase Chain: B: PDB Molecule: tropomyosin 1 alpha; PDBTitle: structure of the actin-tropomyosin-myosin complex (rigor atm 3)

107	c5d6oB_	Alignment	not modelled	93.6	12	PDB header: transferase Chain: B: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acetyler hydrolase from2 corynebacterium glutamicum
108	c2d3eD_	Alignment	not modelled	93.5	14	PDB header: contractile protein Chain: D: PDB Molecule: general control protein gcn4 and tropomyosin 1 alpha chain; PDBTitle: crystal structure of the c-terminal fragment of rabbit skeletal alpha-2 tropomyosin
109	c3qvmA_	Alignment	not modelled	93.5	14	PDB header: hydrolase Chain: A: PDB Molecule: olei00960; PDBTitle: the structure of olei00960, a hydrolase from oleispira antarctica
110	c4qloA_	Alignment	not modelled	93.4	13	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of homoserine o-acetyltransferase from2 staphylococcus aureus
111	c3vvlA_	Alignment	not modelled	93.3	15	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of l-serine-o-acetyltransferase found in d-2 cycloserine biosynthetic pathway
112	c5jxfA_	Alignment	not modelled	93.2	11	PDB header: hydrolase Chain: A: PDB Molecule: asp/glu-specific dipeptidyl-peptidase; PDBTitle: crystal structure of flavobacterium psychrophilum dpp11 in complex2 with dipeptide arg-asp
113	c3q8tB_	Alignment	not modelled	93.2	8	PDB header: apoptosis Chain: B: PDB Molecule: beclin-1; PDBTitle: crystal structure of the coiled coil domain of beclin 1, an essential2 autophagy protein
114	c2zv4O_	Alignment	not modelled	93.2	11	PDB header: structural protein Chain: O: PDB Molecule: major vault protein; PDBTitle: the structure of rat liver vault at 3.5 angstrom resolution
115	d1hpla2	Alignment	not modelled	93.1	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
116	c2pvsB_	Alignment	not modelled	93.1	14	PDB header: hydrolase Chain: B: PDB Molecule: pancreatic lipase-related protein 2; PDBTitle: structure of human pancreatic lipase related protein 22 mutant n336q
117	c5jkjA_	Alignment	not modelled	93.1	19	PDB header: hydrolase Chain: A: PDB Molecule: esterase e22; PDBTitle: crystal structure of esterase e22 l374d mutant
118	d2pl5a1	Alignment	not modelled	93.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
119	c3flaB_	Alignment	not modelled	93.0	19	PDB header: hydrolase Chain: B: PDB Molecule: rifr; PDBTitle: rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1
120	d1pjaa_	Alignment	not modelled	92.9	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases