







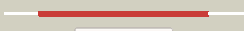
























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1cr6A_	 Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
2	c2qmqa_	 Alignment		100.0	12	PDB header: signaling protein Chain: A: PDB Molecule: protein ndr2; 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
3	c2xmza_	 Alignment		100.0	27	PDB header: lyase Chain: A: PDB Molecule: hydrolase, alpha/beta hydrolase fold family; PDBTitle: structure of menh from s. aureus
4	d1r3da_	 Alignment		100.0	35	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hypothetical protein VC1974
5	c2y6vB_	 Alignment		100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal membrane protein lpx1; PDBTitle: peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from2 saccharomyces cerevisiae (crystal form i)
6	c2vavL_	 Alignment		100.0	13	PDB header: transferase Chain: L: PDB Molecule: acetyl-coa--deacetylcephalosporin c PDBTitle: crystal structure of deacetylcephalosporin c2 acetyltransferase (dac-soak)
7	c3ibtA_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 1h-3-hydroxy-4-oxoquinoline 2,4-dioxygenase; PDBTitle: structure of 1h-3-hydroxy-4-oxoquinoline 2,4-dioxygenase (qdo)
8	c3v48B_	 Alignment		100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: putative aminoacrylate hydrolase rutd; PDBTitle: crystal structure of the putative alpha/beta hydrolase rutd from2 e.coli
9	c2wj4B_	 Alignment		100.0	13	PDB header: oxidoreductase Chain: B: PDB Molecule: 1h-3-hydroxy-4-oxoquinaldine 2,4-dioxygenase; PDBTitle: crystal structure of the cofactor-devoid 1-h-3-hydroxy-4-2 oxoquinaldine 2,4-dioxygenase (hod) from arthrobacter3 nitroguajacolicus ru61a anaerobically complexed with its4 natural substrate 1-h-3-hydroxy-4-oxoquinaldine
10	c3iliA_	 Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
11	d2b61a1	 Alignment		100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase

12	d1m33a_	Alignment		100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Biotin biosynthesis protein BioH
13	c2r11D_	Alignment		100.0	15	PDB header: hydrolase Chain: D: PDB Molecule: carboxylesterase np; PDBTitle: crystal structure of putative hydrolase (2632844) from2 bacillus subtilis at 1.96 a resolution
14	c3om8A_	Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: probable hydrolase; PDBTitle: the crystal structure of a hydrolase from pseudomonas aeruginosa pa01
15	c3oosA_	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase family protein; PDBTitle: the structure of an alpha/beta fold family hydrolase from bacillus2 anthracis str. sterne
16	c2cjpA_	Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: structure of potato (solanum tuberosum) epoxide hydrolase l2 (steh1)
17	c2yysA_	Alignment		100.0	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: proline iminopeptidase-related protein; PDBTitle: crystal structure of the proline iminopeptidase-related protein2 ttha1809 from thermus thermophilus hb8
18	c2e3iA_	Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase ephb; PDBTitle: the crystal structure of epoxide hydrolase b (rv1938) from2 mycobacterium tuberculosis at 2.1 angstrom
19	c3qvmA_	Alignment		100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: olei00960; PDBTitle: the structure of olei00960, a hydrolase from oleispira antarctica
20	d1ehya_	Alignment		100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
21	d1b6ga_	Alignment	not modelled	100.0	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
22	d2vata1	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
23	c2xuaH_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: H: PDB Molecule: 3-oxoadipate enol-lactonase; PDBTitle: crystal structure of the enol-lactonase from burkholderia2 xenovorans lb400
24	c3e3aA_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: possible peroxidase bpoc; PDBTitle: the structure of rv0554 from mycobacterium tuberculosis
25	c3bf7B_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: esterase ybff; PDBTitle: 1.1 resolution structure of ybff, a new esterase from2 escherichia coli: a unique substrate-binding crevice3 generated by domain arrangement
26	d1cr6a2	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
27	d1c4xa_	Alignment	not modelled	100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
28	c2vf2A_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate PDBTitle: x-ray crystal structure of hsd from mycobacterium2 tuberculosis

29	d1zd3a2	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
30	c3a2nF	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: F: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of dbja (wild type type ii p21)
31	c3kxpD	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: D: PDB Molecule: alpha-(n-acetylaminomethylene)succinic acid PDBTitle: crystal structure of e-2-(acetamidomethylene)succinate2 hydrolase
32	c3e0xB	Alignment	not modelled	100.0	19	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
33	c3kdaB	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: cftr inhibitory factor (cif); PDBTitle: crystal structure of the cftr inhibitory factor cif with the h269a2 mutation
34	c3bwxA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase; PDBTitle: crystal structure of an alpha/beta hydrolase (yp_496220.1) from2 novosphingobium aromaticivorans dsm 12444 at 1.50 a resolution
35	c1zoiC	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: C: PDB Molecule: esterase; PDBTitle: crystal structure of a stereoselective esterase from2 pseudomonas putida ifo12996
36	d2rhw1	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
37	d1q0ra	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Aclacinomycin methylesterase RdmC
38	c1u2eA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: 2-hydroxy-6-ketonona-2,4-dienedioic acid PDBTitle: crystal structure of the c-c bond hydrolase mhpc
39	d2pl5a1	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
40	c2xt0A	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: dehalogenase dppa from plasiocystis pacifica sir-i
41	d1a8sa	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
42	d1qo7a	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
43	d1mtza	Alignment	not modelled	100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
44	c1wprA	Alignment	not modelled	100.0	18	PDB header: signaling protein Chain: A: PDB Molecule: sigma factor sigb regulation protein rsbq; PDBTitle: crystal structure of rsbq inhibited by pmsf
45	c3l80A	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1393c; PDBTitle: crystal structure of smu.1393c from streptococcus mutans ua159
46	d1bn7a	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
47	c3u1tA	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: dmma haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase, dmma, of marine microbial origin
48	d1azwa	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
49	c3fsgC	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: C: PDB Molecule: alpha/beta superfamily hydrolase; PDBTitle: crystal structure of alpha/beta superfamily hydrolase from oenococcus2 oeni psu-1
50	d1hkha	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
51	c1y37A	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: fluoroacetate dehalogenase; PDBTitle: structure of fluoroacetate dehalogenase from burkholderia sp. fa1
52	d1brta	Alignment	not modelled	100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
53	c3r0vA	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: the crystal structure of an alpha/beta hydrolase from sphaeobacter2 thermophilus dsm 20745.
54	d1va4a	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase

55	c3fobA	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: bromoperoxidase; PDBTitle: crystal structure of bromoperoxidase from bacillus anthracis
56	d1a8qa	Alignment	not modelled	100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
57	c3qyiB	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: alr0039 protein; PDBTitle: crystal structure of alr0039, a putative alpha/beta hydrolase from2 nostoc sp pcc 7120.
58	d1a88a	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
59	d1xkla	Alignment	not modelled	100.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like
60	c3p2mA	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: possible hydrolase; PDBTitle: crystal structure of a novel esterase rv0045c from mycobacterium2 tuberculosis
61	d1wm1a	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
62	d1e89a	Alignment	not modelled	100.0	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like
63	c3nwoA	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: proline iminopeptidase; PDBTitle: crystal structure of proline iminopeptidase mycobacterium smegmatis
64	c3r3xA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: fluoroacetate dehalogenase; PDBTitle: crystal structure of the fluoroacetate dehalogenase rpa1163 -2 asp110asn/bromoacetate
65	d1mj5a	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
66	c2pseA	Alignment	not modelled	100.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: renilla-luciferin 2-monooxygenase; PDBTitle: crystal structures of the luciferase and green fluorescent2 protein from renilla reniformis
67	c3flaB	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: rifr; PDBTitle: rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1
68	d3c70a1	Alignment	not modelled	100.0	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like
69	c3gzjB	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: B: PDB Molecule: polyneuridine-aldehyde esterase; PDBTitle: crystal structure of polyneuridine aldehyde esterase2 complexed with 16-epi-vellotimine
70	d1uk8a	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
71	c2qvbA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase 3; PDBTitle: crystal structure of haloalkane dehalogenase rv2579 from mycobacterium2 tuberculosis
72	c3dqzB	Alignment	not modelled	100.0	13	PDB header: lyase Chain: B: PDB Molecule: alpha-hydroxynitrile lyase-like protein; PDBTitle: structure of the hydroxynitrile lyase from arabidopsis2 thaliana
73	c2ronA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: surfactin synthetase thioesterase subunit; PDBTitle: the external thioesterase of the surfactin-synthetase
74	c3jw8A	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: mgII protein; PDBTitle: crystal structure of human mono-glyceride lipase
75	c3qitB	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: polyketide synthase; PDBTitle: thioesterase domain from curacin biosynthetic pathway
76	c3c5wP	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: P: PDB Molecule: pp2a-specific methylsterase pme-1; PDBTitle: complex between pp2a-specific methylsterase pme-1 and pp2a core2 enzyme
77	cljliA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: meta cleavage compound hydrolase; PDBTitle: crystal structure of a his-tagged serine hydrolase involved2 in the carbazole degradation (carc enzyme)
78	d1jlia	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
79	d1hlga	Alignment	not modelled	100.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
80	c2ockA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: valacyclovir hydrolase; PDBTitle: crystal structure of valacyclovir hydrolase d123n mutant
81	d1xkta	Alignment	not modelled	100.0	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty

					acid synthases
82	c3hjuB_	Alignment	not modelled	100.0	17 PDB header: hydrolase Chain: B: PDB Molecule: monoglyceride lipase; PDBTitle: crystal structure of human monoglyceride lipase
83	d1k8qa_	Alignment	not modelled	100.0	10 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
84	d1imja_	Alignment	not modelled	100.0	20 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Ccg1/TafII250-interacting factor B (Cib)
85	d1pjaa_	Alignment	not modelled	99.9	12 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases
86	c1pjaa_	Alignment	not modelled	99.9	12 PDB header: hydrolase Chain: A: PDB Molecule: palmitoyl-protein thioesterase 2 precursor; PDBTitle: the crystal structure of palmitoyl protein thioesterase-2 reveals the2 basis for divergent substrate specificities of the two lysosomal3 thioesterases (ppt1 and ppt2)
87	c3dyvA_	Alignment	not modelled	99.9	16 PDB header: hydrolase Chain: A: PDB Molecule: esterase d; PDBTitle: snapshots of esterase d from lactobacillus rhamnosus:2 insights into a rotation driven catalytic mechanism
88	c3bdiA_	Alignment	not modelled	99.9	19 PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ta0194; PDBTitle: crystal structure of predicted cib-like hydrolase (np_393672.1) from2 thermoplasma acidophilum at 1.45 a resolution
89	d1tqha_	Alignment	not modelled	99.9	16 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/lipase
90	c2q0xA_	Alignment	not modelled	99.9	12 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: alpha/beta hydrolase fold protein of unknown function
91	c2px6A_	Alignment	not modelled	99.9	11 PDB header: transferase Chain: A: PDB Molecule: thioesterase domain; PDBTitle: crystal structure of the thioesterase domain of human fatty2 acid synthase inhibited by orlistat
92	c3h04A_	Alignment	not modelled	99.9	13 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
93	c3lcrA_	Alignment	not modelled	99.9	19 PDB header: hydrolase Chain: A: PDB Molecule: tautomycetin biosynthetic pks; PDBTitle: thioesterase from tautomycetin biosynthetic pathway
94	c3qmwD_	Alignment	not modelled	99.9	16 PDB header: hydrolase Chain: D: PDB Molecule: thioesterase; PDBTitle: redj with peg molecule bound in the active site
95	c3qm1A_	Alignment	not modelled	99.9	17 PDB header: hydrolase Chain: A: PDB Molecule: cinnamoyl esterase; PDBTitle: crystal structure of the lactobacillus johnsonii cinnamoyl esterase2 lj0536 s106a mutant in complex with ethylferulate, form ii
96	c3llcA_	Alignment	not modelled	99.9	16 PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of putative hydrolase (yp_002548124.1) from2 agrobacterium vitis s4 at 1.80 a resolution
97	c3ilsA_	Alignment	not modelled	99.9	11 PDB header: hydrolase Chain: A: PDB Molecule: aflatoxin biosynthesis polyketide synthase; PDBTitle: the thioesterase domain from pksa
98	d1ex9a_	Alignment	not modelled	99.9	10 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
99	d1ispa_	Alignment	not modelled	99.9	15 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
100	c2rauA_	Alignment	not modelled	99.9	12 PDB header: hydrolase Chain: A: PDB Molecule: putative esterase; PDBTitle: crystal structure of a putative lipase (np_343859.1) from sulfobolus2 solfataricus at 1.85 a resolution
101	c2wtmC_	Alignment	not modelled	99.9	18 PDB header: hydrolase Chain: C: PDB Molecule: est1e; PDBTitle: est1e from butyrivibrio proteoclasticus
102	c2hdwB_	Alignment	not modelled	99.9	13 PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein pa2218; PDBTitle: crystal structure of hypothetical protein pa2218 from pseudomonas2 aeruginosa
103	d1mo2a_	Alignment	not modelled	99.9	15 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
104	c1mo2A_	Alignment	not modelled	99.9	15 PDB header: transferase Chain: A: PDB Molecule: erythronolide synthase, modules 5 and 6; PDBTitle: thioesterase domain from 6-deoxyerythronolide synthase2 (debs te), ph 8.5
105	c2h7xA_	Alignment	not modelled	99.9	18 PDB header: hydrolase Chain: A: PDB Molecule: type i polyketide synthase pikaiv; PDBTitle: pikromycin thioesterase adduct with reduced triketide2 affinity label
106	c2qs9A_	Alignment	not modelled	99.9	17 PDB header: structural protein Chain: A: PDB Molecule: retinoblastoma-binding protein 9; PDBTitle: crystal structure of the human retinoblastoma-binding2 protein 9 (rbbp-9). nesg target hr2978
					PDB header: hydrolase

107	c3fcyB_	Alignment	not modelled	99.9	14	Chain: B: PDB Molecule: xylan esterase 1; PDBTitle: crystal structure of acetyl xylan esterase 1 from2 thermoanaerobacterium sp. jw/sl ys485
108	d1l7aa_	Alignment	not modelled	99.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like
109	c3fleB_	Alignment	not modelled	99.9	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: se_1780 protein; PDBTitle: se_1780 protein of unknown function from staphylococcus epidermidis.
110	c3mveB_	Alignment	not modelled	99.9	12	PDB header: lyase Chain: B: PDB Molecule: upf0255 protein vv1_0328; PDBTitle: crystal structure of a novel pyruvate decarboxylase
111	c3fnbB_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: B: PDB Molecule: acylaminoacyl peptidase smu_737; PDBTitle: crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159
112	d2h7xa1	Alignment	not modelled	99.9	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
113	d1ufoa_	Alignment	not modelled	99.9	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hypothetical protein TT1662
114	d1uxoa_	Alignment	not modelled	99.8	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: YdeN-like
115	c2jbwB_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: B: PDB Molecule: 2,6-dihydroxy-pseudo-oxynicotine hydrolase; PDBTitle: crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine2 hydrolase.
116	c3lp5A_	Alignment	not modelled	99.8	15	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
117	d2jbwa1	Alignment	not modelled	99.8	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: 2,6-dihydropseudooxynicotine hydrolase-like
118	c3ksrA_	Alignment	not modelled	99.8	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
119	d1qlwa_	Alignment	not modelled	99.8	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: A novel bacterial esterase
120	c2hu7A_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: acylamino-acid-releasing enzyme; PDBTitle: binding of inhibitors by acylaminoacyl peptidase