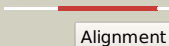

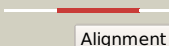
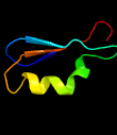





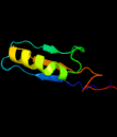
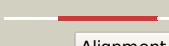


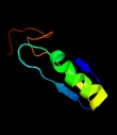







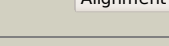
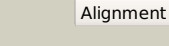

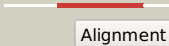



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3337 (-) _3723827_3724213
Date	Thu Aug 8 16:20:55 BST 2019
Unique Job ID	6dd9c1652a313d9c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3i28A_	 Alignment		97.7	36	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
2	c1cr6A_	 Alignment		97.7	36	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
3	c4d9jl_	 Alignment		97.7	30	PDB header: de novo protein Chain: I: PDB Molecule: designed 16nm tetrahedral protein cage containing non-haem PDBTitle: structure of a 16 nm protein cage designed by fusing symmetric2 oligomeric domains
4	d1xkla_	 Alignment		97.7	25	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like
5	c2cjpA_	 Alignment		97.6	27	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: structure of potato (solanum tuberosum) epoxide hydrolase i (steh1)
6	d1va4a_	 Alignment		97.6	28	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
7	d1tqha_	 Alignment		97.6	28	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/lipase
8	d1a8sa_	 Alignment		97.6	26	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
9	c3wibB_	 Alignment		97.5	23	PDB header: hydrolase Chain: B: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of y109w mutant haloalkane dehalogenase data from2 agrobacterium tumefaciens c58
10	c4uhhA_	 Alignment		97.5	35	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural studies of a thermophilic esterase from2 thermogutta terrifontis (cacodylate complex)
11	d1a8qa_	 Alignment		97.5	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase

12	c5h3hB_	 Alignment		97.5	25	PDB header: hydrolase Chain: B: PDB Molecule: abhydrolase domain-containing protein; PDBTitle: esterase (eaest) from exiguobacterium antarcticum
13	c3fobA_	 Alignment		97.5	30	PDB header: oxidoreductase Chain: A: PDB Molecule: bromoperoxidase; PDBTitle: crystal structure of bromoperoxidase from bacillus anthracis
14	c5xmdA_	 Alignment		97.5	30	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase a; PDBTitle: crystal structure of epoxide hydrolase vreh1 from vigna radiata
15	c4y7dA_	 Alignment		97.5	25	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: alpha/beta hydrolase fold protein from nakamurella multipartita
16	c4f0jA_	 Alignment		97.5	23	PDB header: hydrolase Chain: A: PDB Molecule: probable hydrolytic enzyme; PDBTitle: crystal structure of a probable hydrolytic enzyme (pa3053) from2 pseudomonas aeruginosa pao1 at 1.50 a resolution
17	d1hkha_	 Alignment		97.5	28	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
18	d1brta_	 Alignment		97.5	30	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
19	d1zd3a2	 Alignment		97.4	36	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
20	c3wz1B_	 Alignment		97.4	27	PDB header: hydrolase Chain: B: PDB Molecule: zearalenone hydrolase; PDBTitle: zen lactonase
21	c4fbmA_	 Alignment	not modelled	97.4	33	PDB header: hydrolase Chain: A: PDB Molecule: lips lipolytic enzyme; PDBTitle: lips and lipt, two metagenome-derived lipolytic enzymes increase the2 diversity of known lipase and esterase families
22	c4inzB_	 Alignment	not modelled	97.4	28	PDB header: hydrolase Chain: B: PDB Molecule: soluble epoxide hydrolase; PDBTitle: the crystal structure of m145a mutant of an epoxide hydrolase from2 bacillus megaterium
23	c5xksB_	 Alignment	not modelled	97.4	26	PDB header: hydrolase Chain: B: PDB Molecule: thermostable monoacylglycerol lipase; PDBTitle: crystal structure of monoacylglycerol lipase from thermophilic2 geobacillus sp. 12amor
24	c3dyvA_	 Alignment	not modelled	97.4	29	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
25	c5xo6F_	 Alignment	not modelled	97.4	30	PDB header: hydrolase Chain: F: PDB Molecule: lactonase for protein; PDBTitle: crystal structure of a novel zen lactonase mutant
26	c4b9aA_	 Alignment	not modelled	97.4	31	PDB header: hydrolase Chain: A: PDB Molecule: probable epoxide hydrolase; PDBTitle: structure of a putative epoxide hydrolase from pseudomonas2 aeruginosa.
27	c3u1tA_	 Alignment	not modelled	97.3	26	PDB header: hydrolase Chain: A: PDB Molecule: dmma haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase, dmma, of marine microbial origin
28	d1cr6a2	 Alignment	not modelled	97.3	36	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase PDB header: hydrolase

29	c3kxpD	Alignment	not modelled	97.3	28	Chain: D: PDB Molecule: alpha-(n-acetylaminoethylene)succinic acid hydrolase; PDBTitle: crystal structure of e-2-(acetamidomethylene)succinate hydrolase
30	d1ehya	Alignment	not modelled	97.3	28	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
31	c5egnB	Alignment	not modelled	97.2	25	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: est816 as an n-acyl homoserine lactone degrading enzyme
32	c2qvba	Alignment	not modelled	97.2	23	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase 3; PDBTitle: crystal structure of haloalkane dehalogenase rv2579 from mycobacterium2 tuberculosis
33	c5jd6A	Alignment	not modelled	97.2	18	PDB header: hydrolase Chain: A: PDB Molecule: mgs-mche2; PDBTitle: crystal structure of mgs-mche2, an alpha/beta hydrolase enzyme from2 the metagenome of sediments from the lagoon of mar chica, morocco
34	c5z89A	Alignment	not modelled	97.2	33	PDB header: hydrolase Chain: A: PDB Molecule: hyposensitive to light 7; PDBTitle: structural basis for specific inhibition of highly sensitive shhl72 receptor
35	c2pseA	Alignment	not modelled	97.2	20	PDB header: oxidoreductase Chain: A: PDB Molecule: renilla-luciferin 2-monooxygenase; PDBTitle: crystal structures of the luciferase and green fluorescent2 protein from renilla reniformis
36	c3qyb	Alignment	not modelled	97.2	32	PDB header: hydrolase Chain: B: PDB Molecule: alr0039 protein; PDBTitle: crystal structure of alr0039, a putative alpha/beta hydrolase from2 nostoc sp pcc 7120.
37	c6brtB	Alignment	not modelled	97.2	32	PDB header: ligase Chain: B: PDB Molecule: d3-cth-d14-d-ring; PDBTitle: f-box protein cth with hydrolase
38	d1mj5a	Alignment	not modelled	97.2	28	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
39	c5h6bA	Alignment	not modelled	97.2	27	PDB header: hydrolase Chain: A: PDB Molecule: putative secreted lipase; PDBTitle: crystal structure of a thermostable lipase from marine streptomyces
40	c5ng7B	Alignment	not modelled	97.2	38	PDB header: hydrolase Chain: B: PDB Molecule: epoxide hydrolase; PDBTitle: novel epoxide hydrolases belonging to the alpha/beta hydrolases2 superfamily in metagenomes from hot environments
41	c5v3yA	Alignment	not modelled	97.1	23	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: polyketide synthase pks13 (termination polyketide PDBTitle: crystal structure of mtb pks13 thioesterase domain in complex with2 inhibitor tam16
42	c3kdaB	Alignment	not modelled	97.1	30	PDB header: hydrolase Chain: B: PDB Molecule: cftr inhibitory factor (cif); PDBTitle: crystal structure of the cftr inhibitory factor cif with the h269a2 mutation
43	c4dnqA	Alignment	not modelled	97.1	25	PDB header: hydrolase Chain: A: PDB Molecule: dad2; PDBTitle: crystal structure of dad2 s96a mutant
44	c3w06A	Alignment	not modelled	97.1	34	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, alpha/beta fold family protein; PDBTitle: crystal structure of arabidopsis thaliana dwarf14 like (atd14)
45	d1e89a	Alignment	not modelled	97.1	26	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like
46	c5w15D	Alignment	not modelled	97.1	28	PDB header: hydrolase Chain: D: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: crystal structure of an alpha/beta hydrolase fold protein from2 burkholderia ambifaria.
47	c4g9gA	Alignment	not modelled	97.1	22	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: crystal structures of n-acyl homoserine lactonase aidh e219g mutant
48	c4c6hA	Alignment	not modelled	97.1	35	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase with 1-hexanol
49	c5bovD	Alignment	not modelled	97.1	33	PDB header: hydrolase Chain: D: PDB Molecule: putative epoxide hydrolase protein; PDBTitle: crystal structure of a putative epoxide hydrolase (kpn_01808) from2 klebsiella pneumoniae subsp. pneumoniae mgh 78578 at 1.60 a3 resolution
50	c6azdA	Alignment	not modelled	97.1	25	PDB header: hydrolase Chain: A: PDB Molecule: ppkai2-like h; PDBTitle: crystal structure of physcomitrella patens kai2-like h
51	c4nvrC	Alignment	not modelled	97.1	40	PDB header: transferase Chain: C: PDB Molecule: putative acyltransferase; PDBTitle: 2.22 angstrom resolution crystal structure of a putative2 acyltransferase from salmonella enterica
52	d1r3da	Alignment	not modelled	97.1	31	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hypothetical protein VC1974
53	c4rpcA	Alignment	not modelled	97.1	33	PDB header: hydrolase Chain: A: PDB Molecule: putative alpha/beta hydrolase; PDBTitle: crystal structure of the putative alpha/beta hydrolase family protein2 from desulfitobacterium hafniense
54	c4l0cA	Alignment	not modelled	97.1	26	PDB header: hydrolase Chain: A: PDB Molecule: deformylase;

54	c4vca_	Alignment	not modelled	97.1	20	PDBTitle: crystal structure of the n-fopmylmaaleamic acid deformylase nfo(s94a)2 from pseudomonas putida s16 PDB header: hydrolase
55	c3v48B_	Alignment	not modelled	97.0	19	Chain: B: PDB Molecule: putative aminoacrylate hydrolase rutd; PDBTitle: crystal structure of the putative alpha/beta hydrolase rutd from 2 e.coli
56	c3fsgC_	Alignment	not modelled	97.0	13	PDB header: hydrolase Chain: C: PDB Molecule: alpha/beta superfamily hydrolase; PDBTitle: crystal structure of alpha/beta superfamily hydrolase from oenococcus2 oeni psu-1
57	c3r3xA_	Alignment	not modelled	97.0	36	PDB header: hydrolase Chain: A: PDB Molecule: fluoroacetate dehalogenase; PDBTitle: crystal structure of the fluoroacetate dehalogenase rpa1163 -2 asp110asn/bromoacetate
58	c2wj4B_	Alignment	not modelled	97.0	30	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
59	c5esrA_	Alignment	not modelled	97.0	25	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of haloalkane dehalogenase (dcca) from caulobacter2 crescentus
60	d2rhw1	Alignment	not modelled	97.0	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
61	c1y37A_	Alignment	not modelled	97.0	35	PDB header: hydrolase Chain: A: PDB Molecule: fluoroacetate dehalogenase; PDBTitle: structure of fluoroacetate dehalogenase from burkholderia sp. fa1
62	c3rm3A_	Alignment	not modelled	96.9	28	PDB header: hydrolase Chain: A: PDB Molecule: thermostable monoacylglycerol lipase; PDBTitle: crystal structure of monoacylglycerol lipase from bacillus sp. h257
63	c5cbkA_	Alignment	not modelled	96.9	35	PDB header: signaling protein Chain: A: PDB Molecule: shhtl5; PDBTitle: crystal structure of the strigolactone receptor shhtl5 from striga2 hermonthica
64	c4mj3B_	Alignment	not modelled	96.9	28	PDB header: hydrolase Chain: B: PDB Molecule: haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase dmra from mycobacterium rhodesiae js60
65	d1b6ga_	Alignment	not modelled	96.9	24	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
66	c6f9oA_	Alignment	not modelled	96.9	30	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of cold-adapted haloalkane dehalogenase dpca from 2 psychrobacter cryohalolentis k5
67	c3e3aA_	Alignment	not modelled	96.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: possible peroxidase bpo; PDBTitle: the structure of rv0554 from mycobacterium tuberculosis
68	c5dnvA_	Alignment	not modelled	96.9	33	PDB header: hydrolase Chain: A: PDB Molecule: shkai2ib; PDBTitle: crystal structure of kai2-like protein from striga (apo state 2)
69	c3stxB_	Alignment	not modelled	96.8	17	PDB header: hydrolase Chain: B: PDB Molecule: methylketone synthase 1; PDBTitle: crystal structure of tomato methylketone synthase i h243a variant2 complexed with beta-ketoheptanoate
70	c3ibtA_	Alignment	not modelled	96.8	23	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)
71	d1a88a_	Alignment	not modelled	96.8	24	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
72	c5mxB_	Alignment	not modelled	96.8	25	PDB header: hydrolase Chain: B: PDB Molecule: alpha/beta hydrolase; PDBTitle: haloalkane dehalogenase dmxa from marinobacter sp. elb17 possessing a2 unique catalytic residue
73	c5a62A_	Alignment	not modelled	96.8	28	PDB header: hydrolase Chain: A: PDB Molecule: putative alpha/beta hydrolase fold protein; PDBTitle: hydrolytic potential of the ammonia-oxidizing thaumarchaeon2 nitrososphaera gargensis - crystal structure and activity profiles of 3 carboxylesterases linked to their metabolic function
74	c5cw2C_	Alignment	not modelled	96.7	30	PDB header: hydrolase Chain: C: PDB Molecule: putative epoxide hydrolase epha; PDBTitle: crystal structure of epoxide hydrolase a from mycobacterium2 thermoresistibile
75	c6ra2E_	Alignment	not modelled	96.7	12	PDB header: hydrolase Chain: E: PDB Molecule: putative dioxygenase (1h-3-hydroxy-4-oxoquinaldine 2,4- PDBTitle: structural basis for recognition and ring-cleavage of the pseudomonas2 quinolone signal (pqs) by aqdc
76	c4ccyA_	Alignment	not modelled	96.7	20	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase ybfb; PDBTitle: crystal structure of carboxylesterase cesb (ybfb) from bacillus2 subtilis
77	c2e3jA_	Alignment	not modelled	96.7	33	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase ephb; PDBTitle: the crystal structure of epoxide hydrolase b (rv1938) from 2 mycobacterium tuberculosis at 2.1 angstrom
78	c4lxgA_	Alignment	not modelled	96.7	22	PDB header: hydrolase Chain: A: PDB Molecule: mcp hydrolase; PDBTitle: crystal structure of dxnb2, a carbon - carbon bond

					hydrolase from2 sphingomonas wittichii rw1
79	c5uroA_	Alignment	not modelled	96.7	26 PDB header: hydrolase Chain: A: PDB Molecule: predicted protein; PDBTitle: structure of a soluble epoxide hydrolase identified in trichoderma2 reesei
80	c2xt0A_	Alignment	not modelled	96.7	23 PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: dehalogenase dppa from plesiocystis pacifica sir-i
81	c3qitB_	Alignment	not modelled	96.7	30 PDB header: hydrolase Chain: B: PDB Molecule: polyketide synthase; PDBTitle: thioesterase domain from curacin biosynthetic pathway
82	c1zoiC_	Alignment	not modelled	96.7	16 PDB header: hydrolase Chain: C: PDB Molecule: esterase; PDBTitle: crystal structure of a stereoselective esterase from2 pseudomonas putida ifo12996
83	c4opmB_	Alignment	not modelled	96.6	27 PDB header: hydrolase Chain: B: PDB Molecule: lipase; PDBTitle: crystal structure of a putative lipase (lip1) from acinetobacter2 baumannii aye at 1.70 a resolution
84	c1wprA_	Alignment	not modelled	96.6	26 PDB header: signaling protein Chain: A: PDB Molecule: sigma factor sigb regulation protein rsbq; PDBTitle: crystal structure of rsbq inhibited by pmsf
85	c3bf7B_	Alignment	not modelled	96.6	18 PDB header: hydrolase Chain: B: PDB Molecule: esterase ybff; PDBTitle: 1.1 resolution structure of ybff, a new esterase from escherichia2 coli: a unique substrate-binding crevice generated by domain3 arrangement
86	d1m33a_	Alignment	not modelled	96.6	25 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Biotin biosynthesis protein BioH
87	c3oosA_	Alignment	not modelled	96.6	19 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
88	c2xmzA_	Alignment	not modelled	96.5	20 PDB header: lyase Chain: A: PDB Molecule: hydrolase, alpha/beta hydrolase fold family; PDBTitle: structure of menh from s. aureus
89	c5nfgA_	Alignment	not modelled	96.5	28 PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase belonging to alpha/beta hydrolase PDBTitle: novel epoxide hydrolases belonging to the alpha/beta hydrolases2 superfamily in metagenomes from hot environments
90	c1qgeD_	Alignment	not modelled	96.5	24 PDB header: hydrolase Chain: D: PDB Molecule: protein (triacylglycerol hydrolase); PDBTitle: new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
91	d1qo7a_	Alignment	not modelled	96.5	22 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
92	c3qvmA_	Alignment	not modelled	96.5	29 PDB header: hydrolase Chain: A: PDB Molecule: olei00960; PDBTitle: the structure of olei00960, a hydrolase from oleispira antarctica
93	c4x00D_	Alignment	not modelled	96.5	20 PDB header: hydrolase Chain: D: PDB Molecule: putative hydrolase; PDBTitle: x-ray crystal structure of a putative aryl esterase from burkholderia2 cenocepacia
94	c5f4zB_	Alignment	not modelled	96.5	18 PDB header: hydrolase Chain: B: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus
95	c4psuA_	Alignment	not modelled	96.4	33 PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase; PDBTitle: crystal structure of alpha/beta hydrolase from rhodospseudomonas2 palustris cga009
96	c4q3lC_	Alignment	not modelled	96.4	10 PDB header: hydrolase Chain: C: PDB Molecule: mgs-m2; PDBTitle: crystal structure of mgs-m2, an alpha/beta hydrolase enzyme from a2 medee basin deep-sea metagenome library
97	c3dqzB_	Alignment	not modelled	96.4	23 PDB header: lyase Chain: B: PDB Molecule: alpha-hydroxynitrile lyase-like protein; PDBTitle: structure of the hydroxynitrile lyase from arabidopsis thaliana
98	c2r11D_	Alignment	not modelled	96.4	28 PDB header: hydrolase Chain: D: PDB Molecule: carboxylesterase np; PDBTitle: crystal structure of putative hydrolase (2632844) from bacillus2 subtilis at 1.96 a resolution
99	c6g75B_	Alignment	not modelled	96.4	23 PDB header: hydrolase Chain: B: PDB Molecule: common ancestor of haloalkane dehalogenase and renilla PDBTitle: crystal structure of the common ancestor of haloalkane dehalogenases2 and renilla luciferase (anchld-rluc)
100	c3a2nF_	Alignment	not modelled	96.4	23 PDB header: hydrolase Chain: F: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of dbja (wild type type ii p21)
101	d1bn7a_	Alignment	not modelled	96.4	26 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
102	c6ba8A_	Alignment	not modelled	96.4	15 PDB header: hydrolase Chain: A: PDB Molecule: iron acquisition yersiniabactin synthesis enzyme, ybtt; PDBTitle: ybtt - type ii thioesterase from yersiniabactin nrps/pks biosynthetic2 pathway
103	c3qzjB_	Alignment	not modelled	96.4	21 PDB header: hydrolase Chain: B: PDB Molecule: polyneuridine-aldehyde esterase; PDBTitle: crystal structure of polyneuridine aldehyde esterase complexed with2 16-epi-vellosimine

104	c2xuaH_	Alignment	not modelled	96.3	18	PDB header: hydrolase Chain: H: PDB Molecule: 3-oxoadipate enol-lactonase; PDBTitle: crystal structure of the eno-lactonase from burkholderia2 xenovorans lb400
105	d1q0ra_	Alignment	not modelled	96.3	24	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: AcIacinomycin methylesterase RdmC
106	c3e0xB_	Alignment	not modelled	96.3	20	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
107	c3fleB_	Alignment	not modelled	96.3	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: se_1780 protein; PDBTitle: se_1780 protein of unknown function from staphylococcus epidermidis.
108	c3r0vA_	Alignment	not modelled	96.3	27	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: the crystal structure of an alpha/beta hydrolase from sphaerobacter2 thermophilus dsm 20745.
109	c2px6A_	Alignment	not modelled	96.3	26	PDB header: transferase Chain: A: PDB Molecule: thioesterase domain; PDBTitle: crystal structure of the thioesterase domain of human fatty2 acid synthase inhibited by orlistat
110	c3wwoA_	Alignment	not modelled	96.3	19	PDB header: lyase Chain: A: PDB Molecule: (s)-hydroxynitrile lyase; PDBTitle: s-selective hydroxynitrile lyase from baliospermum montanum (apo1)
111	c6ecfB_	Alignment	not modelled	96.3	20	PDB header: hydrolase Chain: B: PDB Molecule: vlm2; PDBTitle: vlm2 thioesterase domain with genetically encoded 2,3-diaminopropionic2 acid bound with a dodecadesipeptide, space group p1
112	c3c5wP_	Alignment	not modelled	96.3	18	PDB header: hydrolase Chain: P: PDB Molecule: pp2a-specific methylesterase pme-1; PDBTitle: complex between pp2a-specific methylesterase pme-1 and pp2a core2 enzyme
113	c1pjaA_	Alignment	not modelled	96.3	16	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)
114	d1pjaa_	Alignment	not modelled	96.3	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases
115	c4qlaA_	Alignment	not modelled	96.3	32	PDB header: hydrolase Chain: A: PDB Molecule: juvenile hormone epoxide hydrolase; PDBTitle: crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
116	c5oluA_	Alignment	not modelled	96.2	22	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase family protein; PDBTitle: the crystal structure of a highly thermostable carboxyl esterase from2 bacillus coagulans in complex with glycerol
117	c4oseA_	Alignment	not modelled	96.2	16	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: x-ray crystal structure of a putative hydrolase from rickettsia typhi
118	c5hk8A_	Alignment	not modelled	96.2	15	PDB header: hydrolase Chain: A: PDB Molecule: probable pheophorbidase; PDBTitle: crystal structure of a methylesterase protein mes16 from arabidopsis
119	c1jlia_	Alignment	not modelled	96.2	26	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)
120	d1jlia_	Alignment	not modelled	96.2	26	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase