Phyre^2

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Description	RVBD0554_(bpoC)_645470_646258
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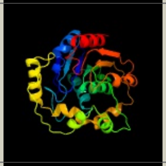
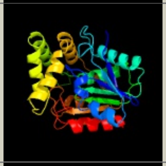
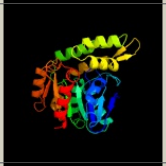
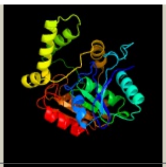
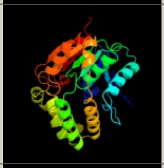
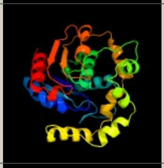
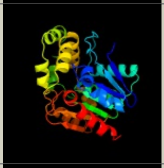
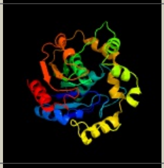
Unique Job ID	e1663c9801b58160

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3i28A_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**epoxide hydrolase 2; **PDBTitle:** crystal structure of soluble epoxide hydrolase
2	c3e3aA_	Alignment		100.0	100	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**possible peroxidase bpoc; **PDBTitle:** the structure of rv0554 from mycobacterium tuberculosis
3	c1cr6A_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**epoxide hydrolase; **PDBTitle:** crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
4	c4d9jI_	Alignment		100.0	25	**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
5	c4y7dA_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha/beta hydrolase fold protein; **PDBTitle:** alpha/beta hydrolase fold protein from nakamurella multipartita
6	c4uhhA_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase; **PDBTitle:** structural studies of a thermophilic esterase from2 thermogutta terrifontis (cacodylate complex)
7	c5h3hB_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**abhydrolase domain-containing protein; **PDBTitle:** esterase (eaest) from exiguobacterium antarcticum
8	d2rhwa1	Alignment		100.0	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carbon-carbon bond hydrolase
9	c3wibB_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**haloalkane dehalogenase; **PDBTitle:** crystal structure of y109w mutant haloalkane dehalogenase data from2 agrobacterium tumefaciens c58
10	c3kxpD_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**alpha-(n-acetylaminomethylene)succinic acid hydrolase; **PDBTitle:** crystal structure of e-2-(acetamidomethylene)succinate hydrolase
11	c4pw0A_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha/beta hydrolase fold protein; **PDBTitle:** alpha/beta hydrolase fold protein from chitinophaga pinensis

12	c3oosA_	Alignment		100.0	13	**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
13	c4q3lC_	Alignment		100.0	21	**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
14	d1m33a_	Alignment		100.0	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Biotin biosynthesis protein BioH
15	d1zd3a2	Alignment		100.0	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Epoxide hydrolase
16	d1q0ra_	Alignment		100.0	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Aclacinomycin methylesterase RdmC
17	c4psuA_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha/beta hydrolase; **PDBTitle:** crystal structure of alpha/beta hydrolase from rhodopseudomonas2 palustris cga009
18	d1cr6a2	Alignment		100.0	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Epoxide hydrolase
19	c3kdaB_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cftr inhibitory factor (cif); **PDBTitle:** crystal structure of the cftr inhibitory factor cif with the h269a2 mutation
20	c4lxgA_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mcp hydrolase; **PDBTitle:** crystal structure of dxnb2, a carbon - carbon bond hydrolase from2 sphingomonas wittichii rw1
21	c3u1tA_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dmma haloalkane dehalogenase; **PDBTitle:** haloalkane dehalogenase, dmma, of marine microbial origin
22	c5egnB_	Alignment	not modelled	100.0	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**esterase; **PDBTitle:** est816 as an n-acyl homoserine lactone degrading enzyme
23	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
24	c1u2eA_	Alignment	not modelled	100.0	20	**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
25	c3fobA_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bromoperoxidase; **PDBTitle:** crystal structure of bromoperoxidase from bacillus anthracis
26	c4rncB_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**esterase; **PDBTitle:** crystal structure of an esterase rhest1 from rhodococcus sp. ecu1013
27	d1hkha_	Alignment	not modelled	100.0	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
28	d1b6ga_	Alignment	not modelled	100.0	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloalkane dehalogenase
						Fold:alpha/beta-Hydrolases

29	d1brta_	Alignment	not modelled	100.0	21	**Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
30	c5w15D_	Alignment	not modelled	100.0	20	**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.
31	d1ehya_	Alignment	not modelled	100.0	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Epoxide hydrolase
32	c5a62A_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative alpha/beta hydrolase fold protein; **PDBTitle:** hydrolytic potential of the ammonia-oxidizing thaumarchaeon2 nitrososphaera gargenis - crystal structure and activity profiles of3 carboxylesterases linked to their metabolic function
33	c4qloA_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine o-acetyltransferase; **PDBTitle:** crystal structure of homoserine o-acetyltransferase from2 staphylococcus aureus
34	c2cjpA_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**epoxide hydrolase; **PDBTitle:** structure of potato (solanum tuberosum) epoxide hydrolase i (steh1)
35	d1a8qa_	Alignment	not modelled	100.0	25	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
36	c5xmdA_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**epoxide hydrolase a; **PDBTitle:** crystal structure of epoxide hydrolase vreh1 from vigna radiata
37	c3a2nF_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**haloalkane dehalogenase; **PDBTitle:** crystal structure of dbja (wild type type ii p21)
38	c4f0jA_	Alignment	not modelled	100.0	20	**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
39	c4l0cA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**deformylase; **PDBTitle:** crystal structure of the n-fopmylmaleamic acid deformylase nfo(s94a)2 from pseudomonas putida s16
40	d1a8sa_	Alignment	not modelled	100.0	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
41	c5esrA_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloalkane dehalogenase; **PDBTitle:** crystal structure of haloalkane dehalogenase (dcca) from caulobacter2 crescentus
42	c4rpcA_	Alignment	not modelled	100.0	14	**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
43	c2e3jA_	Alignment	not modelled	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
44	d1va4a_	Alignment	not modelled	100.0	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
45	c4inzB_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**soluble epoxide hydrolase; **PDBTitle:** the crystal structure of m145a mutant of an epoxide hydrolase from2 bacillus megaterium
46	c3v48B_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative aminoacrylate hydrolase rutd; **PDBTitle:** crystal structure of the putative alpha/beta hydrolase rutd from2 e.coli
47	c1wprA_	Alignment	not modelled	100.0	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sigma factor sigb regulation protein rsbq; **PDBTitle:** crystal structure of rsbq inhibited by pmsf
48	c4opmB_	Alignment	not modelled	100.0	18	**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
49	d2b61a1	Alignment	not modelled	100.0	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
50	c2vavL_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** L: **PDB Molecule:**acetyl-coa--deacetylcephalosporin c acetyltransferase; **PDBTitle:** crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)
51	c3om8A_	Alignment	not modelled	100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable hydrolase; **PDBTitle:** the crystal structure of a hydrolase from pseudomonas aeruginosa pa01
52	c4nvrC_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** C: **PDB Molecule:**putative acyltransferase; **PDBTitle:** 2.22 angstrom resolution crystal structure of a putative2 acyltransferase from salmonella enterica
53	c5d6oB_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**homoserine o-acetyltransferase; **PDBTitle:** orthorhombic crystal structure of an acetylester hydrolase from2 corynebacterium glutamicum
54	c4oseA_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase; **PDBTitle:** x-ray crystal structure of a putative hydrolase from rickettsia typhi

55	d1c4xa_	Alignment	not modelled	100.0	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carbon-carbon bond hydrolase
56	c5mxpB_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha/beta hydrolase; **PDBTitle:** haloalkane dehalogenase dmxa from marinobacter sp. elb17 possessing a2 unique catalytic residue
57	d1uk8a_	Alignment	not modelled	100.0	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carbon-carbon bond hydrolase
58	c2xt0A_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloalkane dehalogenase; **PDBTitle:** dehalogenase dppa from plesiocystis pacifica sir-i
59	c2vf2A_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate **PDBTitle:** x-ray crystal structure of hsad from mycobacterium2 tuberculosis
60	c6brtB_	Alignment	not modelled	100.0	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d3-cth-d14-d-ring; **PDBTitle:** f-box protein cth with hydrolase
61	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 from escherichia2 coli: a unique substrate-binding crevice generated by domain3 arrangement
62	c2wj4B_	Alignment	not modelled	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
63	c3i1iA_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine o-acetyltransferase; **PDBTitle:** x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
64	c2r11D_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**carboxylesterase np; **PDBTitle:** crystal structure of putative hydrolase (2632844) from bacillus2 subtilis at 1.96 a resolution
65	c1y37A_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fluoroacetate dehalogenase; **PDBTitle:** structure of fluoroacetate dehalogenase from burkholderia sp. fa1
66	d1bn7a_	Alignment	not modelled	100.0	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloalkane dehalogenase
67	c2y6vB_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peroxisomal membrane protein lpx1; **PDBTitle:** peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from saccharomyces2 cerevisiae (crystal form i)
68	c5ng7B_	Alignment	not modelled	100.0	20	**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
69	c4i3fA_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine hydrolase ccsp0084; **PDBTitle:** crystal structure of serine hydrolase ccsp0084 from the polyaromatic2 hydrocarbon (pah)-degrading bacterium cycloclasticus zankles
70	c3qyjB_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alr0039 protein; **PDBTitle:** crystal structure of alr0039, a putative alpha/beta hydrolase from2 nostoc sp pcc 7120.
71	c1zoiC_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**esterase; **PDBTitle:** crystal structure of a stereoselective esterase from2 pseudomonas putida ifo12996
72	c3qvmA_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**olei00960; **PDBTitle:** the structure of olei00960, a hydrolase from oleispira antarctica
73	c5efzC_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**homoserine o-acetyltransferase; **PDBTitle:** monoclinic structure of the acetyl esterase mekb
74	c5z89A_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyposensitive to light 7; **PDBTitle:** structural basis for specific inhibition of highly sensitive shhtl72 receptor
75	c5cbkA_	Alignment	not modelled	100.0	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**shhtl5; **PDBTitle:** crystal structure of the strigolactone receptor shhtl5 from striga2 hermonthica
76	c5cw2C_	Alignment	not modelled	100.0	22	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**putative epoxide hydrolase epha; **PDBTitle:** crystal structure of epoxide hydrolase a from mycobacterium2 thermoresistibile
77	c2xuaH_	Alignment	not modelled	100.0	23	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**3-oxoadipate enol-lactonase; **PDBTitle:** crystal structure of the enol-lactonase from burkholderia2 xenovorans lb400
78	c6f9oA_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloalkane dehalogenase; **PDBTitle:** crystal structure of cold-adapted haloalkane dehalogenase dpca from2 psychrobacter cryohalolentis k5
79	d2vata1	Alignment	not modelled	100.0	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases

						Family:O-acetyltransferase
80	c4c6hA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloalkane dehalogenase; **PDBTitle:** haloalkane dehalogenase with 1-hexanol
81	c2qmqA_	Alignment	not modelled	100.0	11	**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
82	c2xmzA_	Alignment	not modelled	100.0	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydrolase, alpha/beta hydrolase fold family; **PDBTitle:** structure of menh from s. aureus
83	c4b9aA_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable epoxide hydrolase; **PDBTitle:** structure of a putative epoxide hydrolase from pseudomonas2 aeruginosa.
84	c5nfqA_	Alignment	not modelled	100.0	23	**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
85	c4dnqA_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dad2; **PDBTitle:** crystal structure of dad2 s96a mutant
86	d1mj5a_	Alignment	not modelled	100.0	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloalkane dehalogenase
87	c4ccyA_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxylesterase ybfk; **PDBTitle:** crystal structure of carboxylesterase cesb (ybfk) from bacillus2 subtilis
88	c3ibtA_	Alignment	not modelled	100.0	14	**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)
89	d1j1ia_	Alignment	not modelled	100.0	22	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carbon-carbon bond hydrolase
90	c1j1iA_	Alignment	not modelled	100.0	22	**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)
91	c5frdA_	Alignment	not modelled	100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxylesterase (est-2); **PDBTitle:** structure of a thermophilic esterase
92	c2yysA_	Alignment	not modelled	100.0	20	**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
93	d1a88a_	Alignment	not modelled	100.0	23	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
94	c2qvbA_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloalkane dehalogenase 3; **PDBTitle:** crystal structure of haloalkane dehalogenase rv2579 from mycobacterium2 tuberculosis
95	c5jkjA_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase e22; **PDBTitle:** crystal structure of esterase e22 l374d mutant
96	c5dnvA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**shkai2ib; **PDBTitle:** crystal structure of kai2-like protein from striga (apo state 2)
97	c5w8pA_	Alignment	not modelled	100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine o-acetyltransferase; **PDBTitle:** homoserine transacetylase meta from mycobacterium abscessus
98	c3r0vA_	Alignment	not modelled	100.0	19	**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.
99	c4mj3B_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**haloalkane dehalogenase; **PDBTitle:** haloalkane dehalogenase dmra from mycobacterium rhodesiae js60
100	c3vvlA_	Alignment	not modelled	100.0	19	**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
101	c4x00D_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative hydrolase; **PDBTitle:** x-ray crystal structure of a putative aryl esterase from burkholderia2 cenocepacia
102	d1azwa_	Alignment	not modelled	100.0	22	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Proline iminopeptidase-like
103	c2pseA_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**renilla-luciferin 2-monooxygenase; **PDBTitle:** crystal structures of the luciferase and green fluorescent2 protein from renilla reniformis
104	c5yhpB_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cold active proline iminopeptidase; **PDBTitle:** proline iminopeptidase from psychrophilic yeast glaciozyma antarctica
						PDB header:hydrolase

105	c4ns4A_	Alignment	not modelled	100.0	16	**Chain:** A: **PDB Molecule:**alpha/beta hydrolase fold protein; **PDBTitle:** crystal structure of cold-active estarase from psychrobacter2 cryohalolentis k5t
106	d1mtza_	Alignment	not modelled	100.0	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Proline iminopeptidase-like
107	c3w06A_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, alpha/beta fold family protein; **PDBTitle:** crystal structure of arabidopsis thaliana dwarf14 like (atd14l)
108	c3r3xA_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fluoroacetate dehalogenase; **PDBTitle:** crystal structure of the fluoroacetate dehalogenase rpa1163 -2 asp110asn/bromoacetate
109	c3p2mA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**possible hydrolase; **PDBTitle:** crystal structure of a novel esterase rv0045c from mycobacterium2 tuberculosis
110	c4qlaA_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**juvenile hormone epoxide hydrolase; **PDBTitle:** crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
111	c3bwxA_	Alignment	not modelled	100.0	15	**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
112	d1xkla_	Alignment	not modelled	100.0	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hydroxynitrile lyase-like
113	c5uroA_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**predicted protein; **PDBTitle:** structure of a soluble epoxide hydrolase identified in trichoderma2 reesei
114	c5jd6A_	Alignment	not modelled	100.0	20	**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
115	c4qlaB_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**juvenile hormone epoxide hydrolase; **PDBTitle:** crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
116	c5bovD_	Alignment	not modelled	100.0	20	**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
117	c4g9gA_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha/beta hydrolase fold protein; **PDBTitle:** crystal structures of n-acyl homoserine lactonase aidh e219g mutant
118	c3e0xB_	Alignment	not modelled	100.0	17	**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
119	d1r3da_	Alignment	not modelled	100.0	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hypothetical protein VC1974
120	c6azdA_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ppkai2-like h; **PDBTitle:** crystal structure of physcomitrella patens kai2-like h