




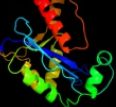















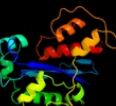






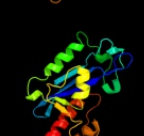




# Phyre2

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Description	Q2A0K9
Date	Thu Jan 5 12:33:36 GMT 2012
Unique Job ID	44f0d769d0e32fb4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2qxfa1</a>	 Alignment		100.0	100	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
2	<a href="#">d1y97a1</a>	 Alignment		100.0	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
3	<a href="#">d1j9aa_</a>	 Alignment		100.0	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
4	<a href="#">d2f96a1</a>	 Alignment		100.0	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
5	<a href="#">d3b6oa1</a>	 Alignment		100.0	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
6	<a href="#">c3u6fA_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> three prime repair exonuclease 1; <b>PDBTitle:</b> mouse trex1 d200n mutant
7	<a href="#">c3tr8A_</a>	 Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oligoribonuclease; <b>PDBTitle:</b> structure of an oligoribonuclease (orn) from coxiella burnetii
8	<a href="#">d2igia1</a>	 Alignment		100.0	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
9	<a href="#">d1w0ha_</a>	 Alignment		100.0	11	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
10	<a href="#">c2gbzA_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oligoribonuclease; <b>PDBTitle:</b> the crystal structure of xc847 from xanthomonas campestris: a 3-52 oligoribonuclease of dnaq fold family with a novel opposingly-shifted3 helix
11	<a href="#">c3cm6A_</a>	 Alignment		100.0	16	<b>PDB header:</b> hydrolase, apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> cell death-related nuclease 4; <b>PDBTitle:</b> crystal structure of cell-death related nuclease 4 (crn-4)2 bound with er

12	<a href="#">c2pljB_</a>	Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase iii polc-type; <b>PDBTitle:</b> crystal structure of a polc-type dna polymerase iii2 exonuclease domain from thermotoga maritima
13	<a href="#">c2xriA_</a>	Alignment		100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> eri1 exoribonuclease 3; <b>PDBTitle:</b> crystal structure of human eri1 exoribonuclease 3
14	<a href="#">d2guia1</a>	Alignment		100.0	21	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
15	<a href="#">c1zbhA_</a>	Alignment		100.0	13	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> 3'-5' exonuclease eri1; <b>PDBTitle:</b> 3'-end specific recognition of histone mrna stem-loop by 3'-2' exonuclease
16	<a href="#">c1zbuB_</a>	Alignment		99.9	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 3'-5' exonuclease eri1; <b>PDBTitle:</b> crystal structure of full-length 3'-exonuclease
17	<a href="#">c2is3B_</a>	Alignment		99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ribonuclease t; <b>PDBTitle:</b> crystal structure of escherichia coli rnase t
18	<a href="#">d1wlja_</a>	Alignment		99.9	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
19	<a href="#">d1luoca_</a>	Alignment		99.7	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> CAF1-like ribonuclease
20	<a href="#">d2d5ra1</a>	Alignment		99.5	13	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> CAF1-like ribonuclease
21	<a href="#">c2p51A_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> hydrolase, gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> spcc18.06c protein; <b>PDBTitle:</b> crystal structure of the s. pombe pop2p deadenylation2 subunit
22	<a href="#">d1x9ma1</a>	Alignment	not modelled	99.3	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
23	<a href="#">d1kfsa1</a>	Alignment	not modelled	99.1	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
24	<a href="#">c2kzzA_</a>	Alignment	not modelled	99.0	15	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (dna polymerase i); <b>PDBTitle:</b> klenow fragment with normal substrate and zinc only
25	<a href="#">d1qhta1</a>	Alignment	not modelled	99.0	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
26	<a href="#">c1tk0A_</a>	Alignment	not modelled	98.9	15	<b>PDB header:</b> transferase/electron transport/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase; <b>PDBTitle:</b> t7 dna polymerase ternary complex with 8 oxo guanosine and2 ddctp at the insertion site
27	<a href="#">d1wn7a1</a>	Alignment	not modelled	98.9	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
28	<a href="#">c2gv9B_</a>	Alignment	not modelled	98.9	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase; <b>PDBTitle:</b> crystal structure of the herpes simplex virus type 1 dna polymerase
						<b>Fold:</b> Ribonuclease H-like motif

29	<a href="#">dltgoa1</a>	Alignment	not modelled	98.9	19	<b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
30	<a href="#">c2a1sC</a>	Alignment	not modelled	98.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> poly(a)-specific ribonuclease parn; <b>PDBTitle:</b> crystal structure of native parn nuclease domain
31	<a href="#">c3d45B</a>	Alignment	not modelled	98.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> poly(a)-specific ribonuclease parn; <b>PDBTitle:</b> crystal structure of mouse parn in complex with m7gpppg
32	<a href="#">c3iayA</a>	Alignment	not modelled	98.7	21	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase delta catalytic subunit; <b>PDBTitle:</b> ternary complex of dna polymerase delta
33	<a href="#">d1d5aa1</a>	Alignment	not modelled	98.7	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
34	<a href="#">d2hhva1</a>	Alignment	not modelled	98.7	12	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
35	<a href="#">c1njzA</a>	Alignment	not modelled	98.6	17	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase i; <b>PDBTitle:</b> cytosine-thymine mismatch at the polymerase active site
36	<a href="#">c2vwkA</a>	Alignment	not modelled	98.5	18	<b>PDB header:</b> dna replication <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase; <b>PDBTitle:</b> uracil recognition in archaeal dna polymerases captured by2 x-ray crystallography. v93q polymerase variant
37	<a href="#">c1d5aA</a>	Alignment	not modelled	98.4	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (dna polymerase); <b>PDBTitle:</b> crystal structure of an archaeobacterial dna polymerase2 d.tok. deposition of second native structure at 2.43 angstrom
38	<a href="#">d1ih7a1</a>	Alignment	not modelled	98.4	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
39	<a href="#">d1s5ja1</a>	Alignment	not modelled	98.4	12	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
40	<a href="#">d1noya</a>	Alignment	not modelled	98.3	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
41	<a href="#">c1s5jA</a>	Alignment	not modelled	98.1	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase i; <b>PDBTitle:</b> insight in dna replication: the crystal structure of dna2 polymerase b1 from the archaeon sulfolobus solfataricus
42	<a href="#">d1q8ia1</a>	Alignment	not modelled	98.1	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
43	<a href="#">c2dtuA</a>	Alignment	not modelled	98.1	13	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase; <b>PDBTitle:</b> crystal structure of the beta hairpin loop deletion variant2 of rb69 gp43 in complex with dna containing an abasic site3 analog
44	<a href="#">c4ktqA</a>	Alignment	not modelled	98.1	18	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (large fragment of dna polymerase i); <b>PDBTitle:</b> binary complex of the large fragment of dna polymerase i2 from t. aquaticus bound to a primer/template dna
45	<a href="#">c1q8iA</a>	Alignment	not modelled	97.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase ii; <b>PDBTitle:</b> crystal structure of escherichia coli dna polymerase ii
46	<a href="#">c1yt3A</a>	Alignment	not modelled	97.4	18	<b>PDB header:</b> hydrolase,translation <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease d; <b>PDBTitle:</b> crystal structure of escherichia coli rnase d, an2 exoribonuclease involved in structured rna processing
47	<a href="#">d1yt3a3</a>	Alignment	not modelled	97.2	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
48	<a href="#">d2hbka2</a>	Alignment	not modelled	97.1	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
49	<a href="#">c2e6mA</a>	Alignment	not modelled	96.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> werner syndrome atp-dependent helicase homolog; <b>PDBTitle:</b> structure of mouse werner exonuclease domain
50	<a href="#">c2hbka</a>	Alignment	not modelled	93.2	19	<b>PDB header:</b> hydrolase, gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> exosome complex exonuclease rrp6; <b>PDBTitle:</b> structure of the yeast nuclear exosome component, rrp6p,2 reveals an interplay between the active site and the hrdc3 domain; protein in complex with mn
51	<a href="#">c3cymA</a>	Alignment	not modelled	92.5	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein bad_0989; <b>PDBTitle:</b> crystal structure of protein bad_0989 from bifidobacterium2 adolescentis
52	<a href="#">c1cmwA</a>	Alignment	not modelled	76.5	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (dna polymerase i); <b>PDBTitle:</b> crystal structure of taq dna-polymerase shows a new2 orientation for the structure-specific nuclease domain
53	<a href="#">c3ikmD</a>	Alignment	not modelled	72.1	29	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> dna polymerase subunit gamma-1; <b>PDBTitle:</b> crystal structure of human mitochondrial dna polymerase2 holoenzyme
54	<a href="#">d1vk0a</a>	Alignment	not modelled	70.2	12	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
55	<a href="#">c3cshA</a>	Alignment	not modelled	60.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exosome component 10;

55	<a href="#">c3saaA</a>	Alignment	not modelled	50.5	42	<b>PDBTitle:</b> crystal structure of the human rrp6 catalytic domain with y436a2 mutation in the catalytic site <b>PDB header:</b> virus
56	<a href="#">c3iykA</a>	Alignment	not modelled	52.2	19	<b>Chain:</b> A: <b>PDB Molecule:</b> vp5; <b>PDBTitle:</b> bluetongue virus structure reveals a sialic acid binding domain,2 amphipathic helices and a central coiled coil in the outer capsid3 proteins
57	<a href="#">d2py5a1</a>	Alignment	not modelled	49.9	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
58	<a href="#">d1bh9b</a>	Alignment	not modelled	34.2	14	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> TBP-associated factors, TAFs
59	<a href="#">c3nrwA</a>	Alignment	not modelled	30.7	19	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> phage integrase/site-specific recombinase; <b>PDBTitle:</b> crystal structure of the n-terminal domain of phage integrase/site-2 specific recombinase (tnp) from haloarcula marismortui, northeast3 structural genomics consortium target hmr208a
60	<a href="#">c3fleB</a>	Alignment	not modelled	28.6	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> se_1780 protein; <b>PDBTitle:</b> se_1780 protein of unknown function from staphylococcus epidermidis.
61	<a href="#">c3fp5A</a>	Alignment	not modelled	26.4	20	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa binding protein; <b>PDBTitle:</b> crystal structure of acbp from moniliophthora perniciosa
62	<a href="#">d1xkla</a>	Alignment	not modelled	23.5	23	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Hydroxynitrile lyase-like
63	<a href="#">c3p2mA</a>	Alignment	not modelled	14.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> possible hydrolase; <b>PDBTitle:</b> crystal structure of a novel esterase rv0045c from mycobacterium2 tuberculosis
64	<a href="#">c3lp5A</a>	Alignment	not modelled	13.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cell surface hydrolase; <b>PDBTitle:</b> the crystal structure of the putative cell surface hydrolase from2 lactobacillus plantarum wcfs1
65	<a href="#">c2ex3l</a>	Alignment	not modelled	13.0	17	<b>PDB header:</b> transferase/replication <b>Chain:</b> I: <b>PDB Molecule:</b> dna polymerase; <b>PDBTitle:</b> bacteriophage phi29 dna polymerase bound to terminal protein
66	<a href="#">c1pjaA</a>	Alignment	not modelled	13.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> palmitoyl-protein thioesterase 2 precursor; <b>PDBTitle:</b> the crystal structure of palmitoyl protein thioesterase-2 reveals the2 basis for divergent substrate specificities of the two lysosomal3 thioesterases (ppt1 and ppt2)
67	<a href="#">d1pjaa</a>	Alignment	not modelled	13.0	25	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterases
68	<a href="#">c3e3aA</a>	Alignment	not modelled	10.2	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> possible peroxidase bpoc; <b>PDBTitle:</b> the structure of rv0554 from mycobacterium tuberculosis
69	<a href="#">d1q0ra</a>	Alignment	not modelled	10.0	22	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Aclacinomycin methyltransferase RdmC
70	<a href="#">d2rhwa1</a>	Alignment	not modelled	9.8	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carbon-carbon bond hydrolase
71	<a href="#">d1m0da</a>	Alignment	not modelled	9.6	29	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Endonuclease I (Holliday junction resolvase)
72	<a href="#">c3ds8A</a>	Alignment	not modelled	9.1	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin2722 protein; <b>PDBTitle:</b> the crysatl structure of the gene lin2722 products from listeria2 innocua
73	<a href="#">c2y6vB</a>	Alignment	not modelled	8.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal membrane protein lpx1; <b>PDBTitle:</b> peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from2 saccharomyces cerevisiae (crystal form i)
74	<a href="#">c3nwoA</a>	Alignment	not modelled	8.7	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> proline iminopeptidase; <b>PDBTitle:</b> crystal structure of proline iminopeptidase mycobacterium smegmatis
75	<a href="#">c3fsgC</a>	Alignment	not modelled	8.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> alpha/beta superfamily hydrolase; <b>PDBTitle:</b> crystal structure of alpha/beta superfamily hydrolase from oenococcus2 oeni psu-1
76	<a href="#">d1brta</a>	Alignment	not modelled	7.2	24	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
77	<a href="#">d1tqha</a>	Alignment	not modelled	7.1	10	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase/lipase
78	<a href="#">c2k9qB</a>	Alignment	not modelled	7.0	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of hth_xre family transcriptional2 regulator bt_p548217 from bacteroides thetaiotaomicron.3 northeast structural genomics consortium target btr244.
79	<a href="#">d1s2da</a>	Alignment	not modelled	6.9	33	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> N-(deoxy)ribosyltransferase-like <b>Family:</b> N-deoxyribosyltransferase
						<b>PDB header:</b> biosynthetic protein

80	<a href="#">c2d3wB_</a>	Alignment	not modelled	6.9	13	<b>Chain:</b> B: <b>PDB Molecule:</b> probable atp-dependent transporter surc; <b>PDBTitle:</b> crystal structure of escherichia coli sufc, an atpase2 compenent of the suf iron-sulfur cluster assembly machinery
81	<a href="#">c3tovB_</a>	Alignment	not modelled	6.8	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl transferase family 9; <b>PDBTitle:</b> the crystal structure of the glycosyl transferase family 9 from2 veillonella parvula dsm 2008
82	<a href="#">c2px6A_</a>	Alignment	not modelled	6.7	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thioesterase domain; <b>PDBTitle:</b> crystal structure of the thioesterase domain of human fatty2 acid synthase inhibited by orlistat
83	<a href="#">d1mj5a_</a>	Alignment	not modelled	6.6	20	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloalkane dehalogenase
84	<a href="#">c2voyD_</a>	Alignment	not modelled	6.5	57	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> sarcoplasmic/endoplasmic reticulum calcium <b>PDBTitle:</b> cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
85	<a href="#">c2r6fA_</a>	Alignment	not modelled	6.4	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> excinuclease abc subunit a; <b>PDBTitle:</b> crystal structure of bacillus stearothermophilus uvra
86	<a href="#">c2h1fB_</a>	Alignment	not modelled	6.4	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> lipopolysaccharide heptosyltransferase-1; <b>PDBTitle:</b> e. coli heptosyltransferase waac with adp
87	<a href="#">c2zyiB_</a>	Alignment	not modelled	6.3	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lipase, putative; <b>PDBTitle:</b> a. fulgidus lipase with fatty acid fragment and calcium
88	<a href="#">c3hhjA_</a>	Alignment	not modelled	6.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mutator mutt protein; <b>PDBTitle:</b> crystal structure of mutator mutt from bartonella henselae
89	<a href="#">d1z67a1</a>	Alignment	not modelled	6.0	21	<b>Fold:</b> YidB-like <b>Superfamily:</b> YidB-like <b>Family:</b> YidB-like
90	<a href="#">d1j6ua3</a>	Alignment	not modelled	5.9	9	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> MurCDEF
91	<a href="#">c2pseA_</a>	Alignment	not modelled	5.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> renilla-luciferin 2-monooxygenase; <b>PDBTitle:</b> crystal structures of the luciferase and green fluorescent2 protein from renilla reniformis
92	<a href="#">c3r0vA_</a>	Alignment	not modelled	5.6	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha/beta hydrolase fold protein; <b>PDBTitle:</b> the crystal structure of an alpha/beta hydrolase from spheraobacter2 thermophilus dsm 20745.
93	<a href="#">c3r03B_</a>	Alignment	not modelled	5.5	9	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nudix hydrolase; <b>PDBTitle:</b> the crystal structure of nudix hydrolase from rhodospirillum rubrum
94	<a href="#">d1gm5a1</a>	Alignment	not modelled	5.5	21	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> RecG, N-terminal domain <b>Family:</b> RecG, N-terminal domain
95	<a href="#">d1zd3a2</a>	Alignment	not modelled	5.5	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Epoxide hydrolase
96	<a href="#">c2qvba_</a>	Alignment	not modelled	5.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> haloalkane dehalogenase 3; <b>PDBTitle:</b> crystal structure of haloalkane dehalogenase rv2579 from mycobacterium2 tuberculosis
97	<a href="#">c3bf7B_</a>	Alignment	not modelled	5.2	28	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> esterase ybff; <b>PDBTitle:</b> 1.1 resolution structure of ybff, a new esterase from2 escherichia coli: a unique substrate-binding crevice3 generated by domain arrangement
98	<a href="#">d1pswa_</a>	Alignment	not modelled	5.1	14	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> ADP-heptose LPS heptosyltransferase II
99	<a href="#">d1uk8a_</a>	Alignment	not modelled	5.1	20	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carbon-carbon bond hydrolase