Email	l.a.kelley@imperial.ac.uk
Description	P76484
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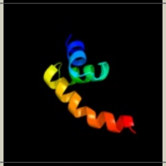
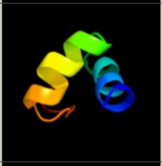
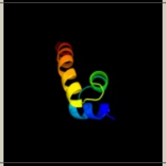
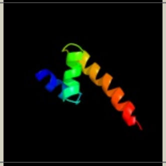
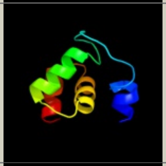
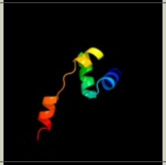
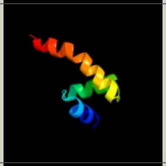
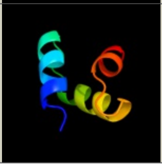
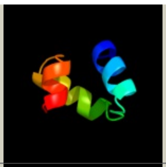
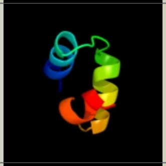
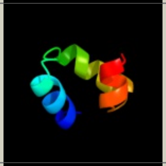
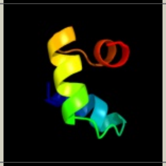
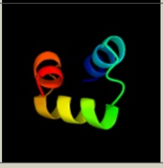
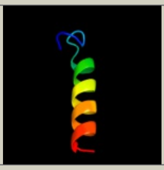
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1efub3	Alignment		95.2	23	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
2	d1xb2b1	Alignment		93.8	25	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
3	d1aipc1	Alignment		93.7	31	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
4	d1v92a_	Alignment		92.2	21	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TAP-C domain-like
5	c1efuB_	Alignment		91.6	23	**PDB header:**complex (two elongation factors) **Chain:** B: **PDB Molecule:**elongation factor ts; **PDBTitle:** elongation factor complex ef-tu/ef-ts from escherichia coli
6	c1aipG_	Alignment		91.4	31	**PDB header:**complex of two elongation factors **Chain:** G: **PDB Molecule:**elongation factor ts; **PDBTitle:** ef-tu ef-ts complex from thermus thermophilus
7	d2cp9a1	Alignment		90.6	26	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
8	d1wj7a1	Alignment		90.5	20	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
9	c1xb2B_	Alignment		87.8	21	**PDB header:**translation **Chain:** B: **PDB Molecule:**elongation factor ts, mitochondrial; **PDBTitle:** crystal structure of bos taurus mitochondrial elongation2 factor tu/ts complex
10	c3mmpC_	Alignment		87.8	23	**PDB header:**transferase **Chain:** C: **PDB Molecule:**elongation factor tu 2, elongation factor ts; **PDBTitle:** structure of the qb replicase, an rna-dependent rna polymerase2 consisting of viral and host proteins
11	d2daha1	Alignment		86.5	27	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain

12	c2dahA_	Alignment		86.4	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ubiquilin-3; **PDBTitle:** solution structure of the c-terminal uba domain in the2 human ubiquilin 3
13	d1veja1	Alignment		86.1	22	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
14	c1wr1B_	Alignment		85.9	22	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ubiquitin-like protein dsk2; **PDBTitle:** the complex sturcture of dsk2p uba with ubiquitin
15	d2bwba1	Alignment		85.4	22	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
16	c2dnaA_	Alignment		85.3	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**unnamed protein product; **PDBTitle:** solution structure of rsgi ruh-056, a uba domain from mouse2 cdna
17	c1tr8A_	Alignment		85.3	27	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**conserved protein (mth177); **PDBTitle:** crystal structure of archaeal nascent polypeptide-associated complex2 (aenac)
18	d1ufza_	Alignment		85.2	23	**Fold:**RuvA C-terminal domain-like **Superfamily:**HBS1-like domain **Family:**HBS1-like domain
19	c2cwbA_	Alignment		85.2	31	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**chimera of immunoglobulin g binding protein g **PDBTitle:** solution structure of the ubiquitin-associated domain of2 human bmsc-ubp and its complex with ubiquitin
20	d2dnaa1	Alignment		84.8	25	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
21	c2jy5A_	Alignment	not modelled	84.4	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquilin-1; **PDBTitle:** nmr structure of ubiquilin 1 uba domain
22	d1ifya_	Alignment	not modelled	84.0	9	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
23	d1wiva_	Alignment	not modelled	80.2	20	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
24	d1oaia_	Alignment	not modelled	77.4	8	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TAP-C domain-like
25	d1oqya1	Alignment	not modelled	77.3	9	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
26	c2jp7A_	Alignment	not modelled	67.9	10	**PDB header:**translation **Chain:** A: **PDB Molecule:**mrna export factor mex67; **PDBTitle:** nmr structure of the mex67 uba domain
27	d1go5a_	Alignment	not modelled	65.4	8	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TAP-C domain-like
28	c3bq3A_	Alignment	not modelled	65.2	19	**PDB header:**cell cycle, ligase **Chain:** A: **PDB Molecule:**defective in cullin neddylation protein 1; **PDBTitle:** crystal structure of s. cerevisiae dcn1
29	c2dakA_	Alignment	not modelled	62.5	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 5; **PDBTitle:** solution structure of the second uba domain in the

						human2 ubiquitin specific protease 5 (isopeptidase 5)
30	d1vega_	Alignment	not modelled	59.5	20	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
31	c2jz1A_	Alignment		57.4	42	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein doublesex; **PDBTitle:** dsx_long
32	c3agqA_	Alignment	not modelled	53.3	22	**PDB header:**translation,transferase **Chain:** A: **PDB Molecule:**elongation factor ts, elongation factor tu 1, linker, q **PDBTitle:** structure of viral polymerase form ii
33	d1wgla_	Alignment	not modelled	51.4	16	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**CUE domain
34	c1umqA_	Alignment	not modelled	41.4	20	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**photosynthetic apparatus regulatory protein; **PDBTitle:** solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
35	d1umqa_	Alignment	not modelled	41.4	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
36	c2dalA_	Alignment	not modelled	37.1	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein kiaa0794; **PDBTitle:** solution structure of the novel identified uba-like domain2 in the n-terminal of human fas associated factor 1 protein
37	d2g3qa1	Alignment	not modelled	32.1	25	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
38	c2l2dA_	Alignment	not modelled	30.3	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**otu domain-containing protein 7a; **PDBTitle:** solution nmr structure of human uba-like domain of otud7a_11_83, nesg2 target ht6304a/ocsp target otud7a_11_83/sgc-toronto
39	c2dhyA_	Alignment	not modelled	29.8	16	**PDB header:**immune system **Chain:** A: **PDB Molecule:**cue domain-containing protein 1; **PDBTitle:** solution structure of the cue domain in the human cue2 domain containing protein 1 (cuedc1)
40	c3qsvD_	Alignment	not modelled	28.0	22	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**mothers against decapentaplegic homolog 4; **PDBTitle:** structural basis for dna recognition by constitutive smad4 mh1 dimers
41	d1b8za_	Alignment	not modelled	28.0	23	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
42	d2dkla1	Alignment	not modelled	23.5	20	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
43	d1mula_	Alignment	not modelled	22.1	26	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
44	c2dagA_	Alignment	not modelled	21.2	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 5; **PDBTitle:** solution structure of the first uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5)
45	c2daiA_	Alignment	not modelled	20.5	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ubiquitin associated domain containing 1; **PDBTitle:** solution structure of the first uba domain in the human2 ubiquitin associated domain containing 1 (ubadc1)
46	c2l3gA_	Alignment	not modelled	20.3	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rho guanine nucleotide exchange factor 7; **PDBTitle:** solution nmr structure of ch domain of rho guanine nucleotide exchange2 factor 7 from homo sapiens, northeast structural genomics consortium3 target hr4495e
47	c2damA_	Alignment	not modelled	20.2	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**etea protein; **PDBTitle:** solution structure of the novel identified uba-like domain2 in the n-terminal of human etea protein
48	c2cfhD_	Alignment	not modelled	20.2	15	**PDB header:**transport **Chain:** D: **PDB Molecule:**trafficking protein particle complex subunit 6b; **PDBTitle:** structure of the bet3-tpc6b core of trapp
49	c2dzlA_	Alignment	not modelled	18.2	26	**PDB header:**structural genomics unknown function **Chain:** A: **PDB Molecule:**protein fam100b; **PDBTitle:** solution structure of the uba domain in human protein2 fam100b
50	d1fipa_	Alignment	not modelled	17.3	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
51	c2iifA_	Alignment	not modelled	17.2	17	**PDB header:**recombination/dna **Chain:** A: **PDB Molecule:**integration host factor; **PDBTitle:** single chain integration host factor mutant protein (scihf2-2 k45ae) in complex with dna
52	d1oiza1	Alignment	not modelled	15.2	16	**Fold:**RuvA C-terminal domain-like **Superfamily:**CRAL/TRIO N-terminal domain **Family:**CRAL/TRIO N-terminal domain
53	c2f46A_	Alignment	not modelled	13.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein;

53	[illegible]	Alignment	not modelled	13.7	18	**PDBTitle:** crystal structure of a putative phosphatase (nma1982) from neisseria2 meningitidis z2491 at 1.41 a resolution
54	c1auaA_	Alignment	not modelled	12.5	15	**PDB header:**phospholipid-binding protein **Chain:** A: **PDB Molecule:**phosphatidylinositol transfer protein sec14p; **PDBTitle:** phosphatidylinositol transfer protein sec14p from2 saccharomyces cerevisiae
55	c1xopA_	Alignment	not modelled	12.4	100	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hemagglutinin; **PDBTitle:** nmr structure of g1v mutant of influenza hemagglutinin2 fusion peptide in dpc micelles at ph 5
56	d2p06a1	Alignment	not modelled	12.4	28	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**AF0060-like
57	c2p06A_	Alignment	not modelled	12.4	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein af_0060; **PDBTitle:** crystal structure of a predicted coding region af_0060 from2 archaeoglobus fulgidus dsm 4304
58	c1xooA_	Alignment	not modelled	12.4	100	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hemagglutinin; **PDBTitle:** nmr structure of g1s mutant of influenza hemagglutinin2 fusion peptide in dpc micelles at ph 5
59	c3g8qA_	Alignment	not modelled	12.4	32	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**predicted rna-binding protein, contains thump **PDBTitle:** a cytidine deaminase edits c-to-u in transfer rnas in2 archaea
60	c1oizA_	Alignment	not modelled	11.6	15	**PDB header:**transport **Chain:** A: **PDB Molecule:**alpha-tocopherol transfer protein; **PDBTitle:** the molecular basis of vitamin e retention: structure of2 human alpha-tocopherol transfer protein
61	c2jrdA_	Alignment	not modelled	11.4	100	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hemagglutinin; **PDBTitle:** influenza hemagglutinin fusion domain mutant f9a
62	c3c4iA_	Alignment	not modelled	10.8	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding protein hu homolog; **PDBTitle:** crystal structure analysis of n terminal region containing the2 dimerization domain and dna binding domain of hu protein(histone like3 protein-dna binding) from mycobacterium tuberculosis [h37rv]
63	c2qhoF_	Alignment	not modelled	10.5	23	**PDB header:**protein binding/ligase **Chain:** F: **PDB Molecule:**e3 ubiquitin-protein ligase edd1; **PDBTitle:** crystal structure of the uba domain from edd ubiquitin2 ligase in complex with ubiquitin
64	d1p71a_	Alignment	not modelled	10.4	31	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
65	d1etxa_	Alignment	not modelled	10.4	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
66	d2o97b1	Alignment	not modelled	10.2	26	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
67	c1ibnA_	Alignment	not modelled	9.7	100	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hemagglutinin ha2 chain peptide; **PDBTitle:** nmr structure of hemagglutinin fusion peptide in dpc2 micelles at ph 5
68	c1iboA_	Alignment	not modelled	9.7	100	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hemagglutinin ha2 chain peptide; **PDBTitle:** nmr structure of hemagglutinin fusion peptide in dpc2 micelles at ph 7.4
69	d1veka_	Alignment	not modelled	9.7	11	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
70	c3qheB_	Alignment	not modelled	9.6	40	**PDB header:**signaling protein/splicing **Chain:** B: **PDB Molecule:**kh domain-containing, rna-binding, signal transduction- **PDBTitle:** crystal structure of the complex between the armadillo repeat domain2 of adenomatous polyposis coli and the tyrosine-rich domain of sam68
71	d1exea_	Alignment	not modelled	9.5	14	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
72	d1huua_	Alignment	not modelled	9.4	26	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
73	c2kq9A_	Alignment	not modelled	9.3	36	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dnak suppressor protein; **PDBTitle:** solution structure of dnak suppressor protein from2 agrobacterium tumefaciens c58. northeast structural3 genomics consortium target att12/ontario center for4 structural proteomics target atc0888
74	c3e21A_	Alignment	not modelled	9.2	19	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fas-associated factor 1; **PDBTitle:** crystal structure of faf-1 uba domain
75	c3ltiA_	Alignment	not modelled	9.2	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit beta; **PDBTitle:** crystal structure of the escherichia coli rna polymerase beta subunit2 beta2-betai4 domains
76	c3b7qA_	Alignment	not modelled	9.1	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**uncharacterized protein ykl091c; **PDBTitle:** crystal structure of yeast sec14 homolog sfh1 in complex with2 phosphatidylcholine
77	d1oqya2	Alignment	not modelled	9.0	13	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like

						Family:UBA domain
78	d2crna1	Alignment	not modelled	8.8	22	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
79	c2rd9C_	Alignment	not modelled	8.6	22	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**bh0186 protein; **PDBTitle:** crystal structure of a putative yfit-like metal-dependent hydrolase2 (bh0186) from bacillus halodurans c-125 at 2.30 a resolution
80	c3e7lD_	Alignment	not modelled	8.6	21	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
81	c1z9eA_	Alignment	not modelled	8.3	25	**PDB header:**protein binding/transcription **Chain:** A: **PDB Molecule:**pc4 and sfrs1 interacting protein 2; **PDBTitle:** solution structure of the hiv-1 integrase-binding domain in2 ledgf/p75
82	d1ntca_	Alignment	not modelled	8.2	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
83	d2k0bx1	Alignment	not modelled	8.0	32	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
84	c3iz6M_	Alignment	not modelled	7.9	15	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**40s ribosomal protein s18 (s13p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
85	d2b4jc1	Alignment	not modelled	7.8	25	**Fold:**N-cbl like **Superfamily:**HIV integrase-binding domain **Family:**HIV integrase-binding domain
86	c3db3A_	Alignment	not modelled	7.8	43	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase uhrf1; **PDBTitle:** crystal structure of the tandem tudor domains of the e3 ubiquitin-2 protein ligase uhrf1 in complex with trimethylated histone h3-k93 peptide
87	c2zkqm_	Alignment	not modelled	7.7	15	**PDB header:**ribosomal protein/rna **Chain:** M: **PDB Molecule:** **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
88	d1olma1	Alignment	not modelled	7.5	17	**Fold:**RuvA C-terminal domain-like **Superfamily:**CRAL/TRIO N-terminal domain **Family:**CRAL/TRIO N-terminal domain
89	d1hlva2	Alignment	not modelled	7.4	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
90	c1o5zA_	Alignment	not modelled	7.3	30	**PDB header:**ligase **Chain:** A: **PDB Molecule:**folylpolyglutamate synthase/dihydrofolate synthase; **PDBTitle:** crystal structure of folylpolyglutamate synthase (tm0166) from2 thermotoga maritima at 2.10 a resolution
91	c2lahA_	Alignment	not modelled	7.1	30	**PDB header:**cell cycle, apoptosis **Chain:** A: **PDB Molecule:**mitotic checkpoint serine/threonine-protein kinase bub1; **PDBTitle:** solution nmr structure of mitotic checkpoint serine/threonine-protein2 kinase bub1 n-terminal domain from homo sapiens, northeast structural3 genomics consortium target hr5460a (methods development)
92	d1tjla1	Alignment	not modelled	6.8	20	**Fold:**Long alpha-hairpin **Superfamily:**DnaK suppressor protein DksA, alpha-hairpin domain **Family:**DnaK suppressor protein DksA, alpha-hairpin domain
93	c3hy5A_	Alignment	not modelled	6.7	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**retinaldehyde-binding protein 1; **PDBTitle:** crystal structure of cralbp
94	d1whca_	Alignment	not modelled	6.6	23	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
95	d1iyca_	Alignment	not modelled	6.4	40	**Fold:**Invertebrate chitin-binding proteins **Superfamily:**Invertebrate chitin-binding proteins **Family:**Antifungal peptide scarabaecin
96	c2jvwA_	Alignment	not modelled	6.3	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of uncharacterized protein q5e7h1 from vibrio2 fischeri. northeast structural genomics target vfr117
97	c2xznM_	Alignment	not modelled	6.3	23	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**rps18e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
98	c2cpwA_	Alignment	not modelled	6.3	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cbl-interacting protein sts-1 variant; **PDBTitle:** solution structure of rsgi ruh-031, a uba domain from human2 cdna
99	d1d1na_	Alignment	not modelled	6.2	40	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors