Phyre^2

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Date	Sun Sep 7 17:02:59 BST 2014
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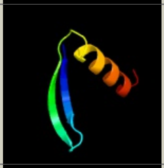
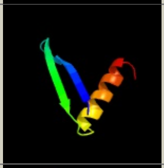
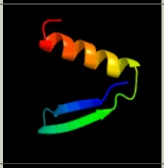
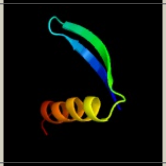
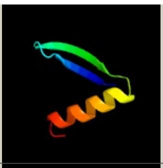
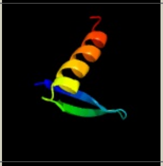
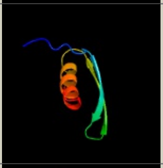
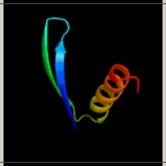
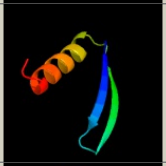
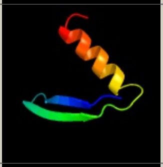
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3g5pB_	Alignment		85.1	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptide deformylase, mitochondrial; **PDBTitle:** structure and activity of human mitochondrial peptide deformylase, a2 novel cancer target
2	d1xeoa1	Alignment		82.0	25	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
3	c2w3tA_	Alignment		81.7	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide deformylase; **PDBTitle:** chloro complex of the ni-form of e.coli deformylase
4	d1lmea_	Alignment		80.5	27	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
5	c1ws1A_	Alignment		80.2	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide deformylase 1; **PDBTitle:** structure analysis of peptide deformylase from bacillus2 cereus
6	c3uwaA_	Alignment		80.1	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**riia-riib membrane-associated protein; **PDBTitle:** crystal structure of a probable peptide deformylase from synechococcus2 phage s-ssm7
7	c3e3uA_	Alignment		79.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide deformylase; **PDBTitle:** crystal structure of mycobacterium tuberculosis peptide2 deformylase in complex with inhibitor
8	d1lqya_	Alignment		78.7	25	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
9	d2defa_	Alignment		78.4	25	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
10	c3cpmA_	Alignment		78.4	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide deformylase, chloroplast; **PDBTitle:** plant peptide deformylase pdf1b crystal structure
11	d1y6ha_	Alignment		78.3	17	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase

12	d1rl4a_	Alignment		78.1	19	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
13	c1zy1B_	Alignment		78.0	33	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptide deformylase, mitochondrial; **PDBTitle:** x-ray structure of peptide deformylase from arabidopsis2 thaliana (atpdf1a) in complex with met-ala-ser
14	d1lm4a_	Alignment		77.6	16	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
15	c3dldA_	Alignment		77.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide deformylase; **PDBTitle:** crystal structure of peptide deformylase, xoo1075, from2 xanthomonas oryzae pv. oryzae kacc10331
16	c3qu1B_	Alignment		76.7	22	**PDB header:**hydrolase, metal binding protein **Chain:** B: **PDB Molecule:**peptide deformylase 2; **PDBTitle:** peptide deformylase from vibrio cholerae
17	d1lm6a_	Alignment		76.5	22	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
18	c3g6nA_	Alignment		75.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide deformylase; **PDBTitle:** crystal structure of an efpdf complex with met-ala-ser
19	c2ew7A_	Alignment		74.7	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide deformylase; **PDBTitle:** crystal structure of helicobacter pylori peptide deformylase
20	d1ix1a_	Alignment		71.5	22	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
21	d1v3ya_	Alignment	not modelled	71.2	19	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
22	c3l87A_	Alignment	not modelled	70.4	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide deformylase; **PDBTitle:** the crystal structure of smu.143c from streptococcus mutans ua159
23	c3ocaB_	Alignment	not modelled	69.7	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptide deformylase; **PDBTitle:** crystal structure of peptide deformylase from ehrlichia chaffeensis
24	c4dr9C_	Alignment	not modelled	62.6	25	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** C: **PDB Molecule:**peptide deformylase; **PDBTitle:** crystal structure of a peptide deformylase from synechococcus2 elongatus in complex with actinonin
25	d1jyma_	Alignment	not modelled	61.8	19	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
26	c2jh9A_	Alignment	not modelled	19.2	38	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**vp4 core protein; **PDBTitle:** the structure of bluetongue virus vp4 reveals a2 multifunctional rna-capping production-line
27	d1xdpa4	Alignment	not modelled	18.9	46	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
28	d1pjwa_	Alignment	not modelled	17.1	53	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Class II viral fusion proteins C-terminal domain
						PDB header:toxin/toxin repressor

29	c4q2uH_	Alignment	not modelled	16.7	31	**Chain:** H: **PDB Molecule:**mrna interferase yafq; **PDBTitle:** crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
30	c2h0pA_	Alignment	not modelled	16.4	54	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope glycoprotein; **PDBTitle:** nmr structure of the dengue-4 virus envelope protein domain2 iii
31	c2ipxA_	Alignment	not modelled	15.3	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rrna 2'-o-methyltransferase fibrillarin; **PDBTitle:** human fibrillarin
32	c4b03A_	Alignment	not modelled	15.2	38	**PDB header:**virus **Chain:** A: **PDB Molecule:**dengue virus 1 e protein; **PDBTitle:** 6a electron cryomicroscopy structure of immature2 dengue virus serotype 1
33	c1jlxB_	Alignment	not modelled	15.0	26	**PDB header:**lectin **Chain:** B: **PDB Molecule:**agglutinin; **PDBTitle:** agglutinin in complex with t-disaccharide
34	d1g8sa_	Alignment	not modelled	15.0	26	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
35	d1b8ta1	Alignment	not modelled	15.0	62	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
36	d1ok8a1	Alignment	not modelled	14.8	42	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Class II viral fusion proteins C-terminal domain
37	d1g8aa_	Alignment	not modelled	14.0	42	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
38	c3id5F_	Alignment	not modelled	14.0	37	**PDB header:**transferase/ribosomal protein/rna **Chain:** F: **PDB Molecule:**fibrillarin-like rrna/trna 2'-o-methyltransferase; **PDBTitle:** crystal structure of sulfolobus solfataricus c/d rnp assembled with2 nop5, fibrillarin, l7ae and a split half c/d rna
39	d1byra_	Alignment	not modelled	12.9	27	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Nuclease
40	c1xdoB_	Alignment	not modelled	12.8	46	**PDB header:**transferase **Chain:** B: **PDB Molecule:**polyphosphate kinase; **PDBTitle:** crystal structure of escherichia coli polyphosphate kinase
41	d1krha3	Alignment	not modelled	12.8	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
42	c3egpA_	Alignment	not modelled	12.0	42	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope protein; **PDBTitle:** crystal structure analysis of dengue-1 envelope protein2 domain iii
43	c4df3B_	Alignment	not modelled	11.8	42	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fibrillarin-like rrna/trna 2'-o-methyltransferase; **PDBTitle:** crystal structure of aeropyrum pernix fibrillarin in complex with2 natively bound s-adenosyl-l-methionine at 1.7a
44	d2o8ra4	Alignment	not modelled	11.6	23	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
45	d1w8oa1	Alignment	not modelled	11.1	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
46	d1jsxa_	Alignment	not modelled	11.0	33	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glucose-inhibited division protein B (GidB)
47	c2jqmA_	Alignment	not modelled	10.9	47	**PDB header:**transferase **Chain:** A: **PDB Molecule:**envelope protein e; **PDBTitle:** yellow fever envelope protein domain iii nmr structure2 (s288-k398)
48	c2pkpA_	Alignment	not modelled	10.9	45	**PDB header:**lyase **Chain:** A: **PDB Molecule:**homoaconitase small subunit; **PDBTitle:** crystal structure of 3-isopropylmalate dehydratase (leud)2 from methhanocaldococcus jannaschii dsm2661 (mj1271)
49	c1p58C_	Alignment	not modelled	10.2	42	**PDB header:**virus **Chain:** C: **PDB Molecule:**major envelope protein e; **PDBTitle:** complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
50	d1wzaa1	Alignment	not modelled	10.0	34	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
51	d1jq4a_	Alignment	not modelled	9.9	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
52	c2otrA_	Alignment	not modelled	9.6	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hp0892; **PDBTitle:** solution structure of conserved hypothetical protein hp0892 from2 helicobacter pylori
53	c4fc2C_	Alignment	not modelled	9.6	67	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**poly(adp-ribose) glycohydrolase; **PDBTitle:** crystal structure of mouse poly(adp-ribose) glycohydrolase (parg)2 catalytic domain
54	c3uekA_	Alignment	not modelled	9.4	67	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**poly(adp-ribose) glycohydrolase; **PDBTitle:** crystal structure of the catalytic domain of rat poly (adp-ribose)2 glycohydrolase
						PDB header:chaperone

55	c3gw6F_	Alignment	not modelled	9.1	38	**Chain:** F: **PDB Molecule:**endo-n-acetylneuraminidase; **PDBTitle:** intramolecular chaperone
56	c4o96D_	Alignment	not modelled	9.1	9	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**type iii effector protein kinase; **PDBTitle:** 2.60 angstrom resolution crystal structure of a protein kinase domain2 of type iii effector nleh2 (ecs1814) from escherichia coli o157:h73 str. sakai
57	c4epqA_	Alignment	not modelled	8.8	56	**PDB header:**hydrolase/inhibitor **Chain:** A: **PDB Molecule:**poly(adp-ribose) glycohydrolase; **PDBTitle:** canonical poly(adp-ribose) glycohydrolase rbpi inhibitor complex from2 tetrahymena thermophila
58	d1frra_	Alignment	not modelled	8.8	33	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
59	c3ah7A_	Alignment	not modelled	8.7	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**[2fe-2s]ferredoxin; **PDBTitle:** crystal structure of the isc-like [2fe-2s] ferredoxin (fdxb) from2 pseudomonas putida jcm 20004
60	d2b3ya1	Alignment	not modelled	8.6	32	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
61	d1prya_	Alignment	not modelled	8.6	42	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
62	d1wvha1	Alignment	not modelled	8.5	43	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Phosphotyrosine-binding domain (PTB)
63	c4ggkA_	Alignment	not modelled	8.3	45	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mitochondrial cardiolipin hydrolase; **PDBTitle:** crystal structure of zucchini from mouse (mzuc / pld6 / mitopld) bound2 to tungstate
64	c2y5cB_	Alignment	not modelled	8.3	38	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**adrenodoxin-like protein, mitochondrial; **PDBTitle:** structure of human ferredoxin 2 (fdx2)in complex with 2fe2s2 cluster
65	c3uzeC_	Alignment	not modelled	8.3	42	**PDB header:**immune system **Chain:** C: **PDB Molecule:**envelope protein; **PDBTitle:** crystal structure of the dengue virus serotype 3 envelope protein2 domain iii in complex with the variable domains of mab 4e11
66	c3cjhK_	Alignment	not modelled	8.1	30	**PDB header:**protein transport **Chain:** K: **PDB Molecule:**mitochondrial import inner membrane translocase subunit **PDBTitle:** tim8-tim13 complex
67	d1z8ma1	Alignment	not modelled	7.7	25	**Fold:**RelE-like **Superfamily:**RelE-like **Family:**RelE-like
68	d1ztxe1	Alignment	not modelled	7.6	50	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Class II viral fusion proteins C-terminal domain
69	d1doia_	Alignment	not modelled	7.6	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
70	c2luwA_	Alignment	not modelled	7.4	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metalloprotease; **PDBTitle:** solution structure of vep c-ter 100
71	c3k1qB_	Alignment	not modelled	7.3	35	**PDB header:**virus **Chain:** B: **PDB Molecule:**vp3a, the building block protein of inner shell; **PDBTitle:** backbone model of an aquareovirus virion by cryo-electron2 microscopy and bioinformatics
72	c4orkB_	Alignment	not modelled	7.2	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional aac/aph; **PDBTitle:** crystal structure of the phosphotransferase domain of the bifunctional2 aminoglycoside resistance enzyme aac(6')-ie-aph(2'')-ia
73	d1s6na_	Alignment	not modelled	7.1	53	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Class II viral fusion proteins C-terminal domain
74	d1sioa_	Alignment	not modelled	7.0	39	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Serine-carboxyl proteinase, SCP
75	d2bs2b2	Alignment	not modelled	6.9	63	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
76	d1li4a1	Alignment	not modelled	6.9	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
77	c1krhA_	Alignment	not modelled	6.7	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**benzoate 1,2-dioxygenase reductase; **PDBTitle:** x-ray stucture of benzoate dioxygenase reductase
78	c4n58A_	Alignment	not modelled	6.7	44	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pectocin m2; **PDBTitle:** crystal structure of pectocin m2 at 1.86 angstroms
79	d1fxia_	Alignment	not modelled	6.5	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
80	d1kf6b2	Alignment	not modelled	6.4	50	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
						PDB header:transferase **Chain:** A: **PDB Molecule:**protein (thymidine kinase);

81	c1qhiA_	Alignment	not modelled	6.3	17	**PDBTitle:** herpes simplex virus type-i thymidine kinase complexed with2 a novel non-substrate inhibitor, 9-(4-hydroxybutyl)-n2-3 phenylguanine
82	c4g5aB_	Alignment	not modelled	6.2	50	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative member of duf 3244 protein family2 (bt_1867) from bacteroides thetaiotaomicron vpi-5482 at 1.69 a3 resolution
83	d2ba0a2	Alignment	not modelled	6.2	41	**Fold:**Barrel-sandwich hybrid **Superfamily:**Ribosomal L27 protein-like **Family:**ECR1 N-terminal domain-like
84	c3uajA_	Alignment	not modelled	6.1	54	**PDB header:**viral protein/immune system **Chain:** A: **PDB Molecule:**envelope protein; **PDBTitle:** crystal structure of the envelope glycoprotein ectodomain from dengue2 virus serotype 4 in complex with the fab fragment of the chimpanzee3 monoclonal antibody 5h2
85	d1ibxb_	Alignment	not modelled	6.0	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**CAD domain
86	c1ibxB_	Alignment	not modelled	6.0	16	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**chimera of igg binding protein g and dna **PDBTitle:** nmr structure of dff40 and dff45 n-terminal domain complex
87	c2ww1B_	Alignment	not modelled	5.9	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-1,2-mannosidase; **PDBTitle:** structure of the family gh92 inverting mannosidase bt39902 from bacteroides thetaiotaomicron vpi-5482 in complex with3 thiomannobioside
88	d1e0za_	Alignment	not modelled	5.9	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
89	d2py5a1	Alignment	not modelled	5.9	50	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
90	d1nekb2	Alignment	not modelled	5.9	38	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
91	d2nn6h2	Alignment	not modelled	5.8	26	**Fold:**Barrel-sandwich hybrid **Superfamily:**Ribosomal L27 protein-like **Family:**ECR1 N-terminal domain-like
92	d2b3za2	Alignment	not modelled	5.8	19	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
93	c3zyyX_	Alignment	not modelled	5.7	40	**PDB header:**iron-sulfur-binding protein **Chain:** X: **PDB Molecule:**iron-sulfur cluster binding protein; **PDBTitle:** reductive activator for corrinoid,iron-sulfur protein
94	c4cbfE_	Alignment	not modelled	5.7	50	**PDB header:**virus **Chain:** E: **PDB Molecule:**envelope protein e; **PDBTitle:** near-atomic resolution cryo-em structure of dengue2 serotype 4 virus
95	d1vpta_	Alignment	not modelled	5.6	45	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**mRNA cap methylase
96	c3huiA_	Alignment	not modelled	5.6	22	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**ferredoxin; **PDBTitle:** crystal structure of the mutant a105r of [2fe-2s] ferredoxin in the2 class i cyp199a2 system from rhodopseudomonas palustris
97	d1acoa1	Alignment	not modelled	5.6	32	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
98	c2o8rA_	Alignment	not modelled	5.6	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polyphosphate kinase; **PDBTitle:** crystal structure of polyphosphate kinase from2 porphyromonas gingivalis
99	c3q3wB_	Alignment	not modelled	5.6	36	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** isopropylmalate isomerase small subunit from campylobacter jejuni.