







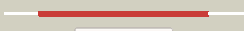




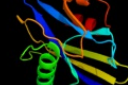



















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3n77B_</a>	 Alignment		100.0	86	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nucleoside triphosphatase nudi; <b>PDBTitle:</b> crystal structure of idp01880, putative ntp pyrophosphohydrolase of2 salmonella typhimurium lt2
2	<a href="#">c3gwyA_</a>	 Alignment		99.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative ctp pyrophosphohydrolase; <b>PDBTitle:</b> crystal structure of putative ctp pyrophosphohydrolase from2 bacteroides fragilis
3	<a href="#">d1puna_</a>	 Alignment		99.9	20	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MuT-like
4	<a href="#">c3hhjA_</a>	 Alignment		99.9	27	<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
5	<a href="#">c3ef5A_</a>	 Alignment		99.9	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable pyrophosphohydrolase; <b>PDBTitle:</b> structure of the rna pyrophosphohydrolase bdrpph in complex with dgtg
6	<a href="#">c2pq1B_</a>	 Alignment		99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ap4a hydrolase; <b>PDBTitle:</b> crystal structure of ap4a hydrolase complexed with amp and2 atp (aq_158) from aquifex aeolicus vf5
7	<a href="#">c3grnB_</a>	 Alignment		99.9	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mutt related protein; <b>PDBTitle:</b> crystal structure of mutt protein from methanosarcina mazei go1
8	<a href="#">c3fk9B_</a>	 Alignment		99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mutator mutt protein; <b>PDBTitle:</b> crystal structure of mmutator mutt protein from bacillus2 halodurans
9	<a href="#">d1ryaa_</a>	 Alignment		99.9	22	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> GDP-mannose mannosyl hydrolase NudD
10	<a href="#">c3exqA_</a>	 Alignment		99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nudix family hydrolase; <b>PDBTitle:</b> crystal structure of a nudix family hydrolase from2 lactobacillus brevis
11	<a href="#">d2b0va1</a>	 Alignment		99.9	20	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MuT-like

12	<a href="#">c3q4iA_</a>	Alignment		99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphohydrolase (mutt/nudix family protein); <b>PDBTitle:</b> crystal structure of cdp-chase in complex with gd3+
13	<a href="#">c3r03B_</a>	Alignment		99.9	31	<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
14	<a href="#">c2o1cB_</a>	Alignment		99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> datp pyrophosphohydrolase; <b>PDBTitle:</b> structure of the e. coli dihydroneopterin triphosphate2 pyrophosphohydrolase
15	<a href="#">c3cngC_</a>	Alignment		99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> nudix hydrolase; <b>PDBTitle:</b> crystal structure of nudix hydrolase from nitrosomonas europaea
16	<a href="#">c3h95A_</a>	Alignment		99.9	25	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoside diphosphate-linked moiety x motif 6; <b>PDBTitle:</b> crystal structure of the nudix domain of nudt6
17	<a href="#">d2fkba1</a>	Alignment		99.9	26	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> IPP isomerase-like
18	<a href="#">dlppva_</a>	Alignment		99.9	25	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> IPP isomerase-like
19	<a href="#">c2qioB_</a>	Alignment		99.9	18	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional nmh adenylyltransferase/nudix hydrolase; <b>PDBTitle:</b> crystal structure of a bifunctional nmh adenylyltransferase/adp ribose2 pyrophosphatase (nadm) complexed with adprp and nad from3 synechocystis sp.
20	<a href="#">c3dkuB_</a>	Alignment		99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphohydrolase; <b>PDBTitle:</b> crystal structure of nudix hydrolase orf153, ymf6, from2 escherichia coli k-1
21	<a href="#">d1k2ea_</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
22	<a href="#">d1hzta_</a>	Alignment	not modelled	99.9	25	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> IPP isomerase-like
23	<a href="#">c3o8sA_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adp-ribose pyrophosphatase; <b>PDBTitle:</b> crystal structure of an adp-ribose pyrophosphatase (ssu98_1448) from2 streptococcus suis 89-1591 at 2.27 a resolution
24	<a href="#">d2b06a1</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
25	<a href="#">dlirya_</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
26	<a href="#">c2kdvA_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> rna pyrophosphohydrolase; <b>PDBTitle:</b> solution structure of rna pyrophosphohydrolase rpph from2 escherichia coli
27	<a href="#">c2r5wA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinamide-nucleotide adenylyltransferase; <b>PDBTitle:</b> crystal structure of a bifunctional nmh2 adenylyltransferase/adp ribose pyrophosphatase from3 francisella tularensis
28	<a href="#">c3gz8C_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> cocrystal structure of nudix domain of shewanella

					oneidensis2 nrtr complexed with adp ribose
29	<a href="#">d1vk6a2</a>	Alignment	not modelled	99.9	19 <b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> NADH pyrophosphatase
30	<a href="#">d1sjya</a>	Alignment	not modelled	99.9	19 <b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
31	<a href="#">c3f6aA</a>	Alignment	not modelled	99.9	18 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase, nudix family; <b>PDBTitle:</b> crystal structure of a hydrolase, nudix family from2 clostridium perfringens
32	<a href="#">c3sonB</a>	Alignment	not modelled	99.8	17 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical nudix hydrolase; <b>PDBTitle:</b> crystal structure of a hypothetical nudix hydrolase (lmof2365_2679)2 from listeria monocytogenes (atcc 19115) at 1.70 a resolution
33	<a href="#">d1vcda1</a>	Alignment	not modelled	99.8	19 <b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
34	<a href="#">d1xsba</a>	Alignment	not modelled	99.8	24 <b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
35	<a href="#">c3gg6A</a>	Alignment	not modelled	99.8	20 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoside diphosphate-linked moiety x motif 18; <b>PDBTitle:</b> crystal structure of the nudix domain of human nudt18
36	<a href="#">d1x51a1</a>	Alignment	not modelled	99.8	15 <b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutY C-terminal domain-like
37	<a href="#">c3i9xA</a>	Alignment	not modelled	99.8	21 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of a mutt/nudix family protein from listeria innocua
38	<a href="#">c2gb5B</a>	Alignment	not modelled	99.8	19 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nadh pyrophosphatase; <b>PDBTitle:</b> crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
39	<a href="#">c3fcmA</a>	Alignment	not modelled	99.8	12 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase, nudix family; <b>PDBTitle:</b> crystal structure of a nudix hydrolase from clostridium2 perfringens
40	<a href="#">c2pqvA</a>	Alignment	not modelled	99.8	23 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of mutt/nudix family protein from streptococcus2 pneumoniae
41	<a href="#">d1ktga</a>	Alignment	not modelled	99.8	21 <b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
42	<a href="#">d2azwa1</a>	Alignment	not modelled	99.8	21 <b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
43	<a href="#">d2fb1a2</a>	Alignment	not modelled	99.8	18 <b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> BT0354 N-terminal domain-like
44	<a href="#">c1rrqA</a>	Alignment	not modelled	99.8	16 <b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> muty; <b>PDBTitle:</b> muty adenine glycosylase in complex with dna containing an2 a:oxog pair
45	<a href="#">c2yyhC</a>	Alignment	not modelled	99.8	25 <b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> 8-oxo-dgtpase domain; <b>PDBTitle:</b> crystal structure of nudix family protein from aquifex aeolicus
46	<a href="#">d1jkna</a>	Alignment	not modelled	99.8	21 <b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
47	<a href="#">c2i6kA</a>	Alignment	not modelled	99.8	21 <b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> isopentenyl-diphosphate delta-isomerase 1; <b>PDBTitle:</b> crystal structure of human type i iip isomerase complexed2 with a substrate analog
48	<a href="#">c3gz6A</a>	Alignment	not modelled	99.8	15 <b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of shewanella oneidensis nrtr complexed2 with a 27mer dna
49	<a href="#">c2fb1A</a>	Alignment	not modelled	99.8	19 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> crystal structure of protein bt0354 from bacteroides thetaiotaomicron
50	<a href="#">c2jvbA</a>	Alignment	not modelled	99.8	15 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mrna-decapping enzyme subunit 2; <b>PDBTitle:</b> solution structure of catalytic domain of ydcp2
51	<a href="#">d1nqza</a>	Alignment	not modelled	99.8	20 <b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
52	<a href="#">c3fjyB</a>	Alignment	not modelled	99.8	18 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable mutt1 protein; <b>PDBTitle:</b> crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
53	<a href="#">d2fvva1</a>	Alignment	not modelled	99.8	20 <b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
54	<a href="#">c2fvvA</a>	Alignment	not modelled	99.8	20 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> diphosphoinositol polyphosphate phosphohydrolase

						<b>PDBTitle:</b> human diphosphoinositol polyphosphate phosphohydrolase 1
55	<a href="#">c2pnyA_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> isopentenyl-diphosphate delta-isomerase 2; <b>PDBTitle:</b> structure of human isopentenyl-diphosphate delta-isomerase 2
56	<a href="#">c3edsA_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of a mut/nudix family protein from bacillus2 thuringiensis
57	<a href="#">d2a6ta2</a>	Alignment	not modelled	99.8	15	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> mRNA decapping enzyme-like
58	<a href="#">d1rrqa2</a>	Alignment	not modelled	99.8	15	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutY C-terminal domain-like
59	<a href="#">c2qkmF_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> spac19a8.12 protein; <b>PDBTitle:</b> the crystal structure of fission yeast mrna decapping enzyme dcp1-dcp22 complex
60	<a href="#">d2o5fa1</a>	Alignment	not modelled	99.8	27	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> IPP isomerase-like
61	<a href="#">d2fmla2</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> BT0354 N-terminal domain-like
62	<a href="#">c3rh7A_</a>	Alignment	not modelled	99.8	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical oxidoreductase; <b>PDBTitle:</b> crystal structure of a hypothetical oxidoreductase (sma0793) from2 sinorhizobium meliloti 1021 at 3.00 a resolution
63	<a href="#">c3id9B_</a>	Alignment	not modelled	99.8	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of a mutt/nudix family protein from2 bacillus thuringiensis
64	<a href="#">c3f13A_</a>	Alignment	not modelled	99.7	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative nudix hydrolase family member; <b>PDBTitle:</b> crystal structure of putative nudix hydrolase family member2 from chromobacterium violaceum
65	<a href="#">c2yvoA_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of ndx2 in complex with mg2+ and amp from thermus2 thermophilus hb8
66	<a href="#">d1vhza_</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
67	<a href="#">c2w4eA_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> structure of an n-terminally truncated nudix hydrolase2 dr2204 from deinococcus radiodurans
68	<a href="#">d1v8ya_</a>	Alignment	not modelled	99.7	24	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
69	<a href="#">c2fmlB_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of mutt/nudix family protein from enterococcus2 faecalis
70	<a href="#">c3bm4B_</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> adp-sugar pyrophosphatase; <b>PDBTitle:</b> crystal structure of human adp-ribose pyrophosphatase nudt52 in complex with magnesium and ampcpr
71	<a href="#">d1g0sa_</a>	Alignment	not modelled	99.6	22	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
72	<a href="#">c3e57A_</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein tm1382; <b>PDBTitle:</b> crystal structure of tm1382, a putative nudix hydrolase
73	<a href="#">d1mqea_</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
74	<a href="#">c3dupB_</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of mutt/nudix family hydrolase from rhodospirillum2 rubrum atcc 11170
75	<a href="#">d1q33a_</a>	Alignment	not modelled	99.5	28	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
76	<a href="#">c3qsjA_</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nudix hydrolase; <b>PDBTitle:</b> crystal structure of nudix hydrolase from alicyclobacillus2 acidocaldarius
77	<a href="#">c3q91D_</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> uridine diphosphate glucose pyrophosphatase; <b>PDBTitle:</b> crystal structure of human uridine diphosphate glucose pyrophosphatase2 (nudt14)
78	<a href="#">c2j8qB_</a>	Alignment	not modelled	99.5	21	<b>PDB header:</b> nuclear protein <b>Chain:</b> B: <b>PDB Molecule:</b> cleavage and polyadenylation specificity factor 5; <b>PDBTitle:</b> crystal structure of human cleavage and polyadenylation2 specificity factor 5 (cpsf5) in complex with a sulphate3 ion.
79	<a href="#">d1viua_</a>	Alignment	not modelled	99.4	12	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like

80	<a href="#">d1u20a1</a>	Alignment	not modelled	99.3	24	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MuTf-like
81	<a href="#">c3couA</a>	Alignment	not modelled	98.1	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoside diphosphate-linked moiety x motif 16; <b>PDBTitle:</b> crystal structure of human nudix motif 16 (nudt16)
82	<a href="#">c3kvhA</a>	Alignment	not modelled	97.0	26	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein syndesmos; <b>PDBTitle:</b> crystal structure of human protein syndesmos (nudt16-like protein)
83	<a href="#">c3p5tE</a>	Alignment	not modelled	96.7	21	<b>PDB header:</b> rna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> cleavage and polyadenylation specificity factor subunit 5; <b>PDBTitle:</b> cfim25-cfim68 complex
84	<a href="#">d1aopa2</a>	Alignment	not modelled	11.1	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> Duplicated SiR/NiR-like domains 1 and 3
85	<a href="#">d1g8ta</a>	Alignment	not modelled	7.0	7	<b>Fold:</b> His-Me finger endonucleases <b>Superfamily:</b> His-Me finger endonucleases <b>Family:</b> DNA/RNA non-specific endonuclease
86	<a href="#">c2hdnE</a>	Alignment	not modelled	6.7	18	<b>PDB header:</b> translation <b>Chain:</b> E: <b>PDB Molecule:</b> elongation factor ef-tu; <b>PDBTitle:</b> trypsin-modified elongation factor tu in complex with2 tetracycline at 2.8 angstrom resolution
87	<a href="#">d2dsya1</a>	Alignment	not modelled	5.9	29	<b>Fold:</b> TTHA1013/TTHA0281-like <b>Superfamily:</b> TTHA1013/TTHA0281-like <b>Family:</b> TTHA0281-like
88	<a href="#">d2a2la1</a>	Alignment	not modelled	5.9	25	<b>Fold:</b> Profilin-like <b>Superfamily:</b> GlcG-like <b>Family:</b> GlcG-like
89	<a href="#">d1tnsa</a>	Alignment	not modelled	5.6	22	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> Excisionase-like
90	<a href="#">c3fpvC</a>	Alignment	not modelled	5.6	17	<b>PDB header:</b> heme binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> extracellular haem-binding protein; <b>PDBTitle:</b> crystal structure of hbps