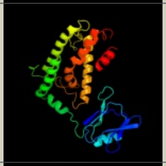
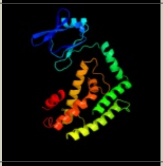
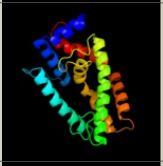
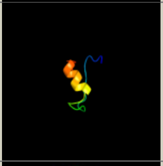
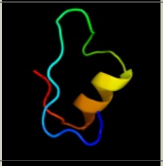
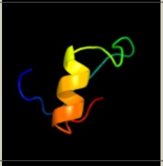
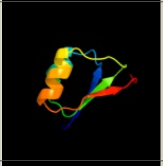
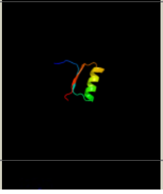
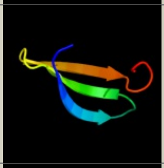
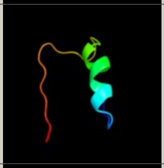
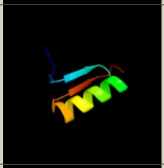
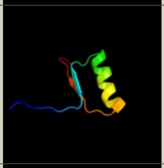
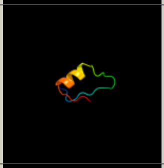
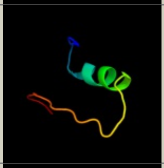
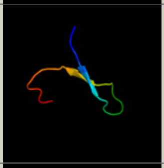
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	Q46896
Date	Thu Jan 5 12:35:36 GMT 2012
Unique Job ID	be002e84e4cf9d7f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3nkdB_	Alignment		100.0	99	**PDB header:**immune system **Chain:** B: **PDB Molecule:**crispr-associated protein cas1; **PDBTitle:** structure of crisp-associated protein cas1 from escherichia coli str.2 k-12
2	c3godA_	Alignment		100.0	25	**PDB header:**immune system **Chain:** A: **PDB Molecule:**cas1; **PDBTitle:** structural basis for dnase activity of a conserved protein2 implicated in crispr-mediated antiviral defense
3	c3lfxE_	Alignment		100.0	18	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**uncharacterized protein; **PDBTitle:** structure of tm1797, a cas1 protein from thermotoga maritima
4	c2yzsB_	Alignment		100.0	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 aquifex aeolicus
5	c3pv9D_	Alignment		100.0	17	**PDB header:**immune system **Chain:** D: **PDB Molecule:**putative uncharacterized protein ph1245; **PDBTitle:** structure of ph1245, a cas1 from pyrococcus horikoshii
6	c3nkeA_	Alignment		100.0	99	**PDB header:**immune system **Chain:** A: **PDB Molecule:**protein ygbt; **PDBTitle:** high resolution structure of the c-terminal domain crisp-associated2 protein cas1 from escherichia coli str. k-12
7	d1p3da1	Alignment		73.8	3	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
8	d2jfga1	Alignment		71.5	26	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
9	d1j6ua1	Alignment		63.4	10	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
10	d2ioja1	Alignment		48.3	13	**Fold:**MurF and HprK N-domain-like **Superfamily:**HprK N-terminal domain-like **Family:**DRTGG domain
11	c1jrxA_	Alignment		42.1	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavocytochrome c; **PDBTitle:** crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina

12	c3nixF_	Alignment		39.1	20	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**flavoprotein/dehydrogenase; **PDBTitle:** crystal structure of flavoprotein/dehydrogenase from cytophaga2 hutchinsonii. northeast structural genomics consortium target chr43.
13	c2hbpA_	Alignment		37.0	13	**PDB header:**endocytosis, protein binding **Chain:** A: **PDB Molecule:**cytoskeleton assembly control protein sla1; **PDBTitle:** solution structure of sla1 homology domain 1
14	c3lhlA_	Alignment		33.6	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative agmatinase; **PDBTitle:** crystal structure of a putative agmatinase from clostridium difficile
15	c1qo8A_	Alignment		33.3	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavocytochrome c3 fumarate reductase; **PDBTitle:** the structure of the open conformation of a flavocytochrome2 c3 fumarate reductase
16	c2aczA_	Alignment		27.2	18	**PDB header:**oxidoreductase/electron transport **Chain:** A: **PDB Molecule:**succinate dehydrogenase flavoprotein subunit; **PDBTitle:** complex ii (succinate dehydrogenase) from e. coli with atpenin a52 inhibitor co-crystallized at the ubiquinone binding site
17	c2f00A_	Alignment		26.7	6	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate--l-alanine ligase; **PDBTitle:** escherichia coli murc
18	d1woha_	Alignment		26.6	19	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
19	c3mlqH_	Alignment		22.8	20	**PDB header:**transferase/transcription **Chain:** H: **PDB Molecule:**transcription-repair coupling factor; **PDBTitle:** crystal structure of the thermus thermophilus transcription-repair2 coupling factor rna polymerase interacting domain with the thermus3 aquaticus rna polymerase beta1 domain
20	c1yq4A_	Alignment		21.6	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**succinate dehydrogenase flavoprotein subunit; **PDBTitle:** avian respiratory complex ii with 3-nitropropionate and ubiquinone
21	c3nipB_	Alignment	not modelled	20.6	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3-guanidinopropionase; **PDBTitle:** crystal structure of pseudomonas aeruginosa guanidinopropionase2 complexed with 1,6-diaminohexane
22	c3m1rF_	Alignment	not modelled	20.1	17	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**formimidoylglutamase; **PDBTitle:** the crystal structure of formimidoylglutamase from bacillus2 subtilis subsp. subtilis str. 168
23	c3ff4A_	Alignment	not modelled	19.8	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein chu_1412
24	d1neka2	Alignment	not modelled	19.6	18	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
25	d2aeba1	Alignment	not modelled	19.6	13	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
26	d1xfka_	Alignment	not modelled	18.5	23	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
27	d2d59a1	Alignment	not modelled	18.5	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
28	d1gq6a_	Alignment	not modelled	18.4	23	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
29	c1jqoA_	Alignment	not modelled	18.3	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate carboxylase; **PDBTitle:** crystal structure of c4-form phosphoenolpyruvate

						carboxylase from2 maize
30	d1jqoa_	Alignment	not modelled	18.3	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate carboxylase
31	d1pq3a_	Alignment	not modelled	17.6	17	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
32	d1zhva2	Alignment	not modelled	17.2	11	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Atu0741-like
33	c1d4cB_	Alignment	not modelled	16.6	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**flavocytochrome c fumarate reductase; **PDBTitle:** crystal structure of the uncomplexed form of the2 flavocytochrome c fumarate reductase of shewanella3 putrefaciens strain mr-1
34	c2cunA_	Alignment	not modelled	16.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of phosphoglycerate kinase from pyrococcus2 horikoshii ot3
35	c3bioB_	Alignment	not modelled	15.5	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of oxidoreductase (gfo/idh/moca family member) from2 porphyromonas gingivalis w83
36	c1j6uA_	Alignment	not modelled	15.0	9	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate-alanine ligase murc; **PDBTitle:** crystal structure of udp-n-acetylmuramate-alanine ligase2 murc (tm0231) from thermotoga maritima at 2.3 a resolution
37	c3ihgA_	Alignment	not modelled	15.0	21	**PDB header:**flavoprotein, oxidoreductase **Chain:** A: **PDB Molecule:**rdme; **PDBTitle:** crystal structure of a ternary complex of aklavinone-112 hydroxylase with fad and aklavinone
38	c2e1mA_	Alignment	not modelled	15.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-glutamate oxidase; **PDBTitle:** crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
39	d2q4qa1	Alignment	not modelled	14.3	16	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
40	d1w4xa1	Alignment	not modelled	13.8	22	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
41	d1cr6a2	Alignment	not modelled	13.7	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Epoxide hydrolase
42	d2a0ma1	Alignment	not modelled	13.3	13	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
43	d1vpea_	Alignment	not modelled	13.0	15	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
44	d1ko7a1	Alignment	not modelled	12.9	15	**Fold:**MurF and HprK N-domain-like **Superfamily:**HprK N-terminal domain-like **Family:**HPr kinase/phoshatase HprK N-terminal domain
45	d2ceva_	Alignment	not modelled	12.9	13	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
46	d2ooxe2	Alignment	not modelled	12.8	14	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
47	c3mlqE_	Alignment	not modelled	12.8	26	**PDB header:**transferase/transcription **Chain:** E: **PDB Molecule:**transcription-repair coupling factor; **PDBTitle:** crystal structure of the thermus thermophilus transcription-repair2 coupling factor rna polymerase interacting domain with the thermus3 aquaticus rna polymerase beta1 domain
48	c2eivH_	Alignment	not modelled	12.7	30	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**arginase; **PDBTitle:** crystal structure of the arginase from thermus thermophilus
49	d2fvta1	Alignment	not modelled	12.6	13	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
50	c2kbrA_	Alignment	not modelled	12.5	8	**PDB header:**structural protein/cell adhesion **Chain:** A: **PDB Molecule:**harmonin; **PDBTitle:** solution structure of harmonin n terminal domain in complex2 with a internal peptide of cadherin23
51	d1iuka_	Alignment	not modelled	12.5	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
52	d1v6sa_	Alignment	not modelled	12.5	22	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
53	c2pd2A_	Alignment	not modelled	12.1	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein st0148; **PDBTitle:** crystal structure of (st0148) conserved hypothetical from sulfolobus2 tokodaii strain7
54	d1phpa_	Alignment	not modelled	12.1	15	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
55	d1gsoa2	Alignment	not modelled	12.0	10	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like

56	d1ybha1	Alignment	not modelled	12.0	9	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
57	d1zvpa2	Alignment	not modelled	11.8	13	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**VC0802-like
58	d1zd3a2	Alignment	not modelled	11.7	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Epoxide hydrolase
59	c3do5A_	Alignment	not modelled	11.5	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** crystal structure of putative homoserine dehydrogenase (np_069768.1)2 from archaeoglobus fulgidus at 2.20 a resolution
60	d1d3va_	Alignment	not modelled	11.3	13	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
61	c3mmrA_	Alignment	not modelled	11.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**arginase; **PDBTitle:** structure of plasmodium falciparum arginase in complex with abh
62	c3cpiH_	Alignment	not modelled	11.1	14	**PDB header:**protein transport **Chain:** H: **PDB Molecule:**rab gdp-dissociation inhibitor; **PDBTitle:** crystal structure of yeast rab-gdi
63	c2qa2A_	Alignment	not modelled	10.9	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**polyketide oxygenase cabe; **PDBTitle:** crystal structure of cabe, an aromatic hydroxylase from angucycline2 biosynthesis, determined to 2.7 a resolution
64	c1zmrA_	Alignment	not modelled	10.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of the e. coli phosphoglycerate kinase
65	c1s1hB_	Alignment	not modelled	10.8	12	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**40s ribosomal protein s0-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
66	c2duwA_	Alignment	not modelled	10.7	11	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**putative coa-binding protein; **PDBTitle:** solution structure of putative coa-binding protein of2 klebsiella pneumoniae
67	d2eyqa1	Alignment	not modelled	10.6	20	**Fold:**SH3-like barrel **Superfamily:**CarD-like **Family:**CarD-like
68	d2gf3a1	Alignment	not modelled	10.4	18	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
69	c2dkhA_	Alignment	not modelled	10.4	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxybenzoate hydroxylase; **PDBTitle:** crystal structure of 3-hydroxybenzoate hydroxylase from comamonas2 testosteroni, in complex with the substrate
70	d2fi9a1	Alignment	not modelled	10.2	9	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
71	c3pzlA_	Alignment	not modelled	10.1	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**agmatine ureohydrolase; **PDBTitle:** the crystal structure of agmatine ureohydrolase of thermoplasma2 volcanium
72	d2nmla1	Alignment	not modelled	10.1	24	**Fold:**ERH-like **Superfamily:**ERH-like **Family:**ERH-like
73	c3q3vA_	Alignment	not modelled	9.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of phosphoglycerate kinase from campylobacter2 jejuni.
74	c2r4jA_	Alignment	not modelled	9.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aerobic glycerol-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of escherichia coli semet substituted2 glycerol-3-phosphate dehydrogenase in complex with dhap
75	c3fwzA_	Alignment	not modelled	9.7	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**inner membrane protein ybal; **PDBTitle:** crystal structure of trka-n domain of inner membrane protein ybal from2 escherichia coli
76	c3nioF_	Alignment	not modelled	9.6	21	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**guanidinobutyrase; **PDBTitle:** crystal structure of pseudomonas aeruginosa guanidinobutyrase
77	d1otha2	Alignment	not modelled	9.5	19	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
78	d2bcgg1	Alignment	not modelled	9.2	14	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GDI-like N domain
79	d1euca1	Alignment	not modelled	9.1	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
80	c2yg4B_	Alignment	not modelled	9.0	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putrescine oxidase; **PDBTitle:** structure-based redesign of cofactor binding in putrescine2 oxidase: wild type bound to putrescine
81	c1oy5B_	Alignment	not modelled	8.7	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of trna (m1g37) methyltransferase from aquifex2 aeolicus

82	d1oy5a_	Alignment	not modelled	8.7	16	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**tRNA(m1G37)-methyltransferase TrmD
83	c3mpoD_	Alignment	not modelled	8.7	24	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**predicted hydrolase of the had superfamily; **PDBTitle:** the crystal structure of a hydrolase from lactobacillus brevis
84	c2rgoA_	Alignment	not modelled	8.6	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alpha-glycerophosphate oxidase; **PDBTitle:** structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
85	d1y81a1	Alignment	not modelled	8.5	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
86	c2p58A_	Alignment	not modelled	8.4	15	**PDB header:**transport protein/chaperone **Chain:** A: **PDB Molecule:**putative type iii secretion protein ysce; **PDBTitle:** structure of the yersinia pestis type iii secretion system2 needle protein yscf in complex with its chaperones3 ysce/yscg
87	c3fmwC_	Alignment	not modelled	8.3	9	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxygenase; **PDBTitle:** the crystal structure of mtmoiv, a baeyer-villiger2 monooxygenase from the mithramycin biosynthetic pathway in3 streptomyces argillaceus.
88	d2ozga1	Alignment	not modelled	8.3	13	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**EF1021 C-terminal domain-like
89	c3nyeA_	Alignment	not modelled	8.3	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-arginine dehydrogenase; **PDBTitle:** crystal structure of pseudomonas aeruginosa d-arginine dehydrogenase2 in complex with imino-arginine
90	d1zcza2	Alignment	not modelled	8.2	12	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
91	c1zvpB_	Alignment	not modelled	8.1	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein vc0802; **PDBTitle:** crystal structure of a protein of unknown function vc0802 from vibrio2 cholerae, possible transport protein
92	c2l2qA_	Alignment	not modelled	8.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, cellobiose-specific iib component (cela); **PDBTitle:** solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi
93	d3coxa1	Alignment	not modelled	8.1	26	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
94	c2d6fA_	Alignment	not modelled	7.9	20	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit d; **PDBTitle:** crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln)
95	d1rlga_	Alignment	not modelled	7.9	9	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
96	d2cvza1	Alignment	not modelled	7.8	22	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain
97	d2npta1	Alignment	not modelled	7.7	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
98	c3l78A_	Alignment	not modelled	7.6	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein spx; **PDBTitle:** the crystal structure of smu.1142c from streptococcus mutans ua159
99	c3nbmA_	Alignment	not modelled	7.5	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, lactose-specific iibc components; **PDBTitle:** the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.