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Description	P33644
Date	Thu Jan 5 11:52:29 GMT 2012
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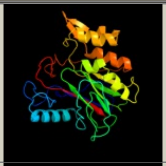
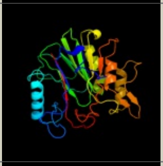
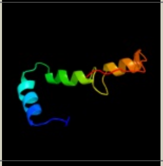
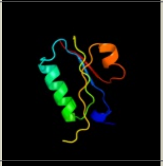
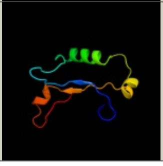
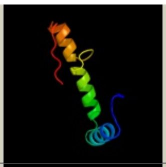
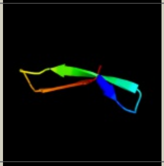
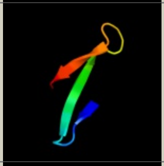
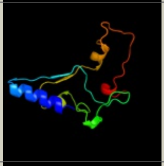
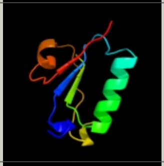
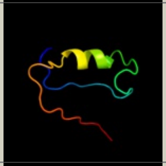
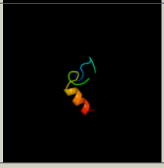
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1rw0a_	Alignment		100.0	87	**Fold:**CNF1/YfiH-like putative cysteine hydrolases **Superfamily:**CNF1/YfiH-like putative cysteine hydrolases **Family:**YfiH-like
2	d1xafa_	Alignment		100.0	97	**Fold:**CNF1/YfiH-like putative cysteine hydrolases **Superfamily:**CNF1/YfiH-like putative cysteine hydrolases **Family:**YfiH-like
3	d1rv9a_	Alignment		100.0	50	**Fold:**CNF1/YfiH-like putative cysteine hydrolases **Superfamily:**CNF1/YfiH-like putative cysteine hydrolases **Family:**YfiH-like
4	d1t8ha_	Alignment		100.0	36	**Fold:**CNF1/YfiH-like putative cysteine hydrolases **Superfamily:**CNF1/YfiH-like putative cysteine hydrolases **Family:**YfiH-like
5	d1xfja_	Alignment		100.0	38	**Fold:**CNF1/YfiH-like putative cysteine hydrolases **Superfamily:**CNF1/YfiH-like putative cysteine hydrolases **Family:**YfiH-like
6	d2f9zc1	Alignment		93.2	17	**Fold:**CNF1/YfiH-like putative cysteine hydrolases **Superfamily:**CNF1/YfiH-like putative cysteine hydrolases **Family:**CheD-like
7	d1np7a2	Alignment		49.0	12	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
8	c3sdsA_	Alignment		46.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase, mitochondrial; **PDBTitle:** crystal structure of a mitochondrial ornithine carbamoyltransferase2 from coccidioides immitis
9	c3giwA_	Alignment		38.1	9	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein of unknown function duf574; **PDBTitle:** crystal structure of a duf574 family protein (sav_2177) from2 streptomyces avermitilis ma-4680 at 1.45 a resolution
10	c3grfA_	Alignment		35.2	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** x-ray structure of ornithine transcarbamoylase from giardia2 lamblia
11	c3g7kD_	Alignment		33.4	25	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**3-methylitaconate isomerase; **PDBTitle:** crystal structure of methylitaconate-delta-isomerase

12	c2qe6B_	Alignment		28.1	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uncharacterized protein tfu_2867; **PDBTitle:** crystal structure of a putative methyltransferase (tfu_2867) from2 thermobifida fusca yx at 1.95 a resolution
13	c1kjkA_	Alignment		26.8	33	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** solution structure of the lambda integrase amino-terminal2 domain
14	d1z1ba1	Alignment		24.4	33	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**lambda integrase N-terminal domain
15	d1owla2	Alignment		23.8	12	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
16	c1ecjB_	Alignment		22.4	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutamine phosphoribosylpyrophosphate **PDBTitle:** escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
17	c2otcA_	Alignment		21.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** ornithine transcarbamoylase complexed with n-2 (phosphonacetyl)-l-ornithine
18	d1duvg2	Alignment		20.3	18	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
19	c3bd0D_	Alignment		19.4	21	**PDB header:**peptide binding protein **Chain:** D: **PDB Molecule:**protein memo1; **PDBTitle:** crystal structure of memo, form ii
20	c2jblC_	Alignment		17.3	26	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**photosynthetic reaction center cytochrome c **PDBTitle:** photosynthetic reaction center from blastochloris viridis
21	d2i5nc1	Alignment	not modelled	17.3	26	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Photosynthetic reaction centre (cytochrome subunit)
22	d2bo9b1	Alignment	not modelled	16.1	14	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**Latexin-like
23	c2w37A_	Alignment	not modelled	16.1	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase, catabolic; **PDBTitle:** crystal structure of the hexameric catabolic ornithine2 transcarbamylase from lactobacillus hilgardii
24	d1otfa_	Alignment	not modelled	15.3	15	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
25	c1zrtD_	Alignment	not modelled	14.4	19	**PDB header:**oxidoreductase/metal transport **Chain:** D: **PDB Molecule:**cytochrome c1; **PDBTitle:** rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound
26	c2fynH_	Alignment	not modelled	14.3	19	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**cytochrome c1; **PDBTitle:** crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
27	c1a1sA_	Alignment	not modelled	13.6	17	**PDB header:**transcarbamylase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** ornithine carbamoyltransferase from pyrococcus furiosus
28	d2nvma1	Alignment	not modelled	13.6	21	**Fold:**XisI-like **Superfamily:**XisI-like **Family:**XisI-like

29	d1dxha2	Alignment	not modelled	13.4	14	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
30	c2pw0A_	Alignment	not modelled	12.9	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**prpf methylaconitate isomerase; **PDBTitle:** crystal structure of trans-aconitate bound to methylaconitate2 isomerase prpf from shewanella oneidensis
31	c3lyvF_	Alignment	not modelled	12.4	63	**PDB header:**chaperone **Chain:** F: **PDB Molecule:**ribosome-associated factor y; **PDBTitle:** crystal structure of a domain of ribosome-associated factor y from2 streptococcus pyogenes serotype m6. northeast structural genomics3 consortium target id dr64a
32	d1vlva2	Alignment	not modelled	12.1	18	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
33	d2nlva1	Alignment	not modelled	11.9	21	**Fold:**XisI-like **Superfamily:**XisI-like **Family:**XisI-like
34	c2qlcC_	Alignment	not modelled	11.8	15	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**dna repair protein radc homolog; **PDBTitle:** the crystal structure of dna repair protein radc from chlorobium2 tepidum tls
35	d1xbta2	Alignment	not modelled	11.5	21	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Type II thymidine kinase zinc finger
36	d2b8ta2	Alignment	not modelled	11.3	25	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Type II thymidine kinase zinc finger
37	d2h9fa1	Alignment	not modelled	11.1	24	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PA0793-like
38	c1eysC_	Alignment	not modelled	10.5	22	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**photosynthetic reaction center; **PDBTitle:** crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
39	d1eysc_	Alignment	not modelled	10.5	22	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Photosynthetic reaction centre (cytochrome subunit)
40	c2hfqA_	Alignment	not modelled	10.1	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** nmr structure of protein ne1680 from nitrosomonas europaea:2 northeast structural genomics consortium target net5
41	d2hfqa1	Alignment	not modelled	10.1	21	**Fold:**NE1680-like **Superfamily:**NE1680-like **Family:**NE1680-like
42	c1p84D_	Alignment	not modelled	9.8	13	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**cytochrome c1, heme protein; **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
43	d1wjpa2	Alignment	not modelled	9.8	45	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
44	d1xkia_	Alignment	not modelled	9.8	16	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
45	d1otha2	Alignment	not modelled	9.6	13	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
46	c3d7qB_	Alignment	not modelled	9.5	11	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**xisi protein-like; **PDBTitle:** crystal structure of a xisi-like protein (npun_ar114) from nostoc2 punctiforme pcc 73102 at 2.30 a resolution
47	d1bjpa_	Alignment	not modelled	9.5	12	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
48	c2f9iC_	Alignment	not modelled	9.1	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl **PDBTitle:** crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus
49	d2hrva_	Alignment	not modelled	9.1	28	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral cysteine protease of trypsin fold
50	c3by0B_	Alignment	not modelled	8.8	18	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**neutrophil gelatinase-associated lipocalin; **PDBTitle:** crystal structure of siderocalin (ngal, lipocalin 2) w79a-r81a2 complexed with ferric enterobactin
51	c1z8rA_	Alignment	not modelled	8.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**coxsackievirus b4 polyprotein; **PDBTitle:** 2a cysteine proteinase from human coxsackievirus b4 (strain2 jvb / benschoten / new york / 51)
52	d2ch5a2	Alignment	not modelled	8.6	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
53	c3rlhA_	Alignment	not modelled	8.5	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sphingomyelin phosphodiesterase d lisictox-alphaia1a; **PDBTitle:** crystal structure of a class ii phospholipase d from loxosceles2 intermedia venom
54	c3updA_	Alignment	not modelled	8.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** 2.9 angstrom crystal structure of ornithine carbamoyltransferase2 (argf) from vibrio vulnificus
						PDB header:hydrolase

55	c3ot4F_	Alignment	not modelled	8.4	23	**Chain:** F: **PDB Molecule:**putative isochorismatase; **PDBTitle:** structure and catalytic mechanism of bordetella bronchiseptica nicf
56	c3tvsA_	Alignment	not modelled	8.3	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cryptochrome-1; **PDBTitle:** structure of full-length drosophila cryptochrome
57	d1b0aa2	Alignment	not modelled	8.1	16	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Tetrahydrofolate dehydrogenase/cyclohydrolase
58	d2nwva1	Alignment	not modelled	8.0	13	**Fold:**XisI-like **Superfamily:**XisI-like **Family:**XisI-like
59	c3gbcA_	Alignment	not modelled	7.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pyrazinamidase/nicotinamidas pnca; **PDBTitle:** determination of the crystal structure of the pyrazinamidase from2 m.tuberculosis : a structure-function analysis for prediction3 resistance to pyrazinamide
60	c2op8A_	Alignment	not modelled	7.9	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable tautomerase ywhb; **PDBTitle:** crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
61	c3m20A_	Alignment	not modelled	7.6	8	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**4-oxalocrotonate tautomerase, putative; **PDBTitle:** crystal structure of dmpi from archaeoglobus fulgidus determined to2 2.37 angstroms resolution
62	d1ppjd1	Alignment	not modelled	7.6	19	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Cytochrome bc1 domain
63	d3cx5d1	Alignment	not modelled	7.6	13	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Cytochrome bc1 domain
64	c3ecyA_	Alignment	not modelled	7.5	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cg4584-pa, isoform a (bcdna.ld08534); **PDBTitle:** crystal structural analysis of drosophila melanogaster dutpase
65	c1gph1_	Alignment	not modelled	7.3	11	**PDB header:**transferase(glutamine amidotransferase) **Chain:** 1: **PDB Molecule:**glutamine phosphoribosyl-pyrophosphate amidotransferase; **PDBTitle:** structure of the allosteric regulatory enzyme of purine biosynthesis
66	d1ml4a2	Alignment	not modelled	7.0	16	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
67	d1mwwa_	Alignment	not modelled	6.7	8	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**Hypothetical protein HI1388.1
68	c3ry0A_	Alignment	not modelled	6.6	8	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tautomerase; **PDBTitle:** crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in2 tomaymycin biosynthetic pathway
69	c3cwbQ_	Alignment	not modelled	6.5	13	**PDB header:**oxidoreductase **Chain:** Q: **PDB Molecule:**mitochondrial cytochrome c1, heme protein; **PDBTitle:** chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
70	d2f9ya1	Alignment	not modelled	6.4	11	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
71	c2rgwD_	Alignment	not modelled	6.3	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** catalytic subunit of m. jannaschii aspartate2 transcarbamoylase
72	c2l5pA_	Alignment	not modelled	6.2	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**lipocalin 12; **PDBTitle:** solution nmr structure of protein lipocalin 12 from rat epididymis
73	c3gd5D_	Alignment	not modelled	6.2	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from gloeobacter2 violaceus
74	c3uzuA_	Alignment	not modelled	6.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal rna small subunit methyltransferase a; **PDBTitle:** the structure of the ribosomal rna small subunit methyltransferase a2 from burkholderia pseudomallei
75	c2f9rC_	Alignment	not modelled	6.1	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**sphingomyelinase d 1; **PDBTitle:** crystal structure of the inactive state of the smase i, a2 sphingomyelinase d from loxosceles laeta venom
76	c2ormA_	Alignment	not modelled	6.0	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable tautomerase hp0924; **PDBTitle:** crystal structure of the 4-oxalocrotonate tautomerase homologue dmpi2 from helicobacter pylori.
77	c2z8nB_	Alignment	not modelled	5.9	24	**PDB header:**lyase **Chain:** B: **PDB Molecule:**27.5 kda virulence protein; **PDBTitle:** structural basis for the catalytic mechanism of phosphothreonine lyase
78	c2bo9B_	Alignment	not modelled	5.9	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**human latexin; **PDBTitle:** human carboxypeptidase a4 in complex with human latexin.
79	c3mb2G_	Alignment	not modelled	5.9	8	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**4-oxalocrotonate tautomerase family enzyme - alpha subunit; **PDBTitle:** kinetic and structural characterization of a heterohexamer 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural

						diversity in the4 tautomerase superfamily
80	c2x4kB_	Alignment	not modelled	5.8	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-oxalocrotonate tautomerase; **PDBTitle:** crystal structure of sar1376, a putative 4-oxalocrotonate2 tautomerase from the methicillin-resistant staphylococcus3 aureus (mrsa)
81	c2orvB_	Alignment	not modelled	5.8	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymidine kinase; **PDBTitle:** human thymidine kinase 1 in complex with tp4a
82	d1x71a1	Alignment	not modelled	5.7	18	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
83	c3nglA_	Alignment	not modelled	5.7	16	**PDB header:**oxidoreductase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of bifunctional 5,10-methylenetetrahydrofolate2 dehydrogenase / cyclohydrolase from thermoplasma acidophilum
84	c1hynQ_	Alignment	not modelled	5.7	15	**PDB header:**membrane protein **Chain:** Q: **PDB Molecule:**band 3 anion transport protein; **PDBTitle:** crystal structure of the cytoplasmic domain of human2 erythrocyte band-3 protein
85	c1jmxA_	Alignment	not modelled	5.7	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**amine dehydrogenase; **PDBTitle:** crystal structure of a quinohemoprotein amine dehydrogenase2 from pseudomonas putida
86	c3hcyB_	Alignment	not modelled	5.7	29	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative two-component sensor histidine kinase protein; **PDBTitle:** the crystal structure of the domain of putative two-component sensor2 histidine kinase protein from sinorhizobium meliloti 1021
87	d1gph11	Alignment	not modelled	5.7	11	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
88	c3uinD_	Alignment	not modelled	5.6	50	**PDB header:**ligase/isomerase/protein binding **Chain:** D: **PDB Molecule:**e3 sumo-protein ligase ranbp2; **PDBTitle:** complex between human rangap1-sumo2, ubc9 and the ir1 domain from2 ranbp2
89	c3abfB_	Alignment	not modelled	5.5	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-oxalocrotonate tautomerase; **PDBTitle:** crystal structure of a 4-oxalocrotonate tautomerase homologue2 (tthb242)
90	d1pvva2	Alignment	not modelled	5.4	20	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
91	c3bmaC_	Alignment	not modelled	5.4	57	**PDB header:**ligase **Chain:** C: **PDB Molecule:**d-alanyl-lipoteichoic acid synthetase; **PDBTitle:** crystal structure of d-alanyl-lipoteichoic acid synthetase from2 streptococcus pneumoniae r6
92	d1yupa1	Alignment	not modelled	5.3	9	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
93	c2h0rD_	Alignment	not modelled	5.3	5	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nicotinamidase; **PDBTitle:** structure of the yeast nicotinamidase pnc1p
94	c2kswA_	Alignment	not modelled	5.2	33	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**oryctin; **PDBTitle:** backbone 1h, 13c, and 15n chemical shift assignments for oryctin
95	c3on9B_	Alignment	not modelled	5.2	22	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**tumour necrosis factor receptor; **PDBTitle:** the secret domain from ectromelia virus
96	c3e2iA_	Alignment	not modelled	5.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidine kinase; **PDBTitle:** crystal structure of thymidine kinase from s. aureus
97	d1ecfa1	Alignment	not modelled	5.1	11	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
98	d1hynp_	Alignment	not modelled	5.0	15	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**Anion transport protein, cytoplasmic domain