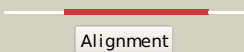

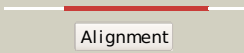







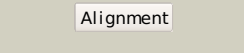

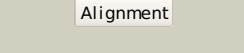
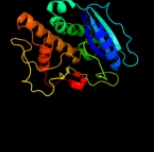
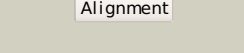
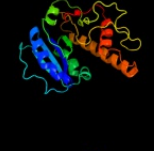




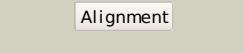



Phyre2

| | |
|---------------|------------------------------|
| Email | I.a.kelley@imperial.ac.uk |
| Description | A0PJZ3 |
| Date | Sat Jun 16 10:31:38 BST 2012 |
| Unique Job ID | eab9cd653f9ed7b9 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c1ga8A_ |  Alignment |  | 100.0 | 20 | PDB header: transferase Chain: A; PDB Molecule: galactosyl transferase Igtc; PDBTitle: crystal structure of galactosyltransferase Igtc in complex2 with donor and acceptor sugar analogs. |
| 2 | d1ga8a_ |  Alignment |  | 100.0 | 20 | Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Galactosyltransferase LgtC |
| 3 | c3tzB_ |  Alignment |  | 99.9 | 19 | PDB header: transferase Chain: B; PDB Molecule: glycosyl transferase family 8; PDBTitle: the structure of a protein in glycosyl transferase family 8 from2 anaerococcus prevotii. |
| 4 | c1zcyA_ |  Alignment |  | 99.9 | 16 | PDB header: transferase Chain: A; PDB Molecule: glycogenin-1; PDBTitle: apo form of a mutant of glycogenin in which asp159 is replaced by ser |
| 5 | d1l12a_ |  Alignment |  | 99.9 | 16 | Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Glycogenin |
| 6 | c1zctB_ |  Alignment |  | 99.9 | 16 | PDB header: transferase Chain: B; PDB Molecule: glycogenin-1; PDBTitle: structure of glycogenin truncated at residue 270 in a2 complex with udp |
| 7 | d1o7qa_ |  Alignment |  | 96.6 | 17 | Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: alpha-1,3-galactosyltransferase-like |
| 8 | d1lzia_ |  Alignment |  | 94.8 | 16 | Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: alpha-1,3-galactosyltransferase-like |
| 9 | c2vg2C_ |  Alignment |  | 84.0 | 25 | PDB header: transferase Chain: C; PDB Molecule: undecaprenyl pyrophosphate synthetase; PDBTitle: rv2361 with ipp |
| 10 | d1qg8a_ |  Alignment |  | 56.5 | 11 | Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Spore coat polysaccharide biosynthesis protein SpsA |
| 11 | c2z86D_ |  Alignment |  | 44.4 | 11 | PDB header: transferase Chain: D; PDB Molecule: chondroitin synthase; PDBTitle: crystal structure of chondroitin polymerase from2 escherichia coli strain k4 (k4cp) complexed with udp-glucua3 and udp |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 12 | c3bcvA_ | Alignment | | 38.0 | 10 | PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase protein; PDBTitle: crystal structure of a putative glycosyltransferase from bacteroides2 fragilis |
| 13 | c2x5sB_ | Alignment | | 34.4 | 15 | PDB header: transferase Chain: B: PDB Molecule: mannose-1-phosphate guanylyltransferase; PDBTitle: crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state. |
| 14 | d2py5a2 | Alignment | | 29.8 | 26 | Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I |
| 15 | c3oj6C_ | Alignment | | 27.5 | 15 | PDB header: hydrolase Chain: C: PDB Molecule: blastidicin-s deaminase; PDBTitle: crystal structure of blastidicin s deaminase from coccidioides immitis |
| 16 | d2bmwa2 | Alignment | | 26.0 | 12 | Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases |
| 17 | d1wn7a2 | Alignment | | 24.1 | 28 | Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I |
| 18 | d1tvca2 | Alignment | | 21.7 | 12 | Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Aromatic dioxygenase reductase-like |
| 19 | c4a69A_ | Alignment | | 20.6 | 30 | PDB header: transcription Chain: A: PDB Molecule: histone deacetylase 3,; PDBTitle: structure of hdac3 bound to corepressor and inositol tetraphosphate |
| 20 | c3ckvA_ | Alignment | | 20.4 | 11 | PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a mycobacterial protein |
| 21 | d1wiwa_ | Alignment | not modelled | 19.0 | 45 | Fold: SIS domain Superfamily: SIS domain Family: double-SIS domain |
| 22 | d1fnda2 | Alignment | not modelled | 18.5 | 12 | Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases |
| 23 | d2d30a1 | Alignment | not modelled | 17.8 | 20 | Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase |
| 24 | c3dmoD_ | Alignment | not modelled | 17.5 | 17 | PDB header: hydrolase Chain: D: PDB Molecule: cytidine deaminase; PDBTitle: 1.6 a crystal structure of cytidine deaminase from2 burkholderia pseudomallei |
| 25 | d1gawa2 | Alignment | not modelled | 17.2 | 13 | Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases |
| 26 | c3ew8A_ | Alignment | not modelled | 17.1 | 30 | PDB header: hydrolase Chain: A: PDB Molecule: histone deacetylase 8; PDBTitle: crystal structure analysis of human hdac8 d101I variant |
| 27 | c3maxB_ | Alignment | not modelled | 17.0 | 35 | PDB header: hydrolase Chain: B: PDB Molecule: histone deacetylase 2; PDBTitle: crystal structure of human hdac2 complexed with an n-(2-aminophenyl)2 benzamide |
| 28 | c2w7tA_ | Alignment | not modelled | 16.6 | 19 | PDB header: ligase Chain: A: PDB Molecule: putative cytidine triphosphate synthase; PDBTitle: trypanosoma brucei ctps - glutaminase domain in bound2 acivicin |
| | | | | | | Fold: Heme-dependent peroxidases |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|---|
| 29 | d1ub2a1 | Alignment | not modelled | 16.3 | 14 | Superfamily: Heme-dependent peroxidases Family: Catalase-peroxidase KatG |
| 30 | c2ffuA | Alignment | not modelled | 15.9 | 14 | PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 2; PDBTitle: crystal structure of human ppgalnact-2 complexed with udp2 and ea2 |
| 31 | c3b8fB | Alignment | not modelled | 15.8 | 14 | PDB header: hydrolase Chain: B: PDB Molecule: putative blasticidin s deaminase; PDBTitle: crystal structure of the cytidine deaminase from bacillus anthracis |
| 32 | d1qhta2 | Alignment | not modelled | 15.7 | 29 | Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I |
| 33 | d1qfza2 | Alignment | not modelled | 15.5 | 12 | Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases |
| 34 | c2vwkA | Alignment | not modelled | 15.3 | 32 | PDB header: dna replication Chain: A: PDB Molecule: dna polymerase; PDBTitle: uracil recognition in archaeal dna polymerases captured by2 x-ray crystallography. v93q polymerase variant |
| 35 | c1omxB | Alignment | not modelled | 14.7 | 9 | PDB header: transferase Chain: B: PDB Molecule: alpha-1,4-n-acetylhexosaminyltransferase extl2; PDBTitle: crystal structure of mouse alpha-1,4-n-2 acetylhexosaminyltransferase (extl2) |
| 36 | c2p73A | Alignment | not modelled | 14.5 | 20 | PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase (mannosyltransferase) involved PDBTitle: crystal structure of a glycosyltransferase involved in the2 glycosylation of the major capsid of pbcv-1 |
| 37 | d1d5aa2 | Alignment | not modelled | 14.5 | 28 | Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I |
| 38 | c1xhbA | Alignment | not modelled | 14.2 | 13 | PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 1; PDBTitle: the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylgalactosaminyltransferase-t1 |
| 39 | d1ep3b2 | Alignment | not modelled | 14.1 | 5 | Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Dihydroorotate dehydrogenase B, PyrK subunit |
| 40 | d1p35a | Alignment | not modelled | 13.7 | 26 | Fold: Baculovirus p35 protein Superfamily: Baculovirus p35 protein Family: Baculovirus p35 protein |
| 41 | c1d5aA | Alignment | not modelled | 13.4 | 28 | PDB header: transferase Chain: A: PDB Molecule: protein (dna polymerase); PDBTitle: crystal structure of an archaeobacterial dna polymerase2 d.tok. deposition of second native structure at 2.43 angstrom |
| 42 | d2piaa2 | Alignment | not modelled | 13.2 | 20 | Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Aromatic dioxygenase reductase-like |
| 43 | d1s5ja2 | Alignment | not modelled | 12.9 | 62 | Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I |
| 44 | c2ex3l | Alignment | not modelled | 12.8 | 26 | PDB header: transferase/replication Chain: I: PDB Molecule: dna polymerase; PDBTitle: bacteriophage phi29 dna polymerase bound to terminal protein |
| 45 | d1ddga2 | Alignment | not modelled | 12.3 | 10 | Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: NADPH-cytochrome p450 reductase-like |
| 46 | c2dogD | Alignment | not modelled | 12.3 | 31 | PDB header: cell cycle Chain: D: PDB Molecule: sfi1p; PDBTitle: crystal structure of sfi1p/cdc31p complex |
| 47 | d3bl9a1 | Alignment | not modelled | 12.2 | 20 | Fold: HIT-like Superfamily: HIT-like Family: mRNA decapping enzyme DcpS C-terminal domain |
| 48 | d2fr5a1 | Alignment | not modelled | 12.2 | 20 | Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase |
| 49 | c1fncA | Alignment | not modelled | 12.1 | 11 | PDB header: oxidoreductase (nadp+(a),ferredoxin(a)) Chain: A: PDB Molecule: ferredoxin-nadp+ reductase; PDBTitle: refined crystal structure of spinach ferredoxin reductase2 at 1.7 angstroms resolution: oxidized, reduced, and 2'-3 phospho-5'-amp bound states |
| 50 | d1xhba2 | Alignment | not modelled | 11.7 | 10 | Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain |
| 51 | c4f7dA | Alignment | not modelled | 11.3 | 8 | PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of ferredoxin-nadp reductase from burkholderia2 thailandensis e264 |
| 52 | d1qasa3 | Alignment | not modelled | 11.1 | 27 | Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Mammalian PLC |
| 53 | d1uwza | Alignment | not modelled | 10.9 | 27 | Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase |
| 54 | d1omza | Alignment | not modelled | 10.8 | 9 | Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases |

| | | | | | Family:Exostosin |
|----|-------------------------|-----------|--------------|------|--|
| 55 | d2z3ga1 | Alignment | not modelled | 10.2 | 11 Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase |
| 56 | c3bg3B | Alignment | not modelled | 10.0 | 13 PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase, mitochondrial; PDBTitle: crystal structure of human pyruvate carboxylase (missing2 the biotin carboxylase domain at the n-terminus) |
| 57 | d1j7ga | Alignment | not modelled | 9.8 | 15 Fold: DTD-like Superfamily: DTD-like Family: DTD-like |
| 58 | d1pzta | Alignment | not modelled | 9.6 | 16 Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: beta 1,4 galactosyltransferase (b4GalT1) |
| 59 | d1c3pa | Alignment | not modelled | 9.4 | 25 Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Histone deacetylase, HDAC |
| 60 | d1r5ta | Alignment | not modelled | 9.3 | 11 Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase |
| 61 | c2d7iA | Alignment | not modelled | 9.2 | 13 PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 10; PDBTitle: crystal structure of pp-galnac-t10 with udp, galnac and mn2+ |
| 62 | d1mq0a | Alignment | not modelled | 9.2 | 16 Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase |
| 63 | d1t64a | Alignment | not modelled | 9.1 | 27 Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Histone deacetylase, HDAC |
| 64 | d1cqxa3 | Alignment | not modelled | 9.0 | 22 Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Flavo-hemoglobin, C-terminal domain |
| 65 | d1tgoa2 | Alignment | not modelled | 8.9 | 32 Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I |
| 66 | c4eh1A | Alignment | not modelled | 8.8 | 8 PDB header: oxidoreductase Chain: A: PDB Molecule: flavo-hemoprotein; PDBTitle: crystal structure of the flavo-hem-like-fad/nad binding domain of2 nitric oxide dioxygenase from vibrio cholerae o1 biovar el tor |
| 67 | c2gv9B | Alignment | not modelled | 8.3 | 29 PDB header: transferase Chain: B: PDB Molecule: dna polymerase; PDBTitle: crystal structure of the herpes simplex virus type 1 dna polymerase |
| 68 | d1ih7a2 | Alignment | not modelled | 8.3 | 38 Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I |
| 69 | c2vqqA | Alignment | not modelled | 8.1 | 55 PDB header: hydrolase Chain: A: PDB Molecule: histone deacetylase 4; PDBTitle: structure of hdac4 catalytic domain (a double cysteine-to-2 alanine mutant) bound to a trifluoromethylketone inhibitor |
| 70 | c2v8wA | Alignment | not modelled | 7.9 | 21 PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 4e; PDBTitle: crystallographic and mass spectrometric characterisation of2 eif4e with n7-cap derivatives |
| 71 | d1jkea | Alignment | not modelled | 7.8 | 15 Fold: DTD-like Superfamily: DTD-like Family: DTD-like |
| 72 | d3c10a1 | Alignment | not modelled | 7.7 | 45 Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Histone deacetylase, HDAC |
| 73 | d1q8ia2 | Alignment | not modelled | 7.6 | 17 Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I |
| 74 | c2j83B | Alignment | not modelled | 7.5 | 19 PDB header: hydrolase Chain: B: PDB Molecule: ulilysin; PDBTitle: ulilysin metalloprotease in complex with batimastat. |
| 75 | c2j7pA | Alignment | not modelled | 7.4 | 16 PDB header: signal recognition Chain: A: PDB Molecule: signal recognition particle protein; PDBTitle: gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy |
| 76 | c2zjtB | Alignment | not modelled | 7.3 | 60 PDB header: isomerase Chain: B: PDB Molecule: dna gyrase subunit b; PDBTitle: crystal structure of dna gyrase b' domain sheds lights on2 the mechanism for t-segment navigation |
| 77 | d2j07a2 | Alignment | not modelled | 7.3 | 36 Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain |
| 78 | d1fo8a | Alignment | not modelled | 7.3 | 12 Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: N-acetylglucosaminyltransferase I |
| 79 | d1yuaa2 | Alignment | not modelled | 7.2 | 38 Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Prokaryotic DNA topoisomerase I, a C-terminal fragment |
| 80 | d1u5tb1 | Alignment | not modelled | 7.2 | 25 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain |

| | | | | | | |
|----|-------------------------|-----------|--------------|-----|----|--|
| 81 | d2ccaa1 | Alignment | not modelled | 7.2 | 15 | Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: Catalase-peroxidase KatG |
| 82 | c3anwB_ | Alignment | not modelled | 7.1 | 19 | PDB header: replication Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: a protein complex essential initiation of dna replication |
| 83 | c3fkqA_ | Alignment | not modelled | 7.1 | 6 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ntrc-like two-domain protein; PDBTitle: crystal structure of ntrc-like two-domain protein (rer070207001320)2 from eubacterium rectale at 2.10 a resolution |
| 84 | c1txlA_ | Alignment | not modelled | 7.0 | 26 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: metal-binding protein yoda; PDBTitle: crystal structure of metal-binding protein yoda from e.2 coli, pfam duf149 |
| 85 | d1bxa_ | Alignment | not modelled | 7.0 | 26 | Fold: Lipocalins Superfamily: Lipocalins Family: Hypothetical protein YodA |
| 86 | c2eixA_ | Alignment | not modelled | 6.9 | 11 | PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-cytochrome b5 reductase; PDBTitle: the structure of physarum polycephalum cytochrome b5 reductase |
| 87 | c3bg5C_ | Alignment | not modelled | 6.9 | 16 | PDB header: ligase Chain: C: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate2 carboxylase |
| 88 | c1cqxB_ | Alignment | not modelled | 6.9 | 19 | PDB header: lipid binding protein Chain: B: PDB Molecule: flavo-hemoglobin; PDBTitle: crystal structure of the flavo-hemoglobin from alcaligenes eutrophus at2 1.75 a resolution |
| 89 | d1nowa1 | Alignment | not modelled | 6.8 | 15 | Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain |
| 90 | d1mwva1 | Alignment | not modelled | 6.5 | 18 | Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: Catalase-peroxidase KatG |
| 91 | d1rz3a_ | Alignment | not modelled | 6.5 | 21 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase |
| 92 | c1s5jA_ | Alignment | not modelled | 6.4 | 62 | PDB header: transferase Chain: A: PDB Molecule: dna polymerase i; PDBTitle: insight in dna replication: the crystal structure of dna2 polymerase b1 from the archaeon sulfolobus solfataricus |
| 93 | d2ccva1 | Alignment | not modelled | 6.3 | 7 | Fold: HPA-like Superfamily: Agglutinin HPA-like Family: Agglutinin HPA-like |
| 94 | d1a8pa2 | Alignment | not modelled | 6.2 | 10 | Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases |
| 95 | c2k0mA_ | Alignment | not modelled | 6.2 | 11 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the uncharacterized protein from2 rhodospirillum rubrum gene locus rru_a0810. northeast3 structural genomics target rrr43 |
| 96 | c1qfjD_ | Alignment | not modelled | 6.2 | 11 | PDB header: oxidoreductase Chain: D: PDB Molecule: protein (flavin reductase); PDBTitle: crystal structure of nad(p)h:flavin oxidoreductase from escherichia2 coli |
| 97 | c2vldA_ | Alignment | not modelled | 6.1 | 24 | PDB header: hydrolase Chain: A: PDB Molecule: upf0286 protein pyrab01260; PDBTitle: crystal structure of a repair endonuclease from pyrococcus2 abyssi |
| 98 | d1rgoa1 | Alignment | not modelled | 6.1 | 33 | Fold: CCCH zinc finger Superfamily: CCCH zinc finger Family: CCCH zinc finger |
| 99 | c1y6gB_ | Alignment | not modelled | 5.8 | 50 | PDB header: transferase/dna Chain: B: PDB Molecule: dna alpha-glucosyltransferase; PDBTitle: alpha-glucosyltransferase in complex with udp and a 13_mer2 dna containing a hmu base at 2.8 a resolution |