

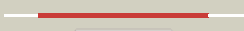



























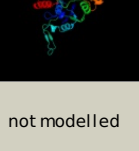


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2pa4B_	 Alignment		100.0	33	PDB header: transferase Chain: B: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of udp-glucose pyrophosphorylase from corynebacteria2 glutamicum in complex with magnesium and udp-glucose
2	c2e3dB_	 Alignment		100.0	51	PDB header: transferase Chain: B: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of e. coli glucose-1-phosphate2 uridylyltransferase
3	c2ux8G_	 Alignment		100.0	40	PDB header: transferase Chain: G: PDB Molecule: glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of sphingomonas elodea atcc 31461 glucose-2 1-phosphate uridylyltransferase in complex with glucose-3 1-phosphate.
4	d1mc3a_	 Alignment		100.0	21	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
5	d1fxoa_	 Alignment		100.0	23	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
6	d1iina_	 Alignment		100.0	24	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
7	d1h5ra_	 Alignment		100.0	24	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
8	d1lvwa_	 Alignment		100.0	24	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
9	c3jukA_	 Alignment		100.0	35	PDB header: transferase Chain: A: PDB Molecule: udp-glucose pyrophosphorylase (galu); PDBTitle: the crystal structure of udp-glucose pyrophosphorylase complexed with2 udp-glucose
10	c1yp3C_	 Alignment		100.0	22	PDB header: transferase Chain: C: PDB Molecule: glucose-1-phosphate adenyltransferase small PDBTitle: crystal structure of potato tuber adp-glucose2 pyrophosphorylase in complex with atp
11	c3hl3A_	 Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: glucose-1-phosphate thymidyltransferase; PDBTitle: 2.76 angstrom crystal structure of a putative glucose-1-phosphate2 thymidyltransferase from bacillus anthracis in complex with a3 sucrose.

12	d1yp2a2	Alignment		100.0	20	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
13	c3brkX	Alignment		100.0	15	PDB header: transferase Chain: X: PDB Molecule: glucose-1-phosphate adenylyltransferase; PDBTitle: crystal structure of adp-glucose pyrophosphorylase from2 agrobacterium tumefaciens
14	c2x5sB	Alignment		100.0	18	PDB header: transferase Chain: B: PDB Molecule: mannose-1-phosphate guanylyltransferase; PDBTitle: crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
15	c2cu2A	Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: putative mannose-1-phosphate guanylyl transferase; PDBTitle: crystal structure of mannose-1-phosphate geranyltransferase from2 thermus thermophilus hb8
16	c3pnnA	Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
17	d2cu2a2	Alignment		100.0	21	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: mannose-1-phosphate guanylyl transferase
18	c1hm8A	Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine-1-phosphate uridylyltransferase; PDBTitle: crystal structure of s.pneumoniae n-acetylglucosamine-1-phosphate2 uridylyltransferase, glmu, bound to acetyl coenzyme a
19	c3d98A	Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
20	d1tzfa	Alignment		100.0	21	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: Cytidylyltransferase
21	c2oi6A	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: e. coli glmu- complex with udp-glcna, coa and glcn-1-po4
22	c2qkxA	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: n-acetyl glucosamine 1-phosphate uridylyltransferase from mycobacterium2 tuberculosis complex with n-acetyl glucosamine 1-phosphate
23	c2v0hA	Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: characterization of substrate binding and catalysis of the2 potential antibacterial target n-acetylglucosamine-1-3 phosphate uridylyltransferase (glmu)
24	c2ggqA	Alignment	not modelled	100.0	24	PDB header: transferase Chain: A: PDB Molecule: 401aa long hypothetical glucose-1-phosphate PDBTitle: complex of hypothetical glucose-1-phosphate thymidyltransferase from2 sulfolobus tokodaii
25	c1fwyA	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of n-acetylglucosamine 1-phosphate2 uridylyltransferase bound to udp-glcna
26	d2oi6a2	Alignment	not modelled	100.0	21	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: UDP-glucose pyrophosphorylase
27	d1g97a2	Alignment	not modelled	100.0	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: UDP-glucose pyrophosphorylase
						Fold: Nucleotide-diphospho-sugar transferases

28	dljka_	Alignment	not modelled	100.0	16	Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
29	cljylC_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: C: PDB Molecule: ctp:phosphocholine cytidylyltransferase; PDBTitle: catalytic mechanism of ctp:phosphocholine2 cytidylyltransferase from streptococcus pneumoniae (liicc)
30	c2xmhB_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: B: PDB Molecule: ctp-inositol-1-phosphate cytidylyltransferase; PDBTitle: the x-ray structure of ctp:inositol-1-phosphate2 cytidylyltransferase from archaeoglobus fulgidus
31	dlvica_	Alignment	not modelled	100.0	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
32	c2qh5B_	Alignment	not modelled	100.0	12	PDB header: isomerase Chain: B: PDB Molecule: mannose-6-phosphate isomerase; PDBTitle: crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
33	c3oamD_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: D: PDB Molecule: 3-deoxy-manno-octulosonate cytidylyltransferase; PDBTitle: crystal structure of cytidylyltransferase from vibrio cholerae
34	c2xwlB_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; PDBTitle: crystal structure of ispd from mycobacterium smegmatis in complex2 with ctp and mg
35	c3tqdA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidylyltransferase; PDBTitle: structure of the 3-deoxy-d-manno-octulosonate cytidylyltransferase2 (kdsb) from coxiella burnetii
36	c3polA_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidylyltransferase; PDBTitle: 2.3 angstrom crystal structure of 3-deoxy-manno-octulosonate2 cytidylyltransferase (kdsb) from acinetobacter baumannii.
37	dlh7ea_	Alignment	not modelled	99.9	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
38	c2y6pC_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: C: PDB Molecule: 3-deoxy-manno-octulosonate cytidylyltransferase; PDBTitle: evidence for a two-metal-ion-mechanism in the2 kdo-cytidylyltransferase kdsb
39	dli52a_	Alignment	not modelled	99.9	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
40	dlvh1a_	Alignment	not modelled	99.9	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
41	dlvpaa_	Alignment	not modelled	99.9	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
42	dlw55a1	Alignment	not modelled	99.9	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
43	dle5ka_	Alignment	not modelled	99.9	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Molybdenum cofactor biosynthesis protein MobA
44	dleyra_	Alignment	not modelled	99.9	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
45	dlqwja_	Alignment	not modelled	99.9	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
46	c2we9A_	Alignment	not modelled	99.9	25	PDB header: unknown function Chain: A: PDB Molecule: moba-related protein; PDBTitle: crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
47	c2wawA_	Alignment	not modelled	99.9	15	PDB header: unknown function Chain: A: PDB Molecule: moba relate protein; PDBTitle: crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
48	c3f1cB_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: B: PDB Molecule: putative 2-c-methyl-d-erythritol 4-phosphate PDBTitle: crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidylyltransferase from listeria monocytogenes
49	d2dpwa1	Alignment	not modelled	99.9	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: TTHA0179-like
50	dlvh3a_	Alignment	not modelled	99.9	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
51	dlw77a1	Alignment	not modelled	99.9	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
52	c3rsbB_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: B: PDB Molecule: adenosyl cobinamide-phosphate guanylyltransferase; PDBTitle: structure of the archaeal gtp:adocbi-p

						guanylyltransferase (coby) from2 methanocaldococcus jannaschii
53	c3ngwA	Alignment	not modelled	99.8	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis protein a PDBTitle: crystal structure of molybdopterin-guanine dinucleotide biosynthesis2 protein a from archaeoglobus fulgidus, northeast structural genomics3 consortium target gr189
54	c2vshB	Alignment	not modelled	99.8	14	PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate PDBTitle: synthesis of cdp-activated ribitol for teichoic acid2 precursors in streptococcus pneumoniae
55	c3okrA	Alignment	not modelled	99.8	13	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
56	c2px7A	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate PDBTitle: crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase from thermus thermophilus hb8
57	d1vgwa	Alignment	not modelled	99.8	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: Cytidyltransferase
58	c1w57A	Alignment	not modelled	99.8	10	PDB header: transferase Chain: A: PDB Molecule: ispd/ispf bifunctional enzyme; PDBTitle: structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
59	c2e8bA	Alignment	not modelled	99.7	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: probable molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of the putative protein (aq1419) from aquifex2 aeolicus vf5
60	c3okrC	Alignment	not modelled	99.6	15	PDB header: transferase Chain: C: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
61	c3d5nB	Alignment	not modelled	99.3	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: q97w15_sulso; PDBTitle: crystal structure of the q97w15_sulso protein from2 sulfolobus solfataricus. nesg target ssr125.
62	c3oc9A	Alignment	not modelled	99.0	15	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of putative udp-n-acetylglucosamine2 pyrophosphorylase from entamoeba histolytica
63	d2icya2	Alignment	not modelled	98.8	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: UDP-glucose pyrophosphorylase
64	d1vm8a	Alignment	not modelled	98.8	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: UDP-glucose pyrophosphorylase
65	d1jv1a	Alignment	not modelled	98.8	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: UDP-glucose pyrophosphorylase
66	c3gueB	Alignment	not modelled	98.7	10	PDB header: transferase Chain: B: PDB Molecule: utp-glucose-1-phosphate uridylyltransferase 2; PDBTitle: crystal structure of udp-glucose phosphorylase from trypanosoma2 brucei, (tb10.389.0330)
67	c2yqsA	Alignment	not modelled	98.6	16	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of uridine-diphospho-n-acetylglucosamine2 pyrophosphorylase from candida albicans, in the product-binding form
68	c2i5kB	Alignment	not modelled	98.5	13	PDB header: transferase Chain: B: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of ugp1p
69	c2q4jB	Alignment	not modelled	98.4	12	PDB header: transferase Chain: B: PDB Molecule: probable utp-glucose-1-phosphate uridylyltransferase 2; PDBTitle: ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at3g03250, a putative udp-glucose3 pyrophosphorylase
70	c2oefA	Alignment	not modelled	98.3	11	PDB header: transferase Chain: A: PDB Molecule: utp-glucose-1-phosphate uridylyltransferase 2, PDBTitle: open and closed structures of the udp-glucose2 pyrophosphorylase from leishmania major
71	c3ogzA	Alignment	not modelled	98.2	13	PDB header: transferase Chain: A: PDB Molecule: udp-sugar pyrophosphorylase; PDBTitle: protein structure of usp from l. major in apo-form
72	c2ffuA	Alignment	not modelled	90.5	14	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 2; PDBTitle: crystal structure of human ppgalnact-2 complexed with udp2 and ea2
73	c2d7iA	Alignment	not modelled	90.5	17	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 10; PDBTitle: crsytal structure of pp-galnac-t10 with udp, galnac and mn2+
74	c1xhbA	Alignment	not modelled	76.2	18	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 1; PDBTitle: the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylgalactosaminyltransferase-t1 Fold: Nucleotide-diphospho-sugar transferases

75	d1xhba2	Alignment	not modelled	63.1	13	Superfamily: Nucleotide-diphospho-sugar transferases Family: Polypeptide N-acetylglactosaminyltransferase 1, N-terminal domain
76	d1omza	Alignment	not modelled	60.8	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Exostosin
77	c1omxB	Alignment	not modelled	53.9	14	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)
78	c2v3wC	Alignment	not modelled	51.1	8	PDB header: lyase Chain: C: PDB Molecule: benzoylformate decarboxylase; PDBTitle: crystal structure of the benzoylformate decarboxylase2 variant l461a from pseudomonas putida
79	d1q6za2	Alignment	not modelled	45.6	8	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
80	d1v7za	Alignment	not modelled	45.1	22	Fold: Creatininase Superfamily: Creatininase Family: Creatininase
81	d2i5ea1	Alignment	not modelled	42.3	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: MM2497-like
82	c3no4A	Alignment	not modelled	39.9	15	PDB header: hydrolase Chain: A: PDB Molecule: creatinine amidohydrolase; PDBTitle: crystal structure of a creatinine amidohydrolase (npun_f1913) from2 nostoc punctiforme pcc 73102 at 2.00 a resolution
83	d1nh9a	Alignment	not modelled	38.3	26	Fold: IF3-like Superfamily: AlbA-like Family: DNA-binding protein AlbA
84	c2z86D	Alignment	not modelled	29.1	13	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
85	c3lubE	Alignment	not modelled	27.3	16	PDB header: hydrolase Chain: E: PDB Molecule: putative creatinine amidohydrolase; PDBTitle: crystal structure of putative creatinine amidohydrolase2 (yp_211512.1) from bacteroides fragilis nctc 9343 at 2.11 a3 resolution
86	c2nxwB	Alignment	not modelled	22.0	7	PDB header: lyase Chain: B: PDB Molecule: phenyl-3-pyruvate decarboxylase; PDBTitle: crystal structure of phenylpyruvate decarboxylase of azospirillum2 brasilense
87	d1ozha2	Alignment	not modelled	21.7	16	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
88	c2hunB	Alignment	not modelled	21.4	31	PDB header: lyase Chain: B: PDB Molecule: 336aa long hypothetical dtdp-glucose 4,6-dehydratase; PDBTitle: crystal structure of hypothetical protein ph0414 from pyrococcus2 horikoshii ot3
89	c2xdoC	Alignment	not modelled	20.7	17	PDB header: oxidoreductase Chain: C: PDB Molecule: tetx2 protein; PDBTitle: structure of the tetracycline degrading monooxygenase tetx2 from2 bacteroides thetaiotaomicron
90	d1d5ga	Alignment	not modelled	20.0	12	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
91	c3cgxA	Alignment	not modelled	19.4	11	PDB header: transferase Chain: A: PDB Molecule: putative nucleotide-diphospho-sugar transferase; PDBTitle: crystal structure of putative nucleotide-diphospho-sugar transferase2 (yp_389115.1) from desulfovibrio desulfuricans g20 at 1.90 a3 resolution
92	c1nwaA	Alignment	not modelled	18.5	33	PDB header: oxidoreductase Chain: A: PDB Molecule: peptide methionine sulfoxide reductase msra; PDBTitle: structure of mycobacterium tuberculosis methionine2 sulfoxide reductase a in complex with protein-bound3 methionine
93	d1nwaa	Alignment	not modelled	18.5	33	Fold: Ferredoxin-like Superfamily: Peptide methionine sulfoxide reductase Family: Peptide methionine sulfoxide reductase
94	d3bofa2	Alignment	not modelled	18.2	12	Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase
95	c1upaC	Alignment	not modelled	17.4	6	PDB header: synthase Chain: C: PDB Molecule: carboxyethylarginine synthase; PDBTitle: carboxyethylarginine synthase from streptomyces2 clavuligerus (semet structure)
96	c1ze2B	Alignment	not modelled	15.0	14	PDB header: lyase/rna Chain: B: PDB Molecule: trna pseudouridine synthase b; PDBTitle: conformational change of pseudouridine 55 synthase upon its2 association with rna substrate
97	d2i7na2	Alignment	not modelled	14.6	7	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
98	c2zqeA	Alignment	not modelled	14.1	15	PDB header: dna binding protein Chain: A: PDB Molecule: muts2 protein; PDBTitle: crystal structure of the smr domain of thermus thermophilus muts2
99	d2ihta2	Alignment	not modelled	13.9	6	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module

