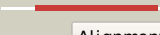























Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	O05154
Date	Tue Jul 17 17:05:01 BST 2012
Unique Job ID	acbb5c26848b3b4f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2z86D_	 Alignment		100.0	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-gluc4 and udp
2	d1xhba2	 Alignment		100.0	15	Fold: Nucleotide-di-phospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: Polypeptide N-acetylglucosaminyltransferase 1, N-terminal domain
3	c2d7iA_	 Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylglucosaminyltransferase 10; PDBTitle: crsytal structure of pp-galnac-t10 with udp, galnac and mn2+
4	c2ffuA_	 Alignment		100.0	13	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylglucosaminyltransferase 2; PDBTitle: crystal structure of human ppgalnact-2 complexed with udp2 and ea2
5	c1xhba_	 Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylglucosaminyltransferase 1; PDBTitle: the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylglucosaminyltransferase-t1
6	d1qq8a_	 Alignment		100.0	9	Fold: Nucleotide-di-phospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: Spore coat polysaccharide biosynthesis protein SpsA
7	c3f1yC_	 Alignment		100.0	9	PDB header: transferase Chain: C: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
8	c3bcvA_	 Alignment		99.9	16	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase protein; PDBTitle: crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
9	c1omxB_	 Alignment		99.9	12	PDB header: transferase Chain: B: PDB Molecule: alpha-1,4-n-acetylhexosaminyltransferase ext12; PDBTitle: crystal structure of mouse alpha-1,4-n-2 acetylhexosaminyltransferase (ext12)
10	d1omza_	 Alignment		99.9	12	Fold: Nucleotide-di-phospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: Exostosin
11	c4fixA_	 Alignment		99.9	12	PDB header: transferase Chain: A: PDB Molecule: udp-galactofuranosyl transferase glft2; PDBTitle: crystal structure of glft2

12	c3ckvA_	Alignment		99.9	11	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a mycobacterial protein
13	c2qgiA_	Alignment		99.9	11	PDB header: transferase Chain: A: PDB Molecule: atp synthase subunits region orf 6; PDBTitle: the udp complex structure of the sixth gene product of the f1-atpase2 operon of rhodobacter blasticus
14	d2bo4a1	Alignment		99.0	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: MGS-like
15	d1pzta_	Alignment		98.3	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: beta 1,4 galactosyltransferase (b4GalT1)
16	d1fo8a_	Alignment		98.0	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: N-acetylglucosaminyltransferase I
17	c2wvmA_	Alignment		97.5	13	PDB header: transferase Chain: A: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: h309a mutant of mannosyl-3-phosphoglycerate synthase from2 thermus thermophilus hb27 in complex with3 gdp-alpha-d-mannose and mg(ii)
18	c2zu8A_	Alignment		97.3	12	PDB header: transferase Chain: A: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: crystal structure of mannosyl-3-phosphoglycerate synthase2 from pyrococcus horikoshii
19	c3lw6A_	Alignment		97.2	15	PDB header: transferase Chain: A: PDB Molecule: beta-4-galactosyltransferase 7; PDBTitle: crystal structure of drosophila beta1,4-galactosyltransferase-7
20	c2px7A_	Alignment		97.0	14	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase from thermus thermophilus hb8
21	d3cu0a1	Alignment	not modelled	96.4	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: 1,3-glucuronyltransferase
22	d1i52a_	Alignment	not modelled	96.1	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
23	c2d0jD_	Alignment	not modelled	95.6	12	PDB header: transferase Chain: D: PDB Molecule: galactosylgalactosylxylosylprotein 3-beta- PDBTitle: crystal structure of human glcat-s apo form
24	c3oamD_	Alignment	not modelled	94.6	11	PDB header: transferase Chain: D: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: crystal structure of cytidyltransferase from vibrio cholerae
25	d1fxoa_	Alignment	not modelled	94.3	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
26	d1v82a_	Alignment	not modelled	94.1	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: 1,3-glucuronyltransferase
27	c3okrA_	Alignment	not modelled	94.0	10	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)
28	d1w55a1	Alignment	not modelled	93.9	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase

29	d1w77a1	Alignment	not modelled	93.8	7	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-de-diphospho-sugar transferases Family: Cytidylyltransferase
30	c2wawA	Alignment	not modelled	93.6	7	PDB header: unknown function Chain: A: PDB Molecule: moba relate protein; PDBTitle: crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
31	d1lvwa	Alignment	not modelled	92.6	9	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-de-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
32	d1vgwa	Alignment	not modelled	91.6	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-de-diphospho-sugar transferases Family: Cytidylyltransferase
33	d1h5ra	Alignment	not modelled	91.4	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-de-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
34	d1iina	Alignment	not modelled	91.0	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-de-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
35	c2gamA	Alignment	not modelled	90.5	8	PDB header: transferase Chain: A: PDB Molecule: beta-1,6-n-acetylglucosaminyltransferase; PDBTitle: x-ray crystal structure of murine leukocyte-type core 2 b1,2 6-n-acetylglucosaminyltransferase (c2gnt-1) in complex3 with galb1,3galnac
36	d1vh3a	Alignment	not modelled	90.3	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-de-diphospho-sugar transferases Family: Cytidylyltransferase
37	c2xwlB	Alignment	not modelled	90.0	12	PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: crystal structure of ispd from mycobacterium smegmatis in complex2 with ctp and mg
38	c1jylC	Alignment	not modelled	89.7	17	PDB header: transferase Chain: C: PDB Molecule: ctp:phosphocholine cytidyltransferase; PDBTitle: catalytic mechanism of ctp:phosphocholine2 cytidyltransferase from streptococcus pneumoniae (licc)
39	d1mc3a	Alignment	not modelled	89.4	7	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-de-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
40	c2e8bA	Alignment	not modelled	87.3	8	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
41	c2vshB	Alignment	not modelled	87.0	11	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
42	c3d5nB	Alignment	not modelled	86.3	21	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.
43	d1h7ea	Alignment	not modelled	85.2	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-de-diphospho-sugar transferases Family: Cytidylyltransferase
44	c1w57A	Alignment	not modelled	81.5	18	PDB header: transferase Chain: A: PDB Molecule: ispd/ispf bifunctional enzyme; PDBTitle: structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
45	c3ngwA	Alignment	not modelled	80.8	11	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
46	c3brcA	Alignment	not modelled	79.8	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein of unknown function; PDBTitle: crystal structure of a conserved protein of unknown function from2 methanobacterium thermoautotrophicum
47	c3polA	Alignment	not modelled	79.4	11	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: 2.3 angstrom crystal structure of 3-deoxy-manno-octulosonate2 cytidyltransferase (kdsb) from acinetobacter baumannii.
48	c3okrC	Alignment	not modelled	77.8	13	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)
49	d1vpaa	Alignment	not modelled	77.3	7	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-de-diphospho-sugar transferases Family: Cytidylyltransferase
50	d1eyra	Alignment	not modelled	76.4	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-de-diphospho-sugar transferases Family: Cytidylyltransferase
51	c2we9A	Alignment	not modelled	73.7	9	PDB header: unknown function Chain: A: PDB Molecule: moba-related protein; PDBTitle: crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
52	d1vica	Alignment	not modelled	73.0	8	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-de-diphospho-sugar transferases Family: Cytidylyltransferase
						Fold: Nucleotide-diphospho-sugar transferases

53	d1jyka_	Alignment	not modelled	71.9	18	Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
54	d2czwa1	Alignment	not modelled	68.4	7	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
55	d1rlga_	Alignment	not modelled	68.1	11	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
56	d2oi6a2	Alignment	not modelled	67.6	9	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
57	d1jj2f_	Alignment	not modelled	67.0	12	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
58	d2aifa1	Alignment	not modelled	66.1	6	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
59	c3ktsA_	Alignment	not modelled	65.8	14	PDB header: transcriptional regulator Chain: A: PDB Molecule: glycerol uptake operon antiterminator regulatory protein; PDBTitle: crystal structure of glycerol uptake operon antiterminator regulatory2 protein from listeria monocytogenes str. 4b f2365
60	d1xbia1	Alignment	not modelled	63.9	8	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
61	d1vqof1	Alignment	not modelled	62.4	11	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
62	c3pnnA_	Alignment	not modelled	61.2	9	PDB header: transferase Chain: A: PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
63	c3o85A_	Alignment	not modelled	58.9	6	PDB header: ribosomal protein Chain: A: PDB Molecule: ribosomal protein l7ae; PDBTitle: giardia lamblia 15.5kd rna binding protein
64	d1e5ka_	Alignment	not modelled	58.2	9	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Molybdenum cofactor biosynthesis protein MobA
65	c3hl3A_	Alignment	not modelled	57.6	12	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.
66	d1ll2a_	Alignment	not modelled	56.8	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Glycogenin
67	c3rsbB_	Alignment	not modelled	53.3	13	PDB header: transferase Chain: B: PDB Molecule: adenosylcobinamide-phosphate guanylyltransferase; PDBTitle: structure of the archaeal gtp:adocbi-p guanylyltransferase (coby) from2 methanocaldococcus jannaschii
68	c2xmhB_	Alignment	not modelled	53.0	4	PDB header: transferase Chain: B: PDB Molecule: ctp-inositol-1-phosphate cytidyltransferase; PDBTitle: the x-ray structure of ctp:inositol-1-phosphate2 cytidyltransferase from archaeoglobus fulgidus
69	c3f1cB_	Alignment	not modelled	52.8	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 cytidyltransferase from listeria monocytogenes
70	c3tqdA_	Alignment	not modelled	51.4	10	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: structure of the 3-deoxy-d-manno-octulosonate cytidyltransferase2 (kdsb) from coxiella burnetii
71	c2qh5B_	Alignment	not modelled	49.7	8	PDB header: isomerase Chain: B: PDB Molecule: mannose-6-phosphate isomerase; PDBTitle: crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
72	d2dpwa1	Alignment	not modelled	49.5	4	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: TTHA0179-like
73	c1zcyA_	Alignment	not modelled	48.5	11	PDB header: transferase Chain: A: PDB Molecule: glycogenin-1; PDBTitle: apo form of a mutant of glycogenin in which asp159 is replaced by ser
74	c2y6pC_	Alignment	not modelled	47.8	14	PDB header: transferase Chain: C: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: evidence for a two-metal-ion-mechanism in the2 kdcy:cytidyltransferase kdsb
75	d2fc3a1	Alignment	not modelled	42.4	9	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
76	d1xkna_	Alignment	not modelled	41.0	16	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
77	d2ozba1	Alignment	not modelled	39.4	8	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
						Fold: Nucleotide-diphospho-sugar transferases

78	d1qwja_	Alignment	not modelled	38.3	14	Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylytransferase
79	c2zkr6_	Alignment	not modelled	37.8	17	PDB header: ribosomal protein/rna Chain: 6: PDB Molecule: 60s ribosomal protein l30e; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
80	c4evwB_	Alignment	not modelled	37.7	9	PDB header: transferase Chain: B: PDB Molecule: nucleoside-diphosphate-sugar pyrophosphorylase; PDBTitle: crystal structure of the nucleoside-diphosphate-sugar2 pyrophosphorylase from vibrio cholerae rc9. northeast structural3 genomics consortium (nesg) target vcr193.
81	d2alea1	Alignment	not modelled	36.7	5	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
82	d1g97a2	Alignment	not modelled	35.8	8	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
83	c3d98A_	Alignment	not modelled	35.0	14	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
84	d1t0ia_	Alignment	not modelled	33.1	16	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
85	c3ssoE_	Alignment	not modelled	32.7	20	PDB header: transferase Chain: E: PDB Molecule: methyltransferase; PDBTitle: myce methyltransferase from the mycinamycin biosynthetic pathway in2 complex with mg and sah, crystal form 2
86	d2cu2a2	Alignment	not modelled	32.4	8	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: mannose-1-phosphate guanylyl transferase
87	c2j0bA_	Alignment	not modelled	30.0	23	PDB header: transferase Chain: A: PDB Molecule: beta-1,3-n-acetylglucosaminyltransferase manic fringe; PDBTitle: structure of the catalytic domain of mouse manic fringe in2 complex with udp and manganese
88	c1zctB_	Alignment	not modelled	29.3	10	PDB header: transferase Chain: B: PDB Molecule: glycogenin-1; PDBTitle: structure of glycogenin truncated at residue 270 in a2 complex with udp
89	d1vh1a_	Alignment	not modelled	28.5	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylytransferase
90	c3tztB_	Alignment	not modelled	27.2	9	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.
91	c2pa4B_	Alignment	not modelled	26.8	16	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
92	d1egoa_	Alignment	not modelled	25.3	10	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
93	c3io3A_	Alignment	not modelled	25.2	18	PDB header: chaperone Chain: A: PDB Molecule: deha2d07832p; PDBTitle: get3 with adp from d. hansenii in closed form
94	c2e3dB_	Alignment	not modelled	25.2	12	PDB header: transferase Chain: B: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of e. coli glucose-1-phosphate2 uridylyltransferase
95	d1dxya2	Alignment	not modelled	24.4	7	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
96	d1vqom1	Alignment	not modelled	23.6	18	Fold: Ribosomal proteins S24e, L23 and L15e Superfamily: Ribosomal proteins S24e, L23 and L15e Family: L15e
97	d1ffki_	Alignment	not modelled	23.3	7	Fold: Ribosomal proteins S24e, L23 and L15e Superfamily: Ribosomal proteins S24e, L23 and L15e Family: L15e
98	d1jj2l_	Alignment	not modelled	22.7	13	Fold: Ribosomal proteins S24e, L23 and L15e Superfamily: Ribosomal proteins S24e, L23 and L15e Family: L15e
99	c1vl6C_	Alignment	not modelled	22.6	14	PDB header: oxidoreductase Chain: C: PDB Molecule: malate oxidoreductase; PDBTitle: crystal structure of nad-dependent malic enzyme (tm0542) from2 thermotoga maritima at 2.61 a resolution
100	c4a1cL_	Alignment	not modelled	22.3	18	PDB header: ribosome Chain: L: PDB Molecule: ribosomal protein l15; PDBTitle: t thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
101	c3k9gA_	Alignment	not modelled	22.0	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: pf-32 protein; PDBTitle: crystal structure of a plasmid partition protein from borrelia2 burgdorferi at 2.25a resolution, iodide soak PDB header: transferase Chain: A: PDB Molecule: putative mannose-1-phosphate quanylyl

102	c2cu2A_	Alignment	not modelled	21.6	10	transferase; PDBTitle: crystal structure of mannose-1-phosphate geranyltransferase from2 thermus thermophilus hb8
103	c2c0nA_	Alignment	not modelled	21.2	14	PDB header: viral protein/transferase Chain: A: PDB Molecule: a197; PDBTitle: crystal structure of a197 from stiv
104	c3ma0A_	Alignment	not modelled	20.9	10	PDB header: sugar binding protein Chain: A: PDB Molecule: d-xylose-binding periplasmic protein; PDBTitle: closed liganded crystal structure of xylose binding protein from2 escherichia coli
105	c1s1iL_	Alignment	not modelled	20.7	7	PDB header: ribosome Chain: L: PDB Molecule: 60s ribosomal protein l15-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, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.