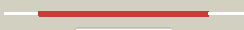


Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1trea_	 Alignment		100.0	100	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
2	d1aw1a_	 Alignment		100.0	66	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
3	c1yyaA_	 Alignment		100.0	42	PDB header: isomerase Chain: A: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of tt0473, putative triosephosphate isomerase from2 thermus thermophilus hb8
4	c2dp3A_	 Alignment		100.0	42	PDB header: isomerase Chain: A: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of a double mutant (c202a/a198v) of triosephosphate2 isomerase from giardia lamblia
5	d1b9ba_	 Alignment		100.0	43	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
6	c3m9yB_	 Alignment		100.0	42	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from methicillin2 resistant staphylococcus aureus at 1.9 angstrom resolution
7	d2btma_	 Alignment		100.0	41	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
8	d1mo0a_	 Alignment		100.0	48	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
9	c3gvga_	 Alignment		100.0	42	PDB header: isomerase Chain: A: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from mycobacterium2 tuberculosis
10	d1m6ja_	 Alignment		100.0	43	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
11	d1kv5a_	 Alignment		100.0	43	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)

12	dlsuxa_	Alignment		100.0	43	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
13	dln55a_	Alignment		100.0	43	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
14	dlsw3a_	Alignment		100.0	46	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
15	dlo5xa_	Alignment		100.0	40	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
16	dlr2ra_	Alignment		100.0	45	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
17	c3krsB_	Alignment		100.0	42	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: structure of triosephosphate isomerase from cryptosporidium parvum at2 1.55a resolution
18	dlneya_	Alignment		100.0	45	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
19	c3s6dA_	Alignment		100.0	28	PDB header: isomerase Chain: A: PDB Molecule: putative triosephosphate isomerase; PDBTitle: crystal structure of a putative triosephosphate isomerase from2 coccidioides immitis
20	c3th6B_	Alignment		100.0	46	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from rhipicephalus2 (boophilus) microplus.
21	dlttja_	Alignment	not modelled	100.0	42	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
22	c3kxqB_	Alignment	not modelled	100.0	39	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from bartonella2 henselae at 1.6a resolution
23	c2jgqB_	Alignment	not modelled	100.0	32	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: kinetics and structural properties of triosephosphate2 isomerase from helicobacter pylori
24	dlhg3a_	Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
25	dlw0ma_	Alignment	not modelled	100.0	25	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
26	c2h6rG_	Alignment	not modelled	100.0	24	PDB header: isomerase Chain: G: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
27	dlrpxa_	Alignment	not modelled	98.4	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
28	dltqja_	Alignment	not modelled	98.2	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
						Fold: TIM beta/alpha-barrel

29	d1j5ta_	Alignment	not modelled	97.8	13	Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
30	c3ct7E_	Alignment	not modelled	97.7	21	PDB header: isomerase Chain: E: PDB Molecule: d-allulose-6-phosphate 3-epimerase; PDBTitle: crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12
31	d1tqxa_	Alignment	not modelled	97.5	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
32	c3inpA_	Alignment	not modelled	97.5	16	PDB header: isomerase Chain: A: PDB Molecule: d-ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
33	d1qopa_	Alignment	not modelled	97.5	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
34	c3qc3B_	Alignment	not modelled	97.4	14	PDB header: isomerase Chain: B: PDB Molecule: d-ribulose-5-phosphate-3-epimerase; PDBTitle: crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution
35	d1rd5a_	Alignment	not modelled	97.4	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
36	c3qjaA_	Alignment	not modelled	97.4	13	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
37	c2c3zA_	Alignment	not modelled	97.3	11	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus
38	c3f4wA_	Alignment	not modelled	97.3	17	PDB header: synthase, lyase Chain: A: PDB Molecule: putative hexulose 6 phosphate synthase; PDBTitle: the 1.65a crystal structure of 3-hexulose-6-phosphate2 synthase from salmonella typhimurium
39	d2flia1	Alignment	not modelled	97.3	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
40	c3ajxA_	Alignment	not modelled	97.3	20	PDB header: lyase Chain: A: PDB Molecule: 3-hexulose-6-phosphate synthase; PDBTitle: crystal structure of 3-hexulose-6-phosphate synthase
41	d1q6oa_	Alignment	not modelled	97.3	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
42	d1i4na_	Alignment	not modelled	97.3	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
43	d1vc4a_	Alignment	not modelled	97.2	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
44	c3igsB_	Alignment	not modelled	97.1	16	PDB header: isomerase Chain: B: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase 2; PDBTitle: structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase
45	d1h1ya_	Alignment	not modelled	97.0	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
46	d1a53a_	Alignment	not modelled	97.0	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
47	d1yxva1	Alignment	not modelled	96.5	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
48	c3q58A_	Alignment	not modelled	96.3	12	PDB header: isomerase Chain: A: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
49	c3navB_	Alignment	not modelled	96.3	17	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
50	c3thaB_	Alignment	not modelled	96.3	20	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
51	d1wv2a_	Alignment	not modelled	96.2	18	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
52	d1xcfa_	Alignment	not modelled	96.2	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
53	d1piia2	Alignment	not modelled	95.7	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
54	d1ka9f_	Alignment	not modelled	95.1	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
55	d1h5ya_	Alignment	not modelled	94.4	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes

56	d1xi3a_	Alignment	not modelled	93.9	18	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
57	c3tdmD_	Alignment	not modelled	93.8	17	PDB header: de novo protein Chain: D: PDB Molecule: computationally designed two-fold symmetric tim-barrel PDBTitle: computationally designed tim-barrel protein, halfflr
58	c2ekcA_	Alignment	not modelled	93.8	23	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
59	c3cu2A_	Alignment	not modelled	93.7	16	PDB header: isomerase Chain: A: PDB Molecule: ribulose-5-phosphate 3-epimerase; PDBTitle: crystal structure of ribulose-5-phosphate 3-epimerase (yp_718263.1)2 from haemophilus somnus 129pt at 1.91 a resolution
60	d2tpsa_	Alignment	not modelled	93.7	20	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
61	c2y85D_	Alignment	not modelled	93.5	17	PDB header: isomerase Chain: D: PDB Molecule: phosphoribosyl isomerase a; PDBTitle: crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
62	d1thfd_	Alignment	not modelled	93.5	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Histidine biosynthesis enzymes
63	d1jvna1	Alignment	not modelled	93.4	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Histidine biosynthesis enzymes
64	d1vzwa1	Alignment	not modelled	93.3	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Histidine biosynthesis enzymes
65	c3exsB_	Alignment	not modelled	93.2	12	PDB header: lyase Chain: B: PDB Molecule: rmpr (hexulose-6-phosphate synthase); PDBTitle: crystal structure of kgpdc from streptococcus mutans in2 complex with d-r5p
66	c2bdqA_	Alignment	not modelled	93.1	17	PDB header: metal transport Chain: A: PDB Molecule: copper homeostasis protein cutc; PDBTitle: crystal structure of the putative copper homeostasis2 protein cutc from streptococcus agalactiae, northeast3 strucural genomics target sar15.
67	d1y0ea_	Alignment	not modelled	93.0	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: NanE-like
68	c2v82A_	Alignment	not modelled	93.0	21	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpgal complexed to kdpgal
69	d1xm3a_	Alignment	not modelled	92.5	18	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
70	d1geqa_	Alignment	not modelled	92.5	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
71	d1wa3a1	Alignment	not modelled	92.4	23	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
72	c3gkaB_	Alignment	not modelled	92.1	11	PDB header: oxidoreductase Chain: B: PDB Molecule: n-ethylmaleimide reductase; PDBTitle: crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei
73	c2h90A_	Alignment	not modelled	91.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
74	c2vwtA_	Alignment	not modelled	91.7	20	PDB header: lyase Chain: A: PDB Molecule: yfau, 2-keto-3-deoxy sugar aldolase; PDBTitle: crystal structure of yfau, a metal ion dependent class ii2 aldolase from escherichia coli k12 - mg-pyruvate product3 complex
75	d1dvja_	Alignment	not modelled	91.3	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Decarboxylase
76	c3gr7A_	Alignment	not modelled	91.3	18	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
77	d1wbha1	Alignment	not modelled	90.3	22	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
78	c3jr2D_	Alignment	not modelled	90.2	12	PDB header: biosynthetic protein Chain: D: PDB Molecule: hexulose-6-phosphate synthase sgbh; PDBTitle: x-ray crystal structure of the mg-bound 3-keto-l-gulonate-6-phosphate2 decarboxylase from vibrio cholerae o1 biovar el tor str. n16961
79	c3hf3A_	Alignment	not modelled	89.5	20	PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
80	d1viza_	Alignment	not modelled	89.1	22	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
81	c2w6rA_	Alignment	not modelled	88.9	20	PDB header: lyase Chain: A: PDB Molecule: imidazole glycerol phosphate synthase subunit PDBTitle: crystal structure of an artificial (ba)8-barrel protein2

						designed from identical half barrels
82	d1o4ua1	Alignment	not modelled	88.7	21	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
83	c1yadD	Alignment	not modelled	88.4	10	PDB header: transcription Chain: D: PDB Molecule: regulatory protein teni; PDBTitle: structure of teni from bacillus subtilis
84	d1ojxa	Alignment	not modelled	88.2	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
85	d1km4a	Alignment	not modelled	88.1	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
86	d1vhna	Alignment	not modelled	88.1	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
87	d1qo2a	Alignment	not modelled	87.9	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
88	d2czda1	Alignment	not modelled	86.9	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
89	d2f6ua1	Alignment	not modelled	86.9	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
90	c2wwcA	Alignment	not modelled	86.6	11	PDB header: hydrolase Chain: A: PDB Molecule: 1,4-beta-n-acetylmuramidase; PDBTitle: 3d-structure of the modular autolysin lytc from2 streptococcus pneumoniae in complex with synthetic3 peptidoglycan ligand
91	d1wkya2	Alignment	not modelled	86.6	10	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
92	d1ytda1	Alignment	not modelled	86.1	14	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
93	c3o63B	Alignment	not modelled	85.8	18	PDB header: transferase Chain: B: PDB Molecule: probable thiamine-phosphate pyrophosphorylase; PDBTitle: crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
94	c2gq8A	Alignment	not modelled	85.6	27	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, fmn-binding; PDBTitle: structure of sye1, an oye homologue from s. ondeidensis, in complex2 with p-hydroxyacetophenone
95	d1djqa1	Alignment	not modelled	85.1	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
96	d1qapa1	Alignment	not modelled	84.0	22	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
97	c3kruC	Alignment	not modelled	83.9	13	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: crystal structure of the thermostable old yellow enzyme from2 thermoanaerobacter pseudethanolicus e39
98	d1qpoa1	Alignment	not modelled	83.4	19	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
99	d1q45a	Alignment	not modelled	83.2	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
100	c2jbmA	Alignment	not modelled	82.6	15	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: qprtase structure from human
101	c2nv2U	Alignment	not modelled	80.3	29	PDB header: lyase/transferase Chain: U: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis
102	c1djinB	Alignment	not modelled	79.7	12	PDB header: oxidoreductase Chain: B: PDB Molecule: trimethylamine dehydrogenase; PDBTitle: structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylophilus methylotrophus (sp.3 w3a1)
103	c3femB	Alignment	not modelled	79.5	20	PDB header: biosynthetic protein, transferase Chain: B: PDB Molecule: pyridoxine biosynthesis protein snz1; PDBTitle: structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae
104	c2htmB	Alignment	not modelled	79.4	19	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
105	d1znna1	Alignment	not modelled	79.1	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: PdxS-like
106	c2zbtB	Alignment	not modelled	78.7	26	PDB header: lyase Chain: B: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8
						Fold: TIM beta/alpha-barrel

107	dloyaa_	Alignment	not modelled	78.4	15	Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
108	dlgwja_	Alignment	not modelled	78.2	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
109	dlps9a1	Alignment	not modelled	77.6	11	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
110	dlvhca_	Alignment	not modelled	77.4	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
111	c1o4uA_	Alignment	not modelled	77.1	20	PDB header: transferase Chain: A: PDB Molecule: type ii quinolic acid phosphoribosyltransferase; PDBTitle: crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution
112	c1wkYA_	Alignment	not modelled	76.8	14	PDB header: hydrolase Chain: A: PDB Molecule: endo-beta-1,4-mannanase; PDBTitle: crystal structure of alkaline mannanase from bacillus sp. strain jamb-2 602: catalytic domain and its carbohydrate binding module
113	c2b7pA_	Alignment	not modelled	76.3	15	PDB header: transferase Chain: A: PDB Molecule: probable nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori
114	dlmxsa_	Alignment	not modelled	76.2	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
115	c3tqvA_	Alignment	not modelled	75.8	12	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: structure of the nicotinate-nucleotide pyrophosphorylase from2 francisella tularensis.
116	c2agkA_	Alignment	not modelled	75.6	13	PDB header: isomerase Chain: A: PDB Molecule: 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) PDBTitle: structure of s. cerevisiae his6 protein
117	c3l0gD_	Alignment	not modelled	75.2	14	PDB header: transferase Chain: D: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution
118	c1x1oC_	Alignment	not modelled	75.2	14	PDB header: transferase Chain: C: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of project id tt0268 from thermus thermophilus hb8
119	c3ncoA_	Alignment	not modelled	75.1	14	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase fncel5a; PDBTitle: crystal structure of fncel5a from f. nodosum rt17-b1
120	c2i14B_	Alignment	not modelled	74.2	24	PDB header: transferase Chain: B: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide2 pyrophosphorylase from pyrococcus furiosus