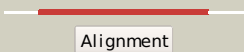

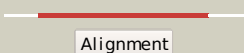

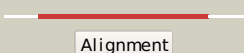

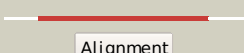



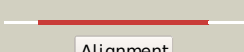

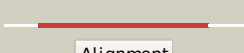

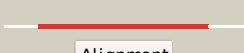


















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1m5wa_	 Alignment		100.0	100	Fold: TIM beta/alpha-barrel Superfamily: Pyridoxine 5'-phosphate synthase Family: Pyridoxine 5'-phosphate synthase
2	c3gk0H_	 Alignment		100.0	67	PDB header: transferase Chain: H: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: crystal structure of pyridoxal phosphate biosynthetic protein from burkholderia pseudomallei
3	c3o6cA_	 Alignment		100.0	48	PDB header: transferase Chain: A: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: pyridoxal phosphate biosynthetic protein pdxj from campylobacter2 jejuni
4	c3igsB_	 Alignment		98.3	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
5	c3qjaA_	 Alignment		97.9	16	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
6	d2flia1	 Alignment		97.8	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
7	d1xya1	 Alignment		97.8	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
8	c3q58A_	 Alignment		97.6	16	PDB header: isomerase Chain: A: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
9	c3lotC_	 Alignment		97.4	21	PDB header: structure genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein of unknown function (np_070038.1) from2 archaeoglobus fulgidus at 1.89 a resolution
10	c3gr7A_	 Alignment		97.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
11	d1xcfa_	 Alignment		97.3	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes

12	c3e02A_	Alignment		97.3	20	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf849; PDBTitle: crystal structure of a duf849 family protein (bx_e_c0271) from2 burkholderia xenovorans lb400 at 1.90 a resolution
13	d1tqja_	Alignment		97.3	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
14	d1vc4a_	Alignment		97.3	21	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
15	c2c3zA_	Alignment		97.2	15	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
16	d1rd5a_	Alignment		97.1	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
17	d1wv2a_	Alignment		97.1	16	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
18	d1wbha1	Alignment		97.1	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
19	d1q6oa_	Alignment		97.0	22	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
20	c3inpA_	Alignment		96.8	15	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.
21	c3hf3A_	Alignment	not modelled	96.8	20	PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
22	d1rpxa_	Alignment	not modelled	96.8	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
23	d1h1ya_	Alignment	not modelled	96.8	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
24	c3c6cA_	Alignment	not modelled	96.7	23	PDB header: hydrolase Chain: A: PDB Molecule: 3-keto-5-amino-hexanoate cleavage enzyme; PDBTitle: crystal structure of a putative 3-keto-5-amino-hexanoate cleavage2 enzyme (reut_c6226) from ralstonia eutropha jmp134 at 1.72 a3 resolution
25	c3e49A_	Alignment	not modelled	96.7	25	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf849 with a tim barrel fold; PDBTitle: crystal structure of a prokaryotic domain of unknown function (duf849)2 with a tim barrel fold (bx_e_c0966) from burkholderia xenovorans lb4003 at 1.75 a resolution
26	c3ct7E_	Alignment	not modelled	96.6	14	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
27	d1y0ea_	Alignment	not modelled	96.6	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
						Fold: TIM beta/alpha-barrel

28	d1thfd_	Alignment	not modelled	96.4	11	Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
29	d1tqxa_	Alignment	not modelled	96.3	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
30	c2v82A_	Alignment	not modelled	96.2	14	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpgal complexed to kdpgal
31	c2htmB_	Alignment	not modelled	96.1	16	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
32	c3l5aA_	Alignment	not modelled	95.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh/flavin oxidoreductase/nadh oxidase; PDBTitle: crystal structure of a probable nadh-dependent flavin oxidoreductase2 from staphylococcus aureus
33	c2y7eA_	Alignment	not modelled	95.9	19	PDB header: lyase Chain: A: PDB Molecule: 3-keto-5-aminohexanoate cleavage enzyme; PDBTitle: crystal structure of the 3-keto-5-aminohexanoate cleavage enzyme2 (kce) from candidatus cloacamonas acidaminovorans (tetragonal form)
34	d1wa3a1	Alignment	not modelled	95.9	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
35	d1i4na_	Alignment	not modelled	95.7	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
36	c2h90A_	Alignment	not modelled	95.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
37	d1j5ta_	Alignment	not modelled	95.5	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
38	c2bdqA_	Alignment	not modelled	95.4	19	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 structural genomics target sar15.
39	d1a53a_	Alignment	not modelled	95.3	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
40	d1tv5a1	Alignment	not modelled	95.2	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
41	c1tv5A_	Alignment	not modelled	95.2	14	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase homolog, mitochondrial; PDBTitle: plasmodium falciparum dihydroorotate dehydrogenase with a bound2 inhibitor
42	c3chvA_	Alignment	not modelled	95.1	15	PDB header: metal binding protein Chain: A: PDB Molecule: prokaryotic domain of unknown function (duf849) with a tim PDBTitle: crystal structure of a prokaryotic domain of unknown function (duf849)2 member (spoa0042) from silicibacter pomeroyi dss-3 at 1.45 a3 resolution
43	d1piia2	Alignment	not modelled	95.1	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
44	d1vhca_	Alignment	not modelled	95.1	22	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
45	c3ajxA_	Alignment	not modelled	95.1	19	PDB header: lyase Chain: A: PDB Molecule: 3-hexulose-6-phosphate synthase; PDBTitle: crystal structure of 3-hexulose-6-phosphate synthase
46	c3jr2D_	Alignment	not modelled	95.1	20	PDB header: biosynthetic protein Chain: D: PDB Molecule: hexulose-6-phosphate synthase sgbb; 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
47	c3f4wA_	Alignment	not modelled	95.0	14	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
48	d1z41a1	Alignment	not modelled	94.9	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
49	c3cixA_	Alignment	not modelled	94.8	21	PDB header: adomet binding protein Chain: A: PDB Molecule: fe(II)-hydrogenase maturase; PDBTitle: x-ray structure of the [fe(II)]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
50	d1q45a_	Alignment	not modelled	94.7	13	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
51	d1bxca_	Alignment	not modelled	94.7	21	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
52	c3dx5A_	Alignment	not modelled	94.7	18	PDB header: lyase Chain: A: PDB Molecule: uncharacterized protein asbf; PDBTitle: crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis PDB header: lyase

53	c3thaB_	Alignment	not modelled	94.5	16	Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
54	d1vyra_	Alignment	not modelled	94.5	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
55	d1qt1a_	Alignment	not modelled	94.5	19	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
56	d1muwa_	Alignment	not modelled	94.4	18	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
57	c2fptA_	Alignment	not modelled	94.4	19	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase, mitochondrial; PDBTitle: dual binding mode of a novel series of dhodh inhibitors
58	c3qc3B_	Alignment	not modelled	94.1	13	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
59	c1ps9A_	Alignment	not modelled	94.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,4-dienoyl-coa reductase; PDBTitle: the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
60	d1xima_	Alignment	not modelled	93.9	22	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
61	c3exsB_	Alignment	not modelled	93.8	21	PDB header: lyase Chain: B: PDB Molecule: rmpd (hexulose-6-phosphate synthase); PDBTitle: crystal structure of kgpdc from streptococcus mutans in2 complex with d-r5p
62	d1h5ya_	Alignment	not modelled	93.8	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
63	d1xi3a_	Alignment	not modelled	93.7	15	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
64	d1f76a_	Alignment	not modelled	93.7	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
65	c1yadD_	Alignment	not modelled	93.5	16	PDB header: transcription Chain: D: PDB Molecule: regulatory protein teni; PDBTitle: structure of teni from bacillus subtilis
66	d1ka9f_	Alignment	not modelled	93.5	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
67	d1vhna_	Alignment	not modelled	93.3	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
68	c3kruC_	Alignment	not modelled	93.2	12	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
69	d1r30a_	Alignment	not modelled	93.2	11	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Biotin synthase
70	c1r30A_	Alignment	not modelled	93.2	11	PDB header: transferase Chain: A: PDB Molecule: biotin synthase; PDBTitle: the crystal structure of biotin synthase, an s-2 adenosylmethionine-dependent radical enzyme
71	d1djqa1	Alignment	not modelled	93.2	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
72	c3no5C_	Alignment	not modelled	93.2	20	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a pfam duf849 domain containing protein2 (reut_a1631) from ralstonia eutropha jmp134 at 1.90 a resolution
73	c3gkaB_	Alignment	not modelled	93.2	31	PDB header: oxidoreductase Chain: B: PDB Molecule: n-ethylmaleimide reductase; PDBTitle: crystal structure of n-ethylmaleimide reductase from2 burkholderia pseudomallei
74	c1xrsB_	Alignment	not modelled	93.0	19	PDB header: isomerase Chain: B: PDB Molecule: d-lysine 5,6-aminomutase beta subunit; PDBTitle: crystal structure of lysine 5,6-aminomutase in complex with plp,2 cobalamin, and 5'-deoxyadenosine
75	c3qxbB_	Alignment	not modelled	93.0	24	PDB header: isomerase Chain: B: PDB Molecule: putative xylose isomerase; PDBTitle: crystal structure of a putative xylose isomerase (yp_426450.1) from2 rhodospirillum rubrum atcc 11170 at 1.90 a resolution
76	c2yw3E_	Alignment	not modelled	92.5	14	PDB header: lyase Chain: E: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3- PDBTitle: crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 deydro-3-deoxyphosphogluconate aldolase from tthb1
77	d1ps9a1	Alignment	not modelled	92.1	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
78	d1i60a_	Alignment	not modelled	91.9	11	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: lol1-like

79	c2gq8A	Alignment	not modelled	91.9	20	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, fmn-binding; PDBTitle: structure of sye1, an oye homologue from s. oncidensis, in complex2 with p-hydroxyacetophenone
80	d1uuma	Alignment	not modelled	91.8	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
81	c3aamA	Alignment	not modelled	91.8	20	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease iv; PDBTitle: crystal structure of endonuclease iv from thermus thermophilus hb8
82	d1qf6a1	Alignment	not modelled	91.8	18	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
83	d1bxbA	Alignment	not modelled	91.6	17	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
84	c2ou4C	Alignment	not modelled	91.6	17	PDB header: isomerase Chain: C: PDB Molecule: d-tagatose 3-epimerase; PDBTitle: crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii
85	d1icpa	Alignment	not modelled	91.6	20	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
86	c2ekcA	Alignment	not modelled	91.3	16	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
87	d1xm3a	Alignment	not modelled	91.0	17	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
88	c2zdsB	Alignment	not modelled	90.8	13	PDB header: dna binding protein Chain: B: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of sco6571 from streptomyces coelicolor2 a3(2)
89	c1djnb	Alignment	not modelled	90.7	19	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)
90	d1wx0a1	Alignment	not modelled	90.5	27	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
91	c3o63B	Alignment	not modelled	90.4	20	PDB header: transferase Chain: B: PDB Molecule: probable thiamine-phosphate pyrophosphorylase; PDBTitle: crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
92	d1gwja	Alignment	not modelled	90.4	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
93	c3khjE	Alignment	not modelled	90.3	15	PDB header: oxidoreductase Chain: E: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
94	d1yx1a1	Alignment	not modelled	90.2	18	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: KguE-like
95	d1k77a	Alignment	not modelled	89.8	13	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Hypothetical protein YgbM (EC1530)
96	d1vd6a1	Alignment	not modelled	89.3	12	Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Glycerophosphoryl diester phosphodiesterase
97	c3kwsB	Alignment	not modelled	89.2	23	PDB header: isomerase Chain: B: PDB Molecule: putative sugar isomerase; PDBTitle: crystal structure of putative sugar isomerase (yp_001305149.1) from2 parabacteroides distasonis atcc 8503 at 1.68 a resolution
98	c3s1vD	Alignment	not modelled	88.5	17	PDB header: transferase Chain: D: PDB Molecule: probable transaldolase; PDBTitle: transaldolase from thermoplasma acidophilum in complex with d-fructose2 6-phosphate schiff-base intermediate
99	c2ftpA	Alignment	not modelled	88.2	9	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
100	c2i2xD	Alignment	not modelled	88.1	17	PDB header: transferase Chain: D: PDB Molecule: methyltransferase 1; PDBTitle: crystal structure of methanol: cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
101	d1xrsb1	Alignment	not modelled	87.8	17	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
102	d1un7a2	Alignment	not modelled	87.8	25	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
103	d1oyaa	Alignment	not modelled	87.8	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
104	d1zfja1	Alignment	not modelled	87.8	16	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH)

					Family: Inosine monophosphate dehydrogenase (IMPDH)
105	d2g0wa1	Alignment	not modelled	87.7	15 Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: loli-like
106	c2x7vA	Alignment	not modelled	87.7	10 PDB header: hydrolase Chain: A: PDB Molecule: probable endonuclease 4; PDBTitle: crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
107	c3k30B	Alignment	not modelled	87.6	18 PDB header: oxidoreductase Chain: B: PDB Molecule: histamine dehydrogenase; PDBTitle: histamine dehydrogenase from nocardiods simplex
108	c3cqkB	Alignment	not modelled	87.5	16 PDB header: isomerase Chain: B: PDB Molecule: l-ribulose-5-phosphate 3-epimerase ulae; PDBTitle: crystal structure of l-xylulose-5-phosphate 3-epimerase ulae (form b)2 complex with zn2+ and sulfate
109	d1vjia	Alignment	not modelled	87.5	15 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
110	d1mxsa	Alignment	not modelled	87.5	16 Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
111	d1d3ga	Alignment	not modelled	87.3	14 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
112	c2yciX	Alignment	not modelled	87.0	15 PDB header: transferase Chain: X: PDB Molecule: 5-methyltetrahydrofolate corrinoid/iron sulfur protein PDBTitle: methyltransferase native
113	d1nyra1	Alignment	not modelled	86.5	21 Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
114	c2v5jB	Alignment	not modelled	86.5	19 PDB header: lyase Chain: B: PDB Molecule: 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; PDBTitle: apo class ii aldolase hpch
115	c3pajA	Alignment	not modelled	86.4	16 PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase, carboxylating; PDBTitle: 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961
116	c1qapA	Alignment	not modelled	86.2	13 PDB header: glycosyltransferase Chain: A: PDB Molecule: quinolinic acid phosphoribosyltransferase; PDBTitle: quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
117	d1qopa	Alignment	not modelled	86.2	18 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
118	d1hc7a1	Alignment	not modelled	86.2	20 Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
119	c2zvrA	Alignment	not modelled	85.9	13 PDB header: isomerase Chain: A: PDB Molecule: uncharacterized protein tm_0416; PDBTitle: crystal structure of a d-tagatose 3-epimerase-related2 protein from thermotoga maritima
120	c2kzhA	Alignment	not modelled	85.8	18 PDB header: isomerase Chain: A: PDB Molecule: tryptophan biosynthesis protein trpcf; PDBTitle: three-dimensional structure of a truncated phosphoribosylanthranilate2 isomerase (residues 255-384) from escherichia coli