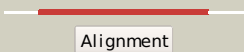

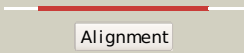


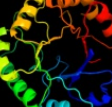
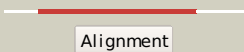

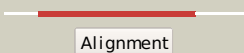

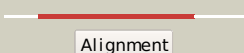

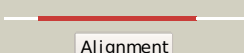

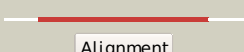

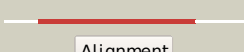

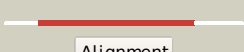

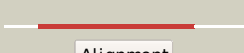












Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1twda_	 Alignment		100.0	94	Fold: TIM beta/alpha-barrel Superfamily: CutC-like Family: CutC-like
2	c3iwpK_	 Alignment		100.0	45	PDB header: metal binding protein Chain: K: PDB Molecule: copper homeostasis protein cutc homolog; PDBTitle: crystal structure of human copper homeostasis protein cutc
3	c2bdqA_	 Alignment		100.0	33	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.
4	d1a53a_	 Alignment		98.9	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
5	c2c3zA_	 Alignment		98.9	16	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
6	d1h1ya_	 Alignment		98.8	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
7	d2flia1	 Alignment		98.8	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
8	d1tqxa_	 Alignment		98.8	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
9	d1j5ta_	 Alignment		98.7	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
10	c3qjaA_	 Alignment		98.7	21	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
11	c3q58A_	 Alignment		98.7	19	PDB header: isomerase Chain: A: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica

12	d1tqja_	Alignment		98.6	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
13	d1vc4a_	Alignment		98.6	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
14	c3qc3B_	Alignment		98.5	16	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
15	d1xcfa_	Alignment		98.5	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
16	dlyxya1	Alignment		98.5	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
17	c3igsB_	Alignment		98.5	18	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
18	d1piia2	Alignment		98.4	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
19	c3inpA_	Alignment		98.4	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.
20	c3ct7E_	Alignment		98.4	12	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
21	d1h5ya_	Alignment	not modelled	98.3	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
22	d1vzwa1	Alignment	not modelled	98.3	21	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
23	d1rpxa_	Alignment	not modelled	98.3	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
24	c2y85D_	Alignment	not modelled	98.3	17	PDB header: isomerase Chain: D: PDB Molecule: phosphoribosyl isomerase a; PDBTitle: crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
25	d1i4na_	Alignment	not modelled	98.3	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
26	d1y0ea_	Alignment	not modelled	98.2	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
27	d1wbha1	Alignment	not modelled	98.2	11	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
28	d2tpsa_	Alignment	not modelled	98.2	20	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
29	d1rd5a_	Alignment	not modelled	98.2	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel

					Family: Tryptophan biosynthesis enzymes
30	c1znnF_	Alignment	not modelled	98.2	16 PDB header: biosynthetic protein Chain: F: PDB Molecule: plp synthase; PDBTitle: structure of the synthase subunit of plp synthase
31	dlznnal	Alignment	not modelled	98.2	16 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: PdxS-like
32	c2v82A_	Alignment	not modelled	98.2	23 PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpgal complexed to kdpgal
33	dlgeqa_	Alignment	not modelled	98.1	18 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
34	dlwa3a1	Alignment	not modelled	98.1	17 Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
35	dlka9f_	Alignment	not modelled	98.1	22 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
36	dlqopa_	Alignment	not modelled	98.1	20 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
37	c3f4wA_	Alignment	not modelled	98.0	12 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
38	dlthfd_	Alignment	not modelled	98.0	14 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
39	dlvhca_	Alignment	not modelled	98.0	18 Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
40	dlmxsa_	Alignment	not modelled	97.9	14 Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
41	c3navB_	Alignment	not modelled	97.8	18 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
42	c2w6rA_	Alignment	not modelled	97.7	13 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
43	c2yw3E_	Alignment	not modelled	97.6	16 PDB header: lyase Chain: E: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase/2-dehydro-3-oxoglutarate aldolase/2-2 dehydro-3-deoxyphosphogluconate aldolase from tthb1
44	c3labA_	Alignment	not modelled	97.5	14 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative kdp (2-keto-3-deoxy-6-phosphogluconate) PDBTitle: crystal structure of a putative kdp (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
45	dlhg3a_	Alignment	not modelled	97.5	19 Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
46	dlxi3a_	Alignment	not modelled	97.4	16 Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
47	c3o63B_	Alignment	not modelled	97.3	17 PDB header: transferase Chain: B: PDB Molecule: probable thiamine-phosphate pyrophosphorylase; PDBTitle: crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
48	dlpia1	Alignment	not modelled	97.2	25 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
49	dlbwva1	Alignment	not modelled	97.1	12 Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
50	c3thaB_	Alignment	not modelled	97.1	16 PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
51	c3ajxA_	Alignment	not modelled	97.0	11 PDB header: lyase Chain: A: PDB Molecule: 3-hexulose-6-phosphate synthase; PDBTitle: crystal structure of 3-hexulose-6-phosphate synthase
52	c2qjhH_	Alignment	not modelled	96.9	17 PDB header: lyase Chain: H: PDB Molecule: putative aldolase mj0400; PDBTitle: m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
53	c2ekcA_	Alignment	not modelled	96.8	17 PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
54	dlw0ma_	Alignment	not modelled	96.8	22 Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
					PDB header: transcription

55	c1yadD_	Alignment	not modelled	96.8	13	Chain: D: PDB Molecule: regulatory protein teni; PDBTitle: structure of teni from bacillus subtilis
56	c3bw2A_	Alignment	not modelled	96.7	27	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-nitropropane dioxygenase; PDBTitle: crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces ansochromogenes
57	d1ojxa_	Alignment	not modelled	96.7	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
58	c1rldB_	Alignment	not modelled	96.6	15	PDB header: lyase(carbon-carbon) Chain: B: PDB Molecule: ribulose 1,5 bisphosphate carboxylase/oxygenase (large PDBTitle: solid-state phase transition in the crystal structure of ribulose 1,5-2 biphosphate carboxylase(/oxygenase
59	c3hf3A_	Alignment	not modelled	96.6	23	PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
60	c3pm6B_	Alignment	not modelled	96.6	12	PDB header: lyase Chain: B: PDB Molecule: putative fructose-bisphosphate aldolase; PDBTitle: crystal structure of a putative fructose-1,6-biphosphate aldolase from2 coccidioides immitis solved by combined sad mr
61	d1wdda1	Alignment	not modelled	96.6	16	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
62	c2gjlA_	Alignment	not modelled	96.5	21	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein pa1024; PDBTitle: crystal structure of 2-nitropropane dioxygenase
63	d1bxna1	Alignment	not modelled	96.5	16	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
64	d1ej7l1	Alignment	not modelled	96.5	15	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
65	c3q94B_	Alignment	not modelled	96.5	16	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase, class ii; PDBTitle: the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
66	d1wv2a_	Alignment	not modelled	96.5	19	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
67	c1rcxH_	Alignment	not modelled	96.4	16	PDB header: lyase (carbon-carbon) Chain: H: PDB Molecule: ribulose bisphosphate carboxylase/oxygenase; PDBTitle: non-activated spinach rubisco in complex with its substrate2 ribulose-1,5-bisphosphate
68	d1qapa1	Alignment	not modelled	96.4	20	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
69	c3qfwB_	Alignment	not modelled	96.3	17	PDB header: lyase Chain: B: PDB Molecule: ribulose-1,5-bisphosphate carboxylase/oxygenase large PDBTitle: crystal structure of rubisco-like protein from rhodopseudomonas2 palustris
70	d1xm3a_	Alignment	not modelled	96.3	18	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
71	c1bwvA_	Alignment	not modelled	96.2	12	PDB header: lyase Chain: A: PDB Molecule: protein (ribulose bisphosphate carboxylase); PDBTitle: activated ribulose 1,5-bisphosphate carboxylase/oxygenase (rubisco)2 complexed with the reaction intermediate analogue 2-carboxyarabinitol3 1,5-bisphosphate
72	d1ru8a_	Alignment	not modelled	96.2	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
73	c2iswB_	Alignment	not modelled	96.2	17	PDB header: lyase Chain: B: PDB Molecule: putative fructose-1,6-bisphosphate aldolase; PDBTitle: structure of giardia fructose-1,6-bisphosphate aldolase in2 complex with phosphoglycolohydroxamate
74	c2d69B_	Alignment	not modelled	96.2	16	PDB header: lyase Chain: B: PDB Molecule: ribulose bisphosphate carboxylase; PDBTitle: crystal structure of the complex of sulfate ion and octameric2 ribulose-1,5-bisphosphate carboxylase/oxygenase (rubisco) from3 pyrococcus horikoshii ot3 (form-2 crystal)
75	c3cu2A_	Alignment	not modelled	96.1	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
76	c3bo9B_	Alignment	not modelled	96.1	26	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nitroalkan dioxygenase; PDBTitle: crystal structure of putative nitroalkan dioxygenase (tm0800) from2 thermotoga maritima at 2.71 a resolution
77	c2h6rG_	Alignment	not modelled	96.1	18	PDB header: isomerase Chain: G: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
78	d1gvfa_	Alignment	not modelled	96.1	12	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
79	d1svda1	Alignment	not modelled	96.1	13	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain

80	dlrblA1	Alignment	not modelled	96.0	14	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
81	c3exsB_	Alignment	not modelled	95.9	13	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
82	d8ruca1	Alignment	not modelled	95.9	14	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
83	d2d69a1	Alignment	not modelled	95.9	16	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
84	c2z6jB_	Alignment	not modelled	95.9	22	PDB header: oxidoreductase Chain: B: PDB Molecule: trans-2-enoyl-acp reductase ii; PDBTitle: crystal structure of s. pneumoniae enoyl-acyl carrier2 protein reductase (fabk) in complex with an inhibitor
85	c3oixA_	Alignment	not modelled	95.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: putative dihydroorotate dehydrogenase; dihydroorotate PDBTitle: crystal structure of the putative dihydroorotate dehydrogenase from2 streptococcus mutans
86	d2d13a1	Alignment	not modelled	95.8	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
87	c3gr7A_	Alignment	not modelled	95.7	22	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
88	dlps9a1	Alignment	not modelled	95.7	25	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
89	c2h90A_	Alignment	not modelled	95.5	20	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
90	dlnsja_	Alignment	not modelled	95.5	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
91	dljuba_	Alignment	not modelled	95.4	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
92	c3nwrA_	Alignment	not modelled	95.4	19	PDB header: lyase Chain: A: PDB Molecule: a rubisco-like protein; PDBTitle: crystal structure of a rubisco-like protein from burkholderia fungorum
93	c9rubB_	Alignment	not modelled	95.4	14	PDB header: lyase(carbon-carbon) Chain: B: PDB Molecule: ribulose-1,5-bisphosphate carboxylase; PDBTitle: crystal structure of activated ribulose-1,5-bisphosphate2 carboxylase complexed with its substrate, ribulose-1,5-3 bisphosphate
94	c3fa4D_	Alignment	not modelled	95.2	11	PDB header: lyase Chain: D: PDB Molecule: 2,3-dimethylmalate lyase; PDBTitle: crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
95	dlv5xa_	Alignment	not modelled	95.2	22	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
96	dlykwa1	Alignment	not modelled	95.1	14	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
97	c2qiwa_	Alignment	not modelled	95.0	14	PDB header: transferase Chain: A: PDB Molecule: pep phosphonmutase; PDBTitle: crystal structure of a putative phosphoenolpyruvate phosphonmutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
98	c2qygC_	Alignment	not modelled	95.0	12	PDB header: unknown function Chain: C: PDB Molecule: ribulose bisphosphate carboxylase-like protein 2; PDBTitle: crystal structure of a rubisco-like protein rlp2 from rhodopseudomonas2 palustris
99	dlgeha1	Alignment	not modelled	94.9	19	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
100	clgthD_	Alignment	not modelled	94.9	26	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpg) from pig, ternary2 complex with nadph and 5-iodouracil
101	clzfjA_	Alignment	not modelled	94.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
102	clgehE_	Alignment	not modelled	94.9	19	PDB header: lyase Chain: E: PDB Molecule: ribulose-1,5-bisphosphate carboxylase/oxygenase; PDBTitle: crystal structure of archaeal rubisco (ribulose 1,5-bisphosphate2 carboxylase/oxygenase)
103	clo4uA_	Alignment	not modelled	94.9	27	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
104	dlvema2	Alignment	not modelled	94.7	10	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain

105	c3gkaB	Alignment	not modelled	94.6	22	PDB header: oxidoreductase Chain: B: PDB Molecule: n-ethylmaleimide reductase; PDBTitle: crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei
106	c1telA	Alignment	not modelled	94.6	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ribulose biphosphate carboxylase, large subunit; PDBTitle: crystal structure of a rubisco-like protein from chlorobium2 tepidum
107	d1rvga	Alignment	not modelled	94.6	22	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
108	d1gk8a1	Alignment	not modelled	94.5	15	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
109	d1o4ua1	Alignment	not modelled	94.5	19	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
110	c2cdh1	Alignment	not modelled	94.5	17	PDB header: transferase Chain: 1: PDB Molecule: enoyl reductase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
111	c1qpoA	Alignment	not modelled	94.3	18	PDB header: transferase Chain: A: PDB Molecule: quinolinate acid phosphoribosyl transferase; PDBTitle: quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
112	d1z41a1	Alignment	not modelled	94.3	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
113	d1q6oa	Alignment	not modelled	94.2	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Decarboxylase
114	c3elfA	Alignment	not modelled	94.1	14	PDB header: lyase Chain: A: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: structural characterization of tetrameric mycobacterium tuberculosis2 fructose 1,6-bisphosphate aldolase - substrate binding and catalysis3 mechanism of a class iia bacterial aldolase
115	c2b7pA	Alignment	not modelled	94.1	32	PDB header: transferase Chain: A: PDB Molecule: probable nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori
116	c1x1oC	Alignment	not modelled	94.0	27	PDB header: transferase Chain: C: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of project id tt0268 from thermus thermophilus hb8
117	d1ujpa	Alignment	not modelled	93.9	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
118	c1piiA	Alignment	not modelled	93.9	16	PDB header: bifunctional (isomerase and synthase) Chain: A: PDB Molecule: n-(5' phosphoribosyl)anthranilate isomerase; PDBTitle: three-dimensional structure of the bifunctional enzyme2 phosphoribosylanthranilate isomerase:3 indoleglycerolphosphate synthase from escherichia coli4 refined at 2.0 angstroms resolution
119	c3tdmD	Alignment	not modelled	93.8	14	PDB header: de novo protein Chain: D: PDB Molecule: computationally designed two-fold symmetric tim-barrel PDBTitle: computationally designed tim-barrel protein, halfflr
120	c3lciA	Alignment	not modelled	93.7	17	PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminate lyase; PDBTitle: the d-sialic acid aldolase mutant v251w