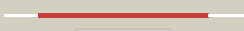
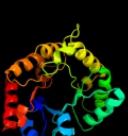
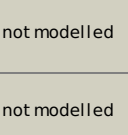


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1eixa_	 Alignment		100.0	100	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
2	d1dbta_	 Alignment		100.0	39	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
3	c3ldvB_	 Alignment		100.0	69	PDB header: lyase Chain: B: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: 1.77 angstrom resolution crystal structure of orotidine 5'-2 phosphate decarboxylase from vibrio cholerae o1 biovar3 eltor str. n16961
4	c3tr2A_	 Alignment		100.0	49	PDB header: lyase Chain: A: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: structure of a orotidine 5'-phosphate decarboxylase (pyrf) from2 coxiella burnetii
5	c2vytA_	 Alignment		100.0	40	PDB header: lyase Chain: A: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus
6	c2qcnaA_	 Alignment		100.0	20	PDB header: lyase Chain: A: PDB Molecule: uridine 5'-monophosphate synthase; PDBTitle: covalent complex of the orotidine-5'-monophosphate decarboxylase2 domain of human ump synthase with 6-iodo-ump
7	c3ru6C_	 Alignment		100.0	34	PDB header: lyase Chain: C: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: 1.8 angstrom resolution crystal structure of orotidine 5'-phosphate2 decarboxylase (pyrf) from campylobacter jejuni subsp. jejuni nctc3 11168
8	c3tfxB_	 Alignment		100.0	38	PDB header: lyase Chain: B: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of orotidine 5'-phosphate decarboxylase from2 lactobacillus acidophilus
9	c3bviA_	 Alignment		100.0	20	PDB header: lyase Chain: A: PDB Molecule: uridine 5'-monophosphate synthase; PDBTitle: crystal structure of human orotidine 5'-monophosphate decarboxylase2 complexed with xmp
10	d1dqwa_	 Alignment		100.0	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
11	c3qw3B_	 Alignment		100.0	20	PDB header: transferase, lyase Chain: B: PDB Molecule: orotidine-5-phosphate decarboxylase/orotate PDBTitle: structure of leishmania donovani omp decarboxylase

12	d1km4a_	Alignment		100.0	25	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
13	d1dvja_	Alignment		100.0	25	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
14	c3qw4B_	Alignment		100.0	23	PDB header: transferase, lyase Chain: B: PDB Molecule: ump synthase; PDBTitle: structure of leishmania donovani ump synthase
15	d2czda1	Alignment		100.0	24	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
16	d2q8za1	Alignment		100.0	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
17	d1losc_	Alignment		100.0	25	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
18	d2ffca1	Alignment		100.0	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
19	c2fdsA_	Alignment		100.0	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of plasmodium berghei orotidine 5'-2 monophosphate decarboxylase (ortholog of plasmodium3 falciparum pf10_0225)
20	d2fdsa1	Alignment		100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
21	c3l52A_	Alignment	not modelled	100.0	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of putative orotidine 5'-phosphate2 decarboxylase from streptomyces avermitilis ma-4680
22	d1vqta1	Alignment	not modelled	100.0	26	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
23	c3r89A_	Alignment	not modelled	100.0	14	PDB header: lyase Chain: A: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of orotidine 5-phosphate decarboxylase from2 anaerococcus prevotii dsm 20548
24	c3exsB_	Alignment	not modelled	100.0	18	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
25	d1q6oa_	Alignment	not modelled	100.0	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
26	c3jr2D_	Alignment	not modelled	100.0	14	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
27	c3ajxA_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: A: PDB Molecule: 3-hexulose-6-phosphate synthase; PDBTitle: crystal structure of 3-hexulose-6-phosphate synthase
28	c3f4wA_	Alignment	not modelled	100.0	19	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

29	c3ct7E_	Alignment	not modelled	100.0	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
30	c3cu2A_	Alignment	not modelled	100.0	11	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
31	d1h1ya_	Alignment	not modelled	100.0	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
32	d1ojxa_	Alignment	not modelled	100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
33	c3qc3B_	Alignment	not modelled	100.0	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
34	c3inpA_	Alignment	not modelled	99.9	13	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.
35	d2flia1	Alignment	not modelled	99.9	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
36	d1rpxa_	Alignment	not modelled	99.9	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
37	d1tqxa_	Alignment	not modelled	99.9	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
38	c2qjhH_	Alignment	not modelled	99.9	15	PDB header: lyase Chain: H: PDB Molecule: putative aldolase mj0400; PDBTitle: m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
39	c3gndC_	Alignment	not modelled	99.9	17	PDB header: lyase Chain: C: PDB Molecule: aldolase lsrf; PDBTitle: crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
40	d1tqja_	Alignment	not modelled	99.9	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
41	c3thaB_	Alignment	not modelled	99.4	13	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
42	d1wbha1	Alignment	not modelled	99.4	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
43	d1wa3a1	Alignment	not modelled	99.3	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
44	c2ekcA_	Alignment	not modelled	99.3	10	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
45	d1xcfa_	Alignment	not modelled	99.3	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
46	d1qopa_	Alignment	not modelled	99.2	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
47	c2bdqA_	Alignment	not modelled	99.2	14	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.
48	d1rd5a_	Alignment	not modelled	99.2	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
49	c2v82A_	Alignment	not modelled	99.1	15	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpgal complexed to kdpgal
50	d1j5ta_	Alignment	not modelled	99.1	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
51	c3navB_	Alignment	not modelled	99.1	21	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
52	d1geqa_	Alignment	not modelled	99.0	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
53	d1vhca_	Alignment	not modelled	99.0	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
54	c3qjaA_	Alignment	not modelled	99.0	12	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
						Fold: TIM beta/alpha-barrel

55	d1piia2	Alignment	not modelled	99.0	12	Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
56	c3igsB	Alignment	not modelled	99.0	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
57	d1mxsa	Alignment	not modelled	99.0	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
58	d1i4na	Alignment	not modelled	98.9	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
59	d2tpsa	Alignment	not modelled	98.9	16	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
60	c3labA	Alignment	not modelled	98.9	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative kdpG (2-keto-3-deoxy-6-phosphogluconate) PDBTitle: crystal structure of a putative kdpG (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
61	c2c3zA	Alignment	not modelled	98.8	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 sulfobolus solfataricus
62	c3o63B	Alignment	not modelled	98.8	15	PDB header: transferase Chain: B: PDB Molecule: probable thiamine-phosphate pyrophosphorylase; PDBTitle: crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
63	c3q58A	Alignment	not modelled	98.8	14	PDB header: isomerase Chain: A: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
64	c1vadD	Alignment	not modelled	98.7	15	PDB header: transcription Chain: D: PDB Molecule: regulatory protein teni; PDBTitle: structure of teni from bacillus subtilis
65	d1xi3a	Alignment	not modelled	98.7	16	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
66	d1y0ea	Alignment	not modelled	98.7	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
67	d1ujpa	Alignment	not modelled	98.7	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
68	d1xya1	Alignment	not modelled	98.6	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
69	c2yw3E	Alignment	not modelled	98.6	15	PDB header: lyase Chain: E: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase/2-dehydro-3- PDBTitle: crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 dehydro-3-deoxyphosphogluconate aldolase from tthb1
70	d1thfd	Alignment	not modelled	98.6	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
71	d1a53a	Alignment	not modelled	98.6	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
72	d1znnal	Alignment	not modelled	98.6	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: PdxS-like
73	d1wv2a	Alignment	not modelled	98.6	19	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
74	c3fokH	Alignment	not modelled	98.5	16	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: uncharacterized protein cgl0159; PDBTitle: crystal structure of cgl0159 from corynebacterium2 glutamicum (brevibacterium flavum). northeast structural 3 genomics target cgr115
75	c1znnF	Alignment	not modelled	98.5	15	PDB header: biosynthetic protein Chain: F: PDB Molecule: plp synthase; PDBTitle: structure of the synthase subunit of plp synthase
76	d1vc4a	Alignment	not modelled	98.5	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
77	d1h5ya	Alignment	not modelled	98.4	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
78	c2htmB	Alignment	not modelled	98.3	17	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
79	d1to3a	Alignment	not modelled	98.3	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
80	d1ka9f	Alignment	not modelled	98.3	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel

						Family: Histidine biosynthesis enzymes
81	c2y85D	Alignment	not modelled	98.3	14	PDB header: isomerase Chain: D: PDB Molecule: phosphoribosyl isomerase a; PDBTitle: crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
82	d1vzwa1	Alignment	not modelled	98.0	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
83	d1xm3a	Alignment	not modelled	98.0	15	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
84	c3nm3D	Alignment	not modelled	97.9	15	PDB header: transferase Chain: D: PDB Molecule: thiamine biosynthetic bifunctional enzyme; PDBTitle: the crystal structure of candida glabrata thi6, a bifunctional enzyme2 involved in thiamin biosynthesis of eukaryotes
85	d1w0ma	Alignment	not modelled	97.9	15	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
86	c1piiA	Alignment	not modelled	97.8	13	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
87	d1hg3a	Alignment	not modelled	97.7	15	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
88	c2h6rG	Alignment	not modelled	97.7	15	PDB header: isomerase Chain: G: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
89	d1vhna	Alignment	not modelled	97.5	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
90	c2d69B	Alignment	not modelled	97.5	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)
91	d2d69a1	Alignment	not modelled	97.4	16	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
92	c3jrkG	Alignment	not modelled	97.3	13	PDB header: lyase Chain: G: PDB Molecule: tagatose 1,6-diphosphate aldolase 2; PDBTitle: a putative tagatose 1,6-diphosphate aldolase from streptococcus2 pyogenes
93	c1bwvA	Alignment	not modelled	97.2	11	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
94	c3ceuA	Alignment	not modelled	97.0	9	PDB header: transferase Chain: A: PDB Molecule: thiamine phosphate pyrophosphorylase; PDBTitle: crystal structure of thiamine phosphate pyrophosphorylase2 (bt_0647) from bacteroides thetaiotaomicron. northeast3 structural genomics consortium target btr268
95	d1o4ua1	Alignment	not modelled	97.0	19	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
96	c2zbtB	Alignment	not modelled	97.0	14	PDB header: lyase Chain: B: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8
97	d1svda1	Alignment	not modelled	97.0	13	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
98	c1qpoA	Alignment	not modelled	96.8	16	PDB header: transferase Chain: A: PDB Molecule: quinolinate acid phosphoribosyl transferase; PDBTitle: quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
99	c2oemA	Alignment	not modelled	96.8	15	PDB header: isomerase Chain: A: PDB Molecule: 2,3-diketo-5-methylthiopentyl-1-phosphate enolase; PDBTitle: crystal structure of a rubisco-like protein from geobacillus2 kaustophilus liganded with mg2+ and 2,3-diketohexane 1-phosphate
100	d1bxna1	Alignment	not modelled	96.8	13	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
101	c3ivuB	Alignment	not modelled	96.8	15	PDB header: transferase Chain: B: PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
102	c1qapA	Alignment	not modelled	96.8	17	PDB header: glycosyltransferase Chain: A: PDB Molecule: quinolinic acid phosphoribosyltransferase; PDBTitle: quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
103	d1qpoa1	Alignment	not modelled	96.8	19	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like

					Family: NadC C-terminal domain-like
104	d8ruca1	Alignment	not modelled	96.6	15 Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
105	dlqapa1	Alignment	not modelled	96.5	16 Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
106	c1rldB_	Alignment	not modelled	96.5	14 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(/slash)oxygenase
107	dlbwva1	Alignment	not modelled	96.5	13 Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
108	c1rcxH_	Alignment	not modelled	96.5	14 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
109	dlgk8a1	Alignment	not modelled	96.4	13 Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
110	c1telA_	Alignment	not modelled	96.4	16 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ribulose bisphosphate carboxylase, large subunit; PDBTitle: crystal structure of a rubisco-like protein from chlorobium2 tepidum
111	c2nv2U_	Alignment	not modelled	96.4	15 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
112	c2yztB_	Alignment	not modelled	96.3	28 PDB header: lyase Chain: B: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxine biosynthesis protein from2 methanocaldococcus jannaschii
113	dlcj7l1	Alignment	not modelled	96.3	14 Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
114	d2f6ua1	Alignment	not modelled	96.3	11 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
115	c3femB_	Alignment	not modelled	96.3	13 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
116	c3fk4A_	Alignment	not modelled	96.2	9 PDB header: isomerase Chain: A: PDB Molecule: rubisco-like protein; PDBTitle: crystal structure of rubisco-like protein from bacillus2 cereus atcc 14579
117	c3ffsC_	Alignment	not modelled	96.1	19 PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
118	c2qygC_	Alignment	not modelled	96.0	16 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
119	dl1kwa1	Alignment	not modelled	95.9	16 Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
120	c1o4uA_	Alignment	not modelled	95.8	18 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