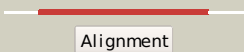

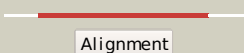

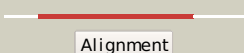

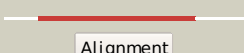



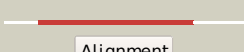

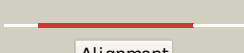

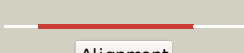


















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1vhna_	 Alignment		100.0	27	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
2	c3b0vD_	 Alignment		100.0	22	PDB header: oxidoreductase/rna Chain: D: PDB Molecule: trna-dihydrouridine synthase; PDBTitle: trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
3	c3hf3A_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
4	c3kruC_	 Alignment		100.0	17	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
5	c3gr7A_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
6	c1ps9A_	 Alignment		100.0	19	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
7	d1z41a1	 Alignment		100.0	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
8	c2h90A_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
9	d1ps9a1	 Alignment		100.0	20	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
10	c1djnB_	 Alignment		100.0	15	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)
11	d1djqa1	 Alignment		100.0	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases

12	d1vyra_	Alignment		100.0	20	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
13	c3k30B_	Alignment		100.0	12	PDB header: oxidoreductase Chain: B: PDB Molecule: histamine dehydrogenase; PDBTitle: histamine dehydrogenase from nocardiothelium simplex
14	c2gq8A_	Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, fmn-binding; PDBTitle: structure of sye1, an oye homologue from s. oncothelium, in complex2 with p-hydroxyacetophenone
15	d1gwja_	Alignment		100.0	20	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
16	c3gkaB_	Alignment		100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: n-ethylmaleimide reductase; PDBTitle: crystal structure of n-ethylmaleimide reductase from2 burkholderia pseudomallei
17	d1icpa_	Alignment		100.0	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
18	d1vjia_	Alignment		100.0	20	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
19	d1oyaa_	Alignment		100.0	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
20	c3atyA_	Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: prostaglandin f2a synthase; PDBTitle: crystal structure of tcoye
21	c3l5aA_	Alignment	not modelled	100.0	20	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
22	d1q45a_	Alignment	not modelled	100.0	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
23	d1gtea2	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
24	d1ep3a_	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
25	d1juba_	Alignment	not modelled	99.9	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
26	c3oixa_	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putative dihydroorotate dehydrogenase; PDBTitle: crystal structure of the putative dihydroorotate dehydrogenase from2 streptococcus mutans
27	d2b4ga1	Alignment	not modelled	99.9	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
28	d1f76a_	Alignment	not modelled	99.9	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases

29	d1d3ga_	Alignment	not modelled	99.9	22	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
30	c2htmB_	Alignment	not modelled	99.8	17	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
31	c2fptA_	Alignment	not modelled	99.8	21	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase, mitochondrial; PDBTitle: dual binding mode of a novel series of dhodh inhibitors
32	c2z6jB_	Alignment	not modelled	99.8	19	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
33	c1gthD_	Alignment	not modelled	99.8	21	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
34	c3bo9B_	Alignment	not modelled	99.8	19	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
35	d1tv5a1	Alignment	not modelled	99.8	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
36	c1tv5A_	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase homolog, mitochondrial; PDBTitle: plasmodium falciparum dihydroorotate dehydrogenase with a bound2 inhibitor
37	c3gyeA_	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase, putative; PDBTitle: dihydroorotate dehydrogenase from leishmania major
38	d1uuma_	Alignment	not modelled	99.8	22	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
39	c2gjlA_	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein pa1024; PDBTitle: crystal structure of 2-nitropropane dioxygenase
40	d1vrda1	Alignment	not modelled	99.7	19	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
41	d1jr1a1	Alignment	not modelled	99.7	20	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
42	d1xm3a_	Alignment	not modelled	99.7	16	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
43	c3ffsC_	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
44	c3khjE_	Alignment	not modelled	99.7	20	PDB header: oxidoreductase Chain: E: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
45	d1tb3a1	Alignment	not modelled	99.7	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
46	d1pvna1	Alignment	not modelled	99.7	21	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
47	c2cdh1_	Alignment	not modelled	99.7	19	PDB header: transferase Chain: 1: PDB Molecule: enoyl reductase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
48	c2a7nA_	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: il(+)-mandelate dehydrogenase; PDBTitle: crystal structure of the g81a mutant of the active chimera of (s)-2 mandelate dehydrogenase
49	c1vrda_	Alignment	not modelled	99.7	22	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase (tm1347)2 from thermotoga maritima at 2.18 a resolution
50	d1jcna1	Alignment	not modelled	99.7	16	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
51	d1goxa_	Alignment	not modelled	99.7	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
52	c3r2gA_	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine 5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
53	d1eepa_	Alignment	not modelled	99.6	19	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
						Fold: TIM beta/alpha-barrel

54	d1p4ca_	Alignment	not modelled	99.6	18	Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
55	c3bw2A_	Alignment	not modelled	99.6	21	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-nitropropane dioxygenase; PDBTitle: crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces ansochromogenes
56	c3tdmD_	Alignment	not modelled	99.6	19	PDB header: de novo protein Chain: D: PDB Molecule: computationally designed two-fold symmetric tim-barrel PDBTitle: computationally designed tim-barrel protein, halflfr
57	c1me9A_	Alignment	not modelled	99.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh) from2 tritrichomonas foetus with imp bound
58	c1ypfB_	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: B: PDB Molecule: gmp reductase; PDBTitle: crystal structure of guac (ba5705) from bacillus anthracis at 1.8 a2 resolution
59	d1zfja1	Alignment	not modelled	99.6	17	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
60	c2y85D_	Alignment	not modelled	99.6	19	PDB header: isomerase Chain: D: PDB Molecule: phosphoribosyl isomerase a; PDBTitle: crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
61	d1geqa_	Alignment	not modelled	99.5	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
62	d1yxva1	Alignment	not modelled	99.5	21	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
63	d1p0ka_	Alignment	not modelled	99.5	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
64	c2e77B_	Alignment	not modelled	99.5	19	PDB header: oxidoreductase Chain: B: PDB Molecule: lactate oxidase; PDBTitle: crystal structure of l-lactate oxidase with pyruvate complex
65	d1kbia1	Alignment	not modelled	99.5	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
66	d1jpma1	Alignment	not modelled	99.5	14	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
67	d2cu0a1	Alignment	not modelled	99.5	18	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
68	d1vcfa1	Alignment	not modelled	99.5	13	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
69	c2zrvC_	Alignment	not modelled	99.5	12	PDB header: isomerase Chain: C: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: crystal structure of sulfolobus shibatae isopentenyl2 diphosphate isomerase in complex with reduced fm.
70	c2cu0B_	Alignment	not modelled	99.5	17	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase from2 pyrococcus horikoshii ot3
71	c1jcnA_	Alignment	not modelled	99.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase i; PDBTitle: binary complex of human type-i inosine monophosphate dehydrogenase2 with 6-cl-imp
72	c2rduA_	Alignment	not modelled	99.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase in complex with2 glyoxylate
73	c1kbiB_	Alignment	not modelled	99.4	14	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome b2; PDBTitle: crystallographic study of the recombinant flavin-binding domain of2 baker's yeast flavocytochrome b2: comparison with the intact wild-3 type enzyme
74	c2a7rD_	Alignment	not modelled	99.4	16	PDB header: oxidoreductase Chain: D: PDB Molecule: gmp reductase 2; PDBTitle: crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2)
75	d1jvna1	Alignment	not modelled	99.4	24	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
76	d1rd5a_	Alignment	not modelled	99.3	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
77	d1xcfa_	Alignment	not modelled	99.3	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
78	d1wv2a_	Alignment	not modelled	99.3	16	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
79	c3q58A_	Alignment	not modelled	99.3	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
80	d2gl5a1	Alignment	not modelled	99.3	15 Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
81	c2qr6A	Alignment	not modelled	99.3	17 PDB header: oxidoreductase Chain: A: PDB Molecule: imp dehydrogenase/gmp reductase; PDBTitle: crystal structure of imp dehydrogenase/gmp reductase-like protein2 (np_599840.1) from corynebacterium glutamicum atcc 13032 kitasato at3 1.50 a resolution
82	d1qo2a	Alignment	not modelled	99.3	22 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
83	d1thfd	Alignment	not modelled	99.3	19 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
84	c1jvnB	Alignment	not modelled	99.2	21 PDB header: transferase Chain: B: PDB Molecule: bifunctional histidine biosynthesis protein hishf; PDBTitle: crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
85	d1qopa	Alignment	not modelled	99.2	13 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
86	c3rcyC	Alignment	not modelled	99.2	15 PDB header: isomerase Chain: C: PDB Molecule: mandelate racemase/muconate lactonizing enzyme-like PDBTitle: crystal structure of mandelate racemase/muconate lactonizing enzyme-2 like protein from roseovarius sp. tm1035
87	c2qjjC	Alignment	not modelled	99.2	13 PDB header: lyase Chain: C: PDB Molecule: mandelate racemase/muconate lactonizing enzyme; PDBTitle: crystal structure of d-mannonate dehydratase from novosphingobium2 aromaticivorans
88	c1zjfA	Alignment	not modelled	99.1	19 PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (imphd; ec 1.1.1.205) from2 streptococcus pyogenes
89	d1ka9f	Alignment	not modelled	99.1	18 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
90	d1vzwa1	Alignment	not modelled	99.1	18 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
91	d1h5ya	Alignment	not modelled	99.1	22 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
92	d1y0ea	Alignment	not modelled	99.1	17 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
93	c3t8qA	Alignment	not modelled	99.1	14 PDB header: isomerase Chain: A: PDB Molecule: mandelate racemase/muconate lactonizing enzyme family PDBTitle: crystal structure of mandelate racemase/muconate lactonizing enzyme2 family protein from hoeflea phototrophica
94	c2ql5A	Alignment	not modelled	99.1	15 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative dehydratase protein; PDBTitle: crystal structure of putative dehydratase from salmonella thyphimurium
95	c2qq6B	Alignment	not modelled	99.1	19 PDB header: isomerase Chain: B: PDB Molecule: mandelate racemase/muconate lactonizing enzyme- PDBTitle: crystal structure of mandelate racemase/muconate2 lactonizing enzyme-like protein from rubrobacter3 xylanophilus dsm 9941
96	c2ox4E	Alignment	not modelled	99.0	14 PDB header: isomerase Chain: E: PDB Molecule: putative mandelate racemase; PDBTitle: crystal structure of putative dehydratase from zymomonas mobilis zm4
97	c3sqsA	Alignment	not modelled	99.0	12 PDB header: isomerase Chain: A: PDB Molecule: mandelate racemase/muconate lactonizing protein; PDBTitle: crystal structure of a putative mandelate racemase/muconate2 lactonizing protein from dinoroseobacter shibae dfl 12
98	c3thuC	Alignment	not modelled	99.0	15 PDB header: lyase Chain: C: PDB Molecule: mandelate racemase / muconate lactonizing enzyme family PDBTitle: crystal structure of an enolase from sphingomonas sp. ska58 (efi2 target efi-501683) with bound mg
99	c2qdeA	Alignment	not modelled	99.0	17 PDB header: lyase Chain: A: PDB Molecule: mandelate racemase/muconate lactonizing enzyme family PDBTitle: crystal structure of mandelate racemase/muconate lactonizing family2 protein from azoarcus sp. ebn1
100	c3tjiA	Alignment	not modelled	99.0	11 PDB header: lyase Chain: A: PDB Molecule: mandelate racemase/muconate lactonizing enzyme, n-terminal PDBTitle: crystal structure of an enolase from enterobacter sp. 638 (efi target2 efi-501662) with bound mg
101	c2p88E	Alignment	not modelled	99.0	20 PDB header: lyase Chain: E: PDB Molecule: mandelate racemase/muconate lactonizing enzyme PDBTitle: crystal structure of n-succinyl arg/lys racemase from2 bacillus cereus atcc 14579
					Fold: TIM beta/alpha-barrel

102	d1nu5a1	Alignment	not modelled	99.0	14	Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
103	c2v82A	Alignment	not modelled	99.0	20	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpGal complexed to kdpGal
104	c3bsmD	Alignment	not modelled	99.0	19	PDB header: lyase Chain: D: PDB Molecule: mandelate racemase/muconate lactonizing enzyme; PDBTitle: crystal structure of d-mannonate dehydratase from2 chromohalobacter salexigens
105	d2mnra1	Alignment	not modelled	99.0	21	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
106	c2o56D	Alignment	not modelled	98.9	14	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative mandelate racemase; PDBTitle: crystal structure of a member of the enolase superfamily from2 salmonella typhimurium
107	d1rvka1	Alignment	not modelled	98.9	17	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
108	c3sjnB	Alignment	not modelled	98.9	14	PDB header: lyase Chain: B: PDB Molecule: mandelate racemase/muconate lactonizing protein; PDBTitle: crystal structure of enolase spea_3858 (target efi-500646) from2 shewanella pealeana with magnesium bound
109	c3jw7E	Alignment	not modelled	98.9	20	PDB header: isomerase Chain: E: PDB Molecule: dipeptide epimerase; PDBTitle: crystal structure of dipeptide epimerase from enterococcus faecalis2 v583 complexed with mg and dipeptide l-ile-l-tyr
110	c3igsB	Alignment	not modelled	98.9	14	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
111	c3dfhC	Alignment	not modelled	98.9	11	PDB header: isomerase Chain: C: PDB Molecule: mandelate racemase; PDBTitle: crystal structure of putative mandelate racemase / muconate2 lactonizing enzyme from vibionales bacterium swat-3
112	c2pozA	Alignment	not modelled	98.9	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative dehydratase; PDBTitle: crystal structure of a putative dehydratase from mesorhizobium loti
113	c2w6rA	Alignment	not modelled	98.9	18	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
114	c3t6cB	Alignment	not modelled	98.9	13	PDB header: lyase Chain: B: PDB Molecule: putative mand family dehydratase; PDBTitle: crystal structure of an enolase from pantoea ananatis (efi target efi-2 501676) with bound d-gluconate and mg
115	d1tza1	Alignment	not modelled	98.9	13	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
116	c2oz8B	Alignment	not modelled	98.9	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ml17089 protein; PDBTitle: crystal structure of putative mandelate racemase from mesorhizobium2 loti
117	c1rvkA	Alignment	not modelled	98.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: isomerase/lactonizing enzyme; PDBTitle: crystal structure of enolase agr_I_2751 from agrobacterium tumefaciens
118	c3fv9D	Alignment	not modelled	98.9	19	PDB header: hydrolase Chain: D: PDB Molecule: mandelate racemase/muconate lactonizing enzyme; PDBTitle: crystal structure of putative mandelate racemase/muconatelactonizing2 enzyme from roseovarius nubihbens ism complexed with magnesium
119	c3tj4B	Alignment	not modelled	98.9	15	PDB header: lyase Chain: B: PDB Molecule: mandelate racemase; PDBTitle: crystal structure of an enolase from agrobacterium tumefaciens (efi2 target efi-502087) no mg
120	c2c3zA	Alignment	not modelled	98.8	13	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