Phyre^2

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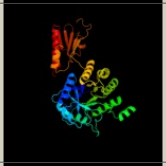
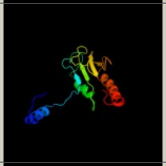
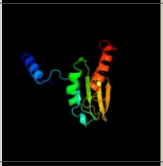
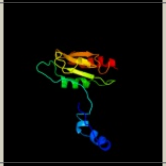
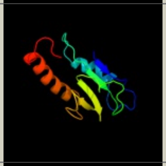
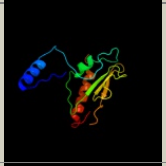
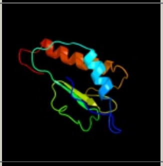
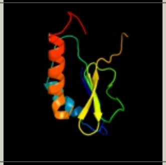
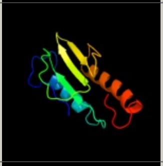
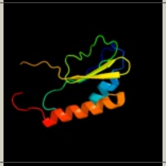
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3noyA_	Alignment		100.0	47	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; **PDBTitle:** crystal structure of ispg (gcpe)
2	c2y0fD_	Alignment		100.0	39	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; **PDBTitle:** structure of gcpe (ispg) from thermus thermophilus hb27
3	c5aopA_	Alignment		99.6	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase hemoprotein; **PDBTitle:** sulfite reductase structure reduced with crii edta, 5-coordinate2 siroheme, siroheme feii, [4fe-4s] +1
4	c1zj8B_	Alignment		99.6	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable ferredoxin-dependent nitrite reductase nira; **PDBTitle:** structure of mycobacterium tuberculosis nira protein
5	c2akjA_	Alignment		99.4	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin--nitrite reductase, chloroplast; **PDBTitle:** structure of spinach nitrite reductase
6	d1aopa4	Alignment		99.4	21	**Fold:**Nitrite and sulphite reductase 4Fe-4S domain-like **Superfamily:**Nitrite and sulphite reductase 4Fe-4S domain-like **Family:**Nitrite and sulphite reductase 4Fe-4S domain-like
7	c2v4jE_	Alignment		99.4	21	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit **PDBTitle:** the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration
8	d3c7bb3	Alignment		99.4	19	**Fold:**Nitrite and sulphite reductase 4Fe-4S domain-like **Superfamily:**Nitrite and sulphite reductase 4Fe-4S domain-like **Family:**Nitrite and sulphite reductase 4Fe-4S domain-like
9	d1zj8a3	Alignment		99.3	22	**Fold:**Nitrite and sulphite reductase 4Fe-4S domain-like **Superfamily:**Nitrite and sulphite reductase 4Fe-4S domain-like **Family:**Nitrite and sulphite reductase 4Fe-4S domain-like
10	d3c7ba3	Alignment		99.3	21	**Fold:**Nitrite and sulphite reductase 4Fe-4S domain-like **Superfamily:**Nitrite and sulphite reductase 4Fe-4S domain-like **Family:**Nitrite and sulphite reductase 4Fe-4S domain-like
11	d2akja3	Alignment		99.2	16	**Fold:**Nitrite and sulphite reductase 4Fe-4S domain-like **Superfamily:**Nitrite and sulphite reductase 4Fe-4S domain-like **Family:**Nitrite and sulphite reductase 4Fe-4S domain-like

12	d2v4jb3	Alignment		99.2	19	**Fold:**Nitrite and sulphite reductase 4Fe-4S domain-like **Superfamily:**Nitrite and sulphite reductase 4Fe-4S domain-like **Family:**Nitrite and sulphite reductase 4Fe-4S domain-like
13	c3c7bE_	Alignment		99.2	24	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit beta; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
14	d2v4ja3	Alignment		99.2	13	**Fold:**Nitrite and sulphite reductase 4Fe-4S domain-like **Superfamily:**Nitrite and sulphite reductase 4Fe-4S domain-like **Family:**Nitrite and sulphite reductase 4Fe-4S domain-like
15	d2akja4	Alignment		99.2	18	**Fold:**Nitrite and sulphite reductase 4Fe-4S domain-like **Superfamily:**Nitrite and sulphite reductase 4Fe-4S domain-like **Family:**Nitrite and sulphite reductase 4Fe-4S domain-like
16	d1aopa3	Alignment		99.2	12	**Fold:**Nitrite and sulphite reductase 4Fe-4S domain-like **Superfamily:**Nitrite and sulphite reductase 4Fe-4S domain-like **Family:**Nitrite and sulphite reductase 4Fe-4S domain-like
17	d1tx2a_	Alignment		99.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
18	c1tx2A_	Alignment		99.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dhps, dihydropteroate synthase; **PDBTitle:** dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
19	c3c7bA_	Alignment		99.2	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit alpha; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
20	d1zj8a4	Alignment		99.1	16	**Fold:**Nitrite and sulphite reductase 4Fe-4S domain-like **Superfamily:**Nitrite and sulphite reductase 4Fe-4S domain-like **Family:**Nitrite and sulphite reductase 4Fe-4S domain-like
21	d1ajza_	Alignment	not modelled	99.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
22	c3tr9A_	Alignment	not modelled	99.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** structure of a dihydropteroate synthase (folp) in complex with pteroic2 acid from coxiella burnetii
23	d1eyea_	Alignment	not modelled	99.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
24	c2v4jA_	Alignment	not modelled	99.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit **PDBTitle:** the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration
25	c3k13A_	Alignment	not modelled	98.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydrofolate-homocysteine methyltransferase; **PDBTitle:** structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron
26	c2vp8A_	Alignment	not modelled	98.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase 2; **PDBTitle:** structure of mycobacterium tuberculosis rv1207
27	c2y5sA_	Alignment	not modelled	98.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
						PDB header:transferase

28	c2yciX_	Alignment	not modelled	98.9	18	**Chain:** X: **PDB Molecule:**5-methyltetrahydrofolate corrinoid/iron sulfur protein **PDBTitle:** methyltransferase native
29	d1f6ya_	Alignment	not modelled	98.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Methyltetrahydrofolate-utiluzing methyltransferases
30	d3bofa1	Alignment	not modelled	98.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Methyltetrahydrofolate-utiluzing methyltransferases
31	d1ad1a_	Alignment	not modelled	98.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
32	c2dzaA_	Alignment	not modelled	98.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of dihydropteroate synthase from thermus2 thermophilus hb8 in complex with 4-aminobenzoate
33	c3bolB_	Alignment	not modelled	98.7	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**5-methyltetrahydrofolate s-homocysteine **PDBTitle:** cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
34	c2vefB_	Alignment	not modelled	98.6	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** dihydropteroate synthase from streptococcus pneumoniae
35	c3pg8B_	Alignment	not modelled	98.4	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phospho-2-dehydro-3-deoxyheptonate aldolase; **PDBTitle:** truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima
36	c2h9aA_	Alignment	not modelled	98.3	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**carbon monoxide dehydrogenase corrinoid/iron- **PDBTitle:** corrinoid iron-sulfur protein
37	c1vs1B_	Alignment	not modelled	98.3	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-deoxy-7-phosphoheptulonate synthase; **PDBTitle:** crystal structure of 3-deoxy-d-arabino-heptulosonate-7-2 phosphate synthase (dahp synthase) from aeropyrum pernix3 in complex with mn2+ and pep
38	c3nvtA_	Alignment	not modelled	98.2	18	**PDB header:**transferase/isomerase **Chain:** A: **PDB Molecule:**3-deoxy-d-arabino-heptulosonate 7-phosphate synthase; **PDBTitle:** 1.95 angstrom crystal structure of a bifunctional 3-deoxy-7-2 phosphoheptulonate synthase/chorismate mutase (aroa) from listeria3 monocytogenes egd-e
39	c2h9aB_	Alignment	not modelled	98.1	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**co dehydrogenase/acetyl-coa synthase, iron- **PDBTitle:** corrinoid iron-sulfur protein
40	d1vr6a1	Alignment	not modelled	97.9	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
41	c3t4cD_	Alignment	not modelled	97.8	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase 1; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia ambifaria
42	c3fs2A_	Alignment	not modelled	97.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate2 aldolase from bruciella melitensis at 1.85a resolution
43	c2bmbA_	Alignment	not modelled	97.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**folic acid synthesis protein fol1; **PDBTitle:** x-ray structure of the bifunctional 6-hydroxymethyl-7,8-2 dihydroxypterin pyrophosphokinase dihydropteroate synthase3 from saccharomyces cerevisiae
44	d2zdra2	Alignment	not modelled	97.6	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
45	c2yr1B_	Alignment	not modelled	97.5	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystal structure of 3-dehydroquinate dehydratase from geobacillus2 kaustophilus hta426
46	c3js3C_	Alignment	not modelled	97.5	21	**PDB header:**lyase **Chain:** C: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystal structure of type i 3-dehydroquinate dehydratase (arod) from2 clostridium difficile with covalent reaction intermediate
47	c3l2iB_	Alignment	not modelled	97.4	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** 1.85 angstrom crystal structure of the 3-dehydroquinate dehydratase2 (arod) from salmonella typhimurium lt2.
48	d1gqna_	Alignment	not modelled	97.3	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
49	c1zfjA_	Alignment	not modelled	97.2	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
50	d1h5ya_	Alignment	not modelled	97.1	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
51	c3mcnA_	Alignment	not modelled	97.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-amino-4-hydroxy-6-hydroxymethyldihydropteridine **PDBTitle:** crystal structure of the 6-hyroxymethyl-7,8-dihydropterin2 pyrophosphokinase dihydropteroate synthase bifunctional enzyme from3 francisella tularensis

52	c3q45E_	Alignment	not modelled	97.0	17	**PDB header:**isomerase **Chain:** E: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme family; **PDBTitle:** crystal structure of dipeptide epimerase from cytophaga hutchinsonii2 complexed with mg and dipeptide d-ala-l-val
53	c2pa6A_	Alignment	not modelled	97.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enolase; **PDBTitle:** crystal structure of mj0232 from methanococcus jannaschii
54	c1l8pC_	Alignment	not modelled	97.0	16	**PDB header:**lyase **Chain:** C: **PDB Molecule:**enolase 1; **PDBTitle:** mg-phosphonoacetohydroxamate complex of s39a yeast enolase 1
55	c1zcoA_	Alignment	not modelled	96.9	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphoheptonate aldolase; **PDBTitle:** crystal structure of pyrococcus furiosus 3-deoxy-d-arabino-2 heptulosonate 7-phosphate synthase
56	d1o60a_	Alignment	not modelled	96.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
57	d1jpma1	Alignment	not modelled	96.7	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
58	c3q58A_	Alignment	not modelled	96.7	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase; **PDBTitle:** structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
59	d2al1a1	Alignment	not modelled	96.7	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
60	d1nu5a1	Alignment	not modelled	96.6	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
61	d1d9ea_	Alignment	not modelled	96.6	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
62	c1wueA_	Alignment	not modelled	96.6	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme family **PDBTitle:** crystal structure of protein gi:29375081, unknown member of enolase2 superfamily from enterococcus faecalis v583
63	c3ijlA_	Alignment	not modelled	96.5	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**muconate cycloisomerase; **PDBTitle:** structure of dipeptide epimerase from bacteroides thetaiotaomicron2 complexed with l-pro-d-glu; nonproductive substrate binding.
64	c2fkpC_	Alignment	not modelled	96.5	22	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**n-acylamino acid racemase; **PDBTitle:** the mutant g127c-t313c of deinococcus radiodurans n-2 acylamino acid racemase
65	c2zc8B_	Alignment	not modelled	96.5	24	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**n-acylamino acid racemase; **PDBTitle:** crystal structure of n-acylamino acid racemase from thermus2 thermophilus hb8
66	d1wbha1	Alignment	not modelled	96.4	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
67	c2ps2A_	Alignment	not modelled	96.4	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative mandelate racemase/muconate lactonizing **PDBTitle:** crystal structure of putative mandelate racemase/muconate2 lactonizing enzyme from aspergillus oryzae
68	c3dipA_	Alignment	not modelled	96.4	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enolase; **PDBTitle:** crystal structure of an enolase protein from the2 environmental genome shotgun sequencing of the sargasso sea
69	c2y7eA_	Alignment	not modelled	96.4	16	**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)
70	c2akmA_	Alignment	not modelled	96.3	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**gamma enolase; **PDBTitle:** fluoride inhibition of enolase: crystal structure of the2 inhibitory complex
71	c3i4kA_	Alignment	not modelled	96.3	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**muconate lactonizing enzyme; **PDBTitle:** crystal structure of muconate lactonizing enzyme from2 corynebacterium glutamicum
72	d1rvka1	Alignment	not modelled	96.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
73	d1r0ma1	Alignment	not modelled	96.3	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
74	c3qc3B_	Alignment	not modelled	96.3	15	**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
75	d1tqja_	Alignment	not modelled	96.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
						Fold:TIM beta/alpha-barrel

76	d2akza1	Alignment	not modelled	96.3	17	**Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
77	c1jpdX_	Alignment	not modelled	96.3	21	**PDB header:**isomerase **Chain:** X: **PDB Molecule:**l-ala-d/l-glu epimerase; **PDBTitle:** l-ala-d/l-glu epimerase
78	d1pdza1	Alignment	not modelled	96.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
79	d1yx1a1	Alignment	not modelled	96.2	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**KguE-like
80	d1jpdx1	Alignment	not modelled	96.2	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
81	c3stgA_	Alignment	not modelled	96.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase; **PDBTitle:** crystal structure of a58p, del(n59), and loop 7 truncated mutant of 3-2 deoxy-d-manno-octulosonate 8-phosphate synthase (kdo8ps) from3 neisseria meningitidis
82	c3sz8D_	Alignment	not modelled	96.1	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase 2; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei
83	c1rvkA_	Alignment	not modelled	96.1	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**isomerase/lactonizing enzyme; **PDBTitle:** crystal structure of enolase agr_l_2751 from agrobacterium tumefaciens
84	c2podA_	Alignment	not modelled	96.1	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**mandelate racemase / muconate lactonizing enzyme; **PDBTitle:** crystal structure of a member of enolase superfamily from burkholderia2 pseudomallei k96243
85	c3qldB_	Alignment	not modelled	96.1	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**mandelate racemase/muconate lactonizing protein; **PDBTitle:** structure of probable mandelate racemase (aalaa1draft_2112) from2 alicyclobacillus acidocaldarius
86	c2pgwC_	Alignment	not modelled	96.1	18	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**muconate cycloisomerase; **PDBTitle:** crystal structure of a putative muconate cycloisomerase from2 sinorhizobium meliloti 1021
87	c3mqtV_	Alignment	not modelled	96.1	13	**PDB header:**isomerase **Chain:** V: **PDB Molecule:** **PDBTitle:** crystal structure of a mandelate racemase/muconate lactonizing enzyme2 from shewanella pealeana
88	c2qdeA_	Alignment	not modelled	96.0	20	**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
89	c1jpmB_	Alignment	not modelled	96.0	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**l-ala-d/l-glu epimerase; **PDBTitle:** l-ala-d/l-glu epimerase
90	c3ddmD_	Alignment	not modelled	96.0	14	**PDB header:**lyase **Chain:** D: **PDB Molecule:**putative mandelate racemase/muconate lactonizing **PDBTitle:** crystal structure of mandelate racemase/muconate2 lactonizing enzyme from bordetella bronchiseptica rb50
91	c2pozA_	Alignment	not modelled	96.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative dehydratase; **PDBTitle:** crystal structure of a putative dehydratase from mesorhizobium loti
92	c2p88E_	Alignment	not modelled	96.0	19	**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
93	c3px5A_	Alignment	not modelled	95.9	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**enzyme of enolase superfamily; **PDBTitle:** structure of efi enolase target en500555, a putative dipeptide2 epimerase: apo structure
94	c3mkcA_	Alignment	not modelled	95.9	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**racemase; **PDBTitle:** crystal structure of a putative racemase
95	c3msyC_	Alignment	not modelled	95.8	13	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme; **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing enzyme2 from a marine actinobacterium
96	c3rcyC_	Alignment	not modelled	95.8	18	**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
97	d1vlia2	Alignment	not modelled	95.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
98	c3igsB_	Alignment	not modelled	95.8	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
99	d2mnra1	Alignment	not modelled	95.8	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like

100	d1ka9f_	Alignment	not modelled	95.7	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
101	c2ovlA_	Alignment	not modelled	95.7	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative racemase; **PDBTitle:** crystal structure of a racemase from streptomyces2 coelicolor a3(2)
102	d1muca1	Alignment	not modelled	95.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
103	c3fv9D_	Alignment	not modelled	95.7	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme; **PDBTitle:** crystal structure of putative mandelate racemase/muconatelactonizing2 enzyme from roseovarius nubinhibens ism complexed with magnesium
104	c2o56D_	Alignment	not modelled	95.6	17	**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
105	c3dfhC_	Alignment	not modelled	95.6	15	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**mandelate racemase; **PDBTitle:** crystal structure of putative mandelate racemase / muconate2 lactonizing enzyme from vibrionales bacterium swat-3
106	c3sjnB_	Alignment	not modelled	95.6	12	**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
107	c3dfyJ_	Alignment	not modelled	95.6	21	**PDB header:**isomerase **Chain:** J: **PDB Molecule:**muconate cycloisomerase; **PDBTitle:** crystal structure of apo dipeptide epimerase from2 thermotoga maritima
108	d1h1ya_	Alignment	not modelled	95.6	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
109	d1mxsa_	Alignment	not modelled	95.6	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
110	d1rpxa_	Alignment	not modelled	95.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
111	c2c3zA_	Alignment	not modelled	95.5	17	**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
112	c3i6eA_	Alignment	not modelled	95.5	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**muconate cycloisomerase i; **PDBTitle:** crystal structure of muconate lactonizing enzyme from2 ruegeria pomeroyi.
113	d1sjda1	Alignment	not modelled	95.4	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
114	c1sjaA_	Alignment	not modelled	95.4	19	**PDB header:**lyase, isomerase **Chain:** A: **PDB Molecule:**n-acylamino acid racemase; **PDBTitle:** x-ray structure of o-succinylbenzoate synthase complexed2 with n-acetylmethionine
115	c2oqhD_	Alignment	not modelled	95.4	13	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative isomerase; **PDBTitle:** crystal structure of an isomerase from streptomyces coelicolor a3(2)
116	d1thfd_	Alignment	not modelled	95.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
117	c3cb3B_	Alignment	not modelled	95.4	9	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme; **PDBTitle:** crystal structure of l-talarate dehydratase from polaromonas sp. js6662 complexed with mg and l-glucarate
118	d1wufa1	Alignment	not modelled	95.3	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
119	c1nu5A_	Alignment	not modelled	95.3	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**chloromuconate cycloisomerase; **PDBTitle:** crystal structure of pseudomonas sp. p51 chloromuconate lactonizing2 enzyme
120	d1dvja_	Alignment	not modelled	95.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase