Phyre^2

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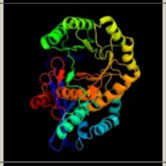
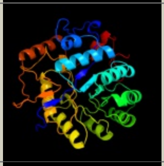
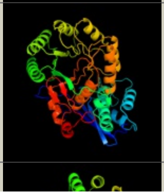
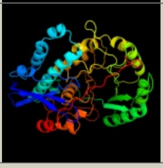
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ec8B_	Alignment		100.0	100	**PDB header:**lyase **Chain:** B: **PDB Molecule:**glucarate dehydratase; **PDBTitle:** e. coli glucarate dehydratase bound to product 2,3-2 dihydroxy-5-oxo-hexanedioate
2	c3nxlD_	Alignment		100.0	65	**PDB header:**lyase **Chain:** D: **PDB Molecule:**glucarate dehydratase; **PDBTitle:** crystal structure of glucarate dehydratase from burkholderia cepacia2 complexed with magnesium
3	c3n6jA_	Alignment		100.0	57	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing protein; **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing protein2 from actinobacillus succinogenes 130z
4	c3mznA_	Alignment		100.0	59	**PDB header:**lyase **Chain:** A: **PDB Molecule:**glucarate dehydratase; **PDBTitle:** crystal structure of probable glucarate dehydratase from2 chromohalobacter salexigens dsm 3043
5	c2nqlB_	Alignment		100.0	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**isomerase/lactonizing enzyme; **PDBTitle:** crystal structure of a member of the enolase superfamily from2 agrobacterium tumefaciens
6	c2pp1C_	Alignment		100.0	20	**PDB header:**lyase **Chain:** C: **PDB Molecule:**l-talarate/galactarate dehydratase; **PDBTitle:** crystal structure of l-talarate/galactarate dehydratase from2 salmonella typhimurium lt2 liganded with mg and l-lyxarohydroxamate
7	c2pgwC_	Alignment		100.0	22	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**muconate cycloisomerase; **PDBTitle:** crystal structure of a putative muconate cycloisomerase from2 sinorhizobium meliloti 1021
8	d1jdfa1	Alignment		100.0	100	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
9	c2oo6A_	Alignment		100.0	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative l-alanine-dl-glutamate epimerase; **PDBTitle:** crystal structure of putative l-alanine-dl-glutamate epimerase from2 burkholderia xenovorans strain lb400
10	c3tjiA_	Alignment		100.0	20	**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
11	c2qgyA_	Alignment		100.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**enolase from the environmental genome shotgun **PDBTitle:** crystal structure of an enolase from the environmental2 genome shotgun sequencing of the sargasso sea
						

12	c2hxtA_	Alignment		100.0	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**l-fuconate dehydratase; **PDBTitle:** crystal structure of l-fuconate dehydratase from xanthomonas2 campestris liganded with mg++ and d-erythronohydroxamate
13	c2o56D_	Alignment		100.0	20	**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
14	c2chrA_	Alignment		100.0	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**chloromuconate cycloisomerase; **PDBTitle:** a re-evaluation of the crystal structure of chloromuconate2 cycloisomerase
15	c2ox4E_	Alignment		100.0	19	**PDB header:**isomerase **Chain:** E: **PDB Molecule:**putative mandelate racemase; **PDBTitle:** crystal structure of putative dehydratase from zymomonas mobilis zm4
16	c3t6cB_	Alignment		100.0	21	**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
17	c3rcyC_	Alignment		100.0	22	**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
18	c2gl5A_	Alignment		100.0	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative dehydratase protein; **PDBTitle:** crystal structure of putative dehydratase from salmonella thyphimurium
19	c3rr1B_	Alignment		100.0	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative d-galactonate dehydratase; **PDBTitle:** crystal structure of enolase prk14017 (target efi-500653) from2 ralstonia pickettii 12j
20	c3thuC_	Alignment		100.0	21	**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
21	c3i6eA_	Alignment	not modelled	100.0	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**muconate cycloisomerase i; **PDBTitle:** crystal structure of muconate lactonizing enzyme from2 ruegeria pomeroyi.
22	c1nu5A_	Alignment	not modelled	100.0	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**chloromuconate cycloisomerase; **PDBTitle:** crystal structure of pseudomonas sp. p51 chloromuconate lactonizing2 enzyme
23	c3h12B_	Alignment	not modelled	100.0	23	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**mandelate racemase; **PDBTitle:** crystal structure of putative mandelate racemase from bordetella2 bronchiseptica rb50
24	c1rvkA_	Alignment	not modelled	100.0	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**isomerase/lactonizing enzyme; **PDBTitle:** crystal structure of enolase agr_l_2751 from agrobacterium tumefaciens
25	c3dg7B_	Alignment	not modelled	100.0	23	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**muconate cycloisomerase; **PDBTitle:** crystal structure of muconate lactonizing enzyme from mucobacterium2 smegmatis complexed with muconolactone
26	c3my9A_	Alignment	not modelled	100.0	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**muconate cycloisomerase; **PDBTitle:** crystal structure of a muconate cycloisomerase from azorhizobium2 caulinodans
27	c2qddA_	Alignment	not modelled	100.0	20	**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 roseovarius2 nubinhibens ism
28	c2oqhD_	Alignment	not modelled	100.0	26	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative isomerase; **PDBTitle:** crystal structure of an isomerase from streptomyces coelicolor a3(2)
						PDB header:structural genomics, unknown function

29	c2ps2A_	Alignment	not modelled	100.0	21	**Chain:** A: **PDB Molecule:**putative mandelate racemase/muconate lactonizing **PDBTitle:** crystal structure of putative mandelate racemase/muconate2 lactonizing enzyme from aspergillus oryzae
30	c2qjjC_	Alignment	not modelled	100.0	20	**PDB header:**lyase **Chain:** C: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme; **PDBTitle:** crystal structure of d-mannonate dehydratase from novosphingobium2 aromaticivorans
31	c3fv9D_	Alignment	not modelled	100.0	19	**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
32	c1f9cA_	Alignment	not modelled	100.0	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein (muconate cycloisomerase i); **PDBTitle:** crystal structure of mle d178n variant
33	c3i4kA_	Alignment	not modelled	100.0	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**muconate lactonizing enzyme; **PDBTitle:** crystal structure of muconate lactonizing enzyme from2 corynebacterium glutamicum
34	c3mkcA_	Alignment	not modelled	100.0	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**racemase; **PDBTitle:** crystal structure of a putative racemase
35	c2qdeA_	Alignment	not modelled	100.0	21	**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
36	c3sqsA_	Alignment	not modelled	100.0	18	**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
37	c3sjnB_	Alignment	not modelled	100.0	22	**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
38	c3es8D_	Alignment	not modelled	100.0	19	**PDB header:**isomerase, lyase **Chain:** D: **PDB Molecule:**muconate cycloisomerase; **PDBTitle:** crystal structure of divergent enolase from oceanobacillus2 iheyensis complexed with mg and l-malate.
39	c3n4eA_	Alignment	not modelled	100.0	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme, c-terminal **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing protein2 from paracoccus denitrificans pd1222
40	c3dipA_	Alignment	not modelled	100.0	20	**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
41	c3bsmD_	Alignment	not modelled	100.0	20	**PDB header:**lyase **Chain:** D: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme; **PDBTitle:** crystal structure of d-mannonate dehydratase from2 chromohalobacter salexigens
42	c2qq6B_	Alignment	not modelled	100.0	20	**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
43	c3bjsB_	Alignment	not modelled	100.0	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme; **PDBTitle:** crystal structure of a member of enolase superfamily from polaromonas2 sp. js666
44	c3eezA_	Alignment	not modelled	100.0	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative mandelate racemase/muconate lactonizing **PDBTitle:** crystal structure of a putative mandelate racemase/muconate2 lactonizing enzyme from silicibacter pomeroyi
45	c2rdxG_	Alignment	not modelled	100.0	19	**PDB header:**structural genomics, unknown function **Chain:** G: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme, putative; **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing enzyme2 from roseovarius nubinhibens ism
46	c3tj4B_	Alignment	not modelled	100.0	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**mandelate racemase; **PDBTitle:** crystal structure of an enolase from agrobacterium tumefaciens (efi2 target efi-502087) no mg
47	c3q45E_	Alignment	not modelled	100.0	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
48	c2gdqB_	Alignment	not modelled	100.0	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**yitf; **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing enzyme2 from bacillus subtilis at 1.8 a resolution
49	c2pmqA_	Alignment	not modelled	100.0	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme; **PDBTitle:** crystal structure of a mandelate racemase/muconate lactonizing enzyme2 from roseovarius sp. htcc2601
50	c2pozA_	Alignment	not modelled	100.0	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative dehydratase; **PDBTitle:** crystal structure of a putative dehydratase from

						mesorhizobium loti
51	c3mqtV_	Alignment	not modelled	100.0	20	**PDB header:**isomerase **Chain:** V: **PDB Molecule:** **PDBTitle:** crystal structure of a mandelate racemase/muconate lactonizing enzyme2 from shewanella pealeana
52	c2ppgB_	Alignment	not modelled	100.0	24	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative isomerase; **PDBTitle:** crystal structure of putative isomerase from sinorhizobium meliloti
53	c2podA_	Alignment	not modelled	100.0	17	**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
54	c3t8qA_	Alignment	not modelled	100.0	21	**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
55	c2oz3F_	Alignment	not modelled	100.0	18	**PDB header:**lyase **Chain:** F: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme; **PDBTitle:** crystal structure of l-rhamnonate dehydratase from azotobacter2 vinelandii
56	c3dfhC_	Alignment	not modelled	100.0	17	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**mandelate racemase; **PDBTitle:** crystal structure of putative mandelate racemase / muconate2 lactonizing enzyme from vibrionales bacterium swat-3
57	c1mraA_	Alignment	not modelled	100.0	19	**PDB header:**racemase **Chain:** A: **PDB Molecule:**mandelate racemase; **PDBTitle:** mandelate racemase mutant d270n co-crystallized with (s)-atrolactate
58	c3toyC_	Alignment	not modelled	100.0	22	**PDB header:**lyase **Chain:** C: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme family **PDBTitle:** crystal structure of enolase brado_4202 (target efi-501651) from2 bradyrhizobium sp. ors278 with calcium and acetate bound
59	c2hzgB_	Alignment	not modelled	100.0	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme/enolase **PDBTitle:** crystal stucture of predicted mandelate racemase from rhodobacter2 sphaeroides
60	c3ugvE_	Alignment	not modelled	100.0	20	**PDB header:**lyase **Chain:** E: **PDB Molecule:**enolase; **PDBTitle:** crystal structure of an enolase from alpha pretobacterium bal199 (efi2 target efi-501650) with bound mg
61	c2p88E_	Alignment	not modelled	100.0	22	**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
62	c3cxoA_	Alignment	not modelled	100.0	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative galactonate dehydratase; **PDBTitle:** crystal structure of l-rhamnonate dehydratase from2 salmonella typhimurium complexed with mg and 3-deoxy-l-3 rhamnonate
63	c3cb3B_	Alignment	not modelled	100.0	21	**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
64	c1wueA_	Alignment	not modelled	100.0	19	**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
65	c3t9pB_	Alignment	not modelled	100.0	23	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme family **PDBTitle:** crystal structure of a putative mandelate racemase/muconate2 lactonizing enzyme family protein from roseovarius
66	c2ovlA_	Alignment	not modelled	100.0	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative racemase; **PDBTitle:** crystal structure of a racemase from streptomyces2 coelicolor a3(2)
67	c2fkpC_	Alignment	not modelled	100.0	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
68	c3fcpF_	Alignment	not modelled	100.0	19	**PDB header:**isomerase **Chain:** F: **PDB Molecule:**l-ala-d/l-glu epimerase, a muconate lactonizing **PDBTitle:** crystal structure of muconate lactonizing enzyme from2 klebsiella pneumoniae
69	c3cyjA_	Alignment	not modelled	100.0	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme-like **PDBTitle:** crystal structure of a mandelate racemase/muconate lactonizing enzyme-2 like protein from rubrobacter xylanophilus
70	c3ik4A_	Alignment	not modelled	100.0	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing protein; **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing protein2 from herpetosiphon aurantiacus
71	c2zc8B_	Alignment	not modelled	100.0	23	**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
72	c3mwcA_	Alignment	not modelled	100.0	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing protein;

						PDBTitle: crystal structure of probable o-succinylbenzoic acid synthetase from2 kosmotoga olearia
73	c2p0iA_	Alignment	not modelled	100.0	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-rhamnonate dehydratase; **PDBTitle:** crystal structure of l-rhamnonate dehydratase from gibberella zeae
74	c1wufB_	Alignment	not modelled	100.0	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein lin2664; **PDBTitle:** crystal structure of protein gi:16801725, member of enolase2 superfamily from listeria innocua clip11262
75	c3ddmD_	Alignment	not modelled	100.0	20	**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
76	c3n4fD_	Alignment	not modelled	100.0	20	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**mandelate racemase/muconate lactonizing protein; **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing protein2 from geobacillus sp. y412mc10
77	c2dw7G_	Alignment	not modelled	100.0	16	**PDB header:**lyase **Chain:** G: **PDB Molecule:**bll6730 protein; **PDBTitle:** crystal structure of d-tartrate dehydratase from2 bradyrhizobium japonicum complexed with mg++ and meso-3 tartrate
78	c1sjaA_	Alignment	not modelled	100.0	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
79	c2oz8B_	Alignment	not modelled	100.0	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**mll7089 protein; **PDBTitle:** crystal structure of putative mandelate racemase from mesorhizobium2 loti
80	c3msyC_	Alignment	not modelled	100.0	17	**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
81	c3px5A_	Alignment	not modelled	100.0	15	**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
82	c1jpmB_	Alignment	not modelled	100.0	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**l-ala-d/l-glu epimerase; **PDBTitle:** l-ala-d/l-glu epimerase
83	c3jw7E_	Alignment	not modelled	100.0	19	**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
84	c3qldB_	Alignment	not modelled	100.0	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**mandelate racemase/muconate lactonizing protein; **PDBTitle:** structure of probable mandelate racemase (aalaa1draft_2112) from2 alicyclobacillus acidocaldarius
85	c3ritE_	Alignment	not modelled	100.0	16	**PDB header:**isomerase **Chain:** E: **PDB Molecule:**dipeptide epimerase; **PDBTitle:** crystal structure of dipeptide epimerase from methylococcus capsulatus2 complexed with mg and dipeptide l-arg-d-lys
86	c3dfyJ_	Alignment	not modelled	100.0	20	**PDB header:**isomerase **Chain:** J: **PDB Molecule:**muconate cycloisomerase; **PDBTitle:** crystal structure of apo dipeptide epimerase from2 thermotoga maritima
87	c3ijlA_	Alignment	not modelled	100.0	18	**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.
88	c2oktA_	Alignment	not modelled	100.0	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**o-succinylbenzoic acid synthetase; **PDBTitle:** crystal structure of o-succinylbenzoic acid synthetase from2 staphylococcus aureus, ligand-free form
89	d1bqga1	Alignment	not modelled	100.0	74	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
90	c2pgeA_	Alignment	not modelled	100.0	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**menc; **PDBTitle:** crystal structure of menc from desulfotalea psychrophila2 lsv54
91	c1jpdX_	Alignment	not modelled	100.0	14	**PDB header:**isomerase **Chain:** X: **PDB Molecule:**l-ala-d/l-glu epimerase; **PDBTitle:** l-ala-d/l-glu epimerase
92	d1muca1	Alignment	not modelled	100.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
93	d2gl5a1	Alignment	not modelled	100.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
94	d2chra1	Alignment	not modelled	100.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
95	d1nu5a1	Alignment	not modelled	100.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
96	c3cawB_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**o-succinylbenzoate synthase; **PDBTitle:** crystal structure of o-succinylbenzoate synthase from2

						bdellovibrio bacteriovorus liganded with mg
97	d1rvka1	Alignment	not modelled	100.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
98	d1r0ma1	Alignment	not modelled	100.0	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
99	d1wuea1	Alignment	not modelled	100.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
100	d2gdqa1	Alignment	not modelled	100.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
101	d1wufa1	Alignment	not modelled	100.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
102	d1sjda1	Alignment	not modelled	100.0	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
103	d1yeya1	Alignment	not modelled	100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
104	d1tzza1	Alignment	not modelled	100.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
105	c2oztA_	Alignment	not modelled	100.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tlr1174 protein; **PDBTitle:** crystal structure of o-succinylbenzoate synthase from2 thermosynechococcus elongatus bp-1
106	d2mnra1	Alignment	not modelled	100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
107	c1kczA_	Alignment	not modelled	100.0	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**beta-methylaspartase; **PDBTitle:** crystal structure of beta-methylaspartase from clostridium2 tetanomorphum. mg-complex.
108	d1jpma1	Alignment	not modelled	100.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
109	c1kkoB_	Alignment	not modelled	100.0	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-methylaspartate ammonia-lyase; **PDBTitle:** crystal structure of citrobacter amalonaticus2 methylaspartate ammonia lyase
110	c2qvhB_	Alignment	not modelled	100.0	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**o-succinylbenzoate-coa synthase; **PDBTitle:** crystal structure of o-succinylbenzoate synthase complexed with o-2 succinyl benzoate (osb)
111	c3gc2A_	Alignment	not modelled	100.0	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**o-succinylbenzoate synthase; **PDBTitle:** 1.85 angstrom crystal structure of o-succinylbenzoate synthase from2 salmonella typhimurium in complex with succinic acid
112	c2pa6A_	Alignment	not modelled	100.0	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enolase; **PDBTitle:** crystal structure of mj0232 from methanococcus jannaschii
113	c3uj2C_	Alignment	not modelled	100.0	16	**PDB header:**lyase **Chain:** C: **PDB Molecule:**enolase 1; **PDBTitle:** crystal structure of an enolase from anaerostipes caccae (efi target2 efi-502054) with bound mg and sulfate
114	c3qn3B_	Alignment	not modelled	100.0	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**enolase; **PDBTitle:** phosphopyruvate hydratase from campylobacter jejuni.
115	c1l8pC_	Alignment	not modelled	100.0	16	**PDB header:**lyase **Chain:** C: **PDB Molecule:**enolase 1; **PDBTitle:** mg-phosphonoacetohydroxamate complex of s39a yeast enolase 1
116	c3tqpA_	Alignment	not modelled	100.0	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enolase; **PDBTitle:** structure of an enolase (eno) from coxiella burnetii
117	c1iyxA_	Alignment	not modelled	100.0	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enolase; **PDBTitle:** crystal structure of enolase from enterococcus hirae
118	c2akmA_	Alignment	not modelled	100.0	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**gamma enolase; **PDBTitle:** fluoride inhibition of enolase: crystal structure of the2 inhibitory complex
119	c2fymA_	Alignment	not modelled	100.0	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enolase; **PDBTitle:** crystal structure of e. coli enolase complexed with the2 minimal binding segment of rnase e.
120	c2ptwA_	Alignment	not modelled	100.0	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enolase; **PDBTitle:** crystal structure of the t. brucei enolase complexed with2 sulphate, identification of a metal binding site iv