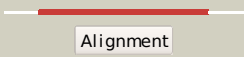

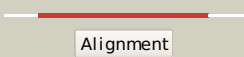

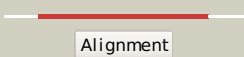

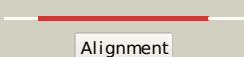

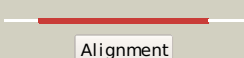

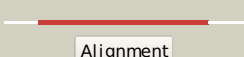

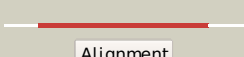

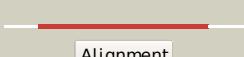

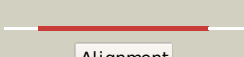

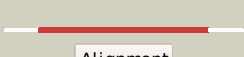






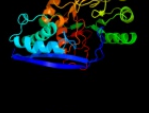




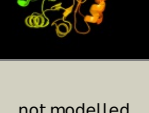









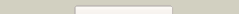















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1jpdX_	 Alignment		100.0	100	PDB header: isomerase Chain: X: PDB Molecule: l-ala-d/l-glu epimerase; PDBTitle: l-ala-d/l-glu epimerase
2	c3q45E_	 Alignment		100.0	26	PDB header: isomerase Chain: E: PDB Molecule: mandelate racemase/muconate lactonizing enzyme family; PDBTitle: crystal structure of dipeptide epimerase from cytophaga hutchinsonii2 complexed with mg and dipeptide d-ala-l-val
3	c2chrA_	 Alignment		100.0	26	PDB header: isomerase Chain: A: PDB Molecule: chloromuconate cycloisomerase; PDBTitle: a re-evaluation of the crystal structure of chloromuconate2 cycloisomerase
4	c1nu5A_	 Alignment		100.0	27	PDB header: isomerase Chain: A: PDB Molecule: chloromuconate cycloisomerase; PDBTitle: crystal structure of pseudomonas sp. p51 chloromuconate lactonizing2 enzyme
5	c2zc8B_	 Alignment		100.0	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
6	c2pgeA_	 Alignment		100.0	19	PDB header: lyase Chain: A: PDB Molecule: menc; PDBTitle: crystal structure of menc from desulfotalea psychrophila2 lsv54
7	c3px5A_	 Alignment		100.0	24	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
8	c1jpmB_	 Alignment		100.0	29	PDB header: isomerase Chain: B: PDB Molecule: l-ala-d/l-glu epimerase; PDBTitle: l-ala-d/l-glu epimerase
9	c1wueA_	 Alignment		100.0	24	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
10	c3ritE_	 Alignment		100.0	33	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
11	c3ijlA_	 Alignment		100.0	34	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.

12	c2p88E_	Alignment		100.0	28	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
13	c2qddA_	Alignment		100.0	24	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
14	c2pgwC_	Alignment		100.0	23	PDB header: isomerase Chain: C: PDB Molecule: muconate cycloisomerase; PDBTitle: crystal structure of a putative muconate cycloisomerase from2 sinorhizobium meliloti 1021
15	c1sjaA_	Alignment		100.0	23	PDB header: lyase, isomerase Chain: A: PDB Molecule: n-acylamino acid racemase; PDBTitle: x-ray structure of o-succinylbenzoate synthase complexed2 with n-acetyl methionine
16	c3fv9D_	Alignment		100.0	23	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
17	c2nqlB_	Alignment		100.0	20	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
18	c1wufB_	Alignment		100.0	24	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
19	c3i4kA_	Alignment		100.0	25	PDB header: isomerase Chain: A: PDB Molecule: muconate lactonizing enzyme; PDBTitle: crystal structure of muconate lactonizing enzyme from2 corynebacterium glutamicum
20	c3dg7B_	Alignment		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
21	c2pmqA_	Alignment	not modelled	100.0	21	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
22	c2ps2A_	Alignment	not modelled	100.0	22	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
23	c3jw7E_	Alignment	not modelled	100.0	33	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
24	c3i6eA_	Alignment	not modelled	100.0	25	PDB header: isomerase Chain: A: PDB Molecule: muconate cycloisomerase i; PDBTitle: crystal structure of muconate lactonizing enzyme from2 ruegeria pomeroyi.
25	c3mwC_A_	Alignment	not modelled	100.0	24	PDB header: ligase Chain: A: PDB Molecule: mandelate racemase/muconate lactonizing protein; PDBTitle: crystal structure of probable o-succinylbenzoic acid synthetase from2 kosmotoga olearia
26	c3ik4A_	Alignment	not modelled	100.0	30	PDB header: isomerase Chain: A: PDB Molecule: mandelate racemase/muconate lactonizing protein; PDBTitle: crystal structure of mandelate racemase/muconate lactonizing protein2 from herpetosiphon aurantiacus
27	c3qldB_	Alignment	not modelled	100.0	23	PDB header: isomerase Chain: B: PDB Molecule: mandelate racemase/muconate lactonizing protein; PDBTitle: structure of probable mandelate racemase (aalaa1draft_2112) from2 alicyclobacillus acidocaldarius

28	c2qdeA	 Alignment	not modelled	100.0	26	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
29	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
30	c2pp1C	 Alignment	not modelled	100.0	23	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
31	c1f9cA	 Alignment	not modelled	100.0	24	PDB header: isomerase Chain: A: PDB Molecule: protein (muconate cycloisomerase i); PDBTitle: crystal structure of mle d178n variant
32	c2rdxG	 Alignment	not modelled	100.0	18	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 nubinhbens ism
33	c3bjsB	 Alignment	not modelled	100.0	22	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
34	c3es8D	 Alignment	not modelled	100.0	21	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.
35	c2gdqB	 Alignment	not modelled	100.0	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: y1f; PDBTitle: crystal structure of mandelate racemase/muconate lactonizing enzyme2 from bacillus subtilis at 1.8 a resolution
36	c1mraA	 Alignment	not modelled	100.0	20	PDB header: racemase Chain: A: PDB Molecule: mandelate racemase; PDBTitle: mandelate racemase mutant d270n co-crystallized with (s)-atrolactate
37	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
38	c1rvkA	 Alignment	not modelled	100.0	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: isomerase/lactonizing enzyme; PDBTitle: crystal structure of enolase agr_I_2751 from agrobacterium tumefaciens
39	c3eezA	 Alignment	not modelled	100.0	25	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
40	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
41	c3toyC	 Alignment	not modelled	100.0	19	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
42	c2oz8B	 Alignment	not modelled	100.0	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: mll7089 protein; PDBTitle: crystal structure of putative mandelate racemase from mesorhizobium2 loti
43	c2hxtA	 Alignment	not modelled	100.0	21	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-erythronehydroxamate
44	c2ovIA	 Alignment	not modelled	100.0	23	PDB header: isomerase Chain: A: PDB Molecule: putative racemase; PDBTitle: crystal structure of a racemase from streptomyces2 coelicolor a3(2)
45	c3fcpF	 Alignment	not modelled	100.0	29	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
46	c3dfyJ	 Alignment	not modelled	100.0	27	PDB header: isomerase Chain: J: PDB Molecule: muconate cycloisomerase; PDBTitle: crystal structure of apo dipeptide epimerase from2 thermotoga maritima
47	c2qgyA	 Alignment	not modelled	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
48	c2ppgB	 Alignment	not modelled	100.0	17	PDB header: isomerase Chain: B: PDB Molecule: putative isomerase; PDBTitle: crystal structure of putative isomerase from sinorhizobium meliloti
49	c2oqhD	 Alignment	not modelled	100.0	23	PDB header: isomerase Chain: D: PDB Molecule: putative isomerase; PDBTitle: crystal structure of an isomerase from streptomyces coelicolor a3(2)
50	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
51	c3ugvE_	Alignment	not modelled	100.0	18	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
52	c2gl5A_	Alignment	not modelled	100.0	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative dehydratase protein; PDBTitle: crystal structure of putative dehydratase from salmonella typhimurium
53	c3tjiA_	Alignment	not modelled	100.0	21	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
54	c3sjnB_	Alignment	not modelled	100.0	20	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
55	c3msyC_	Alignment	not modelled	100.0	20	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
56	c3rcyC_	Alignment	not modelled	100.0	20	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
57	c2oktA_	Alignment	not modelled	100.0	17	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
58	c3bsmD_	Alignment	not modelled	100.0	19	PDB header: lyase Chain: D: PDB Molecule: mandelate racemase/muconate lactonizing enzyme; PDBTitle: crystal structure of d-mannonate dehydratase from2 chromohalobacter salexigens
59	c2hzgB_	Alignment	not modelled	100.0	23	PDB header: isomerase Chain: B: PDB Molecule: mandelate racemase/muconate lactonizing enzyme/enolase PDBTitle: crystal stucture of predicted mandelate racemase from rhodobacter2 sphaeroides
60	c3rr1B_	Alignment	not modelled	100.0	20	PDB header: lyase Chain: B: PDB Molecule: putative d-galactonate dehydratase; PDBTitle: crystal structure of enolase prk14017 (target efi-500653) from2 ralstonia pickettii 12j
61	c2ox4E_	Alignment	not modelled	100.0	20	PDB header: isomerase Chain: E: PDB Molecule: putative mandelate racemase; PDBTitle: crystal structure of putative dehydratase from zymomonas mobilis zm4
62	c3cb3B_	Alignment	not modelled	100.0	25	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
63	c2o56D_	Alignment	not modelled	100.0	23	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
64	c3dfhC_	Alignment	not modelled	100.0	16	PDB header: isomerase Chain: C: PDB Molecule: mandelate racemase; PDBTitle: crystal structure of putative mandelate racemase / muconate2 lactonizing enzyme from vibionales bacterium swat-3
65	c2qjjC_	Alignment	not modelled	100.0	21	PDB header: lyase Chain: C: PDB Molecule: mandelate racemase/muconate lactonizing enzyme; PDBTitle: crystal structure of d-mannonate dehydratase from novosphingobium2 aromaticivorans
66	c3tj4B_	Alignment	not modelled	100.0	23	PDB header: lyase Chain: B: PDB Molecule: mandelate racemase; PDBTitle: crystal structure of an enolase from agrobacterium tumefaciens (efi2 target efi-502087) no mg
67	c3sqsA_	Alignment	not modelled	100.0	19	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
68	c3thuC_	Alignment	not modelled	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
69	c3t6cB_	Alignment	not modelled	100.0	20	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
70	c2pozA_	Alignment	not modelled	100.0	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative dehydratase; PDBTitle: crystal structure of a putative dehydratase from mesorhizobium loti
71	c3n4eA_	Alignment	not modelled	100.0	22	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
72	c3mqtv_	Alignment	not modelled	100.0	19	PDB header: isomerase Chain: V: PDB Molecule: PDBTitle: crystal structure of a mandelate racemase/muconate lactonizing enzyme2 from shewanella pealeana
						PDB header: lyase Chain: G: PDB Molecule: blt6730 protein;

73	c2dw7G_	Alignment	not modelled	100.0	17	PDBTitle: crystal structure of d-tartrate dehydratase from2 bradyrhizobium japonicum complexed with mg++ and meso-3 tartrate
74	c1ec8B_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: B: PDB Molecule: glucarate dehydratase; PDBTitle: e. coli glucarate dehydratase bound to product 2,3-2 dihydroxy-5-oxo-hexanedioate
75	c3ddmD_	Alignment	not modelled	100.0	23	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	c3mznA_	Alignment	not modelled	100.0	19	PDB header: lyase Chain: A: PDB Molecule: glucarate dehydratase; PDBTitle: crystal structure of probable glucarate dehydratase from2 chromohalobacter salexigens dsm 3043
77	c2oo6A_	Alignment	not modelled	100.0	20	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
78	c3gc2A_	Alignment	not modelled	100.0	20	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
79	c3t8qA_	Alignment	not modelled	100.0	22	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
80	c3mkcA_	Alignment	not modelled	100.0	21	PDB header: isomerase Chain: A: PDB Molecule: racemase; PDBTitle: crystal structure of a putative racemase
81	c2podA_	Alignment	not modelled	100.0	22	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
82	c2qq6B_	Alignment	not modelled	100.0	25	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
83	c2p0iA_	Alignment	not modelled	100.0	19	PDB header: lyase Chain: A: PDB Molecule: l-rhamnonate dehydratase; PDBTitle: crystal structure of l-rhamnonate dehydratase from gibberella zeae
84	c3dipA_	Alignment	not modelled	100.0	26	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
85	c3n6jA_	Alignment	not modelled	100.0	18	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
86	c2oztA_	Alignment	not modelled	100.0	22	PDB header: lyase Chain: A: PDB Molecule: thr1174 protein; PDBTitle: crystal structure of o-succinylbenzoate synthase from2 thermosynechococcus elongatus bp-1
87	c3t9pB_	Alignment	not modelled	100.0	16	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
88	c2oz3F_	Alignment	not modelled	100.0	19	PDB header: lyase Chain: F: PDB Molecule: mandelate racemase/muconate lactonizing enzyme; PDBTitle: crystal structure of l-rhamnonate dehydratase from azotobacter2 vinelandii
89	c3nxD_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: D: PDB Molecule: glucarate dehydratase; PDBTitle: crystal structure of glucarate dehydratase from burkholderia cepacia2 complexed with magnesium
90	c3n4fD_	Alignment	not modelled	100.0	18	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
91	c3cxoA_	Alignment	not modelled	100.0	17	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
92	c1kcZa_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: A: PDB Molecule: beta-methylaspartase; PDBTitle: crystal structure of beta-methylaspartase from clostridium2 tetanomorphum. mg-complex.
93	c2qvHb_	Alignment	not modelled	100.0	25	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)
94	c1kkoB_	Alignment	not modelled	100.0	19	PDB header: lyase Chain: B: PDB Molecule: 3-methylaspartate ammonia-lyase; PDBTitle: crystal structure of citrobacter amalonaticus2 methylaspartate ammonia lyase
95	d1jpdX1	Alignment	not modelled	100.0	100	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like

96	c3cawB_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: B: PDB Molecule: o-succinylbenzoate synthase; PDBTitle: crystal structure of o-succinylbenzoate synthase from2 bdellovibrio bacteriovorus liganded with mg
97	d1sjda1	Alignment	not modelled	100.0	25	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
98	d1jpma1	Alignment	not modelled	100.0	31	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
99	d1muca1	Alignment	not modelled	100.0	25	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
100	d1wuea1	Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
101	d2chra1	Alignment	not modelled	100.0	27	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
102	d1wufa1	Alignment	not modelled	100.0	20	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
103	d1r0ma1	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
104	d1nu5a1	Alignment	not modelled	100.0	27	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
105	d2gl5a1	Alignment	not modelled	100.0	20	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
106	d1rvka1	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
107	c2pa6A_	Alignment	not modelled	100.0	19	PDB header: lyase Chain: A: PDB Molecule: enolase; PDBTitle: crystal structure of mj0232 from methanococcus jannaschii
108	d1tzza1	Alignment	not modelled	100.0	15	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
109	d2gdqa1	Alignment	not modelled	100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
110	d2mnra1	Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
111	c1l8pC_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: C: PDB Molecule: enolase 1; PDBTitle: mg-phosphonoaceto-hydroxamate complex of s39a yeast enolase 1
112	c2akmA_	Alignment	not modelled	100.0	20	PDB header: lyase Chain: A: PDB Molecule: gamma enolase; PDBTitle: fluoride inhibition of enolase: crystal structure of the2 inhibitory complex
113	c1iyxA_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: A: PDB Molecule: enolase; PDBTitle: crystal structure of enolase from enterococcus hirae
114	c3qn3B_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: B: PDB Molecule: enolase; PDBTitle: phosphopyruvate hydratase from campylobacter jejuni.
115	c3tqpA_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: A: PDB Molecule: enolase; PDBTitle: structure of an enolase (eno) from coxiella burnetii
116	d1veya1	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
117	c3uj2C_	Alignment	not modelled	100.0	20	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
118	c2ptwA_	Alignment	not modelled	100.0	17	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
119	d1jdfa1	Alignment	not modelled	100.0	12	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
120	c2fymA_	Alignment	not modelled	100.0	23	PDB header: lyase Chain: A: PDB Molecule: enolase; PDBTitle: crystal structure of e. coli enolase complexed with the2 minimal binding segment of rnaase e.