

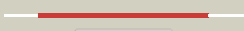


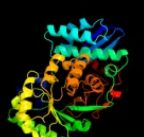


















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3cxoA_</a>	 Alignment		100.0	96	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative galactonate dehydratase; <b>PDBTitle:</b> crystal structure of l-rhamnonate dehydratase from2 salmonella typhimurium complexed with mg and 3-deoxy-l-3 rhamnonate
2	<a href="#">c2oz3F_</a>	 Alignment		100.0	62	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme; <b>PDBTitle:</b> crystal structure of l-rhamnonate dehydratase from azotobacter2 vinelandii
3	<a href="#">c2p0iA_</a>	 Alignment		100.0	43	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> l-rhamnonate dehydratase; <b>PDBTitle:</b> crystal structure of l-rhamnonate dehydratase from gibberella zeae
4	<a href="#">c2o56D_</a>	 Alignment		100.0	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> putative mandelate racemase; <b>PDBTitle:</b> crystal structure of a member of the enolase superfamily from2 salmonella typhimurium
5	<a href="#">c2hxtA_</a>	 Alignment		100.0	18	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> l-fuconate dehydratase; <b>PDBTitle:</b> crystal structure of l-fuconate dehydratase from xanthomonas2 campestris liganded with mg++ and d-erythronohydroxamate
6	<a href="#">c2pp1C_</a>	 Alignment		100.0	24	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> l-talarate/galactarate dehydratase; <b>PDBTitle:</b> crystal structure of l-talarate/galactarate dehydratase from2 salmonella typhimurium lt2 liganded with mg and l-lyxarohydroxamate
7	<a href="#">c2ox4E_</a>	 Alignment		100.0	25	<b>PDB header:</b> isomerase <b>Chain:</b> E: <b>PDB Molecule:</b> putative mandelate racemase; <b>PDBTitle:</b> crystal structure of putative dehydratase from zymomonas mobilis zm4
8	<a href="#">c2nqlB_</a>	 Alignment		100.0	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> isomerase/lactonizing enzyme; <b>PDBTitle:</b> crystal structure of a member of the enolase superfamily from2 agrobacterium tumefaciens
9	<a href="#">c3t6cB_</a>	 Alignment		100.0	25	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative mand family dehydratase; <b>PDBTitle:</b> crystal structure of an enolase from pantoea ananatis (efi target efi-2 501676) with bound d-gluconate and mg
10	<a href="#">c3thuC_</a>	 Alignment		100.0	24	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> mandelate racemase / muconate lactonizing enzyme family <b>PDBTitle:</b> crystal structure of an enolase from sphingomonas sp. ska58 (efi2 target efi-501683) with bound mg
11	<a href="#">c3tjiA_</a>	 Alignment		100.0	25	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme, n-terminal <b>PDBTitle:</b> crystal structure of an enolase from enterobacter sp. 638 (efi target2 efi-501662) with bound mg



28	<a href="#">c2qdeA</a>	Alignment	not modelled	100.0	24	<b>Chain:</b> A: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme family <b>PDBTitle:</b> crystal structure of mandelate racemase/muconate lactonizing family2 protein from azoarcus sp. ebn1
29	<a href="#">c3mkcA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> racemase; <b>PDBTitle:</b> crystal structure of a putative racemase
30	<a href="#">c2pgwC</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> muconate cycloisomerase; <b>PDBTitle:</b> crystal structure of a putative muconate cycloisomerase from2 sinorhizobium meliloti 1021
31	<a href="#">c3bjsB</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme; <b>PDBTitle:</b> crystal structure of a member of enolase superfamily from polaromonas2 sp. js666
32	<a href="#">c3bsmD</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme; <b>PDBTitle:</b> crystal structure of d-mannonate dehydratase from2 chromohalobacter salexigens
33	<a href="#">c2podA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> mandelate racemase / muconate lactonizing enzyme; <b>PDBTitle:</b> crystal structure of a member of enolase superfamily from burkholderia2 pseudomallei k96243
34	<a href="#">c3t8qA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme family <b>PDBTitle:</b> crystal structure of mandelate racemase/muconate lactonizing enzyme2 family protein from hoeflea phototrophica
35	<a href="#">c2chrA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> chloromuconate cycloisomerase; <b>PDBTitle:</b> a re-evaluation of the crystal structure of chloromuconate2 cycloisomerase
36	<a href="#">c3sjnB</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing protein; <b>PDBTitle:</b> crystal structure of enolase spea_3858 (target efi-500646) from2 shewanella pealeana with magnesium bound
37	<a href="#">c3ddmD</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> putative mandelate racemase/muconate lactonizing <b>PDBTitle:</b> crystal structure of mandelate racemase/muconate2 lactonizing enzyme from bordetella bronchiseptica rb50
38	<a href="#">c3dfhC</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> mandelate racemase; <b>PDBTitle:</b> crystal structure of putative mandelate racemase / muconate2 lactonizing enzyme from vibionales bacterium swat-3
39	<a href="#">c3mznA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> glucarate dehydratase; <b>PDBTitle:</b> crystal structure of probable glucarate dehydratase from2 chromohalobacter salexigens dsm 3043
40	<a href="#">c3cb3B</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme; <b>PDBTitle:</b> crystal structure of l-tartrate dehydratase from polaromonas sp. js6662 complexed with mg and l-glucarate
41	<a href="#">c2hzgB</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme/enolase <b>PDBTitle:</b> crystal structure of predicted mandelate racemase from rhodobacter2 sphaeroides
42	<a href="#">c3cyjA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme-like <b>PDBTitle:</b> crystal structure of a mandelate racemase/muconate lactonizing enzyme-2 like protein from rubrobacter xylanophilus
43	<a href="#">c1nu5A</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> chloromuconate cycloisomerase; <b>PDBTitle:</b> crystal structure of pseudomonas sp. p51 chloromuconate lactonizing2 enzyme
44	<a href="#">c3dg7B</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> muconate cycloisomerase; <b>PDBTitle:</b> crystal structure of muconate lactonizing enzyme from mucobacterium2 smegmatis complexed with muconolactone
45	<a href="#">c3my9A</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> muconate cycloisomerase; <b>PDBTitle:</b> crystal structure of a muconate cycloisomerase from azorhizobium2 caulinodans
46	<a href="#">c3es8D</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> isomerase, lyase <b>Chain:</b> D: <b>PDB Molecule:</b> muconate cycloisomerase; <b>PDBTitle:</b> crystal structure of divergent enolase from oceanobacillus2 ihyensensis complexed with mg and l-malate.
47	<a href="#">c3i6eA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> muconate cycloisomerase i; <b>PDBTitle:</b> crystal structure of muconate lactonizing enzyme from2 ruegeria pomeroyi.
48	<a href="#">c3mqtV</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> isomerase <b>Chain:</b> V: <b>PDB Molecule:</b> <b>PDBTitle:</b> crystal structure of a mandelate racemase/muconate lactonizing enzyme2 from shewanella pealeana
49	<a href="#">c3tj4B</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> mandelate racemase; <b>PDBTitle:</b> crystal structure of an enolase from agrobacterium tumefaciens (efi2 target efi-502087) no mg
50	<a href="#">c3t9pB</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme family <b>PDBTitle:</b> crystal structure of a putative mandelate racemase/muconate2 lactonizing enzyme family protein from roseovarius

51	<a href="#">c2oqhD_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> putative isomerase; <b>PDBTitle:</b> crystal structure of an isomerase from streptomyces coelicolor a3(2)
52	<a href="#">c1f9cA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (muconate cycloisomerase i); <b>PDBTitle:</b> crystal structure of mle d178n variant
53	<a href="#">c2ppgB_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative isomerase; <b>PDBTitle:</b> crystal structure of putative isomerase from sinorhizobium meliloti
54	<a href="#">c3ugvE_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> enolase; <b>PDBTitle:</b> crystal structure of an enolase from alpha pretobacterium bal199 (efi2 target efi-501650) with bound mg
55	<a href="#">c3fv9D_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme; <b>PDBTitle:</b> crystal structure of putative mandelate racemase/muconatelactonizing2 enzyme from roseovarius nubinhibens ism complexed with magnesium
56	<a href="#">c2gdqB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> yitf; <b>PDBTitle:</b> crystal structure of mandelate racemase/muconate lactonizing enzyme2 from bacillus subtilis at 1.8 a resolution
57	<a href="#">c3toyC_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme family <b>PDBTitle:</b> crystal structure of enolase brado_4202 (target efi-501651) from2 bradyrhizobium sp. ors278 with calcium and acetate bound
58	<a href="#">c3fcpF_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> F: <b>PDB Molecule:</b> l-ala-d/l-glu epimerase, a muconate lactonizing <b>PDBTitle:</b> crystal structure of muconate lactonizing enzyme from2 klebsiella pneumoniae
59	<a href="#">c2rdxG_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> G: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme, putative; <b>PDBTitle:</b> crystal structure of mandelate racemase/muconate lactonizing enzyme2 from roseovarius nubinhibens ism
60	<a href="#">c2ovlA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative racemase; <b>PDBTitle:</b> crystal structure of a racemase from streptomyces2 coelicolor a3(2)
61	<a href="#">c2ps2A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative mandelate racemase/muconate lactonizing <b>PDBTitle:</b> crystal structure of putative mandelate racemase/muconate2 lactonizing enzyme from aspergillus oryzae
62	<a href="#">c2p88E_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme <b>PDBTitle:</b> crystal structure of n-succinyl arg/lys racemase from2 bacillus cereus atcc 14579
63	<a href="#">c3px5A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> enzyme of enolase superfamily; <b>PDBTitle:</b> structure of efi enolase target en500555, a putative dipeptide2 epimerase: apo structure
64	<a href="#">c3msyC_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme; <b>PDBTitle:</b> crystal structure of mandelate racemase/muconate lactonizing enzyme2 from a marine actinobacterium
65	<a href="#">c1mraA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> racemase <b>Chain:</b> A: <b>PDB Molecule:</b> mandelate racemase; <b>PDBTitle:</b> mandelate racemase mutant d270n co-crystallized with (s)-atrolactate
66	<a href="#">c3q45E_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> isomerase <b>Chain:</b> E: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme family; <b>PDBTitle:</b> crystal structure of dipeptide epimerase from cytophaga hutchinsonii2 complexed with mg and dipeptide d-ala-l-val
67	<a href="#">c3i4kA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> muconate lactonizing enzyme; <b>PDBTitle:</b> crystal structure of muconate lactonizing enzyme from2 corynebacterium glutamicum
68	<a href="#">c2pmqA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme; <b>PDBTitle:</b> crystal structure of a mandelate racemase/muconate lactonizing enzyme2 from roseovarius sp. htcc2601
69	<a href="#">c3eezA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative mandelate racemase/muconate lactonizing <b>PDBTitle:</b> crystal structure of a putative mandelate racemase/muconate2 lactonizing enzyme from silicibacter pomeroyi
70	<a href="#">c2qddA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme; <b>PDBTitle:</b> crystal structure of a member of enolase superfamily from roseovarius2 nubinhibens ism
71	<a href="#">c2dw7G_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> G: <b>PDB Molecule:</b> bl16730 protein; <b>PDBTitle:</b> crystal structure of d-tartrate dehydratase from2 bradyrhizobium japonicum complexed with mg++ and meso-3 tartrate
72	<a href="#">c1sjaA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase, isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acylamino acid racemase; <b>PDBTitle:</b> x-ray structure of o-succinylbenzoate synthase complexed2 with n-acetyl methionine

73	<a href="#">c2oz8B</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> mlf17089 protein; <b>PDBTitle:</b> crystal structure of putative mandelate racemase from mesorhizobium2 loti
74	<a href="#">c1wueA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme family <b>PDBTitle:</b> crystal structure of protein gi:29375081, unknown member of enolase2 superfamily from enterococcus faecalis v583
75	<a href="#">c2fkcC</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> n-acylamino acid racemase; <b>PDBTitle:</b> the mutant g127c-t313c of deinococcus radiodurans n-2 acylamino acid racemase
76	<a href="#">c2zc8B</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> n-acylamino acid racemase; <b>PDBTitle:</b> crystal structure of n-acylamino acid racemase from thermus2 thermophilus hb8
77	<a href="#">c3n4fD</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing protein; <b>PDBTitle:</b> crystal structure of mandelate racemase/muconate lactonizing protein2 from geobacillus sp. y412mc10
78	<a href="#">c3jw7E</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> isomerase <b>Chain:</b> E: <b>PDB Molecule:</b> dipeptide epimerase; <b>PDBTitle:</b> crystal structure of dipeptide epimerase from enterococcus faecalis2 v583 complexed with mg and dipeptide l-ile-l-tyr
79	<a href="#">c1jpmB</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> l-ala-d/l-glu epimerase; <b>PDBTitle:</b> l-ala-d/l-glu epimerase
80	<a href="#">c3mwcA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing protein; <b>PDBTitle:</b> crystal structure of probable o-succinylbenzoic acid synthetase from2 kosmotoga olearia
81	<a href="#">c3ritE</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> E: <b>PDB Molecule:</b> dipeptide epimerase; <b>PDBTitle:</b> crystal structure of dipeptide epimerase from methylococcus capsulatus2 complexed with mg and dipeptide l-arg-d-lys
82	<a href="#">c3ik4A</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing protein; <b>PDBTitle:</b> crystal structure of mandelate racemase/muconate lactonizing protein2 from herpetosiphon aurantiacus
83	<a href="#">c1wufB</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein lin2664; <b>PDBTitle:</b> crystal structure of protein gi:16801725, member of enolase2 superfamily from listeria innocua clip11262
84	<a href="#">c3qldB</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing protein; <b>PDBTitle:</b> structure of probable mandelate racemase (aalaa1draft_2112) from2 alicyclobacillus acidocaldarius
85	<a href="#">c3dfyl</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> J: <b>PDB Molecule:</b> muconate cycloisomerase; <b>PDBTitle:</b> crystal structure of apo dipeptide epimerase from2 thermotoga maritima
86	<a href="#">c3ijlA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> muconate cycloisomerase; <b>PDBTitle:</b> structure of dipeptide epimerase from bacteroides thetaiotaomicron2 complexed with l-pro-d-glu; nonproductive substrate binding.
87	<a href="#">c2pgeA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> menc; <b>PDBTitle:</b> crystal structure of menc from desulfotalea psychrophila2 lsv54
88	<a href="#">c2oktA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> o-succinylbenzoic acid synthetase; <b>PDBTitle:</b> crystal structure of o-succinylbenzoic acid synthetase from2 staphylococcus aureus, ligand-free form
89	<a href="#">c1jpdX</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> isomerase <b>Chain:</b> X: <b>PDB Molecule:</b> l-ala-d/l-glu epimerase; <b>PDBTitle:</b> l-ala-d/l-glu epimerase
90	<a href="#">d2gl5a1</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
91	<a href="#">c1kkoB</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-methylaspartate ammonia-lyase; <b>PDBTitle:</b> crystal structure of citrobacter amalonaticus2 methylaspartate ammonia lyase
92	<a href="#">c1kczA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-methylaspartase; <b>PDBTitle:</b> crystal structure of beta-methylaspartase from clostridium2 tetanomorphum. mg-complex.
93	<a href="#">d1rvka1</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
94	<a href="#">d1yeya1</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
95	<a href="#">d2chra1</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
96	<a href="#">d2gdqa1</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
						<b>Fold:</b> TIM beta/alpha-barrel



97	<a href="#">d1muca1</a>	Alignment	not modelled	100.0	14	<b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
98	<a href="#">c3cawB_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> o-succinylbenzoate synthase; <b>PDBTitle:</b> crystal structure of o-succinylbenzoate synthase from2 bdellovibrio bacteriovorus liganded with mg
99	<a href="#">d1nu5a1</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
100	<a href="#">d1tzza1</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
101	<a href="#">c3qn3B_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> enolase; <b>PDBTitle:</b> phosphopyruvate hydratase from campylobacter jejuni.
102	<a href="#">d1sjda1</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
103	<a href="#">c2pa6A_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enolase; <b>PDBTitle:</b> crystal structure of mj0232 from methanococcus jannaschii
104	<a href="#">c3uj2C_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> enolase 1; <b>PDBTitle:</b> crystal structure of an enolase from anaerostipes cacciae (efi target2 efi-502054) with bound mg and sulfate
105	<a href="#">d1wufa1</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
106	<a href="#">d1wuea1</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
107	<a href="#">d1r0ma1</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
108	<a href="#">c3tqpA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enolase; <b>PDBTitle:</b> structure of an enolase (eno) from coxiella burnetii
109	<a href="#">d2mnra1</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
110	<a href="#">c1l8pC_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> enolase 1; <b>PDBTitle:</b> mg-phosphonoacetohydroxamate complex of s39a yeast enolase 1
111	<a href="#">c2oztA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tlr1174 protein; <b>PDBTitle:</b> crystal structure of o-succinylbenzoate synthase from2 thermosynechococcus elongatus bp-1
112	<a href="#">d1jdfa1</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
113	<a href="#">c2fymA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enolase; <b>PDBTitle:</b> crystal structure of e. coli enolase complexed with the2 minimal binding segment of rnase e.
114	<a href="#">c1iyxA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enolase; <b>PDBTitle:</b> crystal structure of enolase from enterococcus hirae
115	<a href="#">c2ptwA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enolase; <b>PDBTitle:</b> crystal structure of the t. brucei enolase complexed with2 sulphate, identification of a metal binding site iv
116	<a href="#">c2akmA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> gamma enolase; <b>PDBTitle:</b> fluoride inhibition of enolase: crystal structure of the2 inhibitory complex
117	<a href="#">d1jpma1</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
118	<a href="#">d1bqga1</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
119	<a href="#">c3qtpB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> enolase 1; <b>PDBTitle:</b> crystal structure analysis of entamoeba histolytica enolase
120	<a href="#">c3otrC_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> enolase; <b>PDBTitle:</b> 2.75 angstrom crystal structure of enolase 1 from toxoplasma gondii