
































#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2qjjC_</a>	 Alignment		100.0	66	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme; <b>PDBTitle:</b> crystal structure of d-mannonate dehydratase from novosphingobium2 aromaticivorans
2	<a href="#">c3thuC_</a>	 Alignment		100.0	66	<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
3	<a href="#">c3t6cB_</a>	 Alignment		100.0	43	<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
4	<a href="#">c3tjiA_</a>	 Alignment		100.0	37	<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
5	<a href="#">c3bsmD_</a>	 Alignment		100.0	67	<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
6	<a href="#">c3rr1B_</a>	 Alignment		100.0	34	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative d-galactonate dehydratase; <b>PDBTitle:</b> crystal structure of enolase prk14017 (target efi-500653) from2 ralstonia pickettii 12j
7	<a href="#">c2oo6A_</a>	 Alignment		100.0	24	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative l-alanine-dl-glutamate epimerase; <b>PDBTitle:</b> crystal structure of putative l-alanine-dl-glutamate epimerase from2 burkholderia xenovorans strain lb400
8	<a href="#">c2o56D_</a>	 Alignment		100.0	29	<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
9	<a href="#">c2ox4E_</a>	 Alignment		100.0	30	<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
10	<a href="#">c3rcyC_</a>	 Alignment		100.0	28	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme-like <b>PDBTitle:</b> crystal structure of mandelate racemase/muconate lactonizing enzyme-2 like protein from roseovarius sp. tm1035
11	<a href="#">c3dfhC_</a>	 Alignment		100.0	39	<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

12	<a href="#">c2qgyA_</a>	Alignment		100.0	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> enolase from the environmental genome shotgun <b>PDBTitle:</b> crystal structure of an enolase from the environmental2 genome shotgun sequencing of the sargasso sea
13	<a href="#">c3n4eA_</a>	Alignment		100.0	23	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme, c-terminal <b>PDBTitle:</b> crystal structure of mandelate racemase/muconate lactonizing protein2 from paracoccus denitrificans pd1222
14	<a href="#">c2podA_</a>	Alignment		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
15	<a href="#">c2gl5A_</a>	Alignment		100.0	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative dehydratase protein; <b>PDBTitle:</b> crystal structure of putative dehydratase from salmonella thyphimurium
16	<a href="#">c2pozA_</a>	Alignment		100.0	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative dehydratase; <b>PDBTitle:</b> crystal structure of a putative dehydratase from mesorhizobium loti
17	<a href="#">c3h12B_</a>	Alignment		100.0	29	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> mandelate racemase; <b>PDBTitle:</b> crystal structure of putative mandelate racemase from bordetella2 bronchiseptica rb50
18	<a href="#">c2qq6B_</a>	Alignment		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 mandelate racemase/muconate2 lactonizing enzyme-like protein from rubrobacter3 xylanophilus dsm 9941
19	<a href="#">c3t8qA_</a>	Alignment		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 hoeftlea phototrophica
20	<a href="#">c3t9pB_</a>	Alignment		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
21	<a href="#">c2pgwC_</a>	Alignment	not modelled	100.0	24	<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
22	<a href="#">c2qdeA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> lyase <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
23	<a href="#">c2pp1C_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> l-tartrate/galactarate dehydratase; <b>PDBTitle:</b> crystal structure of l-tartrate/galactarate dehydratase from2 salmonella typhimurium lt2 liganded with mg and l-lyxarohydroxamate
24	<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.
25	<a href="#">c3sjnB_</a>	Alignment	not modelled	100.0	29	<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
26	<a href="#">c3dipA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enolase; <b>PDBTitle:</b> crystal structure of an enolase protein from the2 environmental genome shotgun sequencing of the sargasso sea
27	<a href="#">c2chrA_</a>	Alignment	not modelled	100.0	20	<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
28	<a href="#">c2nqlB_</a>	Alignment	not modelled	100.0	24	<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
29	<a href="#">c3bjsB_</a>	Alignment	not modelled	100.0	30	<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
30	<a href="#">c2ps2A_</a>	Alignment	not modelled	100.0	22	<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
31	<a href="#">c3fv9D_</a>	Alignment	not modelled	100.0	23	<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/muconate lactonizing2 enzyme from roseovarius nubinhibens ism complexed with magnesium
32	<a href="#">c3tj4B_</a>	Alignment	not modelled	100.0	27	<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
33	<a href="#">c3mqtV_</a>	Alignment	not modelled	100.0	22	<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
34	<a href="#">c3es8D_</a>	Alignment	not modelled	100.0	27	<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 iheyensis complexed with mg and l-malate.
35	<a href="#">c1nu5A_</a>	Alignment	not modelled	100.0	22	<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
36	<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
37	<a href="#">c2hxtA_</a>	Alignment	not modelled	100.0	23	<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-erythronehydroxamate
38	<a href="#">c3sqsA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing protein; <b>PDBTitle:</b> crystal structure of a putative mandelate racemase/muconate2 lactonizing protein from dinoroseobacter shibae dfl 12
39	<a href="#">c2p88E_</a>	Alignment	not modelled	100.0	26	<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
40	<a href="#">c3mkcA_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> racemase; <b>PDBTitle:</b> crystal structure of a putative racemase
41	<a href="#">c2gdqB_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> yltf; <b>PDBTitle:</b> crystal structure of mandelate racemase/muconate lactonizing enzyme2 from bacillus subtilis at 1.8 a resolution
42	<a href="#">c3dg7B_</a>	Alignment	not modelled	100.0	20	<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
43	<a href="#">c3my9A_</a>	Alignment	not modelled	100.0	22	<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
44	<a href="#">c3q45E_</a>	Alignment	not modelled	100.0	23	<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
45	<a href="#">c1mraA_</a>	Alignment	not modelled	100.0	21	<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
46	<a href="#">c1f9cA_</a>	Alignment	not modelled	100.0	21	<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
47	<a href="#">c2hzgB_</a>	Alignment	not modelled	100.0	20	<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
48	<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
49	<a href="#">c3fcpF_</a>	Alignment	not modelled	100.0	22	<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
50	<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-talarate dehydratase from polaromonas sp. js6662 complexed with mg and l-glucarate
						<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> structural genomics, unknown function

51	<a href="#">c1rvkA_</a>	Alignment	not modelled	100.0	22	<b>Chain:</b> A: <b>PDB Molecule:</b> isomerase/lactonizing enzyme; <b>PDBTitle:</b> crystal structure of enolase agr_l_2751 from agrobacterium tumefaciens
52	<a href="#">c2qddA_</a>	Alignment	not modelled	100.0	21	<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
53	<a href="#">c3eezA_</a>	Alignment	not modelled	100.0	25	<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
54	<a href="#">c3ugvE_</a>	Alignment	not modelled	100.0	25	<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="#">c1ec8B_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> glucarate dehydratase; <b>PDBTitle:</b> e. coli glucarate dehydratase bound to product 2,3-2 dihydroxy-5-oxo-hexanedioate
56	<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)
57	<a href="#">c3toyC_</a>	Alignment	not modelled	100.0	25	<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="#">c2ppgB_</a>	Alignment	not modelled	100.0	23	<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
59	<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
60	<a href="#">c3n6jA_</a>	Alignment	not modelled	100.0	21	<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 actinobacillus succinogenes 130z
61	<a href="#">c1sjaA_</a>	Alignment	not modelled	100.0	19	<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-acetylmethionine
62	<a href="#">c1jpmB_</a>	Alignment	not modelled	100.0	26	<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
63	<a href="#">c2p0iA_</a>	Alignment	not modelled	100.0	23	<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
64	<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)
65	<a href="#">c3jw7E_</a>	Alignment	not modelled	100.0	24	<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
66	<a href="#">c3nxD_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> glucarate dehydratase; <b>PDBTitle:</b> crystal structure of glucarate dehydratase from burkholderia cepacia2 complexed with magnesium
67	<a href="#">c3mznA_</a>	Alignment	not modelled	100.0	20	<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
68	<a href="#">c2fkpC_</a>	Alignment	not modelled	100.0	22	<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
69	<a href="#">c3px5A_</a>	Alignment	not modelled	100.0	21	<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
70	<a href="#">c2oz3F_</a>	Alignment	not modelled	100.0	25	<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
71	<a href="#">c3cxoA_</a>	Alignment	not modelled	100.0	22	<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
72	<a href="#">c1wueA_</a>	Alignment	not modelled	100.0	19	<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
73	<a href="#">c2zc8B_</a>	Alignment	not modelled	100.0	22	<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
						<b>PDB header:</b> lyase <b>Chain:</b> G: <b>PDB Molecule:</b> bl16730 protein;

74	<a href="#">c2dw7G_</a>	Alignment	not modelled	100.0	19	<b>PDBTitle:</b> crystal structure of d-tartrate dehydratase from2 bradyrhizobium japonicum complexed with mg++ and meso-3 tartrate
75	<a href="#">c2oz8B_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ml17089 protein; <b>PDBTitle:</b> crystal structure of putative mandelate racemase from mesorhizobium2 loti
76	<a href="#">c3ritE_</a>	Alignment	not modelled	100.0	23	<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
77	<a href="#">c2pmqA_</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; <b>PDBTitle:</b> crystal structure of a mandelate racemase/muconate lactonizing enzyme2 from roseovarius sp. htcc2601
78	<a href="#">c3msyC_</a>	Alignment	not modelled	100.0	26	<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
79	<a href="#">c3ik4A_</a>	Alignment	not modelled	100.0	19	<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
80	<a href="#">c1wufB_</a>	Alignment	not modelled	100.0	19	<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
81	<a href="#">c3cyjA_</a>	Alignment	not modelled	100.0	26	<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
82	<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
83	<a href="#">c3n4fD_</a>	Alignment	not modelled	100.0	19	<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
84	<a href="#">c3dfyl_</a>	Alignment	not modelled	100.0	22	<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
85	<a href="#">c3qldB_</a>	Alignment	not modelled	100.0	15	<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
86	<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
87	<a href="#">c3ijlA_</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> structure of dipeptide epimerase from bacteroides thetaiotaomicron2 complexed with l-pro-d-glu; nonproductive substrate binding.
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	21	<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	26	<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="#">d2gdqa1</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
92	<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
93	<a href="#">d1muca1</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
94	<a href="#">d1nu5a1</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="#">d1tzza1</a>	Alignment	not modelled	100.0	19	<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="#">d1sjda1</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
97	<a href="#">d1rvka1</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>PDB header:</b> oxidoreductase



98	<a href="#">c3cawB_</a>	Alignment	not modelled	100.0	15	<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="#">dlwufal</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
100	<a href="#">clkczA_</a>	Alignment	not modelled	100.0	17	<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.
101	<a href="#">dlveyal</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
102	<a href="#">d2mnra1</a>	Alignment	not modelled	100.0	22	<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="#">dlr0ma1</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
104	<a href="#">dlwuea1</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
105	<a href="#">c1kkoB_</a>	Alignment	not modelled	100.0	17	<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
106	<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
107	<a href="#">dljpma1</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
108	<a href="#">c2pa6A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enolase; <b>PDBTitle:</b> crystal structure of mj0232 from methanococcus jannaschii
109	<a href="#">c3uj2C_</a>	Alignment	not modelled	100.0	20	<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
110	<a href="#">c2qvB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> o-succinylbenzoate-coa synthase; <b>PDBTitle:</b> crystal structure of o-succinylbenzoate synthase complexed with o-2 succinyl benzoate (osb)
111	<a href="#">c3qn3B_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> enolase; <b>PDBTitle:</b> phosphopyruvate hydratase from campylobacter jejuni.
112	<a href="#">c3tqpA_</a>	Alignment	not modelled	100.0	17	<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
113	<a href="#">dljdfa1</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
114	<a href="#">c1l8pC_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> enolase 1; <b>PDBTitle:</b> mg-phosphonoaceto-hydroxamate complex of s39a yeast enolase 1
115	<a href="#">dlbqga1</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
116	<a href="#">cliyxA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enolase; <b>PDBTitle:</b> crystal structure of enolase from enterococcus hirae
117	<a href="#">c2ptwA_</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 the t. brucei enolase complexed with2 sulphate, identification of a metal binding site iv
118	<a href="#">c2akmA_</a>	Alignment	not modelled	100.0	17	<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
119	<a href="#">c2fymA_</a>	Alignment	not modelled	100.0	22	<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.
120	<a href="#">c3qtpB_</a>	Alignment	not modelled	100.0	16	<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