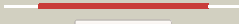



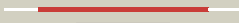


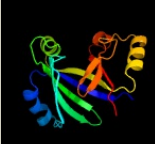
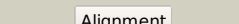

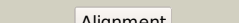

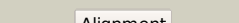











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1322A (-) _1485319_1485777
Date	Wed Jul 31 22:05:42 BST 2019
Unique Job ID	7c496d928ccff39f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6bu2A_</a>	 Alignment		100.0	100	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase; <b>PDBTitle:</b> crystal structure of methylmalonyl-coa epimerase from mycobacterium2 tuberculosis
2	<a href="#">c3rmuD_</a>	 Alignment		99.9	26	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> methylmalonyl-coa epimerase, mitochondrial; <b>PDBTitle:</b> crystal structure of human methylmalonyl-coa epimerase, mcee
3	<a href="#">d1jc4a_</a>	 Alignment		99.9	36	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Methylmalonyl-CoA epimerase
4	<a href="#">c3oa4A_</a>	 Alignment		99.9	34	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase; <b>PDBTitle:</b> crystal structure of hypothetical protein bh1468 from bacillus2 halodurans c-125
5	<a href="#">d1qipa_</a>	 Alignment		99.9	21	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Glyoxalase I (lactoylglutathione lyase)
6	<a href="#">c3gm5A_</a>	 Alignment		99.9	27	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> lactoylglutathione lyase and related lyases; <b>PDBTitle:</b> crystal structure of a putative methylmalonyl-coenzyme a epimerase2 from thermoanaerobacter tengcongensis at 2.0 a resolution
7	<a href="#">c4g6xA_</a>	 Alignment		99.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> crystal structure of glyoxalase/bleomycin resistance protein from2 catenulispora acidiphila.
8	<a href="#">c5umwA_</a>	 Alignment		99.9	20	<b>PDB header:</b> tiancimycin-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> crystal structure of tnms2, an antibiotic binding protein from2 streptomyces sp. cb03234
9	<a href="#">c4mtsA_</a>	 Alignment		99.9	26	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> lactoylglutathione lyase; <b>PDBTitle:</b> ni- and zn-bound gloa2 at high resolution
10	<a href="#">d1f9za_</a>	 Alignment		99.9	22	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Glyoxalase I (lactoylglutathione lyase)
11	<a href="#">c3l7tB_</a>	 Alignment		99.8	21	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of smu.1112c

12	<a href="#">d1ss4a_</a>	Alignment		99.8	19	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Hypothetical protein BC1747
13	<a href="#">d1t47a1</a>	Alignment		99.8	23	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
14	<a href="#">c3huhA_</a>	Alignment		99.8	19	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> virulence protein stm3117; <b>PDBTitle:</b> the structure of biphenyl-2,3-diol 1,2-dioxygenase iii-related protein2 from salmonella typhimurium
15	<a href="#">d1sqia1</a>	Alignment		99.8	17	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
16	<a href="#">c2p25A_</a>	Alignment		99.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase family protein; <b>PDBTitle:</b> the crystal structure of the glyoxalase family protein from2 enterococcus faecalis
17	<a href="#">c5uhjA_</a>	Alignment		99.8	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> the crystal structure of a natural product biosynthetic enzyme from2 streptomyces sp. cb03234
18	<a href="#">c2qh0A_</a>	Alignment		99.8	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> lactoylglutathione lyase; <b>PDBTitle:</b> crystal structure of a glyoxalase from clostridium acetobutylicum
19	<a href="#">c3ey7B_</a>	Alignment		99.8	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> biphenyl-2,3-diol 1,2-dioxygenase iii-related <b>PDBTitle:</b> structure from the mobile metagenome of v. cholerae.2 integron cassette protein vch_cass1
20	<a href="#">c1zswA_</a>	Alignment		99.8	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase family protein; <b>PDBTitle:</b> crystal structure of bacillus cereus metallo protein from glyoxalase2 family
21	<a href="#">d2c21a1</a>	Alignment	not modelled	99.8	21	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Glyoxalase I (lactoylglutathione lyase) <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> crystal structure of member of glyoxalase/bleomycin resistance2 protein/dioxygenase superfamily from sphaerobacter thermophilus dsm3 20745
22	<a href="#">c4hc5A_</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
23	<a href="#">d1mpya2</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
24	<a href="#">d1q0oa2</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
25	<a href="#">d1sp8a1</a>	Alignment	not modelled	99.8	21	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
26	<a href="#">c2r6uB_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of gene product rha04853 from rhodococcus sp. rha1
27	<a href="#">c3ct8A_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative glyoxalase; <b>PDBTitle:</b> crystal structure of a putative glyoxalase (np_243026.1) from bacillus2 halodurans at 2.10 a resolution

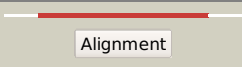
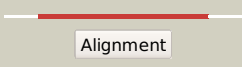
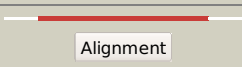
28	<a href="#">c3zw5A</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase domain-containing protein 5; <b>PDBTitle:</b> crystal structure of the human glyoxalase domain-containing protein 5
29	<a href="#">d1lqta2</a>	Alignment	not modelled	99.8	21	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
30	<a href="#">d1sqda1</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
31	<a href="#">d1zswa1</a>	Alignment	not modelled	99.8	15	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> BC1024-like
32	<a href="#">c1mpyD</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> catechol 2,3-dioxygenase; <b>PDBTitle:</b> structure of catechol 2,3-dioxygenase (metapyrocatechase)2 from pseudomonas putida mt-2
33	<a href="#">c3bt3B</a>	Alignment	not modelled	99.8	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxalase-related enzyme, arac type; <b>PDBTitle:</b> crystal structure of a glyoxalase-related enzyme from clostridium2 phytofermentans
34	<a href="#">c3k0a</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance <b>PDBTitle:</b> crystal structure of a glyoxalase/dioxygenase from nostoc2 punctiforme
35	<a href="#">c3zi1A</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase domain-containing protein 4; <b>PDBTitle:</b> crystal structure of human glyoxalase domain-containing protein 42 (glod4)
36	<a href="#">c3e5dA</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative glyoxalase i; <b>PDBTitle:</b> crystal structure of a putative glyoxalase i (lmof2365_0426) from2 listeria monocytogenes str. 4b f2365 at 2.70 a resolution
37	<a href="#">c2qqzB</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxalase family protein, putative; <b>PDBTitle:</b> crystal structure of putative glyoxalase family protein from bacillus2 anthracis
38	<a href="#">c3g12A</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative lactoylglutathione lyase; <b>PDBTitle:</b> crystal structure of a putative lactoylglutathione lyase from2 bdellovibrio bacteriovorus
39	<a href="#">c1t47A</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxyphenylpyruvate dioxygenase; <b>PDBTitle:</b> structure of fe2-hppd bound to ntbc
40	<a href="#">c2p7pB</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> metal binding protein, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxalase family protein; <b>PDBTitle:</b> crystal structure of genomically encoded fosfomycin resistance2 protein, fosx, from listeria monocytogenes complexed with mn(ii) and3 sulfate ion
41	<a href="#">c3bqxA</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase-related enzyme; <b>PDBTitle:</b> high resolution crystal structure of a glyoxalase-related enzyme from2 fulvimarina pelagi
42	<a href="#">d1kw3b2</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
43	<a href="#">c2rk0B</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase domain; <b>PDBTitle:</b> crystal structure of glyoxylase/bleomycin resistance2 protein/dioxygenase domain from frankia sp. ean1pec
44	<a href="#">c3hpyD</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> catechol 2,3-dioxygenase; <b>PDBTitle:</b> crystal structure analysis of the 2,3-dioxygenase lapb from2 pseudomonas in the complex with 4-methylcatechol
45	<a href="#">c6on3C</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> l-dopa extradiol dioxygenase; <b>PDBTitle:</b> a substrate bound structure of l-dopa dioxygenase from streptomyces2 sclerotialis
46	<a href="#">d1sp9a</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
47	<a href="#">c3ghjA</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative integron gene cassette protein; <b>PDBTitle:</b> crystal structure from the mobile metagenome of halifax harbour sewage2 outfall: integron cassette protein hfx_cass4
48	<a href="#">c3rriB</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> crystal structure of glyoxalase/bleomycin resistance2 protein/dioxygenase from alicyclobacillus acidocaldarius
49	<a href="#">c4jh1B</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> metallothiol transferase fosb; <b>PDBTitle:</b> crystal structure of fosb from bacillus cereus with zinc and sulfate2 at 1.55 a resolution -sad phasing
50	<a href="#">d1zswa2</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> BC1024-like
						<b>PDB header:</b> lyase

51	<a href="#">c4ro6A_</a>	Alignment	not modelled	99.7	20	<b>Chain:</b> A: <b>PDB Molecule:</b> lactoylglutathione lyase; <b>PDBTitle:</b> crystal structure of glyoxalase i from zea mays
52	<a href="#">c2zi8A_</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable biphenyl-2,3-diol 1,2-dioxygenase bphc; <b>PDBTitle:</b> crystal structure of the hsaC extradiol dioxygenase from m.2 tuberculosis in complex with 3,4-dihydroxy-9,10-3 seconandrost-1,3,5(10)-triene-9,17-dione (dhsa)
53	<a href="#">c1sqiA_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxyphenylpyruvic acid dioxygenase; <b>PDBTitle:</b> structural basis for inhibitor selectivity revealed by2 crystal structures of plant and mammalian 4-3 hydroxyphenylpyruvate dioxygenases
54	<a href="#">d1nkiA_</a>	Alignment	not modelled	99.7	25	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Antibiotic resistance proteins
55	<a href="#">c3lm4C_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> catechol 2,3-dioxygenase; <b>PDBTitle:</b> crystal structure of 2,3-dihydroxy biphenyl dioxygenase from2 rhodococcus sp. (strain rha1)
56	<a href="#">c3vb0D_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> crystal structure of 2,2',3-trihydroxybiphenyl 1,2-dioxygenase from2 dibenzofuran-degrading sphingomonas wittichii strain rw1
57	<a href="#">c4nvsB_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative enzyme, glyoxalase family; <b>PDBTitle:</b> crystal structure of the q18cp6_clod6 protein from glyoxalase family.2 northeast structural genomics consortium target cfr3
58	<a href="#">c3r4qB_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> lactoylglutathione lyase; <b>PDBTitle:</b> crystal structure of lactoylglutathione lyase from agrobacterium2 tumefaciens
59	<a href="#">d1klla_</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Antibiotic resistance proteins
60	<a href="#">d2i7ra1</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Antibiotic resistance proteins
61	<a href="#">c3itwA_</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein tiox; <b>PDBTitle:</b> crystal structure of tiox from micromonospora sp. m11
62	<a href="#">c3oajA_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative ring-cleaving dioxygenase mhqo; <b>PDBTitle:</b> crystal structure of putative dioxygenase from bacillus subtilis2 subsp. subtilis str. 168
63	<a href="#">d1lqta1</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
64	<a href="#">c4nb2B_</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> metallothiol transferase fosb; <b>PDBTitle:</b> crystal structure of fosb from staphylococcus aureus at 1.89 angstrom2 resolution - apo structure
65	<a href="#">d1r9ca_</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Antibiotic resistance proteins
66	<a href="#">c4z04A_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance /dioxygenase superfamily <b>PDBTitle:</b> crystal structure of a probable lactoylglutathione lyase from brucella2 melitensis in complex with glutathione
67	<a href="#">c3ecjC_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> protein (homoprotocatechuate 2,3-dioxygenase); <b>PDBTitle:</b> structure of e323l mutant of homoprotocatechuate 2,3-dioxygenase from2 brevibacterium fuscum at 1.65a resolution
68	<a href="#">c3r6aB_</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> isomerase, lyase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an uncharacterized protein (hypothetical protein2 mm_3218) from methanosarcina mazei.
69	<a href="#">d1mpya1</a>	Alignment	not modelled	99.7	24	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
70	<a href="#">c5vb0E_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> fosfomycin resistance protein fosa3; <b>PDBTitle:</b> crystal structure of fosfomycin resistance protein fosa3
71	<a href="#">c4gymB_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> crystal structure of glyoxalase/bleomycin resistance2 protein/dioxygenase from conexibacter woesei dsm 14684
72	<a href="#">c2ei2A_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 1,2-dihydroxynaphthalene dioxygenase; <b>PDBTitle:</b> crystal structure analysis of the 1,2-dihydroxynaphthalene dioxygenase2 from pseudomonas sp. stain c18
						<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase

73	<a href="#">d1npba_</a>	Alignment	not modelled	99.7	20	<b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Antibiotic resistance proteins
74	<a href="#">c4mymA_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> crystal structure of a glyoxalase/ bleomycin resistance protein/2 dioxygenase from nocardioides
75	<a href="#">d1f1xa1</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
76	<a href="#">d1twua_</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Hypothetical protein YycE
77	<a href="#">c1knfA_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,3-dihydroxybiphenyl 1,2-dioxygenase; <b>PDBTitle:</b> crystal structure of 2,3-dihydroxybiphenyl 1,2-dioxygenase complexed2 with 3-methyl catechol under anaerobic condition
78	<a href="#">c1sp8A_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxyphenylpyruvate dioxygenase; <b>PDBTitle:</b> 4-hydroxyphenylpyruvate dioxygenase
79	<a href="#">d1kw3b1</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
80	<a href="#">d1f1xa2</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
81	<a href="#">c3m2oB_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein; <b>PDBTitle:</b> crystal structure of a putative glyoxalase/bleomycin resistance2 protein from rhodopseudomonas palustris cga009
82	<a href="#">d1flua1</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
83	<a href="#">d1flua2</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
84	<a href="#">c5znhA_</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> catechol 2,3-dioxygenase, extradiol protein; <b>PDBTitle:</b> catechol 2,3-dioxygenase with 4-methyl catechol from diaphorobacter sp2 ds2
85	<a href="#">c4huzA_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,6-dichloro-p-hydroquinone 1,2-dioxygenase; <b>PDBTitle:</b> 2,6-dichloro-p-hydroquinone 1,2-dioxygenase
86	<a href="#">d1cjax2</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
87	<a href="#">c2rk9B_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> the crystal structure of a glyoxalase/bleomycin resistance2 protein/dioxygenase superfamily member from vibrio splendidus 12b01
88	<a href="#">c4rt5A_</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> the crystal structure of a glyoxalase/bleomycin resistance2 protein/dioxygenase protein from planctomyces limnophilus dsm 3776
89	<a href="#">c4qb5A_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> crystal structure of a glyoxalase/bleomycin resistance protein from2 albidiferax ferrireducens t118
90	<a href="#">c2kjaA_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> atc0852; <b>PDBTitle:</b> solution nmr structure of protein atc0852 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att2.
91	<a href="#">c2rbbB_</a>	Alignment	not modelled	99.7	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> crystal structure of a glyoxalase/bleomycin resistance2 protein/dioxygenase family enzyme from burkholderia phytofirmans psjn
92	<a href="#">d1sp8a2</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
93	<a href="#">c2wl9A_</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> catechol 2,3-dioxygenase; <b>PDBTitle:</b> crystal structure of catechol 2,3-dioxygenase
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxyphenylpyruvate dioxygenase;



94	<a href="#">c1tfzA</a>	Alignment	not modelled	99.7	18	<b>PDBTitle:</b> structural basis for herbicidal inhibitor selectivity revealed by2 comparison of crystal structures of plant and mammalian 4-3 hydroxyphenylpyruvate dioxygenases
95	<a href="#">c5cb9A</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> crystal structure of c-as lyase with mercaptoethonal
96	<a href="#">c4pavA</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase family protein; <b>PDBTitle:</b> structure of hypothetical protein sa1046 from s. aureus.
97	<a href="#">c5ujpB</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> the crystal structure of a glyoxalase/bleomycin resistance protein2 from streptomyces sp. cb03234
98	<a href="#">c1kw3B</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2,3-dihydroxybiphenyl dioxygenase; <b>PDBTitle:</b> crystal structure of 2,3-dihydroxybiphenyl dioxygenase (bphc) at 1.452 a resolution
99	<a href="#">c3pkwA</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> toxoflavin lyase (tfla); <b>PDBTitle:</b> crystal structure of toxoflavin lyase (tfla) bound to mn(ii)
100	<a href="#">d1t47a2</a>	Alignment	not modelled	99.6	23	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
101	<a href="#">c3b59A</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> crystal structure of the mn(ii)-bound glyoxalase from novosphingobium2 aromaticivorans
102	<a href="#">c3uh9B</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> metallothiol transferase fosb 2; <b>PDBTitle:</b> crystal structure of metallothiol transferase fosb 2 from bacillus2 anthracis str. ames
103	<a href="#">c6a4zA</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> chap protein; <b>PDBTitle:</b> oxidase chap
104	<a href="#">c3rheA</a>	Alignment	not modelled	99.6	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent benzaldehyde dehydrogenase; <b>PDBTitle:</b> the crystal structure of nad-dependent benzaldehyde dehydrogenase from2 legionella pneumophila
105	<a href="#">d1sqda2</a>	Alignment	not modelled	99.6	22	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
106	<a href="#">d1cxa1</a>	Alignment	not modelled	99.6	19	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
107	<a href="#">c1fluB</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> homoprotocatechuate 2,3-dioxygenase; <b>PDBTitle:</b> crystal structure of homoprotocatechuate 2,3-dioxygenase from2 arthrobacter globiformis (native, low temperature)
108	<a href="#">c2r5vA</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pcza361.1; <b>PDBTitle:</b> hydroxymandelate synthase crystal structure
109	<a href="#">c1cxC</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 4-hydroxyphenylpyruvate dioxygenase; <b>PDBTitle:</b> crystal structure of pseudomonas fluorescens hppd
110	<a href="#">d1sqia2</a>	Alignment	not modelled	99.6	19	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
111	<a href="#">c6iptB</a>	Alignment	not modelled	99.6	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> all3014 protein; <b>PDBTitle:</b> crystal structure of a fosfomycin and bleomycin resistant protein from2 anabaena/nostoc cyanobacterium at 1.70 a resolution
112	<a href="#">d1xqaa</a>	Alignment	not modelled	99.6	16	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Antibiotic resistance proteins
113	<a href="#">d2pjsa1</a>	Alignment	not modelled	99.6	20	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Antibiotic resistance proteins
114	<a href="#">c6a52A</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> dioxidase chap-h1; <b>PDBTitle:</b> oxidase chap-h1
115	<a href="#">c6a4xA</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> bleomycin resistance protein; <b>PDBTitle:</b> oxidase chap-h2
116	<a href="#">c4n04B</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> the crystal structure of glyoxalase / bleomycin resistance protein2 from catenulispora acidiphila dsm 44928
117	<a href="#">c4lqbA</a>	Alignment	not modelled	99.5	20	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein kfla3161

118	<a href="#">c2qntA_</a>	 Alignment	not modelled	99.5	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein atu1872; <b>PDBTitle:</b> crystal structure of protein of unknown function from agrobacterium2 tumefaciens str. c58
119	<a href="#">c3sk1C_</a>	 Alignment	not modelled	99.5	13	<b>PDB header:</b> griseoluate-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> ehpr; <b>PDBTitle:</b> crystal structure of phenazine resistance protein ehpr from2 enterobacter agglomerans (erwinia herbicola, pantoaea agglomerans)3 eh1087, apo form
120	<a href="#">c3zgjA_</a>	 Alignment	not modelled	99.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxyphenylpyruvic acid dioxygenase; <b>PDBTitle:</b> s221m v223f y359a mutant of 4-hydroxymandelate synthase2 from streptomyces coelicolor