Phyre2

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Description	P0AC81
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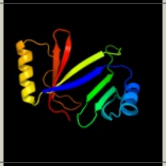
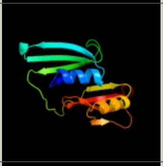
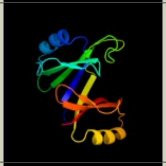
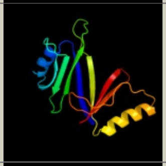
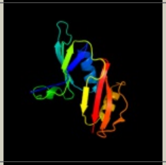
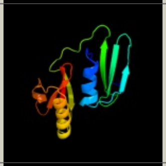
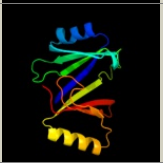
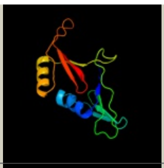
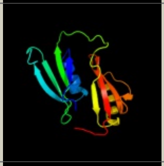
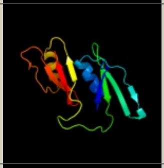
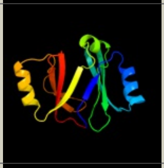
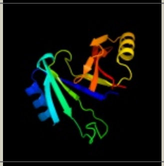
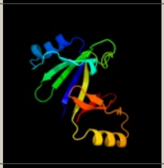
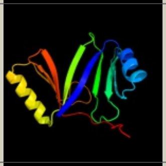
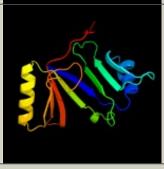
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1f9za_	Alignment		99.9	98	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Glyoxalase I (lactoylglutathione lyase)
2	d1qipa_	Alignment		99.9	33	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Glyoxalase I (lactoylglutathione lyase)
3	d1mpya2	Alignment		99.9	15	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
4	d2c21a1	Alignment		99.9	53	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Glyoxalase I (lactoylglutathione lyase)
5	c3oa4A_	Alignment		99.8	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**glyoxalase; **PDBTitle:** crystal structure of hypothetical protein bh1468 from bacillus2 halodurans c-125
6	c2qh0A_	Alignment		99.8	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**lactoylglutathione lyase; **PDBTitle:** crystal structure of a glyoxalase from clostridium acetobutylicum
7	d1q0oa2	Alignment		99.8	17	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
8	d1jc4a_	Alignment		99.8	18	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Methylmalonyl-CoA epimerase
9	c3bt3B_	Alignment		99.8	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**glyoxalase-related enzyme, arac type; **PDBTitle:** crystal structure of a glyoxalase-related enzyme from clostridium2 phytofermentans
10	d1twua_	Alignment		99.8	15	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Hypothetical protein YycE
11	d1mpya1	Alignment		99.8	18	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases

12	c3l7tB_	Alignment		99.8	21	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of smu.1112c
13	d1zswa1	Alignment		99.8	12	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**BC1024-like
14	c3e5dA_	Alignment		99.8	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative glyoxalase i; **PDBTitle:** crystal structure of a putative glyoxalase i (lmof2365_0426) from2 listeria monocytogenes str. 4b f2365 at 2.70 a resolution
15	d1lgta2	Alignment		99.8	20	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
16	c2r6uB_	Alignment		99.8	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of gene product rha04853 from rhodococcus sp. rha1
17	c3rmuD_	Alignment		99.8	24	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**methylmalonyl-coa epimerase, mitochondrial; **PDBTitle:** crystal structure of human methylmalonyl-coa epimerase, mcee
18	c2p25A_	Alignment		99.8	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glyoxalase family protein; **PDBTitle:** the crystal structure of the glyoxalase family protein from2 enterococcus faecalis
19	d1f1xa1	Alignment		99.8	22	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
20	d1f1ua1	Alignment		99.8	22	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
21	c3rriB_	Alignment	not modelled	99.8	18	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase; **PDBTitle:** crystal structure of glyoxalase/bleomycin resistance2 protein/dioxygenase from alicyclobacillus acidocaldarius
22	c3huhA_	Alignment	not modelled	99.8	19	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**virulence protein stm3117; **PDBTitle:** the structure of biphenyl-2,3-diol 1,2-dioxygenase iii-2 related protein from salmonella typhimurium
23	c3ct8A_	Alignment	not modelled	99.8	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative glyoxalase; **PDBTitle:** crystal structure of a putative glyoxalase (np_243026.1) from bacillus2 halodurans at 2.10 a resolution
24	c3g12A_	Alignment	not modelled	99.8	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative lactoylglutathione lyase; **PDBTitle:** crystal structure of a putative lactoylglutathione lyase2 from bdellovibrio bacteriovorus
25	c1zswA_	Alignment	not modelled	99.8	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**glyoxalase family protein; **PDBTitle:** crystal structure of bacillus cereus metallo protein from glyoxalase2 family
26	d1zswa2	Alignment	not modelled	99.8	12	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**BC1024-like
27	c3zw5A_	Alignment	not modelled	99.8	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**glyoxalase domain-containing protein 5; **PDBTitle:** crystal structure of the human glyoxalase domain-containing2 protein 5
						PDB header:oxidoreductase **Chain:** B: **PDB Molecule:**biphenyl-2,3-diol 1,2-dioxygenase iii-

28	c3ey7B_	Alignment	not modelled	99.8	18	related **PDBTitle:** structure from the mobile metagenome of v. cholerae.2 integron cassette protein vch_cass1
29	d1f1ua2	Alignment	not modelled	99.8	16	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
30	c2qqzB_	Alignment	not modelled	99.8	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**glyoxalase family protein, putative; **PDBTitle:** crystal structure of putative glyoxalase family protein from bacillus2 anthracis
31	d1f1xa2	Alignment	not modelled	99.8	17	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
32	d1ss4a_	Alignment	not modelled	99.8	18	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Hypothetical protein BC1747
33	c3bqxA_	Alignment	not modelled	99.8	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**glyoxalase-related enzyme; **PDBTitle:** high resolution crystal structure of a glyoxalase-related enzyme from2 fulvimarina pelagi
34	c3ghjA_	Alignment	not modelled	99.8	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative integron gene cassette protein; **PDBTitle:** crystal structure from the mobile metagenome of halifax2 harbour sewage outfall: integron cassette protein hfx_cass4
35	c1mpyD_	Alignment	not modelled	99.8	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**catechol 2,3-dioxygenase; **PDBTitle:** structure of catechol 2,3-dioxygenase (metapyrocatechase)2 from pseudomonas putida mt-2
36	d1kw3b2	Alignment	not modelled	99.8	19	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
37	c3pkwA_	Alignment	not modelled	99.8	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**toxoflavin lyase (tfla); **PDBTitle:** crystal structure of toxoflavin lyase (tfla) bound to mn(ii)
38	c2rk0B_	Alignment	not modelled	99.8	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase domain; **PDBTitle:** crystal structure of glyoxylase/bleomycin resistance2 protein/dioxygenase domain from frankia sp. ean1pec
39	d2i7ra1	Alignment	not modelled	99.8	15	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
40	c2kjzA_	Alignment	not modelled	99.8	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**atc0852; **PDBTitle:** solution nmr structure of protein atc0852 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att2.
41	c3r4qB_	Alignment	not modelled	99.8	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**lactoylglutathione lyase; **PDBTitle:** crystal structure of lactoylglutathione lyase from agrobacterium2 tumefaciens
42	c3kolA_	Alignment	not modelled	99.8	24	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**glyoxalase/bleomycin resistance **PDBTitle:** crystal structure of a glyoxalase/dioxygenase from nostoc2 punctiforme
43	c3hpyD_	Alignment	not modelled	99.8	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**catechol 2,3-dioxygenase; **PDBTitle:** crystal structure analysis of the 2,3-dioxygenase lapb from2 pseudomonas in the complex with 4-methylcatechol
44	c3lm4C_	Alignment	not modelled	99.7	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**catechol 2,3-dioxygenase; **PDBTitle:** crystal structure of 2,3-dihydroxy biphenyl dioxygenase from2 rhodococcus sp. (strain rha1)
45	c3r6aB_	Alignment	not modelled	99.7	23	**PDB header:**isomerase, lyase **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein (hypothetical protein2 mm_3218) from methanosarcina mazei.
46	c2rbbB_	Alignment	not modelled	99.7	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase; **PDBTitle:** crystal structure of a glyoxalase/bleomycin resistance2 protein/dioxygenase family enzyme from burkholderia phytofirmans psjn
47	d1kw3b1	Alignment	not modelled	99.7	18	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
48	c3oajA_	Alignment	not modelled	99.7	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative ring-cleaving dioxygenase mhqo; **PDBTitle:** crystal structure of putative dioxygenase from bacillus subtilis2 subsp. subtilis str. 168
49	c3gm5A_	Alignment	not modelled	99.7	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**lactoylglutathione lyase and related lyases; **PDBTitle:** crystal structure of a putative methylmalonyl-coenzyme a2 epimerase from thermoanaerobacter tengcongensis at 2.0 a3 resolution
50	c3itwA_	Alignment	not modelled	99.7	15	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**protein tiox;

						PDBTitle: crystal structure of tiox from micromonospora sp. ml1
51	c3m2oB_	Alignment	not modelled	99.7	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**glyoxalase/bleomycin resistance protein; **PDBTitle:** crystal structure of a putative glyoxalase/bleomycin resistance2 protein from rhodopseudomonas palustris cga009
52	c2p7pB_	Alignment	not modelled	99.7	19	**PDB header:**metal binding protein, hydrolase **Chain:** B: **PDB Molecule:**glyoxalase family protein; **PDBTitle:** crystal structure of genomically encoded fosfomycin resistance2 protein, fosx, from listeria monocytogenes complexed with mn(ii) and3 sulfate ion
53	c3ecjC_	Alignment	not modelled	99.7	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**protein (homoprotocatechuate 2,3-dioxygenase); **PDBTitle:** structure of e323l mutant of homoprotocatechuate 2,3-dioxygenase from2 brevibacterium fuscum at 1.65a resolution
54	c1f1uB_	Alignment	not modelled	99.7	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**homoprotocatechuate 2,3-dioxygenase; **PDBTitle:** crystal structure of homoprotocatechuate 2,3-dioxygenase from2 arthrobacter globiformis (native, low temperature)
55	c3rheA_	Alignment	not modelled	99.7	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad-dependent benzaldehyde dehydrogenase; **PDBTitle:** the crystal structure of nad-dependent benzaldehyde dehydrogenase from2 legionella pneumophila
56	d1lgta1	Alignment	not modelled	99.7	21	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
57	d1klla_	Alignment	not modelled	99.7	16	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
58	d1npba_	Alignment	not modelled	99.7	20	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
59	c2zi8A_	Alignment	not modelled	99.7	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable biphenyl-2,3-diol 1,2-dioxygenase bphc; **PDBTitle:** 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)
60	d1r9ca_	Alignment	not modelled	99.7	17	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
61	d1xqaa_	Alignment	not modelled	99.7	20	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
62	d1sqia1	Alignment	not modelled	99.7	17	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
63	d1nkia_	Alignment	not modelled	99.7	23	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
64	c3b59A_	Alignment	not modelled	99.7	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase; **PDBTitle:** crystal structure of the mn(ii)-bound glyoxalase from novosphingobium2 aromaticivorans
65	d1t47a1	Alignment	not modelled	99.7	16	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
66	c3sk1C_	Alignment	not modelled	99.7	13	**PDB header:**griseoluteate-binding protein **Chain:** C: **PDB Molecule:**ehpr; **PDBTitle:** crystal structure of phenazine resistance protein ehpr from2 enterobacter agglomerans (erwinia herbicola, pantoea agglomerans)3 eh1087, apo form
67	c2qntA_	Alignment	not modelled	99.7	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1872; **PDBTitle:** crystal structure of protein of unknown function from agrobacterium2 tumefaciens str. c58
68	c2rk9B_	Alignment	not modelled	99.7	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase; **PDBTitle:** the crystal structure of a glyoxalase/bleomycin resistance2 protein/dioxygenase superfamily member from vibrio splendidus 12b01
69	d1sp8a1	Alignment	not modelled	99.6	19	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
70	d2pjsa1	Alignment	not modelled	99.6	20	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
						PDB header:oxidoreductase **Chain:** A: **PDB Molecule:**1,2-dihydroxynaphthalene dioxygenase;

71	c2ei2A_	Alignment	not modelled	99.6	16	**PDBTitle:** crystal structure analysis of the 1,2-dihydroxynaphthalene dioxygenase2 from pseudomonas sp. stain c18
72	c2wl9A_	Alignment	not modelled	99.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catechol 2,3-dioxygenase; **PDBTitle:** crystal structure of catechol 2,3-dioxygenase
73	c1knfA_	Alignment	not modelled	99.6	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2,3-dihydroxybiphenyl 1,2-dioxygenase; **PDBTitle:** crystal structure of 2,3-dihydroxybiphenyl 1,2-dioxygenase complexed2 with 3-methyl catechol under anaerobic condition
74	c1sp8A_	Alignment	not modelled	99.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxyphenylpyruvate dioxygenase; **PDBTitle:** 4-hydroxyphenylpyruvate dioxygenase
75	c1kw3B_	Alignment	not modelled	99.6	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2,3-dihydroxybiphenyl dioxygenase; **PDBTitle:** crystal structure of 2,3-dihydroxybiphenyal dioxygenase (bphc) at 1.452 a resolution
76	d1sqda1	Alignment	not modelled	99.6	19	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
77	c1t47A_	Alignment	not modelled	99.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxyphenylpyruvate dioxygenase; **PDBTitle:** structure of fe2-hppd bound to ntbc
78	c2zw7A_	Alignment	not modelled	99.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bleomycin acetyltransferase; **PDBTitle:** crystal structure of bleomycin n-acetyltransferase complexed2 with bleomycin a2 and coenzyme a
79	c3fcdB_	Alignment	not modelled	99.5	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**lyase; **PDBTitle:** crystal structure of a putative glyoxalase from an2 environmental bacteria
80	d1sp9a_	Alignment	not modelled	99.5	18	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
81	c1sqiA_	Alignment	not modelled	99.5	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**4-hydroxyphenylpyruvic acid dioxygenase; **PDBTitle:** structural basis for inhibitor selectivity revealed by2 crystal structures of plant and mammalian 4-3 hydroxyphenylpyruvate dioxygenases
82	d1ecsa_	Alignment	not modelled	99.5	22	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
83	c1tfzA_	Alignment	not modelled	99.5	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxyphenylpyruvate dioxygenase; **PDBTitle:** structural basis for herbicidal inhibitor selectivity revealed by2 comparison of crystal structures of plant and mammalian 4-3 hydroxyphenylpyruvate dioxygenases
84	d1jifa_	Alignment	not modelled	99.5	12	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
85	c2r5vA_	Alignment	not modelled	99.5	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pcza361.1; **PDBTitle:** hydroxymandelate synthase crystal structure
86	d1xy7a_	Alignment	not modelled	99.5	14	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Hypothetical protein At5g48480
87	c2q48A_	Alignment	not modelled	99.5	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein at5g48480; **PDBTitle:** ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at5g48480
88	d1xrka_	Alignment	not modelled	99.4	17	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
89	d1cjxa2	Alignment	not modelled	99.4	21	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
90	c3e0rC_	Alignment	not modelled	99.4	20	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**c3-degrading proteinase (cppa protein); **PDBTitle:** crystal structure of cppa protein from streptococcus pneumoniae tigr4
91	c1cjxC_	Alignment	not modelled	99.4	12	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**4-hydroxyphenylpyruvate dioxygenase; **PDBTitle:** crystal structure of pseudomonas fluorescens hppd
92	d1t47a2	Alignment	not modelled	99.4	20	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
93	d1sqia2	Alignment	not modelled	99.3	18	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
						Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl

94	d1sp8a2	Alignment	not modelled	99.3	19	dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
95	d1cjxa1	Alignment	not modelled	99.3	12	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
96	d1u6la_	Alignment	not modelled	99.2	16	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**3-demethylubiquinone-9 3-methyltransferase
97	d1sqda2	Alignment	not modelled	99.2	18	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
98	c3l20A_	Alignment	not modelled	99.1	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a hypothetical protein from staphylococcus aureus
99	d1u7ia_	Alignment	not modelled	98.9	12	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**3-demethylubiquinone-9 3-methyltransferase
100	c3omsA_	Alignment	not modelled	98.8	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phnb protein; **PDBTitle:** putative 3-demethylubiquinone-9 3-methyltransferase, phnb protein,2 from bacillus cereus.
101	d1tsja_	Alignment	not modelled	97.8	10	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**3-demethylubiquinone-9 3-methyltransferase
102	d1u69a_	Alignment	not modelled	96.2	11	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**3-demethylubiquinone-9 3-methyltransferase
103	c3opyH_	Alignment	not modelled	84.8	20	**PDB header:**transferase **Chain:** H: **PDB Molecule:**6-phosphofructo-1-kinase beta-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
104	c3opyB_	Alignment	not modelled	84.1	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6-phosphofructo-1-kinase beta-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
105	c3opyE_	Alignment	not modelled	67.1	20	**PDB header:**transferase **Chain:** E: **PDB Molecule:**6-phosphofructo-1-kinase alpha-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
106	d2g3aa1	Alignment	not modelled	65.4	7	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
107	d1y9wa1	Alignment	not modelled	42.0	22	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
108	d1ghea_	Alignment	not modelled	37.9	12	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
109	c1ib1E_	Alignment	not modelled	36.1	9	**PDB header:**signaling protein/transferase **Chain:** E: **PDB Molecule:**serotonin n-acetyltransferase; **PDBTitle:** crystal structure of the 14-3-3 zeta:serotonin n-2 acetyltransferase complex
110	d3etja1	Alignment	not modelled	33.3	24	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
111	c3lodA_	Alignment	not modelled	32.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acyl-coa n-acyltransferase; **PDBTitle:** the crystal structure of the putative acyl-coa n-acyltransferase from2 klebsiella pneumoniae subsp.pneumoniae mgh 78578
112	c2qecA_	Alignment	not modelled	25.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone acetyltransferase hpa2 and related **PDBTitle:** crystal structure of histone acetyltransferase hpa2 and related2 acetyltransferase (np_600742.1) from corynebacterium glutamicum atcc3 13032 at 1.90 a resolution