Phyre2

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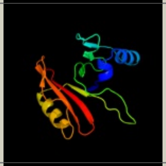
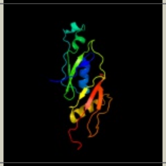
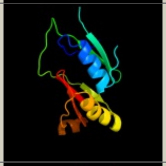
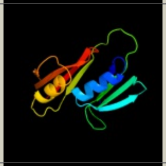
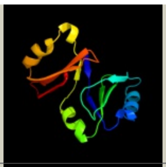
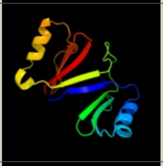
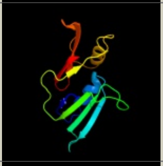
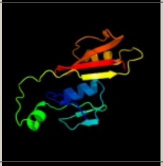
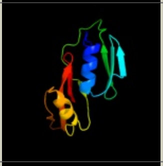
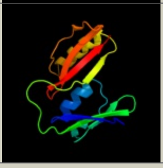
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1u6la_	Alignment		100.0	33	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**3-demethylubiquinone-9 3-methyltransferase
2	c3omsA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phnb protein; **PDBTitle:** putative 3-demethylubiquinone-9 3-methyltransferase, phnb protein,2 from bacillus cereus.
3	d1u7ia_	Alignment		100.0	20	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**3-demethylubiquinone-9 3-methyltransferase
4	d1tsja_	Alignment		100.0	24	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**3-demethylubiquinone-9 3-methyltransferase
5	c3l20A_	Alignment		100.0	26	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a hypothetical protein from staphylococcus aureus
6	d1u69a_	Alignment		100.0	19	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**3-demethylubiquinone-9 3-methyltransferase
7	d1xy7a_	Alignment		99.9	30	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Hypothetical protein At5g48480
8	c2q48A_	Alignment		99.9	30	**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
9	c2zw7A_	Alignment		99.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bleomycin acetyltransferase; **PDBTitle:** crystal structure of bleomycin n-acetyltransferase complexed2 with bleomycin a2 and coenzyme a
10	c3itwA_	Alignment		99.7	19	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**protein tiox; **PDBTitle:** crystal structure of tiox from micromonospora sp. ml1
11	c3fcdB_	Alignment		99.5	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**lyase; **PDBTitle:** crystal structure of a putative glyoxalase from an2 environmental bacteria

12	c3r6aB_	Alignment		99.4	11	**PDB header:**isomerase, lyase **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein (hypothetical protein2 mm_3218) from methanosarcina mazei.
13	c2rk9B_	Alignment		99.4	15	**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
14	d2pjsa1	Alignment		99.4	15	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
15	c3bt3B_	Alignment		99.3	10	**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
16	c2qntA_	Alignment		99.3	13	**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
17	d2i7ra1	Alignment		99.3	17	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
18	d1ecsa_	Alignment		99.2	16	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
19	c3m2oB_	Alignment		99.2	20	**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
20	d1klla_	Alignment		99.2	12	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
21	c3rheA_	Alignment	not modelled	99.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad-dependent benzaldehyde dehydrogenase; **PDBTitle:** the crystal structure of nad-dependent benzaldehyde dehydrogenase from2 legionella pneumophila
22	c2rbbB_	Alignment	not modelled	99.2	19	**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
23	c3bqxA_	Alignment	not modelled	99.2	20	**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
24	c3g12A_	Alignment	not modelled	99.2	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative lactoylglutathione lyase; **PDBTitle:** crystal structure of a putative lactoylglutathione lyase2 from bdellovibrio bacteriovorus
25	c2kjzA_	Alignment	not modelled	99.1	15	**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.
26	d1twua_	Alignment	not modelled	99.1	14	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Hypothetical protein YycE
27	c2r6uB_	Alignment	not modelled	99.1	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of gene product rha04853 from

						rhodococcus sp. rha1
28	c3r4qB_	Alignment	not modelled	99.1	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**lactoylglutathione lyase; **PDBTitle:** crystal structure of lactoylglutathione lyase from agrobacterium2 tumefaciens
29	d1mpya2	Alignment	not modelled	99.0	9	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
30	d1lgta2	Alignment	not modelled	99.0	16	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
31	d1jifa_	Alignment	not modelled	99.0	17	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
32	c3sk1C_	Alignment	not modelled	99.0	8	**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
33	d1f9za_	Alignment	not modelled	99.0	19	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Glyoxalase I (lactoylglutathione lyase)
34	d1xrka_	Alignment	not modelled	98.9	15	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
35	c3e5dA_	Alignment	not modelled	98.9	14	**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
36	c2rk0B_	Alignment	not modelled	98.9	15	**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
37	c3ghjA_	Alignment	not modelled	98.9	12	**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
38	d1xqaa_	Alignment	not modelled	98.9	15	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
39	d1zswa1	Alignment	not modelled	98.9	9	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**BC1024-like
40	c3l7tB_	Alignment	not modelled	98.9	14	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of smu.1112c
41	c2p25A_	Alignment	not modelled	98.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glyoxalase family protein; **PDBTitle:** the crystal structure of the glyoxalase family protein from2 enterococcus faecalis
42	d1nkia_	Alignment	not modelled	98.8	18	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
43	c3rriB_	Alignment	not modelled	98.8	9	**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
44	c3oa4A_	Alignment	not modelled	98.8	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**glyoxalase; **PDBTitle:** crystal structure of hypothetical protein bh1468 from bacillus2 halodurans c-125
45	d1sp8a1	Alignment	not modelled	98.8	21	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
46	d1qipa_	Alignment	not modelled	98.8	13	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Glyoxalase I (lactoylglutathione lyase)
47	c2p7pB_	Alignment	not modelled	98.8	17	**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
48	d1zswa2	Alignment	not modelled	98.8	12	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**BC1024-like
						Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl

49	d1mpya1	Alignment	not modelled	98.8	11	dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
50	c3ey7B_	Alignment	not modelled	98.7	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**biphenyl-2,3-diol 1,2-dioxygenase iii-related **PDBTitle:** structure from the mobile metagenome of v. cholerae.2 integron cassette protein vch_cass1
51	c1zswA_	Alignment	not modelled	98.7	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**glyoxalase family protein; **PDBTitle:** crystal structure of bacillus cereus metallo protein from glyoxalase2 family
52	c3ct8A_	Alignment	not modelled	98.7	12	**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
53	c3zw5A_	Alignment	not modelled	98.7	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**glyoxalase domain-containing protein 5; **PDBTitle:** crystal structure of the human glyoxalase domain-containing2 protein 5
54	c3huhA_	Alignment	not modelled	98.7	16	**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
55	d2c21a1	Alignment	not modelled	98.7	15	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Glyoxalase I (lactoylglutathione lyase)
56	c3rmuD_	Alignment	not modelled	98.7	12	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**methylmalonyl-coa epimerase, mitochondrial; **PDBTitle:** crystal structure of human methylmalonyl-coa epimerase, mcee
57	d1lgta1	Alignment	not modelled	98.7	13	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
58	c3b59A_	Alignment	not modelled	98.6	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase; **PDBTitle:** crystal structure of the mn(ii)-bound glyoxalase from novosphingobium2 aromaticivorans
59	d1npba_	Alignment	not modelled	98.6	14	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
60	d1r9ca_	Alignment	not modelled	98.6	9	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
61	c1mpyD_	Alignment	not modelled	98.6	9	**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
62	d1f1ua1	Alignment	not modelled	98.6	16	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
63	d1sqda1	Alignment	not modelled	98.6	13	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
64	c2qqzB_	Alignment	not modelled	98.6	16	**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
65	d1jc4a_	Alignment	not modelled	98.6	12	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Methylmalonyl-CoA epimerase
66	d1t47a1	Alignment	not modelled	98.6	15	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
67	d1sqia1	Alignment	not modelled	98.6	12	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
68	d1kw3b1	Alignment	not modelled	98.6	17	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
69	c2qh0A_	Alignment	not modelled	98.6	7	**PDB header:**lyase **Chain:** A: **PDB Molecule:**lactoylglutathione lyase; **PDBTitle:** crystal structure of a glyoxalase from clostridium acetobutylicum
70	d1q0oa2	Alignment	not modelled	98.6	11	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
						Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl

71	d1f1xa1	Alignment	not modelled	98.6	11	dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
72	c1sp8A_	Alignment	not modelled	98.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxyphenylpyruvate dioxygenase; **PDBTitle:** 4-hydroxyphenylpyruvate dioxygenase
73	c3kolA_	Alignment	not modelled	98.5	11	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**glyoxalase/bleomycin resistance **PDBTitle:** crystal structure of a glyoxalase/dioxygenase from nostoc2 punctiforme
74	c3oajA_	Alignment	not modelled	98.5	10	**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
75	d1kw3b2	Alignment	not modelled	98.5	16	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
76	c3pkwA_	Alignment	not modelled	98.5	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**toxoflavin lyase (tfla); **PDBTitle:** crystal structure of toxoflavin lyase (tfla) bound to mn(ii)
77	c3hpyD_	Alignment	not modelled	98.5	11	**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
78	c1f1uB_	Alignment	not modelled	98.5	13	**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)
79	d1sp9a_	Alignment	not modelled	98.5	15	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
80	d1ss4a_	Alignment	not modelled	98.5	7	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Hypothetical protein BC1747
81	c3ecjC_	Alignment	not modelled	98.5	11	**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
82	c3lm4C_	Alignment	not modelled	98.4	10	**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)
83	c1knfA_	Alignment	not modelled	98.4	16	**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
84	c1kw3B_	Alignment	not modelled	98.4	18	**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
85	c1sqiA_	Alignment	not modelled	98.4	12	**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
86	c2ei2A_	Alignment	not modelled	98.4	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1,2-dihydroxynaphthalene dioxygenase; **PDBTitle:** crystal structure analysis of the 1,2-dihydroxynaphthalene dioxygenase2 from pseudomonas sp. stain c18
87	c3gm5A_	Alignment	not modelled	98.4	9	**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
88	c2zi8A_	Alignment	not modelled	98.3	11	**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)
89	c2wl9A_	Alignment	not modelled	98.3	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catechol 2,3-dioxygenase; **PDBTitle:** crystal structure of catechol 2,3-dioxygenase
90	c2r5vA_	Alignment	not modelled	98.3	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pcza361.1; **PDBTitle:** hydroxymandelate synthase crystal structure
91	c1t47A_	Alignment	not modelled	98.2	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxyphenylpyruvate dioxygenase; **PDBTitle:** structure of fe2-hppd bound to ntbc
92	d1f1ua2	Alignment	not modelled	98.2	12	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
						PDB header:oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxyphenylpyruvate dioxygenase;

93	c1tfzA_	Alignment	not modelled	98.1	18	**PDBTitle:** structural basis for herbicidal inhibitor selectivity revealed by2 comparison of crystal structures of plant and mammalian 4-3 hydroxyphenylpyruvate dioxygenases
94	d1f1xa2	Alignment	not modelled	98.1	12	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
95	c3e0rC_	Alignment	not modelled	98.1	11	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**c3-degrading proteinase (cppa protein); **PDBTitle:** crystal structure of cppa protein from streptococcus pneumoniae tigr4
96	c1cjxC_	Alignment	not modelled	97.0	8	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**4-hydroxyphenylpyruvate dioxygenase; **PDBTitle:** crystal structure of pseudomonas fluorescens hppd
97	d1t47a2	Alignment	not modelled	97.0	12	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
98	d1cjxa2	Alignment	not modelled	97.0	12	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
99	d1cjxa1	Alignment	not modelled	96.5	6	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
100	d1sp8a2	Alignment	not modelled	96.2	11	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
101	d1sqia2	Alignment	not modelled	95.7	11	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
102	d1sqda2	Alignment	not modelled	93.6	10	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
103	d2joqa1	Alignment	not modelled	77.1	16	**Fold:**Ferredoxin-like **Superfamily:**YbeD/HP0495-like **Family:**HP0495-like
104	c1rwuA_	Alignment	not modelled	57.8	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0250 protein ybed; **PDBTitle:** solution structure of conserved protein ybed from e. coli
105	d1rwua_	Alignment	not modelled	57.8	19	**Fold:**Ferredoxin-like **Superfamily:**YbeD/HP0495-like **Family:**YbeD-like
106	c1dl5A_	Alignment	not modelled	46.2	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein-l-isoaspartate o-methyltransferase; **PDBTitle:** protein-l-isoaspartate o-methyltransferase
107	c1htyA_	Alignment	not modelled	36.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-mannosidase ii; **PDBTitle:** golgi alpha-mannosidase ii
108	c2ow7A_	Alignment	not modelled	30.3	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-mannosidase 2; **PDBTitle:** golgi alpha-mannosidase ii complex with (1r,6s,7r,8s)-1-2 thioniabicyclo[4.3.0]nonan-7,8-diol chloride
109	c2wyhA_	Alignment	not modelled	22.1	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-mannosidase; **PDBTitle:** structure of the streptococcus pyogenes family gh38 alpha-2 mannosidase
110	d1dl5a1	Alignment	not modelled	21.8	11	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Protein-L-isoaspartyl O-methyltransferase