Phyre^2

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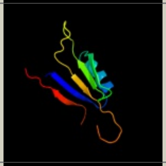
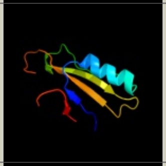
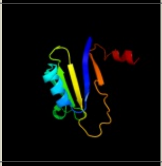
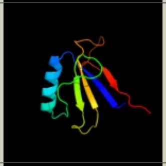
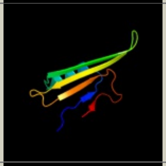
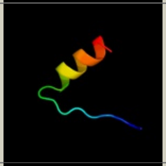
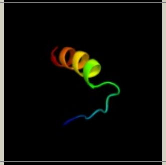
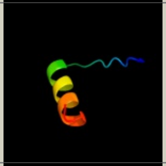
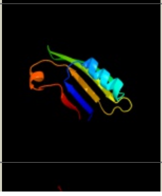
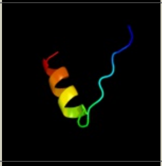
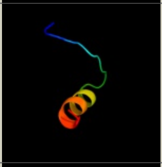
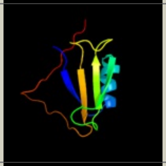
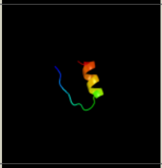
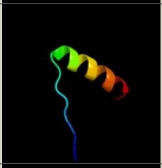
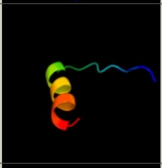
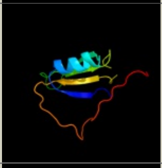
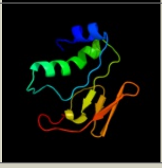
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1k4na_	Alignment		100.0	99	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Hypothetical protein YecM (EC4020)
2	d1sp8a2	Alignment		76.1	20	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
3	d1t47a2	Alignment		75.8	16	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
4	d1sqia1	Alignment		72.7	16	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
5	c1zswA_	Alignment		69.7	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**glyoxalase family protein; **PDBTitle:** crystal structure of bacillus cereus metallo protein from glyoxalase2 family
6	c2qh0A_	Alignment		64.4	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**lactoylglutathione lyase; **PDBTitle:** crystal structure of a glyoxalase from clostridium acetobutylicum
7	d1sqda2	Alignment		60.0	16	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
8	d1sqda1	Alignment		55.6	18	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
9	c3ct8A_	Alignment		53.3	4	**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
10	c3gm5A_	Alignment		52.7	8	**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
11	c2r5vA_	Alignment		50.1	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pcza361.1; **PDBTitle:** hydroxymandelate synthase crystal structure

12	d1klla_	Alignment		49.2	13	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
13	d1sp8a1	Alignment		48.1	23	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
14	c3r4qB_	Alignment		44.9	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**lactoylglutathione lyase; **PDBTitle:** crystal structure of lactoylglutathione lyase from agrobacterium2 tumefaciens
15	d1zswa1	Alignment		42.8	11	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**BC1024-like
16	c3huhA_	Alignment		41.2	23	**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
17	d1lgta2	Alignment		37.4	12	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
18	d1cjxa2	Alignment		36.2	9	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
19	c3oajA_	Alignment		35.6	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
20	c2gcuD_	Alignment		35.4	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative hydroxyacylglutathione hydrolase 3; **PDBTitle:** x-ray structure of gene product from arabidopsis thaliana2 at1g53580
21	c1cjxC_	Alignment	not modelled	34.5	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**4-hydroxyphenylpyruvate dioxygenase; **PDBTitle:** crystal structure of pseudomonas fluorescens hppd
22	d1kw3b2	Alignment	not modelled	34.1	10	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
23	c2p7pB_	Alignment	not modelled	33.6	13	**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
24	d1xqaa_	Alignment	not modelled	33.5	14	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
25	d1qbaa1	Alignment	not modelled	32.5	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
26	c2rk0B_	Alignment	not modelled	32.0	23	**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
27	c2pkaB_	Alignment	not modelled	31.4	18	**PDB header:**serine proteinase **Chain:** B: **PDB Molecule:**kallikrein a; **PDBTitle:** refined 2 angstroms x-ray crystal structure of porcine2 pancreatic kallikrein a, a specific trypsin-like serine3 proteinase. crystallization, structure determination,4 crystallographic refinement, structure and its comparison5 with bovine trypsin

28	c3ghjA_	Alignment	not modelled	31.0	0	**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
29	c1sp8A_	Alignment	not modelled	30.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxyphenylpyruvate dioxygenase; **PDBTitle:** 4-hydroxyphenylpyruvate dioxygenase
30	c2qqzB_	Alignment	not modelled	30.2	15	**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	c3zw5A_	Alignment	not modelled	28.8	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**glyoxalase domain-containing protein 5; **PDBTitle:** crystal structure of the human glyoxalase domain-containing2 protein 5
32	d1e8oa_	Alignment	not modelled	28.0	15	**Fold:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Superfamily:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Family:**Signal recognition particle alu RNA binding heterodimer, SRP9/14
33	c3e5dA_	Alignment	not modelled	28.0	10	**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
34	c3l7tB_	Alignment	not modelled	27.9	9	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of smu.1112c
35	c3pkwA_	Alignment	not modelled	27.8	5	**PDB header:**lyase **Chain:** A: **PDB Molecule:**toxoflavin lyase (tfla); **PDBTitle:** crystal structure of toxoflavin lyase (tfla) bound to mn(ii)
36	d2c21a1	Alignment	not modelled	27.5	9	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Glyoxalase I (lactoylglutathione lyase)
37	d1qipa_	Alignment	not modelled	26.7	9	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Glyoxalase I (lactoylglutathione lyase)
38	c2rbbB_	Alignment	not modelled	26.3	5	**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
39	d1t47a1	Alignment	not modelled	26.2	10	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
40	d1zvpa2	Alignment	not modelled	25.5	23	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**VC0802-like
41	d1914a1	Alignment	not modelled	24.3	15	**Fold:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Superfamily:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Family:**Signal recognition particle alu RNA binding heterodimer, SRP9/14
42	d1h3ga2	Alignment	not modelled	22.7	24	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
43	d1nkia_	Alignment	not modelled	22.4	13	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
44	d1lgta1	Alignment	not modelled	22.1	5	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
45	d1f1xa2	Alignment	not modelled	21.7	10	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
46	c3p3dA_	Alignment	not modelled	21.5	26	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nucleoporin 53; **PDBTitle:** crystal structure of the nup53 rrm domain from pichia guilliermondii
47	d1f9za_	Alignment	not modelled	20.5	10	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Glyoxalase I (lactoylglutathione lyase)
48	d1sqia2	Alignment	not modelled	19.6	23	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
49	c2wl9A_	Alignment	not modelled	19.6	7	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catechol 2,3-dioxygenase; **PDBTitle:** crystal structure of catechol 2,3-dioxygenase
						PDB header:oxidoreductase

50	c1kw3B_	Alignment	not modelled	18.8	12	**Chain:** B: **PDB Molecule:**2,3-dihydroxybiphenyl dioxygenase; **PDBTitle:** crystal structure of 2,3-dihydroxybiphenyal dioxygenase (bphc) at 1.452 a resolution
51	c3rriB_	Alignment	not modelled	18.7	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
52	c3kolA_	Alignment	not modelled	18.6	17	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**glyoxalase/bleomycin resistance **PDBTitle:** crystal structure of a glyoxalase/dioxygenase from nostoc2 punctiforme
53	d1ryua_	Alignment	not modelled	18.4	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**ARID-like **Family:**ARID domain
54	d1npba_	Alignment	not modelled	17.8	7	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
55	c3g12A_	Alignment	not modelled	17.7	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative lactoylglutathione lyase; **PDBTitle:** crystal structure of a putative lactoylglutathione lyase2 from bdellovibrio bacteriovorus
56	c2w00B_	Alignment	not modelled	17.1	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hsdr; **PDBTitle:** crystal structure of the hsdr subunit of the ecor124i2 restriction enzyme in complex with atp
57	c3rmuD_	Alignment	not modelled	17.0	9	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**methylmalonyl-coa epimerase, mitochondrial; **PDBTitle:** crystal structure of human methylmalonyl-coa epimerase, mcee
58	d1jc4a_	Alignment	not modelled	17.0	19	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Methylmalonyl-CoA epimerase
59	c3lm4C_	Alignment	not modelled	16.4	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)
60	d1sp9a_	Alignment	not modelled	15.8	18	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
61	c3oa4A_	Alignment	not modelled	15.6	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**glyoxalase; **PDBTitle:** crystal structure of hypothetical protein bh1468 from bacillus2 halodurans c-125
62	d1c20a_	Alignment	not modelled	15.5	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**ARID-like **Family:**ARID domain
63	c1914A_	Alignment	not modelled	15.4	15	**PDB header:**alu domain **Chain:** A: **PDB Molecule:**signal recognition particle 9/14 fusion protein; **PDBTitle:** signal recognition particle alu rna binding heterodimer, srp9/14
64	c2fupA_	Alignment	not modelled	14.8	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**hypothetical protein pa3352; **PDBTitle:** crystal structure of a putative flagella synthesis protein flgn2 (pa3352) from pseudomonas aeruginosa at 1.48 a resolution
65	d2fupa1	Alignment	not modelled	14.8	18	**Fold:**STAT-like **Superfamily:**FlgN-like **Family:**FlgN-like
66	c2zi8A_	Alignment	not modelled	14.7	10	**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)
67	c3bqxA_	Alignment	not modelled	14.7	14	**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
68	c1zvpB_	Alignment	not modelled	14.4	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein vc0802; **PDBTitle:** crystal structure of a protein of unknown function vc0802 from vibrio2 cholerae, possible transport protein
69	c2jxjA_	Alignment	not modelled	13.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**histone demethylase jarid1a; **PDBTitle:** nmr structure of the arid domain from the histone h3k42 demethylase rbp2
70	d2dyna_	Alignment	not modelled	13.2	23	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
71	c3ktcB_	Alignment	not modelled	13.1	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**xylose isomerase; **PDBTitle:** crystal structure of putative sugar isomerase (yp_050048.1) from2 erwinia carotovora atroseptica scri1043 at 1.54 a resolution
72	c3omsA_	Alignment	not modelled	12.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phnb protein; **PDBTitle:** putative 3-demethylubiquinone-9 3-methyltransferase, phnb protein,2 from bacillus cereus.
73	d1mpya2	Alignment	not modelled	12.5	13	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase

						Family: Extradiol dioxygenases
74	c2ei2A_	Alignment	not modelled	12.5	10	**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
75	c3l9dA_	Alignment	not modelled	12.2	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative gtp pyrophosphokinase; **PDBTitle:** the crystal structure of smu.1046c from streptococcus mutans ua159
76	c2p25A_	Alignment	not modelled	12.2	5	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glyoxalase family protein; **PDBTitle:** the crystal structure of the glyoxalase family protein from2 enterococcus faecalis
77	c1jmtB_	Alignment	not modelled	12.2	63	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**splicing factor u2af 65 kda subunit; **PDBTitle:** x-ray structure of a core u2af65/u2af35 heterodimer
78	c1tfzA_	Alignment	not modelled	12.1	21	**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
79	d1mpya1	Alignment	not modelled	12.0	18	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
80	d1h7sa1	Alignment	not modelled	11.9	67	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
81	d1nxia_	Alignment	not modelled	11.8	10	**Fold:**Ferredoxin-like **Superfamily:**Hypothetical protein VC0424 **Family:**Hypothetical protein VC0424
82	c1knfA_	Alignment	not modelled	11.8	12	**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
83	d1f1ua2	Alignment	not modelled	11.7	10	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
84	d1lnsa2	Alignment	not modelled	11.4	22	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**PepX C-terminal domain-like
85	d1xo8a_	Alignment	not modelled	11.2	21	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**LEA14-like **Family:**LEA14-like
86	d1ig6a_	Alignment	not modelled	10.9	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**ARID-like **Family:**ARID domain
87	d1e5xa_	Alignment	not modelled	10.7	24	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
88	d1hl6a_	Alignment	not modelled	10.2	14	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
89	c2hntE_	Alignment	not modelled	10.2	32	**PDB header:**serine protease **Chain:** E: **PDB Molecule:**gamma-thrombin; **PDBTitle:** crystallographic structure of human gamma-thrombin
90	c1mpyD_	Alignment	not modelled	10.1	10	**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
91	d2ibxa1	Alignment	not modelled	10.0	28	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
92	c3h1tA_	Alignment	not modelled	10.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**type i site-specific restriction-modification **PDBTitle:** the fragment structure of a putative hsdr subunit of a type2 i restriction enzyme from vibrio vulnificus yj016
93	d2dbsa1	Alignment	not modelled	9.8	56	**Fold:**TTHC002-like **Superfamily:**TTHC002-like **Family:**TTHC002-like
94	c2w74B_	Alignment	not modelled	9.6	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**type i restriction enzyme ecor124ii r protein; **PDBTitle:** mutant (k220r) of the hsdr subunit of the ecor124i2 restriction enzyme in complex with atp
95	d2i7ra1	Alignment	not modelled	9.5	0	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
96	c3pyiA_	Alignment	not modelled	9.3	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**spindle assembly abnormal protein 6; **PDBTitle:** structure of the n-terminal domain of c. elegans sas-6
97	d1b63a1	Alignment	not modelled	9.3	50	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain

98	c3ey7B_	Alignment	not modelled	9.2	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
99	d1vjea_	Alignment	not modelled	9.2	30	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS