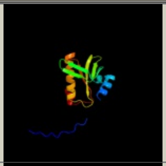
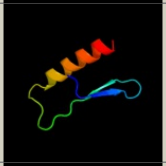
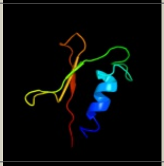
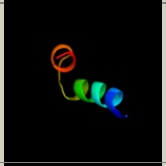
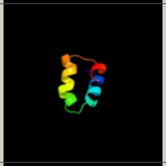
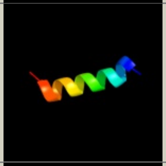
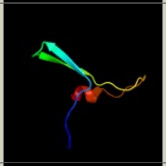
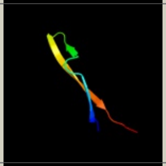
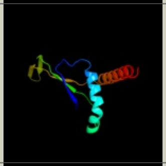
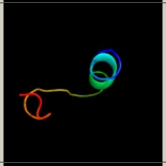
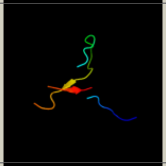
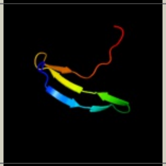
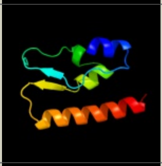
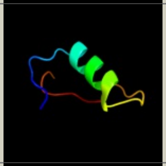
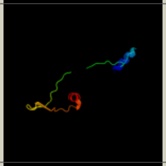
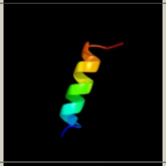
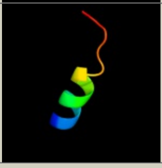
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P45423
Date	Thu Jan 5 12:02:36 GMT 2012
Unique Job ID	42fa58ed444ff121

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vldA_	Alignment		99.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**upf0286 protein pyrab01260; **PDBTitle:** crystal structure of a repair endonuclease from pyrococcus2 abyssi
2	d1w36b3	Alignment		92.9	19	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Exodeoxyribonuclease V beta chain (RecB), C-terminal domain
3	c1w36E_	Alignment		91.9	19	**PDB header:**recombination **Chain:** E: **PDB Molecule:**exodeoxyribonuclease v beta chain; **PDBTitle:** recbcd:dna complex
4	d1az3a_	Alignment		56.3	14	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease EcoRV
5	d1a9xa1	Alignment		54.2	27	**Fold:**Carbamoyl phosphate synthetase, large subunit connection domain **Superfamily:**Carbamoyl phosphate synthetase, large subunit connection domain **Family:**Carbamoyl phosphate synthetase, large subunit connection domain
6	d1vz0a1	Alignment		41.9	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
7	d2btoa1	Alignment		37.4	20	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
8	c3h1tA_	Alignment		36.4	21	**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
9	d1vhsa_	Alignment		34.3	28	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
10	c3h4rA_	Alignment		32.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exodeoxyribonuclease 8; **PDBTitle:** crystal structure of e. coli rece exonuclease
11	c3ot2B_	Alignment		31.9	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative nuclease belonging to duf8202 (ava_3926) from anabaena variabilis atcc 29413 at 1.96 a resolution

12	c3ot2A_	Alignment		31.9	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative nuclease belonging to duf8202 (ava_3926) from anabaena variabilis atcc 29413 at 1.96 a resolution
13	c3njcA_	Alignment		29.6	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**yslb protein; **PDBTitle:** crystal structure of the yslb protein from bacillus subtilis.2 northeast structural genomics consortium target sr460.
14	c3ga2A_	Alignment		29.5	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endonuclease v; **PDBTitle:** crystal structure of the endonuclease_v (bsu36170) from2 bacillus subtilis, northeast structural genomics3 consortium target sr624
15	c3fovA_	Alignment		29.4	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0102 protein rpa0323; **PDBTitle:** crystal structure of protein rpa0323 of unknown function from2 rhodopseudomonas palustris
16	d1yioa2	Alignment		27.6	20	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
17	d2k3ka1	Alignment		26.0	27	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
18	d1m0da_	Alignment		25.1	17	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Endonuclease I (Holliday junction resolvase)
19	d1tuba1	Alignment		22.8	20	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
20	d1w0ba_	Alignment		22.1	40	**Fold:**Spectrin repeat-like **Superfamily:**Alpha-hemoglobin stabilizing protein AHSP **Family:**Alpha-hemoglobin stabilizing protein AHSP
21	d1tubb1	Alignment	not modelled	21.6	15	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
22	d1d2zb_	Alignment	not modelled	21.4	26	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
23	c3cueJ_	Alignment	not modelled	21.4	16	**PDB header:**protein transport **Chain:** J: **PDB Molecule:**transport protein particle 22 kda subunit; **PDBTitle:** crystal structure of a trapp subassembly activating the rab2 ypt1p
24	c2jg6A_	Alignment	not modelled	20.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna-3-methyladenine glycosidase; **PDBTitle:** crystal structure of a 3-methyladenine dna glycosylase i2 from staphylococcus aureus
25	d1sjqa_	Alignment	not modelled	19.7	15	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
26	d1xmxa_	Alignment	not modelled	18.8	10	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hypothetical protein VC1899
27	c2az1B_	Alignment	not modelled	18.7	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** structure of a halophilic nucleoside diphosphate kinase2 from halobacterium salinarum
28	c3edlA_	Alignment	not modelled	18.2	20	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**alpha-tubulin; **PDBTitle:** kinesin13-microtubule ring complex
29	d1z8ua1	Alignment	not modelled	17.9	40	**Fold:**Spectrin repeat-like **Superfamily:**Alpha-hemoglobin stabilizing protein AHSP **Family:**Alpha-hemoglobin stabilizing protein AHSP

30	d1sx5a_	Alignment	not modelled	17.7	14	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease EcoRV
31	c2jlmE_	Alignment	not modelled	17.4	22	**PDB header:**transferase **Chain:** E: **PDB Molecule:**putative phosphinothricin n-acetyltransferase; **PDBTitle:** structure of a putative acetyltransferase (aciad1637) from2 acinetobacter baylyi adp1
32	c1s7fA_	Alignment	not modelled	17.1	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyl transferase; **PDBTitle:** riml- ribosomal l7/l12 alpha-n-protein acetyltransferase crystal form2 i (apo)
33	c2o37A_	Alignment	not modelled	17.0	6	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**protein sis1; **PDBTitle:** j-domain of sis1 protein, hsp40 co-chaperone from2 saccharomyces cerevisiae.
34	c2jh9A_	Alignment	not modelled	16.8	23	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**vp4 core protein; **PDBTitle:** the structure of bluetongue virus vp4 reveals a2 multifunctional rna-capping production-line
35	c2e5jA_	Alignment	not modelled	16.6	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**methenyltetrahydrofolate synthetase domain **PDBTitle:** solution structure of rna binding domain in2 methenyltetrahydrofolate synthetase domain containing
36	c3cxjB_	Alignment	not modelled	15.8	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from2 methanothermobacter thermautotrophicus
37	c3apqB_	Alignment	not modelled	15.7	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dnaj homolog subfamily c member 10; **PDBTitle:** crystal structure of j-trx1 fragment of erdj5
38	d1nkua_	Alignment	not modelled	15.4	26	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**3-Methyladenine DNA glycosylase I (Tag)
39	d1w25a1	Alignment	not modelled	14.9	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
40	c1vbkA_	Alignment	not modelled	14.7	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ph1313; **PDBTitle:** crystal structure of ph1313 from pyrococcus horikoshii ot3
41	d2di0a1	Alignment	not modelled	14.6	33	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**CUE domain
42	c2w4zB_	Alignment	not modelled	14.4	38	**PDB header:**virus **Chain:** B: **PDB Molecule:**caulobacter bacteriophage 5; **PDBTitle:** caulobacter bacteriophage 5
43	c3efcA_	Alignment	not modelled	14.2	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein assembly factor yaet; **PDBTitle:** crystal structure of yaet periplasmic domain
44	d1whya_	Alignment	not modelled	13.9	18	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
45	d1wdjb_	Alignment	not modelled	13.9	16	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hypothetical protein TT1808 (TTHA1514)
46	c1m6vE_	Alignment	not modelled	13.8	27	**PDB header:**ligase **Chain:** E: **PDB Molecule:**carbamoyl phosphate synthetase large chain; **PDBTitle:** crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
47	d2gxba1	Alignment	not modelled	13.1	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
48	d1kxpd3	Alignment	not modelled	13.1	22	**Fold:**Serum albumin-like **Superfamily:**Serum albumin-like **Family:**Serum albumin-like
49	c3pgwP_	Alignment	not modelled	13.0	27	**PDB header:**splicing/dna/rna **Chain:** P: **PDB Molecule:**u1-a; **PDBTitle:** crystal structure of human u1 snrnp
50	c1xaxA_	Alignment	not modelled	13.0	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0054 protein hi0004; **PDBTitle:** nmr structure of hi0004, a putative essential gene product2 from haemophilus influenzae
51	d1qkka_	Alignment	not modelled	12.8	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
52	d1kn0a_	Alignment	not modelled	12.8	30	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**The homologous-pairing domain of Rad52 recombinase
53	c2qv0A_	Alignment	not modelled	12.7	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein mrke; **PDBTitle:** crystal structure of the response regulatory domain of2 protein mrke from klebsiella pneumoniae
54	d1wdja_	Alignment	not modelled	12.6	18	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hypothetical protein TT1808 (TTHA1514)
55	d2b7oa1	Alignment	not modelled	12.6	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class-II DAHP synthetase

56	c3eplA_	Alignment	not modelled	12.4	20	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**trna isopentenyltransferase; **PDBTitle:** crystallographic snapshots of eukaryotic2 dimethylallyltransferase acting on trna: insight into trna3 recognition and reaction mechanism
57	d1xe1a_	Alignment	not modelled	12.3	30	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
58	c1xe1A_	Alignment	not modelled	12.3	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pf0907; **PDBTitle:** hypothetical protein from pyrococcus furiosus pfu-880080-001
59	c2i79B_	Alignment	not modelled	12.3	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetyltransferase, gnat family; **PDBTitle:** the crystal structure of the acetyltransferase of gnat family from2 streptococcus pneumoniae
60	c3hdgE_	Alignment	not modelled	12.2	12	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the n-terminal domain of an2 uncharacterized protein (ws1339) from wolinella3 succinogenes
61	d1gefa_	Alignment	not modelled	12.0	31	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hjc-like
62	c2kqxA_	Alignment	not modelled	11.4	10	**PDB header:**chaperone binding protein **Chain:** A: **PDB Molecule:**curved dna-binding protein; **PDBTitle:** nmr structure of the j-domain (residues 2-72) in the2 escherichia coli cbpa
63	c3qpbB_	Alignment	not modelled	11.4	38	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uridine phosphorylase; **PDBTitle:** crystal structure of streptococcus pyogenes uridine phosphorylase2 reveals a subclass of the np-i superfamily
64	d2rnrb1	Alignment	not modelled	11.4	22	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**TFIIH domain
65	c2pd0D_	Alignment	not modelled	11.1	14	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein; **PDBTitle:** protein cgd2_2020 from cryptosporidium parvum
66	c2oziA_	Alignment	not modelled	11.1	38	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rpa4178; **PDBTitle:** structural genomics, the crystal structure of a putative2 protein rpa4178 from rhodopseudomonas palustris cga009
67	d1vbka2	Alignment	not modelled	10.9	20	**Fold:**THUMP domain **Superfamily:**THUMP domain-like **Family:**THUMP domain
68	d1xm5a_	Alignment	not modelled	10.7	10	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Predicted metal-dependent hydrolase
69	d1mnta_	Alignment	not modelled	10.6	12	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
70	d1fj7a_	Alignment	not modelled	10.6	21	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
71	c3mg9A_	Alignment	not modelled	10.5	30	**PDB header:**transferase/antibiotic **Chain:** A: **PDB Molecule:**teg12; **PDBTitle:** teg 12 binary structure complexed with the teicoplanin aglycone
72	c2dmxA_	Alignment	not modelled	10.3	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily b member 8; **PDBTitle:** solution structure of the j domain of dnaj homolog2 subfamily b member 8
73	d1v4na_	Alignment	not modelled	10.1	33	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
74	c1yewC_	Alignment	not modelled	10.1	29	**PDB header:**oxidoreductase, membrane protein **Chain:** C: **PDB Molecule:**particulate methane monooxygenase subunit c2; **PDBTitle:** crystal structure of particulate methane monooxygenase
75	d1a9nb_	Alignment	not modelled	9.5	18	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
76	c3f6cB_	Alignment	not modelled	9.4	4	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**positive transcription regulator evga; **PDBTitle:** crystal structure of n-terminal domain of positive transcription2 regulator evga from escherichia coli
77	d1tvia_	Alignment	not modelled	9.3	12	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Predicted metal-dependent hydrolase
78	d2g9ha2	Alignment	not modelled	9.0	27	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
79	c1wtaA_	Alignment	not modelled	9.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5'-methylthioadenosine phosphorylase; **PDBTitle:** crystal structure of 5'-deoxy-5'-methylthioadenosine from aeropyrum2 pernix (r32 form)
80	d1hh1a_	Alignment	not modelled	9.0	26	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hjc-like
81	c2btoA_	Alignment	not modelled	8.7	20	**PDB header:**cytoskeletal protein **Chain:** A: **PDB Molecule:**tubulin btuba; **PDBTitle:** structure of btuba from prosthecobacter dejongeii
82	c2p1lF_	Alignment	not modelled	8.6	31	**PDB header:**apoptosis **Chain:** F: **PDB Molecule:**beclin 1;

						PDBTitle: structure of the bcl-xl:beclin 1 complex
83	c1u9pA_	Alignment	not modelled	8.6	28	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**parc; **PDBTitle:** permuted single-chain arc
84	c3pbiA_	Alignment	not modelled	8.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**invasion protein; **PDBTitle:** structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution
85	d1fl0a_	Alignment	not modelled	8.5	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Myf domain
86	d1yr0a1	Alignment	not modelled	8.3	25	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
87	c1vkjA_	Alignment	not modelled	8.2	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**heparan sulfate (glucosamine) 3-o- **PDBTitle:** crystal structure of heparan sulfate 3-o-sulfotransferase2 isoform 1 in the presence of pap
88	d1vkja_	Alignment	not modelled	8.2	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
89	c2hjnA_	Alignment	not modelled	8.2	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**maintenance of ploidy protein mob1; **PDBTitle:** structural and functional analysis of saccharomyces2 cerevisiae mob1
90	d2cq2a1	Alignment	not modelled	8.1	12	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
91	d1wexa_	Alignment	not modelled	8.1	27	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
92	d2ad9a1	Alignment	not modelled	8.0	15	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
93	d1if1a_	Alignment	not modelled	8.0	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Interferon regulatory factor
94	d1qgpa_	Alignment	not modelled	7.9	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
95	d2cpda1	Alignment	not modelled	7.8	27	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
96	c3k44D_	Alignment	not modelled	7.7	24	**PDB header:**nucleic acid binding protein **Chain:** D: **PDB Molecule:**purine-rich binding protein-alpha, isoform b; **PDBTitle:** crystal structure of drosophila melanogaster pur-alpha
97	c3g16A_	Alignment	not modelled	7.7	56	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein with cystatin-like fold; **PDBTitle:** crystal structure of protein of unknown function with cystatin-like2 fold (yp_001022489.1) from methylobium petroleophilum pm1 at 1.45 a3 resolution
98	c3d3qB_	Alignment	not modelled	7.4	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate **PDBTitle:** crystal structure of trna delta(2)-isopentenylpyrophosphate2 transferase (se0981) from staphylococcus epidermidis.3 northeast structural genomics consortium target ser100
99	d1kw3b1	Alignment	not modelled	7.4	25	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases