

Mark G Bartlam

List of Publications by Year in descending order

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73
papers

2,352
citations

236612

25
h-index

214527

47
g-index

78
all docs

78
docs citations

78
times ranked

3122
citing authors

#	ARTICLE	IF	CITATIONS
1	Selective enrichment of bacterial pathogens by microplastic biofilm. <i>Water Research</i> , 2019, 165, 114979.	5.3	408
2	Structural insights into diversity and n-alkane biodegradation mechanisms of alkane hydroxylases. <i>Frontiers in Microbiology</i> , 2013, 4, 58.	1.5	169
3	Crystal Structure of Long-Chain Alkane Monooxygenase (LadA) in Complex with Coenzyme FMN: Unveiling the Long-Chain Alkane Hydroxylase. <i>Journal of Molecular Biology</i> , 2008, 376, 453-465.	2.0	163
4	Crystal structure of the human CNOT6L nuclease domain reveals strict poly(A) substrate specificity. <i>EMBO Journal</i> , 2010, 29, 2566-2576.	3.5	87
5	Structural insights into SARS coronavirus proteins. <i>Current Opinion in Structural Biology</i> , 2005, 15, 664-672.	2.6	75
6	Molecular Characterization of a Class I P450 Electron Transfer System from <i>Novosphingobium aromaticivorans</i> DSM12444. <i>Journal of Biological Chemistry</i> , 2010, 285, 27372-27384.	1.6	74
7	Crystal Structure of an Acylpeptide Hydrolase/Esterase from <i>Aeropyrum pernix</i> K1. <i>Structure</i> , 2004, 12, 1481-1488.	1.6	73
8	A Highly Active Singleâ€Mutation Variant of P450_{BM3} (CYP102A1). <i>ChemBioChem</i> , 2009, 10, 1654-1656.	1.3	72
9	Structural Basis for the Properties of Two Singleâ€Site Proline Mutants of CYP102A1 (P450_{BM3}). <i>ChemBioChem</i> , 2010, 11, 2549-2556.	1.3	63
10	The structural basis for deadenylation by the CCR4-NOT complex. <i>Protein and Cell</i> , 2010, 1, 443-452.	4.8	61
11	Protein recognition in ferredoxinâ€P450 electron transfer in the class I CYP199A2 system from <i>Rhodospseudomonas palustris</i> . <i>Journal of Biological Inorganic Chemistry</i> , 2010, 15, 315-328.	1.1	56
12	Crystal Structure of CYP199A2, a Para-Substituted Benzoic Acid Oxidizing Cytochrome P450 from <i>Rhodospseudomonas palustris</i> . <i>Journal of Molecular Biology</i> , 2008, 383, 561-574.	2.0	55
13	Comparison of ITS and 18S rDNA for estimating fungal diversity using PCRâ€DGGE. <i>World Journal of Microbiology and Biotechnology</i> , 2015, 31, 1387-1395.	1.7	44
14	Six-helix bundle assembly and characterization of heptad repeat regions from the F protein of Newcastle disease virus. <i>Journal of General Virology</i> , 2002, 83, 623-629.	1.3	43
15	Crystal structures of human BTG2 and mouse TIS21 involved in suppression of CAF1 deadenylase activity. <i>Nucleic Acids Research</i> , 2008, 36, 6872-6881.	6.5	43
16	Biodegradation of decabromodiphenyl ether (BDE 209) by a newly isolated bacterium from an e-waste recycling area. <i>AMB Express</i> , 2018, 8, 27.	1.4	41
17	Crystal structure of a ferredoxin reductase for the CYP199A2 system from <i>Rhodospseudomonas palustris</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 867-880.	1.5	40
18	Structure, electronic properties and catalytic behaviour of an activity-enhancing CYP102A1 (P450BM3) variant. <i>Dalton Transactions</i> , 2011, 40, 10383.	1.6	40

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19	Combination of biochar amendment and phytoremediation for hydrocarbon removal in petroleum-contaminated soil. <i>Environmental Science and Pollution Research</i> , 2016, 23, 21219-21228.	2.7	40
20	Insights into the structure and architecture of the CCR4-Not complex. <i>Frontiers in Genetics</i> , 2014, 5, 137.	1.1	37
21	The structure of CYP101D2 unveils a potential path for substrate entry into the active site. <i>Biochemical Journal</i> , 2011, 433, 85-93.	1.7	36
22	Structural proteomics of the SARS coronavirus: a model response to emerging infectious diseases. <i>Journal of Structural and Functional Genomics</i> , 2007, 8, 85-97.	1.2	35
23	Crystal Structure of the C-Terminal Domain of Human DPY-30-Like Protein: A Component of the Histone Methyltransferase Complex. <i>Journal of Molecular Biology</i> , 2009, 390, 530-537.	2.0	33
24	Spatial-Temporal Changes of Bacterioplankton Community along an Exorheic River. <i>Frontiers in Microbiology</i> , 2016, 7, 250.	1.5	32
25	Structural Analysis of CYP101C1 from <i>Novosphingobium aromaticivorans</i> DSM12444. <i>ChemBioChem</i> , 2011, 12, 88-99.	1.3	31
26	Structural basis for the recognition of MucA by MucB and AlgU in <i>Pseudomonas aeruginosa</i> . <i>FEBS Journal</i> , 2019, 286, 4982-4994.	2.2	27
27	Distribution and diversity of fungi in freshwater sediments on a river catchment scale. <i>Frontiers in Microbiology</i> , 2015, 6, 329.	1.5	26
28	PDlim2 Selectively Interacts with the PDZ Binding Motif of Highly Pathogenic Avian H5N1 Influenza A Virus NS1. <i>PLoS ONE</i> , 2011, 6, e19511.	1.1	26
29	Structure and function of CYP108D1 from <i>Novosphingobium aromaticivorans</i> DSM12444: an aromatic hydrocarbon-binding P450 enzyme. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 277-291.	2.5	25
30	Isolation, Characterization, and Antiproliferative Activities of Eudesmanolide Derivatives from the Flowers of <i>Inula japonica</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2015, 63, 9006-9011.	2.4	24
31	Long-Term Effects of Residual Chlorine on <i>Pseudomonas aeruginosa</i> in Simulated Drinking Water Fed With Low AOC Medium. <i>Frontiers in Microbiology</i> , 2018, 9, 879.	1.5	23
32	Crystal structure of human transgelin. <i>Journal of Structural Biology</i> , 2008, 162, 229-236.	1.3	22
33	Sesquiterpenes from <i>Carpesium macrocephalum</i> inhibit <i>Candida albicans</i> biofilm formation and dimorphism. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2015, 25, 5409-5411.	1.0	21
34	Integrated metagenomic and metatranscriptomic analysis reveals actively expressed antibiotic resistomes in the plastisphere. <i>Journal of Hazardous Materials</i> , 2022, 430, 128418.	6.5	21
35	Structural and Biochemical Analysis of Tyrosine Phosphatase Related to Biofilm Formation A (Tpba) from the Opportunistic Pathogen <i>Pseudomonas aeruginosa</i> PAO1. <i>PLoS ONE</i> , 2015, 10, e0124330.	1.1	20
36	Crystal-Structure and Biochemical Characterization of Recombinant Human Calcyphosine Delineates a Novel EF-Hand-Containing Protein Family. <i>Journal of Molecular Biology</i> , 2008, 383, 455-464.	2.0	19

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37	Structural and Functional Changes of Groundwater Bacterial Community During Temperature and pH Disturbances. <i>Microbial Ecology</i> , 2019, 78, 428-445.	1.4	18
38	Different biotransformation of three hexabromocyclododecane diastereoisomers by <i>Pseudomonas</i> sp. under aerobic conditions. <i>Chemical Engineering Journal</i> , 2019, 374, 870-879.	6.6	17
39	Spatio-Temporal Variations of High and Low Nucleic Acid Content Bacteria in an Exorheic River. <i>PLoS ONE</i> , 2016, 11, e0153678.	1.1	17
40	Structural insights into YfiR sequestering by YfiB in <i>Pseudomonas aeruginosa</i> PAO1. <i>Scientific Reports</i> , 2015, 5, 16915.	1.6	16
41	Genome Sequence of a Typical Ultramicrobacterium, <i>Curvibacter</i> sp. Strain PAE-UM, Capable of Phthalate Ester Degradation. <i>Genome Announcements</i> , 2016, 4, .	0.8	16
42	Transport mechanism of a glutamate transporter homologue GltPh. <i>Biochemical Society Transactions</i> , 2016, 44, 898-904.	1.6	15
43	Structural and functional insight into the mechanism of an alkaline exonuclease from <i>Laribacter hongkongensis</i> . <i>Nucleic Acids Research</i> , 2011, 39, 9803-9819.	6.5	13
44	A Versatile Strategy for Production of Membrane Proteins with Diverse Topologies: Application to Investigation of Bacterial Homologues of Human Divalent Metal Ion and Nucleoside Transporters. <i>PLoS ONE</i> , 2015, 10, e0143010.	1.1	12
45	Resistance and resilience of representative low nucleic acid-content bacteria to free chlorine exposure. <i>Journal of Hazardous Materials</i> , 2019, 365, 270-279.	6.5	12
46	Mechanism of Dephosphorylation of Glucosyl-3-phosphoglycerate by a Histidine Phosphatase. <i>Journal of Biological Chemistry</i> , 2014, 289, 21242-21251.	1.6	9
47	Structural basis for inhibition of the deadenylase activity of human CNOT6L. <i>FEBS Letters</i> , 2016, 590, 1270-1279.	1.3	9
48	Structure of the human Ccr4-Not nuclease module using X-ray crystallography and electron paramagnetic resonance spectroscopy distance measurements. <i>Protein Science</i> , 2022, 31, 758-764.	3.1	9
49	Structural basis for prokaryotic calcium-mediated regulation by a <i>Streptomyces coelicolor</i> calcium binding protein. <i>Protein and Cell</i> , 2010, 1, 771-779.	4.8	8
50	Crystal structure of RecR, a member of the RecFOR DNA-repair pathway, from <i>Pseudomonas aeruginosa</i> PAO1. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 222-230.	0.4	7
51	Biogeography and Diversity of Freshwater Bacteria on a River Catchment Scale. <i>Microbial Ecology</i> , 2019, 78, 324-335.	1.4	7
52	Crystallization and preliminary X-ray characterization of an NAD(P)-dependent butanol dehydrogenase A from <i>Geobacillus thermodenitrificans</i> NG80-2. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 184-187.	0.7	5
53	Structure and characterization of a NAD(P)H-dependent carbonyl reductase from <i>Pseudomonas aeruginosa</i> PAO1. <i>FEBS Letters</i> , 2017, 591, 1785-1797.	1.3	5
54	Crystal structure of a glutamate-1-semialdehyde-aminomutase from <i>Pseudomonas aeruginosa</i> PAO1. <i>Biochemical and Biophysical Research Communications</i> , 2018, 500, 804-809.	1.0	5

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55	Structural characterization of an acetolactate decarboxylase from <i>Klebsiella pneumoniae</i> . <i>Biochemical and Biophysical Research Communications</i> , 2019, 509, 154-160.	1.0	5
56	Structure of <i>Pseudomonas aeruginosa</i> spermidine dehydrogenase: a polyamine oxidase with a novel heme-binding fold. <i>FEBS Journal</i> , 2022, 289, 1911-1928.	2.2	5
57	The search for a structural basis for therapeutic intervention against the SARS coronavirus. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2008, 64, 204-213.	0.3	4
58	Complete Genome Sequence of <i>Stenotrophomonas</i> sp. Strain WZN-1, Which Is Capable of Degrading Polybrominated Diphenyl Ethers. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
59	Structure of subunit I of the anthranilate synthase complex of <i>Mycobacterium smegmatis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2020, 527, 37-41.	1.0	3
60	Functional Characterization of the \hat{I}^3 -Aminobutyric Acid Transporter from <i>Mycobacterium smegmatis</i> MC 2 155 Reveals Sodium-Driven GABA Transport. <i>Journal of Bacteriology</i> , 2021, 203, .	1.0	3
61	Structure and mechanism of the \hat{I}^3 -glutamyl- \hat{I}^3 -aminobutyrate hydrolase SpuA from <i>Pseudomonas aeruginosa</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1305-1316.	1.1	3
62	Crystallization and Preliminary Crystallographic Analysis of Transgelin. <i>Protein and Peptide Letters</i> , 2007, 14, 209-211.	0.4	2
63	Structural basis for inhibition of the Tob-CNOT7 interaction by a fragment screening approach. <i>Protein and Cell</i> , 2015, 6, 924-928.	4.8	2
64	Purification, crystallization and X-ray crystallographic analysis of a putative exopolyphosphatase from <i>Zymomonas mobilis</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 172-178.	0.4	2
65	Structural analysis of activating mutants of YfiB from <i>Pseudomonas aeruginosa</i> PAO1. <i>Biochemical and Biophysical Research Communications</i> , 2018, 506, 997-1003.	1.0	2
66	Structural characterization of an isopenicillin N synthase family oxygenase from <i>Pseudomonas aeruginosa</i> PAO1. <i>Biochemical and Biophysical Research Communications</i> , 2019, 514, 1031-1036.	1.0	2
67	Structural characterization of a 2-aminoethylphosphonate:pyruvate aminotransferase from <i>Pseudomonas aeruginosa</i> PAO1. <i>Biochemical and Biophysical Research Communications</i> , 2021, 552, 114-119.	1.0	2
68	Structural characterization of the urease accessory protein UreF from <i>Klebsiella pneumoniae</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2022, 78, 75-80.	0.4	2
69	Structural characterization of the <i>Pseudomonas aeruginosa</i> dehydrogenase AtuB involved in citronellol and geraniol catabolism. <i>Biochemical and Biophysical Research Communications</i> , 2020, 523, 954-960.	1.0	1
70	Structural characterization and Kemp eliminase activity of the <i>Mycobacterium smegmatis</i> Ketosteroid Isomerase. <i>Biochemical and Biophysical Research Communications</i> , 2021, 560, 159-164.	1.0	1
71	Characteristics, Biodiversity, and Cultivation Strategy of Low Nucleic Acid Content Bacteria. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
72	Crystal structure of oligoribonuclease from <i>Vibrio cholerae</i> O1 El Tor with bound peptide. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021, 77, 437-443.	0.4	0

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73	Structural characterization of an L-fucose-1-phosphate aldolase from <i>Klebsiella pneumoniae</i> . Biochemical and Biophysical Research Communications, 2022, 607, 15-19.	1.0	0