

Biswarup Mukhopadhyay

List of Publications by Year in descending order

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68
papers

2,436
citations

218677

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73
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73
docs citations

73
times ranked

2718
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genome of <i>M. acetivorans</i> Reveals Extensive Metabolic and Physiological Diversity. <i>Genome Research</i> , 2002, 12, 532-542.	5.5	573
2	Construction of a hybrid quadrupole/fourier transform ion cyclotron resonance mass spectrometer for versatile MS/MS above 10 kDa. <i>Journal of the American Society for Mass Spectrometry</i> , 2004, 15, 1099-1108.	2.8	107
3	Methanogenic bacteria in human vaginal samples. <i>Journal of Clinical Microbiology</i> , 1990, 28, 1666-1668.	3.9	105
4	Genomic Characterization of Methanomicrobiales Reveals Three Classes of Methanogens. <i>PLoS ONE</i> , 2009, 4, e5797.	2.5	103
5	A New Type of Sulfite Reductase, a Novel Coenzyme F420-dependent Enzyme, from the Methanarchaeon <i>Methanocaldococcus jannaschii</i> *. <i>Journal of Biological Chemistry</i> , 2005, 280, 38776-38786.	3.4	87
6	A novel p _H ² control on the expression of flagella in the hyperthermophilic strictly hydrogenotrophic methanarchaeon <i>Methanococcus jannaschii</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 11522-11527.	7.1	82
7	Ribosomal protein L7Ae is a subunit of archaeal RNase P. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 14573-14578.	7.1	71
8	Conversion of NO ₂ to NO by reduced coenzyme F ₄₂₀ protects mycobacteria from nitrosative damage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6333-6338.	7.1	70
9	Reactor-Scale Cultivation of the Hyperthermophilic Methanarchaeon <i>Methanococcus jannaschii</i> to High Cell Densities. <i>Applied and Environmental Microbiology</i> , 1999, 65, 5059-5065.	3.1	65
10	TmpL, a Transmembrane Protein Required for Intracellular Redox Homeostasis and Virulence in a Plant and an Animal Fungal Pathogen. <i>PLoS Pathogens</i> , 2009, 5, e1000653.	4.7	62
11	Genetic analysis of mch mutants in two Methanosarcina species demonstrates multiple roles for the methanopterin-dependent C-1 oxidation/reduction pathway and differences in H ₂ metabolism between closely related species. <i>Molecular Microbiology</i> , 2005, 55, 1671-1680.	2.5	59
12	Genome Sequence of <i>Thermofilum pendens</i> Reveals an Exceptional Loss of Biosynthetic Pathways without Genome Reduction. <i>Journal of Bacteriology</i> , 2008, 190, 2957-2965.	2.2	53
13	Purification, Regulation, and Molecular and Biochemical Characterization of Pyruvate Carboxylase from <i>Methanobacterium thermoautotrophicum</i> Strain 1 ^H . <i>Journal of Biological Chemistry</i> , 1998, 273, 5155-5166.	3.4	51
14	Aerobic purification of <i>N</i> ⁵ , <i>N</i> ¹⁰ -methylene tetrahydromethanopterin dehydrogenase, separated from <i>N</i> ⁵ , <i>N</i> ¹⁰ -methylene tetrahydromethanopterin cyclohydrolase, from <i>Methanobacterium thermoautotrophicum</i> strain Marburg. <i>Canadian Journal of Microbiology</i> , 1989, 35, 499-507.	1.7	49
15	Cloning, Sequencing, and Transcriptional Analysis of the Coenzyme F420-dependent Methylene-5,6,7,8-tetrahydromethanopterin Dehydrogenase Gene from <i>Methanobacterium thermoautotrophicum</i> Strain Marburg and Functional Expression in <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 1995, 270, 2827-2832.	3.4	46
16	An aminoacyl tRNA synthetase whose sequence fits into neither of the two known classes. <i>Nature</i> , 2001, 411, 110-114.	27.8	46
17	A GTP-dependent Vertebrate-type Phosphoenolpyruvate Carboxykinase from <i>Mycobacterium smegmatis</i> . <i>Journal of Biological Chemistry</i> , 2001, 276, 16137-16145.	3.4	42
18	Coenzyme F ₄₂₀ -Dependent Sulfite Reductase-Enabled Sulfite Detoxification and Use of Sulfite as a Sole Sulfur Source by <i>Methanococcus marisaludis</i> . <i>Applied and Environmental Microbiology</i> , 2008, 74, 3591-3595.	3.1	41

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19	An Intertwined Evolutionary History of Methanogenic Archaea and Sulfate Reduction. PLoS ONE, 2012, 7, e45313.	2.5	41
20	Thioredoxin targets fundamental processes in a methane-producing archaeon, <i>Methanocaldococcus jannaschii</i> . Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2608-2613.	7.1	41
21	Rv0132c of <i>Mycobacterium tuberculosis</i> Encodes a Coenzyme F420-Dependent Hydroxymycolic Acid Dehydrogenase. PLoS ONE, 2013, 8, e81985.	2.5	36
22	Comparative Genomics and Proteomic Analysis of Assimilatory Sulfate Reduction Pathways in Anaerobic Methanotrophic Archaea. Frontiers in Microbiology, 2018, 9, 2917.	3.5	33
23	Effect of temperature on the spectral properties of coenzyme F420 and related compounds. Analytical Biochemistry, 1992, 205, 342-350.	2.4	32
24	Pyruvate carboxylase from <i>Mycobacterium smegmatis</i> : stabilization, rapid purification, molecular and biochemical characterization and regulation of the cellular level. Biochimica Et Biophysica Acta - General Subjects, 2000, 1475, 191-206.	2.4	32
25	Ferredoxin:thioredoxin reductase (FTR) links the regulation of oxygenic photosynthesis to deeply rooted bacteria. Planta, 2013, 237, 619-635.	3.2	31
26	The Phosphoenolpyruvate Carboxylase from <i>Methanothermobacter thermautotrophicus</i> Has a Novel Structure. Journal of Bacteriology, 2004, 186, 5129-5137.	2.2	30
27	Engineered Microbial Production of 2-Pyrone-4,6-Dicarboxylic Acid from Lignin Residues for Use as an Industrial Platform Chemical. BioResources, 2016, 11, .	1.0	30
28	A stable archaeal pyruvate carboxylase from the hyperthermophile <i>Methanococcus jannaschii</i> . Archives of Microbiology, 2000, 174, 406-414.	2.2	26
29	The complete genome sequence of <i>Staphylothermus marinus</i> reveals differences in sulfur metabolism among heterotrophic Crenarchaeota. BMC Genomics, 2009, 10, 145.	2.8	26
30	Oxaloacetate Synthesis in the Methanarchaeon <i>Methanosarcina barkeri</i> : Pyruvate Carboxylase Genes and a Putative <i>Escherichia coli</i> -Type Bifunctional Biotin Protein Ligase Gene (<i>bpl/birA</i>) Exhibit a Unique Organization. Journal of Bacteriology, 2001, 183, 3804-3810.	2.2	24
31	Characterization of an NADH oxidase of the flavin-dependent disulfide reductase family from <i>Methanocaldococcus jannaschii</i> . Microbiology (United Kingdom), 2009, 155, 69-79.	1.8	23
32	A Novel F420-dependent Thioredoxin Reductase Gated by Low Potential FAD. Journal of Biological Chemistry, 2016, 291, 23084-23100.	3.4	22
33	A Genetic System for <i>Methanocaldococcus jannaschii</i> : An Evolutionary Deeply Rooted Hyperthermophilic Methanarchaeon. Frontiers in Microbiology, 2019, 10, 1256.	3.5	22
34	Identification of Pyruvate Carboxylase Genes in <i>Pseudomonas aeruginosa</i> PAO1 and Development of a <i>P. aeruginosa</i> -Based Overexpression System for Γ - and Γ -Type Pyruvate Carboxylases. Applied and Environmental Microbiology, 2006, 72, 7785-7792.	3.1	21
35	Characterization of a <i>Methanosarcina</i> strain isolated from goat feces, and that grows on H ₂ -CO ₂ only after adaptation. Current Microbiology, 1991, 23, 165-173.	2.2	19
36	Genetic resources for advanced biofuel production described with the Gene Ontology. Frontiers in Microbiology, 2014, 5, 528.	3.5	18

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37	Conditions for Vigorous Growth on Sulfide and Reactor-Scale Cultivation Protocols for the Thermophilic Green Sulfur Bacterium <i>Chlorobium tepidum</i> . Applied and Environmental Microbiology, 1999, 65, 301-306.	3.1	18
38	Genetic resources for methane production from biomass described with the Gene Ontology. Frontiers in Microbiology, 2014, 5, 634.	3.5	16
39	Reclassification of <i>Desulfurococcus mobilis</i> as a synonym of <i>Desulfurococcus mucosus</i> , <i>Desulfurococcus fermentans</i> and <i>Desulfurococcus kamchatkensis</i> as synonyms of <i>Desulfurococcus amylolyticus</i> , and emendation of the <i>D. mucosus</i> and <i>D. amylolyticus</i> species descriptions. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 514-517.	1.7	16
40	Proline utilization system is required for infection by the pathogenic $\hat{\alpha}$ -proteobacterium <i>Brucella abortus</i> . Microbiology (United Kingdom), 2017, 163, 970-979.	1.8	16
41	Complete Genome Sequence of <i>Desulfurococcus fermentans</i> , a Hyperthermophilic Cellulolytic Crenarchaeon Isolated from a Freshwater Hot Spring in Kamchatka, Russia. Journal of Bacteriology, 2012, 194, 5703-5704.	2.2	15
42	F ₄₂₀ H ₂ Is Required for Phthiocerol Dimycocerosate Synthesis in Mycobacteria. Journal of Bacteriology, 2016, 198, 2020-2028.	2.2	15
43	Kinetic characterization of recombinant human cytosolic phosphoenolpyruvate carboxykinase with and without a His10-tag. Biochimica Et Biophysica Acta - General Subjects, 2007, 1770, 1576-1584.	2.4	14
44	Effect of methanogenic substrates on coenzyme F ₄₂₀ -dependent N ₅ ,N ₁₀ -methylene-H ₄ MPT dehydrogenase, N ₅ ,N ₁₀ -methenyl-H ₄ MPT cyclohydrolase and F ₄₂₀ -reducing hydrogenase activities in <i>Methanosarcina barkeri</i> . Archives of Microbiology, 1993, 159, 141-146.	2.2	13
45	Tyr235 of human cytosolic phosphoenolpyruvate carboxykinase influences catalysis through an anion- π quadrupole interaction with phosphoenolpyruvate carboxylate. FEBS Journal, 2008, 275, 5810-5819.	4.7	11
46	A Reexamination of Thioredoxin Reductase from <i>Thermoplasma acidophilum</i> , a Thermoacidophilic Euryarchaeon, Identifies It as an NADH-Dependent Enzyme. ACS Omega, 2017, 2, 4180-4187.	3.5	9
47	Tn2008-driven carbapenem resistance in <i>Acinetobacter baumannii</i> isolates from a period of increased incidence of infections in a Southwest Virginia hospital (USA). Journal of Global Antimicrobial Resistance, 2018, 12, 79-87.	2.2	9
48	Roles of Asp75, Asp78, and Glu83 of GTP-dependent Phosphoenolpyruvate Carboxykinase from <i>Mycobacterium smegmatis</i> . Journal of Biological Chemistry, 2006, 281, 39262-39272.	3.4	8
49	Establishment of a Gene Expression System in <i>Ochrobactrum anthropi</i> . Applied and Environmental Microbiology, 2006, 72, 6833-6836.	3.1	8
50	Coenzyme F ₄₂₀ -Dependent Glucose-6-Phosphate Dehydrogenase-Coupled Polyglutamylation of Coenzyme F ₄₂₀ in Mycobacteria. Journal of Bacteriology, 2018, 200, .	2.2	7
51	A Novel Coenzyme F ₄₂₀ Dependent Sulfite Reductase and a Small Sulfite Reductase in Methanogenic Archaea. , 2008, , 202-216.		7
52	Structure of an archaeal α -type phosphoenolpyruvate carboxylase sensitive to inhibition by aspartate. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1820-1829.	2.6	6
53	Whole genome sequence analysis reveals the broad distribution of the RtxA type 1 secretion system and four novel putative type 1 secretion systems throughout the <i>Legionella</i> genus. PLoS ONE, 2020, 15, e0223033.	2.5	5
54	Elucidation of structure-function relationships in <i>Methanocaldococcus jannaschii</i> RNase P, a multi-subunit catalytic ribonucleoprotein. Nucleic Acids Research, 2022, 50, 8154-8167.	14.5	5

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55	A Reduced F ₄₂₀ -Dependent Nitrite Reductase in an Anaerobic Methanotrophic Archaeon. Journal of Bacteriology, 2022, 204, .	2.2	3
56	Expression, purification and crystallization of an archaeal-type phosphoenolpyruvate carboxylase. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1193-1196.	0.7	2
57	Understanding of Genetic Code Degeneracy and New Way of Classifying of Protein Family: A Mathematical Approach. , 2016, , .		2
58	Permanent draft genome sequence of Desulfurococcus mobilis type strain DSM 2161, a thermoacidophilic sulfur-reducing crenarchaeon isolated from acidic hot springs of Hveravellir, Iceland. Standards in Genomic Sciences, 2016, 11, 3.	1.5	2
59	Complete Genome Sequence of Bordetella pertussis Pelita III, the Production Strain for an Indonesian Whole-Cell Pertussis Vaccine. Genome Announcements, 2017, 5, .	0.8	2
60	Permanent Draft Genome Sequence of Desulfurococcus amylolyticus Strain Z-533 ^T , a Peptide and Starch Degradar Isolated from Thermal Springs in the Kamchatka Peninsula and Kunashir Island, Russia. Genome Announcements, 2017, 5, .	0.8	2
61	Dominant remodelling of cattle rumen microbiome by Schedonorus arundinaceus (tall fescue) KY-31 carrying a fungal endophyte. Access Microbiology, 2022, 4, 000322.	0.5	2
62	Reduced protein sequence patterns in identifying key structural elements of dissimilatory sulfite reductase homologs. Computational Biology and Chemistry, 2022, 98, 107691.	2.3	1
63	Characterization of F ₃₉₀ synthetase activity in cell extracts of <i>Methanobacterium thermoautotrophicum</i> Marburg. Canadian Journal of Microbiology, 1994, 40, 306-309.	1.7	0
64	352Clinical and molecular characteristics of NDM-1 harboring Multi-Drug Resistant Gram Negative Bacteria at Carilion Medical Center. Open Forum Infectious Diseases, 2014, 1, S139-S140.	0.9	0
65	Title is missing!. , 2020, 15, e0223033.		0
66	Title is missing!. , 2020, 15, e0223033.		0
67	Title is missing!. , 2020, 15, e0223033.		0
68	Title is missing!. , 2020, 15, e0223033.		0