Biswarup Mukhopadhyay

List of Publications by Year
in descending order

68 papers	2,436 citations	218677 26 h-index	206112 48 g-index
73 all docs	73 docs citations	73 times ranked	2718 citing authors

#	Article	IF	Citations
1	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
2	Reduced protein sequence patterns in identifying key structural elements of dissimilatory sulfite reductase homologs. Computational Biology and Chemistry, 2022, 98, 107691.	2.3	1
3	A Reduced F ₄₂₀ -Dependent Nitrite Reductase in an Anaerobic Methanotrophic Archaeon. Journal of Bacteriology, 2022, 204, .	2.2	3
4	Elucidation of structureâ€“function relationships in Methanocaldococcus jannaschii RNase P, a multi-subunit catalytic ribonucleoprotein. Nucleic Acids Research, 2022, 50, 8154-8167.	14.5	5
5	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 Legionella genus. PLoS ONE, 2020, 15, e0223033.	2.5	5
6	Title is missing!. , 2020, 15, e0223033.		0
7	Title is missing!. , 2020, 15, e0223033.		0
8	Title is missing!. , 2020, 15, e0223033.		0
9	Title is missing!. , 2020, 15, e0223033.		0
10	A Genetic System for Methanocaldococcus jannaschii: An Evolutionary Deeply Rooted Hyperthermophilic Methanarchaeon. Frontiers in Microbiology, 2019, 10, 1256.	3.5	22
11	Tn2008-driven carbapenem resistance in Acinetobacter baumannii 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
12	Comparative Genomics and Proteomic Analysis of Assimilatory Sulfate Reduction Pathways in Anaerobic Methanotrophic Archaea. Frontiers in Microbiology, 2018, 9, 2917.	3.5	33
13	Coenzyme F ₄₂₀ -Dependent Glucose-6-Phosphate Dehydrogenase-Coupled Polyglutamylation of Coenzyme F ₄₂₀ in Mycobacteria. Journal of Bacteriology, 2018, 200, .	2.2	7
14	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
15	Permanent Draft Genome Sequence of Desulfurococcus amylolyticus Strain Z-533 ^T , a Peptide and Starch Degrader Isolated from Thermal Springs in the Kamchatka Peninsula and Kunashir Island, Russia. Genome Announcements, 2017, 5, .	0.8	2
16	A Reexamination of Thioredoxin Reductase from Thermoplasma acidophilum, a Thermoacidophilic Euryarchaeon, Identifies It as an NADH-Dependent Enzyme. ACS Omega, 2017, 2, 4180-4187.	3.5	9
17	Proline utilization system is required for infection by the pathogenic Î±-proteobacterium Brucella abortus. Microbiology (United Kingdom), 2017, 163, 970-979.	1.8	16
18	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

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19	F ₄₂₀ H ₂ Is Required for Phthiocerol Dimycocerosate Synthesis in Mycobacteria. Journal of Bacteriology, 2016, 198, 2020-2028.	2.2	15
20	Understanding of Genetic Code Degeneracy and New Way of Classifying of Protein Family: A Mathematical Approach. , 2016, , .		2
21	A Novel F420-dependent Thioredoxin Reductase Gated by Low Potential FAD. Journal of Biological Chemistry, 2016, 291, 23084-23100.	3.4	22
22	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
23	Reclassification of Desulfurococcus mobilis as a synonym of Desulfurococcus mucosus, Desulfurococcus fermentans and Desulfurococcus kamchatkensis as synonyms of Desulfurococcus amylolyticus, and emendation of the D. mucosus and D. amylolyticus species descriptions. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 514-517.	1.7	16
24	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
25	Thioredoxin targets fundamental processes in a methane-producing archaeon, Methanocaldococcus jannaschii. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2608-2613.	7.1	41
26	Genetic resources for advanced biofuel production described with the Gene Ontology. Frontiers in Microbiology, 2014, 5, 528.	3.5	18
27	Genetic resources for methane production from biomass described with the Gene Ontology. Frontiers in Microbiology, 2014, 5, 634.	3.5	16
28	Ferredoxin:thioredoxin reductase (FTR) links the regulation of oxygenic photosynthesis to deeply rooted bacteria. Planta, 2013, 237, 619-635.	3.2	31
29	Rv0132c of Mycobacterium tuberculosis Encodes a Coenzyme F420-Dependent Hydroxymycolic Acid Dehydrogenase. PLoS ONE, 2013, 8, e81985.	2.5	36
30	Complete Genome Sequence of Desulfurococcus fermentans, a Hyperthermophilic Cellulolytic Crenarchaeon Isolated from a Freshwater Hot Spring in Kamchatka, Russia. Journal of Bacteriology, 2012, 194, 5703-5704.	2.2	15
31	An Intertwined Evolutionary History of Methanogenic Archaea and Sulfate Reduction. PLoS ONE, 2012, 7, e45313.	2.5	41
32	Structure of an archaealâ€type phosphoenolpyruvate carboxylase sensitive to inhibition by aspartate. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1820-1829.	2.6	6
33	Ribosomal protein L7Ae is a subunit of archaeal RNase P. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 14573-14578.	7.1	71
34	Characterization of an NADH oxidase of the flavin-dependent disulfide reductase family from Methanocaldococcus jannaschii. Microbiology (United Kingdom), 2009, 155, 69-79.	1.8	23
35	Conversion of NO ₂ to NO by reduced coenzyme F ₄₂₀ protects mycobacteria from nitrosative damage. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 6333-6338.	7.1	70
36	TmpL, a Transmembrane Protein Required for Intracellular Redox Homeostasis and Virulence in a Plant and an Animal Fungal Pathogen. PLoS Pathogens, 2009, 5, e1000653.	4.7	62

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37	The complete genome sequence of Staphylothermus marinus reveals differences in sulfur metabolism among heterotrophic Crenarchaeota. BMC Genomics, 2009, 10, 145.	2.8	26
38	Expression, purification and crystallization of an archaeal-type phosphoenolpyruvate carboxylase. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1193-1196.	0.7	2
39	Genomic Characterization of Methanomicrobiales Reveals Three Classes of Methanogens. PLoS ONE, 2009, 4, e5797.	2.5	103
40	Tyr235 of human cytosolic phosphoenolpyruvate carboxykinase influences catalysis through an anionâ€“quadrupole interaction with phosphoenolpyruvate carboxylate. FEBS Journal, 2008, 275, 5810-5819.	4.7	11
41	Coenzyme F ₄₂₀ -Dependent Sulfite Reductase-Enabled Sulfite Detoxification and Use of Sulfite as a Sole Sulfur Source by Methanococcus maripaludis. Applied and Environmental Microbiology, 2008, 74, 3591-3595.	3.1	41
42	Genome Sequence of Thermofilum pendens Reveals an Exceptional Loss of Biosynthetic Pathways without Genome Reduction. Journal of Bacteriology, 2008, 190, 2957-2965.	2.2	53
43	A Novel Coenzyme F420 Dependent Sulfite Reductase and a Small Sulfite Reductase in Methanogenic Archaea. , 2008, , 202-216.		7
44	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
45	Roles of Asp75, Asp78, and Glu83 of GTP-dependent Phosphoenolpyruvate Carboxykinase from Mycobacterium smegmatis. Journal of Biological Chemistry, 2006, 281, 39262-39272.	3.4	8
46	Establishment of a Gene Expression System in Ochrobactrum anthropi. Applied and Environmental Microbiology, 2006, 72, 6833-6836.	3.1	8
47	Identification of Pyruvate Carboxylase Genes in Pseudomonas aeruginosa PAO1 and Development of a P. aeruginosa-Based Overexpression System for Î±4- and Î±4Î²4-Type Pyruvate Carboxylases. Applied and Environmental Microbiology, 2006, 72, 7785-7792.	3.1	21
48	Genetic analysis ofmchmutants in twoMethanosarcinaspecies demonstrates multiple roles for the methanopterin-dependent C-1 oxidation/reduction pathway and differences in H2metabolism between closely related species. Molecular Microbiology, 2005, 55, 1671-1680.	2.5	59
49	A New Type of Sulfite Reductase, a Novel Coenzyme F420-dependent Enzyme, from the Methanarchaeon Methanocaldococcus jannaschii*. Journal of Biological Chemistry, 2005, 280, 38776-38786.	3.4	87
50	The Phosphoenolpyruvate Carboxylase from Methanothermobacter thermautotrophicus Has a Novel Structure. Journal of Bacteriology, 2004, 186, 5129-5137.	2.2	30
51	Construction of a hybrid quadrupole/fourier transform ion cyclotron resonance mass spectrometer for versatile MS/MS above 10 kDa. Journal of the American Society for Mass Spectrometry, 2004, 15, 1099-1108.	2.8	107
52	The Genome of M. acetivorans Reveals Extensive Metabolic and Physiological Diversity. Genome Research, 2002, 12, 532-542.	5.5	573
53	An aminoacyl tRNA synthetase whose sequence fits into neither of the two known classes. Nature, 2001, 411, 110-114.	27.8	46
54	A GTP-dependent Vertebrate-type Phosphoenolpyruvate Carboxykinase from Mycobacterium smegmatis. Journal of Biological Chemistry, 2001, 276, 16137-16145.	3.4	42

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55	Oxaloacetate Synthesis in the Methanarchaeon Methanosarcina barkeri : Pyruvate Carboxylase Genes and a Putative Escherichia coli -Type Bifunctional Biotin Protein Ligase Gene (bpl/birA) Exhibit a Unique Organization. Journal of Bacteriology, 2001, 183, 3804-3810.	2.2	24
56	A stable archaeal pyruvate carboxylase from the hyperthermophile Methanococcus jannaschii. Archives of Microbiology, 2000, 174, 406-414.	2.2	26
57	A novel p _{H ₂} control on the expression of flagella in the hyperthermophilic strictly hydrogenotrophic methanarchaeaon Methanococcus jannaschii. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 11522-11527.	7.1	82
58	Pyruvate carboxylase from Mycobacterium smegmatis: 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
59	Conditions for Vigorous Growth on Sulfide and Reactor-Scale Cultivation Protocols for the Thermophilic Green Sulfur Bacterium Chlorobium tepidum. Applied and Environmental Microbiology, 1999, 65, 301-306.	3.1	18
60	Reactor-Scale Cultivation of the Hyperthermophilic Methanarchaeon Methanococcus jannaschii to High Cell Densities. Applied and Environmental Microbiology, 1999, 65, 5059-5065.	3.1	65
61	Purification, Regulation, and Molecular and Biochemical Characterization of Pyruvate Carboxylase from Methanobacterium thermoautotrophicum Strain Î”H. Journal of Biological Chemistry, 1998, 273, 5155-5166.	3.4	51
62	Cloning, Sequencing, and Transcriptional Analysis of the Coenzyme F420-dependent Methylene-5,6,7,8-tetrahydromethanopterin Dehydrogenase Gene from Methanobacterium thermoautotrophicum Strain Marburg and Functional Expression in Escherichia coli. Journal of Biological Chemistry, 1995, 270, 2827-2832.	3.4	46
63	Characterization of F₃₉₀ synthetase activity in cell extracts of Methanobacterium thermoautotrophicum Marburg. Canadian Journal of Microbiology, 1994, 40, 306-309.	1.7	0
64	Effect of methanogenic substrates on coenzyme F420-dependent N5,N10-methylene-H4MPT dehydrogenase, N5,N10-methenyl-H4MPT cyclohydrolase and F420-reducing hydrogenase activities in Methanosarcina barkeri. Archives of Microbiology, 1993, 159, 141-146.	2.2	13
65	Effect of temperature on the spectral properties of coenzyme F420 and related compounds. Analytical Biochemistry, 1992, 205, 342-350.	2.4	32
66	Characterization of aMethanosarcina strain isolated from goat feces, and that grows on H2-CO2 only after adaptation. Current Microbiology, 1991, 23, 165-173.	2.2	19
67	Methanogenic bacteria in human vaginal samples. Journal of Clinical Microbiology, 1990, 28, 1666-1668.	3.9	105
68	Aerobic purification of N⁵,N¹⁰-methylenetetrahydromethanopterin dehydrogenase, separated from N⁵,N¹⁰-methenyltetrahydromethanopterin cyclohydrolase, from Methanobacterium thermoautotrophicum strain Marburg. Canadian Journal of Microbiology, 1989, 35, 499-507.	1.7	49