

Michael A Kertesz

List of Publications by Year in descending order

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73
papers

4,279
citations

101543

36
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114465

63
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74
all docs

74
docs citations

74
times ranked

4467
citing authors

#	ARTICLE	IF	CITATIONS
1	Riding the sulfur cycle – metabolism of sulfonates and sulfate esters in Gram-negative bacteria. FEMS Microbiology Reviews, 2000, 24, 135-175.	8.6	295
2	The role of soil microbes in plant sulphur nutrition. Journal of Experimental Botany, 2004, 55, 1939-1945.	4.8	229
3	Characterization of α -Ketoglutarate-dependent Taurine Dioxygenase from Escherichia coli. Journal of Biological Chemistry, 1997, 272, 23031-23036.	3.4	227
4	<i>phoD</i> Alkaline Phosphatase Gene Diversity in Soil. Applied and Environmental Microbiology, 2015, 81, 7281-7289.	3.1	206
5	1.3 Å... Structure of Arylsulfatase from Pseudomonas aeruginosa Establishes the Catalytic Mechanism of Sulfate Ester Cleavage in the Sulfatase Family. Structure, 2001, 9, 483-491.	3.3	177
6	Riding the sulfur cycle – metabolism of sulfonates and sulfate esters in Gram-negative bacteria. FEMS Microbiology Reviews, 2000, 24, 135-175.	8.6	176
7	Soil <i>phoD</i> and <i>phoX</i> alkaline phosphatase gene diversity responds to multiple environmental factors. FEMS Microbiology Ecology, 2017, 93, fiw212.	2.7	137
8	Effect of Sphingobium yanoikuyae B1 inoculation on bacterial community dynamics and polycyclic aromatic hydrocarbon degradation in aged and freshly PAH-contaminated soils. Environmental Pollution, 2006, 144, 228-237.	7.5	120
9	Posttranslational Formation of Formylglycine in Prokaryotic Sulfatases by Modification of Either Cysteine or Serine. Journal of Biological Chemistry, 1998, 273, 25560-25564.	3.4	113
10	Purification and Characterization of the Arylsulfatase Synthesized by Pseudomonas aeruginosa PAO During Growth in Sulfate-Free Medium and Cloning of the Arylsulfatase Gene (atsA). FEBS Journal, 1995, 229, 385-394.	0.2	107
11	Characterization of a Sulfur-regulated Oxygenative Alkylsulfatase from Pseudomonas putida S-313. Journal of Biological Chemistry, 2000, 275, 31661-31667.	3.4	96
12	Compost bacteria and fungi that influence growth and development of Agaricus bisporus and other commercial mushrooms. Applied Microbiology and Biotechnology, 2018, 102, 1639-1650.	3.6	96
13	Bacterial transporters for sulfate and organosulfur compounds. Research in Microbiology, 2001, 152, 279-290.	2.1	94
14	Total and active microbial communities and <i>phoD</i> as affected by phosphate depletion and pH in soil. Plant and Soil, 2016, 408, 15-30.	3.7	93
15	Pathways of Assimilative Sulfur Metabolism in <i>Pseudomonas putida</i> . Journal of Bacteriology, 1999, 181, 5833-5837.	2.2	89
16	Genotype \times Genotype Interactions Modified by a Third Species in a Plant-Insect System. American Naturalist, 2007, 170, 492-499.	2.1	89
17	Crystal Structure of the Alkylsulfatase AtsK: Insights into the Catalytic Mechanism of the Fe(II) α -Ketoglutarate-Dependent Dioxygenase Superfamily. Biochemistry, 2004, 43, 3075-3088.	2.5	88
18	Transcriptomic Analysis of the Sulfate Starvation Response of <i>Pseudomonas aeruginosa</i> . Journal of Bacteriology, 2007, 189, 6743-6750.	2.2	84

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19	The role of <i>Variovorax</i> and other <i>Comamonadaceae</i> in sulfur transformations by microbial wheat rhizosphere communities exposed to different sulfur fertilization regimes. <i>Environmental Microbiology</i> , 2008, 10, 1486-1500.	3.8	81
20	Analysis of Global Responses by Protein and Peptide Fingerprinting of Proteins Isolated by Two-Dimensional Gel Electrophoresis. Application to the Sulfate-Starvation Response of <i>Escherichia Coli</i> . <i>FEBS Journal</i> , 1996, 239, 773-781.	0.2	78
21	The <i>ssu</i> Locus Plays a Key Role in Organosulfur Metabolism in <i>Pseudomonas putida</i> S-313. <i>Journal of Bacteriology</i> , 2000, 182, 2869-2878.	2.2	75
22	A Novel Reduced Flavin Mononucleotide-Dependent Methanesulfonate Sulfonatase Encoded by the Sulfur-Regulated <i>msu</i> Operon of <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 1999, 181, 1464-1473.	2.2	73
23	Structural studies on the full-length Lys-type regulator TsaR from <i>Comamonas testosteroni</i> reveal a novel open conformation of the tetrameric LTTR fold. <i>Molecular Microbiology</i> , 2010, 75, 1199-1214.	2.5	72
24	Indirect effects of polycyclic aromatic hydrocarbon contamination on microbial communities in legume and grass rhizospheres. <i>Plant and Soil</i> , 2012, 358, 169-182.	3.7	68
25	Desulfonation of Linear Alkylbenzenesulfonate Surfactants and Related Compounds by Bacteria. <i>Applied and Environmental Microbiology</i> , 1994, 60, 2296-2303.	3.1	68
26	Rhizobacteria and Plant Sulfur Supply. <i>Advances in Applied Microbiology</i> , 2007, 62, 235-268.	2.4	64
27	Determination of Cypermethrin Degradation Potential of Soil Bacteria Along with Plant Growth-Promoting Characteristics. <i>Current Microbiology</i> , 2015, 70, 75-84.	2.2	59
28	Effect of crop rotation on mycorrhizal colonization and wheat yield under different fertilizer treatments. <i>Agriculture, Ecosystems and Environment</i> , 2017, 247, 130-136.	5.3	59
29	Genetic organization of sulphur-controlled aryl desulphonation in <i>Pseudomonas putida</i> S-313. <i>Molecular Microbiology</i> , 1999, 32, 913-926.	2.5	57
30	Evidence for two distinct phosphonate-degrading enzymes (C-P lyases) in <i>Arthrobacter</i> sp. GLP-1. <i>Biodegradation</i> , 1991, 2, 53-59.	3.0	51
31	Quantitative trait loci mapping of phenotypic plasticity and genotype-environment interactions in plant and insect performance. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2011, 366, 1368-1379.	4.0	47
32	Proteome mapping, mass spectrometric sequencing and reverse transcription-PCR for characterization of the sulfate starvation-induced response in <i>Pseudomonas aeruginosa</i> PAO1. <i>FEBS Journal</i> , 1999, 266, 986-996.	0.2	45
33	Arbuscular mycorrhizal fungal hyphae mediating acidification can promote phytate mineralization in the hyphosphere of maize (<i>Zea mays</i> L.). <i>Soil Biology and Biochemistry</i> , 2013, 65, 69-74.	8.8	43
34	Effect of twenty four wheat genotypes on soil biochemical and microbial properties. <i>Plant and Soil</i> , 2016, 404, 141-155.	3.7	42
35	Desulfurization of mucin by <i>Pseudomonas aeruginosa</i> : influence of sulfate in the lungs of cystic fibrosis patients. <i>Journal of Medical Microbiology</i> , 2012, 61, 1644-1653.	1.8	40
36	Desulfurization of aromatic sulfonates by rhizosphere bacteria: high diversity of the <i>asfA</i> gene. <i>Environmental Microbiology</i> , 2007, 9, 535-545.	3.8	39

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37	The Sulfur-Regulated Arylsulfatase Gene Cluster of <i>Pseudomonas aeruginosa</i> , a New Member of the <i>cys</i> Regulon. <i>Journal of Bacteriology</i> , 2000, 182, 2055-2058.	2.2	38
38	Construction of improved plasmid vectors for promoter characterization in <i>Pseudomonas aeruginosa</i> and other Gram-negative bacteria. <i>FEMS Microbiology Letters</i> , 1998, 169, 179-183.	1.8	37
39	The LysR-type regulator SftR is involved in soil survival and sulphate ester metabolism in <i>Pseudomonas putida</i> . <i>Environmental Microbiology</i> , 2002, 4, 225-237.	3.8	37
40	Succinate Complex Crystal Structures of the α -Ketoglutarate-dependent Dioxygenase AtsK. <i>Journal of Biological Chemistry</i> , 2005, 280, 5716-5723.	3.4	32
41	Caffeine metabolism during cultivation of oyster mushroom (<i>Pleurotus ostreatus</i>) with spent coffee grounds. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 5831-5841.	3.6	31
42	Autecological properties of soil sphingomonads involved in the degradation of polycyclic aromatic hydrocarbons. <i>Applied Microbiology and Biotechnology</i> , 2006, 72, 1083-1089.	3.6	30
43	Seasonal total methane depletion in limestone caves. <i>Scientific Reports</i> , 2017, 7, 8314.	3.3	30
44	Probing protein function using a combination of gene knockout and proteome analysis by mass spectrometry. <i>Electrophoresis</i> , 1997, 18, 432-442.	2.4	28
45	Effect of inoculum pretreatment on survival, activity and catabolic gene expression of <i>Sphingobium yanoikuyae</i> B1 in an aged polycyclic aromatic hydrocarbon-contaminated soil. <i>FEMS Microbiology Ecology</i> , 2006, 58, 364-372.	2.7	28
46	Bacterial community analysis of cypermethrin enrichment cultures and bioremediation of cypermethrin contaminated soils. <i>Journal of Basic Microbiology</i> , 2015, 55, 819-829.	3.3	28
47	Phosphorus forms affect the rhizosphere bacterial community involved in soil organic phosphorus turnover. <i>Mycorrhiza</i> , 2019, 29, 351-362.	2.8	27
48	Sulfonate desulfurization in <i>Rhodococcus</i> from wheat rhizosphere communities. <i>FEMS Microbiology Ecology</i> , 2009, 67, 140-150.	2.7	26
49	Importance of Organosulfur Utilization for Survival of <i>Pseudomonas putida</i> in Soil and Rhizosphere. <i>Applied and Environmental Microbiology</i> , 2005, 71, 6571-6577.	3.1	25
50	Desulfonation of aliphatic sulfonates by <i>Pseudomonas aeruginosa</i> PAO. <i>FEMS Microbiology Letters</i> , 1996, 137, 221-225.	1.8	24
51	Community genetic interactions mediate indirect ecological effects between a parasitoid wasp and rhizobacteria. <i>Ecology</i> , 2010, 91, 1563-1568.	3.2	24
52	Variation in specific root length among 23 wheat genotypes affects leaf $\delta^{13}C$ and yield. <i>Agriculture, Ecosystems and Environment</i> , 2017, 246, 21-29.	5.3	22
53	Bacterial community analysis in chlorpyrifos enrichment cultures via DGGE and use of bacterial consortium for CP biodegradation. <i>World Journal of Microbiology and Biotechnology</i> , 2014, 30, 2755-2766.	3.6	20
54	Sample handling for proteome analysis. <i>Electrophoresis</i> , 1998, 19, 901-908.	2.4	18

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55	Specific influence of white clover on the rhizosphere microbial community in response to polycyclic aromatic hydrocarbon (PAH) contamination. <i>Plant and Soil</i> , 2016, 401, 365-379.	3.7	18
56	Two-dimensional single strand conformation polymorphism (SSCP) of 16S rRNA gene fragments reveals highly dissimilar bacterial communities in an acidic fen. <i>European Journal of Soil Biology</i> , 2008, 44, 495-500.	3.2	16
57	Metabolism of Sulphur-Containing Organic Compounds. , 2004, , 323-357.		16
58	Sulfate treatment affects desulfonating bacterial community structures in <i>Agrostis</i> rhizospheres as revealed by functional gene analysis based on <i>asfA</i> . <i>European Journal of Soil Biology</i> , 2010, 46, 248-254.	3.2	15
59	Dual-labeling with ^{15}N and H_2^{18}O to investigate water and N uptake of wheat under different water regimes. <i>Plant and Soil</i> , 2016, 408, 429-441.	3.7	15
60	Assessment of functional diversity and structure of phytate-hydrolysing bacterial community in <i>Lolium perenne</i> rhizosphere. <i>Plant and Soil</i> , 2016, 401, 151-167.	3.7	15
61	Studying root water uptake of wheat genotypes in different soils using water ^{18}O stable isotopes. <i>Agriculture, Ecosystems and Environment</i> , 2018, 264, 119-129.	5.3	14
62	Aerobic Hydrocarbon-Degrading Alphaproteobacteria: Sphingomonadales. , 2019, , 105-124.		14
63	Identification of Plant Quantitative Trait Loci Modulating a Rhizobacteria-Aphid Indirect Effect. <i>PLoS ONE</i> , 2012, 7, e41524.	2.5	13
64	Mineral surface reactivity and mass transfer in environmental mineralogy. <i>European Journal of Mineralogy</i> , 2007, 19, 297-307.	1.3	11
65	Transcriptional response of <i>Pseudomonas aeruginosa</i> to a phosphate-deficient <i>Lolium perenne</i> rhizosphere. <i>Plant and Soil</i> , 2012, 359, 25-44.	3.7	11
66	Biological Cycling of Inorganic Nutrients and Metals in Soils and Their Role in Soil Biogeochemistry. , 2015, , 471-503.		11
67	Bacterial population dynamics in recycled mushroom compost leachate. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 5335-5342.	3.6	9
68	Rhizosphere 3: where plants meet soils down-under. <i>Plant and Soil</i> , 2012, 358, 1-5.	3.7	7
69	Aerobic Hydrocarbon-Degrading Alphaproteobacteria: Sphingomonadales. , 2018, , 1-21.		4
70	Comparative effect of alternative fertilisers on pasture production, soil properties and soil microbial community structure. <i>Crop and Pasture Science</i> , 2019, 70, 1110.	1.5	4
71	Construction of improved plasmid vectors for promoter characterization in <i>Pseudomonas aeruginosa</i> and other Gram-negative bacteria. <i>FEMS Microbiology Letters</i> , 1998, 169, 179-183.	1.8	2
72	High crystallizability under air-exclusion conditions of the full-length LysR-type transcriptional regulator <i>TsaR</i> from <i>Comamonas testosteroni</i> T-2 and data-set analysis for a MIRAS structure-solution approach. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 764-769.	0.7	1

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73	Purification and Characterization of the Arylsulfatase Synthesized by <i>Pseudomonas aeruginosa</i> PAO During Growth in Sulfate-Free Medium and Cloning of the Arylsulfatase Gene (<i>atsA</i>). <i>FEBS Journal</i> , 1995, 229, 385-394.	0.2	1