

# Michael A Kertesz

## List of Publications by Year in descending order

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Version: 2024-02-01

73  
papers

4,279  
citations

101543  
36  
h-index

114465  
63  
g-index

74  
all docs

74  
docs citations

74  
times ranked

4467  
citing authors

| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 1  | 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        |
| 2  | Phosphorus forms affect the hyphosphere bacterial community involved in soil organic phosphorus turnover. <i>Mycorrhiza</i> , 2019, 29, 351-362.   | 2.8 | 27        |
| 3  | 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         |
| 4  | Aerobic Hydrocarbon-Degrading Alphaproteobacteria: Sphingomonadales. , 2019, , 105-124.  |     | 14        |
| 5  | Compost bacteria and fungi that influence growth and development of <i>Agaricus bisporus</i> and other commercial mushrooms. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 1639-1650. | 3.6 | 96        |
| 6  | Bacterial population dynamics in recycled mushroom compost leachate. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 5335-5342.   | 3.6 | 9         |
| 7  | Aerobic Hydrocarbon-Degrading Alphaproteobacteria: Sphingomonadales. , 2018, , 1-21.   |     | 4         |
| 8  | Studying root water uptake of wheat genotypes in different soils using water $\delta^{18}\text{O}$ stable isotopes. <i>Agriculture, Ecosystems and Environment</i> , 2018, 264, 119-129.           | 5.3 | 14        |
| 9  | Seasonal total methane depletion in limestone caves. <i>Scientific Reports</i> , 2017, 7, 8314.  | 3.3 | 30        |
| 10 | 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        |
| 11 | Soil <i>phoD</i> and <i>phoX</i> alkaline phosphatase gene diversity responds to multiple environmental factors. <i>FEMS Microbiology Ecology</i> , 2017, 93, fiw212.                              | 2.7 | 137       |
| 12 | Variation in specific root length among 23 wheat genotypes affects leaf $\delta^{13}\text{C}$ and yield. <i>Agriculture, Ecosystems and Environment</i> , 2017, 246, 21-29.                        | 5.3 | 22        |
| 13 | Effect of twenty four wheat genotypes on soil biochemical and microbial properties. <i>Plant and Soil</i> , 2016, 404, 141-155.  | 3.7 | 42        |
| 14 | Total and active microbial communities and <i>phoD</i> as affected by phosphate depletion and pH in soil. <i>Plant and Soil</i> , 2016, 408, 15-30.  | 3.7 | 93        |
| 15 | Dual-labeling with $^{15}\text{N}$ and $\text{H}_2^{18}\text{O}$ to investigate water and N uptake of wheat under different water regimes. <i>Plant and Soil</i> , 2016, 408, 429-441.             | 3.7 | 15        |
| 16 | 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        |
| 17 | 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        |
| 18 | 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        |

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|----|---|-----|-----------|
| 19 | Biological Cycling of Inorganic Nutrients and Metals in Soils and Their Role in Soil Biogeochemistry. , 2015, , 471-503.  |     | 11        |
| 20 | Alkaline Phosphatase Gene Diversity in Soil. Applied and Environmental Microbiology, 2015, 81, 7281-7289.   | 3.1 | 206       |
| 21 | Determination of Cypermethrin Degradation Potential of Soil Bacteria Along with Plant Growth-Promoting Characteristics. Current Microbiology, 2015, 70, 75-84.  | 2.2 | 59        |
| 22 | Bacterial community analysis in chlorpyrifos enrichment cultures via DGGE and use of bacterial consortium for CP biodegradation. World Journal of Microbiology and Biotechnology, 2014, 30, 2755-2766.  | 3.6 | 20        |
| 23 | Arbuscular mycorrhizal fungal hyphae mediating acidification can promote phytate mineralization in the hyphosphere of maize ( <i>Zea mays</i> L.). Soil Biology and Biochemistry, 2013, 65, 69-74.  | 8.8 | 43        |
| 24 | Desulfurization of mucin by <i>Pseudomonas aeruginosa</i> : influence of sulfate in the lungs of cystic fibrosis patients. Journal of Medical Microbiology, 2012, 61, 1644-1653.  | 1.8 | 40        |
| 25 | Rhizosphere 3: where plants meet soils down-under. Plant and Soil, 2012, 358, 1-5.  | 3.7 | 7         |
| 26 | Transcriptional response of <i>Pseudomonas aeruginosa</i> to a phosphate-deficient <i>Lolium perenne</i> rhizosphere. Plant and Soil, 2012, 359, 25-44.   | 3.7 | 11        |
| 27 | Indirect effects of polycyclic aromatic hydrocarbon contamination on microbial communities in legume and grass rhizospheres. Plant and Soil, 2012, 358, 169-182.  | 3.7 | 68        |
| 28 | Identification of Plant Quantitative Trait Loci Modulating a Rhizobacteria-Aphid Indirect Effect. PLoS ONE, 2012, 7, e41524.  | 2.5 | 13        |
| 29 | Quantitative trait loci mapping of phenotypic plasticity and genotype×environment interactions in plant and insect performance. Philosophical Transactions of the Royal Society B: Biological Sciences, 2011, 366, 1368-1379.   | 4.0 | 47        |
| 30 | Structural studies on the full-length LysR-type regulator TsaR from <i>Comamonas testosteroni</i> T-2 reveal a novel open conformation of the tetrameric LTTR fold. Molecular Microbiology, 2010, 75, 1199-1214.  | 2.5 | 72        |
| 31 | Community genetic interactions mediate indirect ecological effects between a parasitoid wasp and rhizobacteria. Ecology, 2010, 91, 1563-1568.   | 3.2 | 24        |
| 32 | Sulfate treatment affects desulfonating bacterial community structures in <i>Agrostis</i> rhizospheres as revealed by functional gene analysis based on <i>asfA</i> . European Journal of Soil Biology, 2010, 46, 248-254.  | 3.2 | 15        |
| 33 | Sulfonate desulfurization in <i>Rhodococcus</i> from wheat rhizosphere communities. FEMS Microbiology Ecology, 2009, 67, 140-150.   | 2.7 | 26        |
| 34 | High crystallizability under air-exclusion conditions of the full-length LysR-type transcriptional regulator TsaR from <i>Comamonas testosteroni</i> T-2 and data-set analysis for a MIRAS structure-solution approach. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 764-769. | 0.7 | 1         |
| 35 | 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. Environmental Microbiology, 2008, 10, 1486-1500.  | 3.8 | 81        |
| 36 | Two-dimensional single strand conformation polymorphism (SSCP) of 16S rRNA gene fragments reveals highly dissimilar bacterial communities in an acidic fen. European Journal of Soil Biology, 2008, 44, 495-500.  | 3.2 | 16        |

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|----|---|-----|-----------|
| 37 | Rhizobacteria and Plant Sulfur Supply. <i>Advances in Applied Microbiology</i> , 2007, 62, 235-268.   | 2.4 | 64        |
| 38 | Transcriptomic Analysis of the Sulfate Starvation Response of <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2007, 189, 6743-6750.  | 2.2 | 84        |
| 39 | Genotype×Genotype Interactions Modified by a Third Species in a Plant-Insect System. <i>American Naturalist</i> , 2007, 170, 492-499.   | 2.1 | 89        |
| 40 | Mineral surface reactivity and mass transfer in environmental mineralogy. <i>European Journal of Mineralogy</i> , 2007, 19, 297-307.  | 1.3 | 11        |
| 41 | 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        |
| 42 | Effect of <i>Sphingobium yanoikuyae</i> B1 inoculation on bacterial community dynamics and polycyclic aromatic hydrocarbon degradation in aged and freshly PAH-contaminated soils. <i>Environmental Pollution</i> , 2006, 144, 228-237.     | 7.5 | 120       |
| 43 | 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        |
| 44 | 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        |
| 45 | 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        |
| 46 | Succinate Complex Crystal Structures of the $\pm$ -Ketoglutarate-dependent Dioxygenase AtsK. <i>Journal of Biological Chemistry</i> , 2005, 280, 5716-5723.   | 3.4 | 32        |
| 47 | The role of soil microbes in plant sulphur nutrition. <i>Journal of Experimental Botany</i> , 2004, 55, 1939-1945.  | 4.8 | 229       |
| 48 | Crystal Structure of the Alkylsulfatase AtsK: Insights into the Catalytic Mechanism of the Fe(II) $\pm$ -Ketoglutarate-Dependent Dioxygenase Superfamily. <i>Biochemistry</i> , 2004, 43, 3075-3088.  | 2.5 | 88        |
| 49 | Metabolism of Sulphur-Containing Organic Compounds. , 2004, , 323-357.  |     | 16        |
| 50 | 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        |
| 51 | Bacterial transporters for sulfate and organosulfur compounds. <i>Research in Microbiology</i> , 2001, 152, 279-290.  | 2.1 | 94        |
| 52 | 1.3 Å... Structure of Arylsulfatase from <i>Pseudomonas aeruginosa</i> Establishes the Catalytic Mechanism of Sulfate Ester Cleavage in the Sulfatase Family. <i>Structure</i> , 2001, 9, 483-491.  | 3.3 | 177       |
| 53 | Riding the sulfur cycle “ metabolism of sulfonates and sulfate esters in Gram-negative bacteria. <i>FEMS Microbiology Reviews</i> , 2000, 24, 135-175.  | 8.6 | 176       |
| 54 | Riding the sulfur cycle “ metabolism of sulfonates and sulfate esters in Gram-negative bacteria. <i>FEMS Microbiology Reviews</i> , 2000, 24, 135-175.  | 8.6 | 295       |

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|----|---|-----|-----------|
| 55 | Characterization of a Sulfur-regulated Oxygenative Alkylsulfatase from <i>Pseudomonas putida</i> S-313. <i>Journal of Biological Chemistry</i> , 2000, 275, 31661-31667.  | 3.4 | 96        |
| 56 | 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        |
| 57 | 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        |
| 58 | Pathways of Assimilative Sulfur Metabolism in <i>Pseudomonas putida</i> . <i>Journal of Bacteriology</i> , 1999, 181, 5833-5837.  | 2.2 | 89        |
| 59 | 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        |
| 60 | 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        |
| 61 | A Novel Reduced Flavin Mononucleotide-Dependent Methanesulfonate Sulfonase 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        |
| 62 | 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        |
| 63 | Sample handling for proteome analysis. <i>Electrophoresis</i> , 1998, 19, 901-908.  | 2.4 | 18        |
| 64 | Posttranslational Formation of Formylglycine in Prokaryotic Sulfatases by Modification of Either Cysteine or Serine. <i>Journal of Biological Chemistry</i> , 1998, 273, 25560-25564.   | 3.4 | 113       |
| 65 | 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         |
| 66 | Characterization of $\alpha$ -Ketoglutarate-dependent Taurine Dioxygenase from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 1997, 272, 23031-23036.   | 3.4 | 227       |
| 67 | 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        |
| 68 | 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        |
| 69 | Desulfonation of aliphatic sulfonates by <i>Pseudomonas aeruginosa</i> PAO. <i>FEMS Microbiology Letters</i> , 1996, 137, 221-225.  | 1.8 | 24        |
| 70 | 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 | 107       |
| 71 | 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         |
| 72 | Desulfonation of Linear Alkylbenzenesulfonate Surfactants and Related Compounds by Bacteria. <i>Applied and Environmental Microbiology</i> , 1994, 60, 2296-2303.   | 3.1 | 68        |

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|----|--|-----|-----------|
| 73 | 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        |