

Sasha G Tetu

List of Publications by Year in descending order

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Version: 2024-02-01

61
papers

3,205
citations

186265

28
h-index

161849

54
g-index

64
all docs

64
docs citations

64
times ranked

4710
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative Genomics of Plant-Associated <i>Pseudomonas</i> spp.: Insights into Diversity and Inheritance of Traits Involved in Multitrophic Interactions. <i>PLoS Genetics</i> , 2012, 8, e1002784.	3.5	578
2	TransportDB 2.0: a database for exploring membrane transporters in sequenced genomes from all domains of life. <i>Nucleic Acids Research</i> , 2017, 45, D320-D324.	14.5	306
3	Complete Genome Sequence of the Multiresistant Taxonomic Outlier <i>Pseudomonas aeruginosa</i> PA7. <i>PLoS ONE</i> , 2010, 5, e8842.	2.5	236
4	Transcriptomic and biochemical analyses identify a family of chlorhexidine efflux proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20254-20259.	7.1	138
5	Plastic leachates impair growth and oxygen production in <i>Prochlorococcus</i> , the ocean's most abundant photosynthetic bacteria. <i>Communications Biology</i> , 2019, 2, 184.	4.4	135
6	Microarray analysis of phosphate regulation in the marine cyanobacterium <i>Synechococcus</i> sp. WH8102. <i>ISME Journal</i> , 2009, 3, 835-849.	9.8	131
7	The Complete Genome and Phenome of a Community-Acquired <i>Acinetobacter baumannii</i> . <i>PLoS ONE</i> , 2013, 8, e58628.	2.5	93
8	Long-Term Irrigation Affects the Dynamics and Activity of the Wheat Rhizosphere Microbiome. <i>Frontiers in Plant Science</i> , 2018, 9, 345.	3.6	73
9	Genomic analyses of <i>Clostridium perfringens</i> isolates from five toxinotypes. <i>Research in Microbiology</i> , 2015, 166, 255-263.	2.1	71
10	Life in the dark: metagenomic evidence that a microbial slime community is driven by inorganic nitrogen metabolism. <i>ISME Journal</i> , 2013, 7, 1227-1236.	9.8	63
11	The Peril and Promise of Integrons: Beyond Antibiotic Resistance. <i>Trends in Microbiology</i> , 2020, 28, 455-464.	7.7	62
12	The Effect of Iron Limitation on the Transcriptome and Proteome of <i>Pseudomonas fluorescens</i> Pf-5. <i>PLoS ONE</i> , 2012, 7, e39139.	2.5	62
13	Ecology and Evolution of the Human Microbiota: Fire, Farming and Antibiotics. <i>Genes</i> , 2015, 6, 841-857.	2.4	61
14	Colony Location and Captivity Influence the Gut Microbial Community Composition of the Australian Sea Lion (<i>Neophoca cinerea</i>). <i>Applied and Environmental Microbiology</i> , 2016, 82, 3440-3449.	3.1	61
15	Conserving the holobiont. <i>Functional Ecology</i> , 2020, 34, 764-776.	3.6	61
16	A synthesis of bacterial and archaeal phenotypic trait data. <i>Scientific Data</i> , 2020, 7, 170.	5.3	59
17	Genomics and the evolution of antibiotic resistance. <i>Annals of the New York Academy of Sciences</i> , 2017, 1388, 92-107.	3.8	50
18	High-Throughput Phenotypic Characterization of <i>Pseudomonas aeruginosa</i> Membrane Transport Genes. <i>PLoS Genetics</i> , 2008, 4, e1000211.	3.5	49

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19	Cereal products derived from wheat, sorghum, rice and oats alter the infant gut microbiota in vitro. <i>Scientific Reports</i> , 2017, 7, 14312.	3.3	48
20	The Flaveria bidentis Î ² -Carbonic Anhydrase Gene Family Encodes Cytosolic and Chloroplastic Isoforms Demonstrating Distinct Organ-Specific Expression Patterns. <i>Plant Physiology</i> , 2007, 144, 1316-1327.	4.8	47
21	Loss of the Transit Peptide and an Increase in Gene Expression of an Ancestral Chloroplastic Carbonic Anhydrase Were Instrumental in the Evolution of the Cytosolic C ₄ Carbonic Anhydrase in <i>Flaveria</i> . <i>Plant Physiology</i> , 2009, 150, 1515-1529.	4.8	47
22	The Coal Seam Microbiome (CSMB) reference set, a lingua franca for the microbial coal-to-methane community. <i>International Journal of Coal Geology</i> , 2018, 186, 41-50.	5.0	46
23	Cell size, genome size, and maximum growth rate are near-independent dimensions of ecological variation across bacteria and archaea. <i>Ecology and Evolution</i> , 2021, 11, 3956-3976.	1.9	43
24	PtrA is required for coordinate regulation of gene expression during phosphate stress in a marine <i>Synechococcus</i> . <i>ISME Journal</i> , 2010, 4, 908-921.	9.8	42
25	Complete Sequence of pJIE143, apir-Type Plasmid Carrying ISEcp1-blaCTX-M-15 from an Escherichia coli ST131 Isolate. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 5933-5935.	3.2	38
26	Effects of low temperature on tropical and temperate isolates of marine <i>Synechococcus</i> . <i>ISME Journal</i> , 2016, 10, 1252-1263.	9.8	36
27	Assessing the Toxicity of Leachates From Weathered Plastics on Photosynthetic Marine Bacteria Prochlorococcus. <i>Frontiers in Marine Science</i> , 2020, 7, .	2.5	36
28	Biolog Phenotype MicroArrays for Phenotypic Characterization of Microbial Cells. <i>Methods in Molecular Biology</i> , 2014, 1096, 123-130.	0.9	35
29	Succession Patterns and Physical Niche Partitioning in Microbial Communities from Subsurface Coal Seams. <i>IScience</i> , 2019, 12, 152-167.	4.1	32
30	The Natural History of Integrons. <i>Microorganisms</i> , 2021, 9, 2212.	3.6	32
31	Who eats what? Unravelling microbial conversion of coal to methane. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	29
32	Revealing colonisation and biofilm formation of an adherent coal seam associated microbial community on a coal surface. <i>International Journal of Coal Geology</i> , 2016, 160-161, 42-50.	5.0	27
33	An unusual integron in <i>Treponema denticola</i> . <i>Microbiology (United Kingdom)</i> , 2004, 150, 3524-3526.	1.8	26
34	A Family of Insertion Sequences That Impacts Integrons by Specific Targeting of Gene Cassette Recombination Sites, the IS ₁₁₁₁ -attC Group. <i>Journal of Bacteriology</i> , 2008, 190, 4959-4970.	2.2	26
35	Impact of DNA damaging agents on genome-wide transcriptional profiles in two marine <i>Synechococcus</i> species. <i>Frontiers in Microbiology</i> , 2013, 4, 232.	3.5	25
36	Fiber Supplements Derived From Sugarcane Stem, Wheat Dextrin and Psyllium Husk Have Different In Vitro Effects on the Human Gut Microbiota. <i>Frontiers in Microbiology</i> , 2018, 9, 1618.	3.5	25

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37	Predicting the taxonomic and environmental sources of integron gene cassettes using structural and sequence homology of attC sites. <i>Communications Biology</i> , 2021, 4, 946.	4.4	23
38	Trait dimensions in bacteria and archaea compared to vascular plants. <i>Ecology Letters</i> , 2021, 24, 1487-1504.	6.4	21
39	Alternative dietary protein and water temperature influence the skin and gut microbial communities of yellowtail kingfish (<i>Seriola lalandi</i>). <i>PeerJ</i> , 2020, 8, e8705.	2.0	21
40	Genomic and phenotypic insights point to diverse ecological strategies by facultative anaerobes obtained from subsurface coal seams. <i>Scientific Reports</i> , 2019, 9, 16186.	3.3	19
41	Aerobic bacteria and archaea tend to have larger and more versatile genomes. <i>Oikos</i> , 2021, 130, 501-511.	2.7	19
42	A Novel Family of Acinetobacter Mega-Plasmids Are Disseminating Multi-Drug Resistance Across the Globe While Acquiring Location-Specific Accessory Genes. <i>Frontiers in Microbiology</i> , 2020, 11, 605952.	3.5	18
43	How will marine plastic pollution affect bacterial primary producers?. <i>Communications Biology</i> , 2020, 3, 55.	4.4	16
44	Application of Transposon Insertion Sequencing to Agricultural Science. <i>Frontiers in Plant Science</i> , 2020, 11, 291.	3.6	16
45	Stress effects caused by the expression of a mutant cellobiohydrolase I and proteasome inhibition in <i>Trichoderma reesei</i> Rut-C30. <i>New Biotechnology</i> , 2013, 30, 183-191.	4.4	14
46	Investigating zinc toxicity responses in marine <i>Prochlorococcus</i> and <i>Synechococcus</i> . <i>Microbiology (United Kingdom)</i> , 2021, 167, .	1.8	13
47	Elucidating Essential Genes in Plant-Associated <i>Pseudomonas protegens</i> Pf-5 Using Transposon Insertion Sequencing. <i>Journal of Bacteriology</i> , 2021, 203, .	2.2	11
48	Genome Sequence of the Neurotoxigenic <i>Clostridium butyricum</i> Strain 5521. <i>Genome Announcements</i> , 2014, 2, .	0.8	10
49	The Transcriptomic Signature of Tigecycline in <i>Acinetobacter baumannii</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 565438.	3.5	10
50	Unravelling Stratified Microbial Assemblages in Australia's Only Deep Anchialine System, The Bundera Sinkhole. <i>Frontiers in Marine Science</i> , 0, 9, .	2.5	10
51	Subsurface Stappia: Success Through Defence, Specialisation and Putative Pressure-Dependent Carbon Fixation. <i>Microbial Ecology</i> , 2020, 80, 34-46.	2.8	9
52	Methods for the targeted sequencing and analysis of integrons and their gene cassettes from complex microbial communities. <i>Microbial Genomics</i> , 2022, 8, .	2.0	9
53	Strategic traits of bacteria and archaea vary widely within substrate-use groups. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	8
54	A Transcriptomic Approach to Identify Novel Drug Efflux Pumps in Bacteria. <i>Methods in Molecular Biology</i> , 2018, 1700, 221-235.	0.9	7

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55	Genome Sequence of the Group III Clostridium botulinum Strain Eklund-C. Genome Announcements, 2013, 1, e0004413.	0.8	5
56	Structure of a short-chain dehydrogenase/reductase (SDR) within a genomic island from a clinical strain of Acinetobacter baumannii. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1318-1323.	0.8	5
57	Delving into defence: identifying the Pseudomonas protegens Pf-5 gene suite involved in defence against secreted products of fungal, oomycete and bacterial rhizosphere competitors. Microbial Genomics, 2021, 7, .	2.0	4
58	Next Generation Barcode Tagged Sequencing for Monitoring Microbial Community Dynamics. Methods in Molecular Biology, 2014, 1096, 101-110.	0.9	2
59	Draft Genome Sequence of Dietzia sp. Strain SYD-A1, Isolated from Coal Seam Formation Water. Microbiology Resource Announcements, 2021, 10, .	0.6	1
60	6. Microbial Slime Curtain Communities of the Nullarbor Caves. , 2015, , 125-136.		0
61	From omics to systems biology: Exploring the mystery box of microbial life. Microbiology Australia, 2011, 32, 147.	0.4	0