

Johannes Sikorski

List of Publications by Year in descending order

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116
papers

5,696
citations

126708

33
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91712

69
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123
all docs

123
docs citations

123
times ranked

8888
citing authors

#	ARTICLE	IF	CITATIONS
1	The Evolution of Ecological Diversity in Acidobacteria. <i>Frontiers in Microbiology</i> , 2022, 13, 715637.	1.5	15
2	Differential Response of Acidobacteria to Water Content, Soil Type, and Land Use During an Extended Drought in African Savannah Soils. <i>Frontiers in Microbiology</i> , 2022, 13, 750456.	1.5	9
3	Biological Soil Crust From Mesic Forests Promote a Specific Bacteria Community. <i>Frontiers in Microbiology</i> , 2022, 13, 769767.	1.5	8
4	The multidimensionality of soil macroecology. <i>Global Ecology and Biogeography</i> , 2021, 30, 4-10.	2.7	16
5	The mineralosphere—interactive zone of microbial colonization and carbon use in grassland soils. <i>Biology and Fertility of Soils</i> , 2021, 57, 587-601.	2.3	11
6	Contrasting responses of above- and belowground diversity to multiple components of land-use intensity. <i>Nature Communications</i> , 2021, 12, 3918.	5.8	81
7	Among stand heterogeneity is key for biodiversity in managed beech forests but does not question the value of unmanaged forests: Response to Bruun and Heilmann—Clausen (2021). <i>Journal of Applied Ecology</i> , 2021, 58, 1817-1826.	1.9	8
8	Phylogenomics reveals the basis of adaptation of <i>Pseudorhizobium</i> species to extreme environments and supports a taxonomic revision of the genus. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126165.	1.2	33
9	Bacterial colonization of minerals in grassland soils is selective and highly dynamic. <i>Environmental Microbiology</i> , 2020, 22, 917-933.	1.8	23
10	Drivers of the composition of active rhizosphere bacterial communities in temperate grasslands. <i>ISME Journal</i> , 2020, 14, 463-475.	4.4	141
11	A single <i>Thaumarchaeon</i> drives nitrification in deep oligotrophic Lake Constance. <i>Environmental Microbiology</i> , 2020, 22, 212-228.	1.8	33
12	Stochastic Dispersal Rather Than Deterministic Selection Explains the Spatio-Temporal Distribution of Soil Bacteria in a Temperate Grassland. <i>Frontiers in Microbiology</i> , 2020, 11, 1391.	1.5	36
13	Blind spots in global soil biodiversity and ecosystem function research. <i>Nature Communications</i> , 2020, 11, 3870.	5.8	192
14	Can multi-taxa diversity in European beech forest landscapes be increased by combining different management systems?. <i>Journal of Applied Ecology</i> , 2020, 57, 1363-1375.	1.9	38
15	The impact of even-aged and uneven-aged forest management on regional biodiversity of multiple taxa in European beech forests. <i>Journal of Applied Ecology</i> , 2018, 55, 267-278.	1.9	188
16	Convergent Loss of ABC Transporter Genes From <i>Clostridioides difficile</i> Genomes Is Associated With Impaired Tyrosine Uptake and p-Cresol Production. <i>Frontiers in Microbiology</i> , 2018, 9, 901.	1.5	30
17	Function of bacterial community dynamics in the formation of cadaveric semiochemicals during <i>in situ</i> carcass decomposition. <i>Environmental Microbiology</i> , 2017, 19, 3310-3322.	1.8	26
18	Present and Future of Culturing Bacteria. <i>Annual Review of Microbiology</i> , 2017, 71, 711-730.	2.9	192

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19	Trajectories and Drivers of Genome Evolution in Surface-Associated Marine Phaeobacter. <i>Genome Biology and Evolution</i> , 2017, 9, 3297-3311.	1.1	13
20	Inferring interactions in complex microbial communities from nucleotide sequence data and environmental parameters. <i>PLoS ONE</i> , 2017, 12, e0173765.	1.1	15
21	Land-use intensification causes multitrophic homogenization of grassland communities. <i>Nature</i> , 2016, 540, 266-269.	13.7	404
22	Locally rare species influence grassland ecosystem multifunctionality. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150269.	1.8	117
23	Biodiversity at multiple trophic levels is needed for ecosystem multifunctionality. <i>Nature</i> , 2016, 536, 456-459.	13.7	526
24	Estimates of Soil Bacterial Ribosome Content and Diversity Are Significantly Affected by the Nucleic Acid Extraction Method Employed. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2595-2607.	1.4	28
25	Mining the phytomicrobiome to understand how bacterial coinoculations enhance plant growth. <i>Frontiers in Plant Science</i> , 2015, 6, 784.	1.7	33
26	Comparison of Rock Varnish Bacterial Communities with Surrounding Non-Varnished Rock Surfaces: Taxon-Specific Analysis and Morphological Description. <i>Microbial Ecology</i> , 2015, 70, 741-750.	1.4	36
27	Spatial Interaction of Archaeal Ammonia-Oxidizers and Nitrite-Oxidizing Bacteria in an Unfertilized Grassland Soil. <i>Frontiers in Microbiology</i> , 2015, 6, 1567.	1.5	40
28	Isolation and Characterization of Numerous Novel Phages Targeting Diverse Strains of the Ubiquitous and Opportunistic Pathogen <i>Achromobacter xylosoxidans</i> . <i>PLoS ONE</i> , 2014, 9, e86935.	1.1	30
29	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. <i>PLoS Biology</i> , 2014, 12, e1001920.	2.6	190
30	Comparative Analysis of Type III Secreted Effector Genes Reflects Divergence of <i>Acidovorax citrulli</i> Strains into Three Distinct Lineages. <i>Phytopathology</i> , 2014, 104, 1152-1162.	1.1	53
31	The Family Segniliparaceae. , 2014, , 877-881.		0
32	From genome mining to phenotypic microarrays: Planctomycetes as source for novel bioactive molecules. <i>Antonie Van Leeuwenhoek</i> , 2013, 104, 551-567.	0.7	99
33	opm: an R package for analysing OmniLog [®] phenotype microarray data. <i>Bioinformatics</i> , 2013, 29, 1823-1824.	1.8	214
34	Impacts of pr-10a Overexpression at the Molecular and the Phenotypic Level. <i>International Journal of Molecular Sciences</i> , 2013, 14, 15141-15166.	1.8	7
35	Phenotypic Variation in the Plant Pathogenic Bacterium <i>Acidovorax citrulli</i> . <i>PLoS ONE</i> , 2013, 8, e73189.	1.1	18
36	Complete genome sequence of the aerobic, heterotroph <i>Marinithermus hydrothermalis</i> type strain (T1T) from a deep-sea hydrothermal vent chimney. <i>Standards in Genomic Sciences</i> , 2012, 6, 21-30.	1.5	8

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37	Complete genome sequence of the aquatic bacterium <i>Runella slithyformis</i> type strain (LSU 4T). Standards in Genomic Sciences, 2012, 6, 145-154.	1.5	24
38	Complete genome sequence of the orange-red pigmented, radioresistant <i>Deinococcus proteolyticus</i> type strain (MRPT). Standards in Genomic Sciences, 2012, 6, 240-250.	1.5	14
39	Complete genome sequence of the sulfur compounds oxidizing chemolithoautotroph <i>Sulfuricumvum kujiense</i> type strain (YK-1T). Standards in Genomic Sciences, 2012, 6, 94-103.	1.5	37
40	<i>Pseudomonas aeruginosa</i> population structure revisited under environmental focus: impact of water quality and phage pressure. Environmental Microbiology, 2012, 14, 1952-1967.	1.8	104
41	Visualization and Curve-Parameter Estimation Strategies for Efficient Exploration of Phenotype Microarray Kinetics. PLoS ONE, 2012, 7, e34846.	1.1	173
42	Complete genome sequence of <i>Hydrogenobacter thermophilus</i> type strain (TK-6T). Standards in Genomic Sciences, 2011, 4, 131-143.	1.5	12
43	Complete genome sequence of <i>Desulfobulbus propionicus</i> type strain (1pr3T). Standards in Genomic Sciences, 2011, 4, 100-110.	1.5	51
44	Complete genome sequence of <i>Marivirga tractuosa</i> type strain (H-43T). Standards in Genomic Sciences, 2011, 4, 154-162.	1.5	18
45	Complete genome sequence of <i>Desulfurococcus mucosus</i> type strain (O7/1T). Standards in Genomic Sciences, 2011, 4, 173-182.	1.5	10
46	Complete genome sequence of the extremely halophilic <i>Halanaerobium praevalens</i> type strain (GSLT). Standards in Genomic Sciences, 2011, 4, 312-321.	1.5	36
47	Complete genome sequence of <i>Nitratifactor salsuginis</i> type strain (E9I37-1T). Standards in Genomic Sciences, 2011, 4, 322-330.	1.5	13
48	Complete genome sequence of <i>Mahella australiensis</i> type strain (50-1 BONT). Standards in Genomic Sciences, 2011, 4, 331-341.	1.5	7
49	Complete genome sequence of <i>Syntrophobotulus glycolicus</i> type strain (FGlyRT). Standards in Genomic Sciences, 2011, 4, 371-380.	1.5	11
50	Complete genome sequence of the hyperthermophilic chemolithoautotroph <i>Pyrolobus fumarii</i> type strain (1AT). Standards in Genomic Sciences, 2011, 4, 381-392.	1.5	13
51	Complete genome sequence of the gliding, heparinolytic <i>Pedobacter saltans</i> type strain (113T). Standards in Genomic Sciences, 2011, 5, 30-40.	1.5	16
52	Complete genome sequence of the thermophilic sulfur-reducer <i>Desulfurobacterium thermolithotrophum</i> type strain (BSAT) from a deep-sea hydrothermal vent. Standards in Genomic Sciences, 2011, 5, 407-415.	1.5	11
53	Complete genome sequence of <i>Calditerrivibrio nitroreducens</i> type strain (Yu37-1T). Standards in Genomic Sciences, 2011, 4, 54-62.	1.5	10
54	Complete genome sequence of <i>Oceanithermus profundus</i> type strain (506T). Standards in Genomic Sciences, 2011, 4, 210-220.	1.5	4

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55	Complete genome sequence of <i>Tsukamurella paurometabola</i> type strain (no. 33T). <i>Standards in Genomic Sciences</i> , 2011, 4, 342-351.	1.5	10
56	Complete genome sequence of the gliding freshwater bacterium <i>Fluviicola taffensis</i> type strain (RW262T). <i>Standards in Genomic Sciences</i> , 2011, 5, 21-29.	1.5	23
57	Identification and Targeted Cultivation of Abundant Novel Freshwater Sphingomonads and Analysis of Their Population Substructure. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7355-7364.	1.4	22
58	Complete genome sequence of <i>Thermomonospora curvata</i> type strain (B9T). <i>Standards in Genomic Sciences</i> , 2011, 4, 13-22.	1.5	35
59	Complete genome sequence of <i>Syntrophobotulus glycolicus</i> type strain (FLGlyR). <i>Standards in Genomic Sciences</i> , 2011, 4, 371-80.	1.5	4
60	Complete genome sequence of <i>Planctomyces limnophilus</i> type strain (MÅ¼ 290T). <i>Standards in Genomic Sciences</i> , 2010, 3, 47-56.	1.5	31
61	Complete genome sequence of <i>Ferrimonas balearica</i> type strain (PATT). <i>Standards in Genomic Sciences</i> , 2010, 3, 174-182.	1.5	14
62	Non-contiguous finished genome sequence of <i>Aminomonas paucivorans</i> type strain (GLU-3T). <i>Standards in Genomic Sciences</i> , 2010, 3, 285-293.	1.5	9
63	Complete genome sequence of <i>Ilyobacter polytropus</i> type strain (CuHbu1T). <i>Standards in Genomic Sciences</i> , 2010, 3, 304-314.	1.5	10
64	Complete genome sequence of <i>Nocardiopsis dassonvillei</i> type strain (IMRU 509T). <i>Standards in Genomic Sciences</i> , 2010, 3, 325-336.	1.5	32
65	Complete genome sequence of <i>Thermocrinis albus</i> type strain (HI 11/12T). <i>Standards in Genomic Sciences</i> , 2010, 2, 194-202.	1.5	18
66	Complete genome sequence of <i>Meiothermus silvanus</i> type strain (VI-R2T). <i>Standards in Genomic Sciences</i> , 2010, 3, 37-46.	1.5	19
67	Complete genome sequence of <i>Olsenella uli</i> type strain (VPI D76D-27CT). <i>Standards in Genomic Sciences</i> , 2010, 3, 76-84.	1.5	43
68	Complete genome sequence of <i>Meiothermus ruber</i> type strain (21T). <i>Standards in Genomic Sciences</i> , 2010, 3, 26-36.	1.5	33
69	Complete genome sequence of <i>Acetohalobium arabaticum</i> type strain (Z-7288T). <i>Standards in Genomic Sciences</i> , 2010, 3, 57-65.	1.5	24
70	Complete genome sequence of <i>Ignisphaera aggregans</i> type strain (AQ1.S1T). <i>Standards in Genomic Sciences</i> , 2010, 3, 66-75.	1.5	15
71	Complete genome sequence of <i>Vulcanisaeta distributa</i> type strain (IC-017T). <i>Standards in Genomic Sciences</i> , 2010, 3, 117-125.	1.5	10
72	Complete genome sequence of <i>Arcanobacterium haemolyticum</i> type strain (11018T). <i>Standards in Genomic Sciences</i> , 2010, 3, 126-135.	1.5	8

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73	Complete genome sequence of <i>Thermosediminibacter oceani</i> type strain (JW/IW-1228PT). <i>Standards in Genomic Sciences</i> , 2010, 3, 108-116.	1.5	12
74	Complete genome sequence of <i>Spirochaeta smaragdinae</i> type strain (SEBR 4228T). <i>Standards in Genomic Sciences</i> , 2010, 3, 1-9.	1.5	18
75	Complete genome sequence of <i>Syntrophothermus lipocalidus</i> type strain (TGB-C1T). <i>Standards in Genomic Sciences</i> , 2010, 3, 268-275.	1.5	13
76	Complete genome sequence of <i>Intrasporangium calvum</i> type strain (7 KIPT). <i>Standards in Genomic Sciences</i> , 2010, 3, 294-303.	1.5	7
77	Complete genome sequence of <i>Methanothermus fervidus</i> type strain (V24ST). <i>Standards in Genomic Sciences</i> , 2010, 3, 315-324.	1.5	17
78	Complete genome sequence of <i>Alicyclobacillus acidocaldarius</i> type strain (104-IAT). <i>Standards in Genomic Sciences</i> , 2010, 2, 9-18.	1.5	24
79	Complete genome sequence of <i>Sphaerobacter thermophilus</i> type strain (S 6022T). <i>Standards in Genomic Sciences</i> , 2010, 2, 49-56.	1.5	27
80	Complete genome sequence of <i>Streptosporangium roseum</i> type strain (NI 9100T). <i>Standards in Genomic Sciences</i> , 2010, 2, 29-37.	1.5	27
81	Complete genome sequence of <i>Sulfurospirillum deleyianum</i> type strain (5175T). <i>Standards in Genomic Sciences</i> , 2010, 2, 149-157.	1.5	29
82	Complete genome sequence of <i>Geodermatophilus obscurus</i> type strain (G-20T). <i>Standards in Genomic Sciences</i> , 2010, 2, 158-167.	1.5	56
83	Complete genome sequence of <i>Spirosoma linguale</i> type strain (1T). <i>Standards in Genomic Sciences</i> , 2010, 2, 176-184.	1.5	40
84	Complete genome sequence of <i>Segniliparus rotundus</i> type strain (CDC 1076T). <i>Standards in Genomic Sciences</i> , 2010, 2, 203-211.	1.5	10
85	Complete genome sequence of <i>Brachyspira murdochii</i> type strain (56-150T). <i>Standards in Genomic Sciences</i> , 2010, 2, 260-269.	1.5	20
86	Complete genome sequence of <i>Aminobacterium colombiense</i> type strain (ALA-1T). <i>Standards in Genomic Sciences</i> , 2010, 2, 280-289.	1.5	32
87	Complete genome sequence of <i>Thermobispora bispora</i> type strain (R51T). <i>Standards in Genomic Sciences</i> , 2010, 2, 318-326.	1.5	23
88	Complete genome sequence of <i>Gordonia bronchialis</i> type strain (3410T). <i>Standards in Genomic Sciences</i> , 2010, 2, 19-28.	1.5	26
89	Characterization of JG024, a <i>Pseudomonas aeruginosa</i> PB1-like broad host range phage under simulated infection conditions. <i>BMC Microbiology</i> , 2010, 10, 301.	1.3	81
90	Ecology of Speciation in the Genus <i>Bacillus</i> . <i>Applied and Environmental Microbiology</i> , 2010, 76, 1349-1358.	1.4	97

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91	A Robust Procedure for Comparing Multiple Means under Heteroscedasticity in Unbalanced Designs. PLoS ONE, 2010, 5, e9788.	1.1	240
92	Complete genome sequence of Sulfurimonas autotrophica type strain (OK10T). Standards in Genomic Sciences, 2010, 3, 194-202.	1.5	37
93	Complete genome sequence of Methanoplanus petrolearius type strain (SEBR 4847T). Standards in Genomic Sciences, 2010, 3, 203-211.	1.5	14
94	Complete genome sequence of Sanguibacter keddieii type strain (ST-74T). Standards in Genomic Sciences, 2009, 1, 110-118.	1.5	16
95	Complete genome sequence of Saccharomonospora viridis type strain (P101T). Standards in Genomic Sciences, 2009, 1, 141-149.	1.5	24
96	Complete genome sequence of Atopobium parvulum type strain (IPP 1246T). Standards in Genomic Sciences, 2009, 1, 166-173.	1.5	30
97	Complete genome sequence of Kangiella koreensis type strain (SW-125T). Standards in Genomic Sciences, 2009, 1, 226-233.	1.5	28
98	Complete genome sequence of Pirellula staleyi type strain (ATCC 27377T). Standards in Genomic Sciences, 2009, 1, 308-316.	1.5	34
99	Complete genome sequence of Thermanaerovibrio acidaminovorans type strain (Su883T). Standards in Genomic Sciences, 2009, 1, 254-261.	1.5	23
100	Carbon source utilization patterns of Bacillus simplex ecotypes do not reflect their adaptation to ecologically divergent slopes in "Evolution Canyon", Israel. FEMS Microbiology Ecology, 2008, 66, 38-44.	1.3	6
101	Identifying the fundamental units of bacterial diversity: A paradigm shift to incorporate ecology into bacterial systematics. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 2504-2509.	3.3	286
102	The temperature-adaptive fatty acid content in Bacillus simplex strains from "Evolution Canyon", Israel. Microbiology (United Kingdom), 2008, 154, 2416-2426.	0.7	25
103	Patterns of thermal adaptation of Bacillus simplex to the microclimatically contrasting slopes of 'Evolution Canyons' I and II, Israel. Environmental Microbiology, 2007, 9, 716-726.	1.8	39
104	Populations under microevolutionary scrutiny: what will we gain?. Archives of Microbiology, 2007, 189, 1-5.	1.0	18
105	On The Necessity to Study Natural Bacterial Populations-The Model of Bacillus Simplex From "Evolution Canyons" I and II, Israel. Israel Journal of Ecology and Evolution, 2006, 52, 527-542.	0.2	8
106	Identifying the Fundamental Units of Diversity Among Bacillus Isolates From "Evolution Canyon" III. Israel Journal of Ecology and Evolution, 2006, 52, 543-552.	0.2	7
107	Adaptive Mutations In RNA-Based Regulatory Mechanisms: Computational and Experimental Investigations. Israel Journal of Ecology and Evolution, 2006, 52, 263-279.	0.2	14
108	Adaptation and incipient sympatric speciation of Bacillus simplex under microclimatic contrast at "Evolution Canyons" I and II, Israel. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 15924-15929.	3.3	104

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109	Genomovars 11 to 18 of <i>Pseudomonas stutzeri</i> , identified among isolates from soil and marine sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2005, 55, 1767-1770.	0.8	28
110	Highly Different Levels of Natural Transformation Are Associated with Genomic Subgroups within a Local Population of <i>Pseudomonas stutzeri</i> from Soil. <i>Applied and Environmental Microbiology</i> , 2002, 68, 865-873.	1.4	69
111	Identification of complex composition, strong strain diversity and directional selection in local <i>Pseudomonas stutzeri</i> populations from marine sediment and soils. <i>Environmental Microbiology</i> , 2002, 4, 465-476.	1.8	47
112	The structure of a local population of phytopathogenic <i>Pseudomonas brassicacearum</i> from agricultural soil indicates development under purifying selection pressure. <i>Environmental Microbiology</i> , 2001, 3, 176-186.	1.8	28
113	The potential for intraspecific horizontal gene exchange by natural genetic transformation: sexual isolation among genomovars of <i>Pseudomonas stutzeri</i> The EMBL accession numbers for the sequences reported in this paper are given in Methods.. <i>Microbiology (United Kingdom)</i> , 2000, 146, 3081-3090.	0.7	30
114	Analysis of Genotypic Diversity and Relationships Among <i>Pseudomonas stutzeri</i> strains by PCR-Based Genomic Fingerprinting and Multilocus Enzyme Electrophoresis. <i>Systematic and Applied Microbiology</i> , 1999, 22, 393-402.	1.2	42
115	Natural genetic transformation of <i>Pseudomonas stutzeri</i> in a non-sterile soil. <i>Microbiology (United Kingdom)</i> , 2000, 146, 3081-3090.	0.7	30
116	Microbial diversity-ecosystem function relationships across environmental gradients. <i>Research Ideas and Outcomes</i> , 2016, 6, .	1.0	8