

Johannes Sikorski

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

119
papers

3,962
citations

29
h-index

58
g-index

123
ext. papers

5,054
ext. citations

6.8
avg, IF

4.93
L-index

#	Paper	IF	Citations
119	The Evolution of Ecological Diversity in .. <i>Frontiers in Microbiology</i> , 2022 , 13, 715637	5.7	4
118	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	5.7	0
117	Biological Soil Crust From Mesic Forests Promote a Specific Bacteria Community.. <i>Frontiers in Microbiology</i> , 2022 , 13, 769767	5.7	0
116	The mineralosphereInteractive zone of microbial colonization and carbon use in grassland soils. <i>Biology and Fertility of Soils</i> , 2021 , 57, 587-601	6.1	3
115	Contrasting responses of above- and belowground diversity to multiple components of land-use intensity. <i>Nature Communications</i> , 2021 , 12, 3918	17.4	13
114	The multidimensionality of soil macroecology. <i>Global Ecology and Biogeography</i> , 2021 , 30, 4-10	6.1	1
113	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	5.8	1
112	Phylogenomics reveals the basis of adaptation of Pseudorhizobium species to extreme environments and supports a taxonomic revision of the genus. <i>Systematic and Applied Microbiology</i> , 2021 , 44, 126165	4.2	8
111	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	5.8	18
110	Drivers of the composition of active rhizosphere bacterial communities in temperate grasslands. <i>ISME Journal</i> , 2020 , 14, 463-475	11.9	65
109	A single Thaumarchaeon drives nitrification in deep oligotrophic Lake Constance. <i>Environmental Microbiology</i> , 2020 , 22, 212-228	5.2	14
108	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	5.7	13
107	Blind spots in global soil biodiversity and ecosystem function research. <i>Nature Communications</i> , 2020 , 11, 3870	17.4	72
106	Bacterial colonization of minerals in grassland soils is selective and highly dynamic. <i>Environmental Microbiology</i> , 2020 , 22, 917-933	5.2	12
105	Convergent Loss of ABC Transporter Genes From Genomes Is Associated With Impaired Tyrosine Uptake and -Cresol Production. <i>Frontiers in Microbiology</i> , 2018 , 9, 901	5.7	21
104	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	5.8	125
103	Function of bacterial community dynamics in the formation of cadaveric semiochemicals during in situ carcass decomposition. <i>Environmental Microbiology</i> , 2017 , 19, 3310-3322	5.2	16

102	Present and Future of Culturing Bacteria. <i>Annual Review of Microbiology</i> , 2017 , 71, 711-730	17.5	113
101	Trajectories and Drivers of Genome Evolution in Surface-Associated Marine Phaeobacter. <i>Genome Biology and Evolution</i> , 2017 , 9, 3297-3311	3.9	8
100	Inferring interactions in complex microbial communities from nucleotide sequence data and environmental parameters. <i>PLoS ONE</i> , 2017 , 12, e0173765	3.7	11
99	Biodiversity at multiple trophic levels is needed for ecosystem multifunctionality. <i>Nature</i> , 2016 , 536, 456-9	50.4	345
98	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	4.8	21
97	Land-use intensification causes multitrophic homogenization of grassland communities. <i>Nature</i> , 2016 , 540, 266-269	50.4	236
96	Schmelztiegel Bodenbakterien. <i>Biologie in Unserer Zeit</i> , 2016 , 46, 358-365	0.1	
95	Locally rare species influence grassland ecosystem multifunctionality. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016 , 371,	5.8	88
94	Comparison of Rock Varnish Bacterial Communities with Surrounding Non-Varnished Rock Surfaces: Taxon-Specific Analysis and Morphological Description. <i>Microbial Ecology</i> , 2015 , 70, 741-50	4.4	23
93	Mining the phytomicrobiome to understand how bacterial coinoculations enhance plant growth. <i>Frontiers in Plant Science</i> , 2015 , 6, 784	6.2	18
92	Spatial Interaction of Archaeal Ammonia-Oxidizers and Nitrite-Oxidizing Bacteria in an Unfertilized Grassland Soil. <i>Frontiers in Microbiology</i> , 2015 , 6, 1567	5.7	32
91	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, 1152-62	3.8	29
90	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	3.7	23
89	Genomic encyclopedia of bacteria and archaea: sequencing a myriad of type strains. <i>PLoS Biology</i> , 2014 , 12, e1001920	9.7	146
88	The Family Segniliparaceae 2014 , 877-881		
87	From genome mining to phenotypic microarrays: Planctomycetes as source for novel bioactive molecules. <i>Antonie Van Leeuwenhoek</i> , 2013 , 104, 551-67	2.1	78
86	opm: an R package for analysing OmniLog(R) phenotype microarray data. <i>Bioinformatics</i> , 2013 , 29, 1823-4	4.2	153
85	Impacts of pr-10a overexpression at the molecular and the phenotypic level. <i>International Journal of Molecular Sciences</i> , 2013 , 14, 15141-66	6.3	7

84	Phenotypic variation in the plant pathogenic bacterium <i>Acidovorax citrulli</i> . <i>PLoS ONE</i> , 2013 , 8, e73189	3.7	11
83	<i>Pseudomonas aeruginosa</i> population structure revisited under environmental focus: impact of water quality and phage pressure. <i>Environmental Microbiology</i> , 2012 , 14, 1952-67	5.2	75
82	Visualization and curve-parameter estimation strategies for efficient exploration of phenotype microarray kinetics. <i>PLoS ONE</i> , 2012 , 7, e34846	3.7	139
81	Complete genome sequence of the aerobic, heterotroph <i>Marinithermus hydrothermalis</i> type strain (T1(T)) from a deep-sea hydrothermal vent chimney. <i>Standards in Genomic Sciences</i> , 2012 , 6, 21-30		6
80	Complete genome sequence of the aquatic bacterium <i>Runella slithyformis</i> type strain (LSU 4(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 145-54		16
79	Complete genome sequence of the orange-red pigmented, radioresistant <i>Deinococcus proteolyticus</i> type strain (MRP(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 240-50		7
78	Complete genome sequence of the sulfur compounds oxidizing chemolithoautotroph <i>Sulfuricum kujiense</i> type strain (YK-1(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 94-103		31
77	Complete genome sequence of <i>Hydrogenobacter thermophilus</i> type strain (TK-6). <i>Standards in Genomic Sciences</i> , 2011 , 4, 131-43		8
76	Complete genome sequence of <i>Desulfobulbus propionicus</i> type strain (1pr3). <i>Standards in Genomic Sciences</i> , 2011 , 4, 100-10		39
75	Complete genome sequence of <i>Marivirga tractuosa</i> type strain (H-43). <i>Standards in Genomic Sciences</i> , 2011 , 4, 154-62		15
74	Complete genome sequence of <i>Desulfurococcus mucosus</i> type strain (O7/1). <i>Standards in Genomic Sciences</i> , 2011 , 4, 173-82		9
73	Complete genome sequence of the extremely halophilic <i>Halanaerobium praevalens</i> type strain (GSL). <i>Standards in Genomic Sciences</i> , 2011 , 4, 312-21		24
72	Complete genome sequence of <i>Nitratifactor salsuginis</i> type strain (E9I37-1). <i>Standards in Genomic Sciences</i> , 2011 , 4, 322-30		10
71	Complete genome sequence of <i>Mahella australiensis</i> type strain (50-1 BON). <i>Standards in Genomic Sciences</i> , 2011 , 4, 331-41		6
70	Complete genome sequence of <i>Syntrophobotulus glycolicus</i> type strain (FlGlyRT). <i>Standards in Genomic Sciences</i> , 2011 , 4, 371-380		9
69	Complete genome sequence of the hyperthermophilic chemolithoautotroph <i>Pyrolobus fumarii</i> type strain (1A). <i>Standards in Genomic Sciences</i> , 2011 , 4, 381-92		10
68	Complete genome sequence of the gliding, heparinolytic <i>Pedobacter saltans</i> type strain (113). <i>Standards in Genomic Sciences</i> , 2011 , 5, 30-40		11
67	Complete genome sequence of the thermophilic sulfur-reducer <i>Desulfurobacterium thermolithotrophum</i> type strain (BSA(T)) from a deep-sea hydrothermal vent. <i>Standards in Genomic Sciences</i> , 2011 , 5, 407-15		10

66	Complete genome sequence of <i>Calditerrivibrio nitroreducens</i> type strain (Yu37-1). <i>Standards in Genomic Sciences</i> , 2011 , 4, 54-62		9
65	Complete genome sequence of <i>Oceanithermus profundus</i> type strain (506). <i>Standards in Genomic Sciences</i> , 2011 , 4, 210-20		3
64	Complete genome sequence of <i>Tsukamurella paurometabola</i> type strain (no. 33). <i>Standards in Genomic Sciences</i> , 2011 , 4, 342-51		8
63	Complete genome sequence of the gliding freshwater bacterium <i>Fluviicola taffensis</i> type strain (RW262). <i>Standards in Genomic Sciences</i> , 2011 , 5, 21-9		19
62	Identification and targeted cultivation of abundant novel freshwater sphingomonads and analysis of their population substructure. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 7355-64	4.8	17
61	Complete genome sequence of <i>Thermomonospora curvata</i> type strain (B9). <i>Standards in Genomic Sciences</i> , 2011 , 4, 13-22		24
60	Complete genome sequence of <i>Syntrophobotulus glycolicus</i> type strain (FLGlyR). <i>Standards in Genomic Sciences</i> , 2011 , 4, 371-80		3
59	Ecology of speciation in the genus <i>Bacillus</i> . <i>Applied and Environmental Microbiology</i> , 2010 , 76, 1349-58	4.8	80
58	A robust procedure for comparing multiple means under heteroscedasticity in unbalanced designs. <i>PLoS ONE</i> , 2010 , 5, e9788	3.7	184
57	Complete genome sequence of <i>Planctomyces limnophilus</i> type strain (M290). <i>Standards in Genomic Sciences</i> , 2010 , 3, 47-56		28
56	Complete genome sequence of <i>Ferrimonas balearica</i> type strain (PAT). <i>Standards in Genomic Sciences</i> , 2010 , 3, 174-82		9
55	Non-contiguous finished genome sequence of <i>Aminomonas paucivorans</i> type strain (GLU-3). <i>Standards in Genomic Sciences</i> , 2010 , 3, 285-93		8
54	Complete genome sequence of <i>Ilyobacter polytropus</i> type strain (CuHbu1). <i>Standards in Genomic Sciences</i> , 2010 , 3, 304-14		7
53	Complete genome sequence of <i>Nocardiopsis dassonvillei</i> type strain (IMRU 509). <i>Standards in Genomic Sciences</i> , 2010 , 3, 325-36		27
52	Complete genome sequence of <i>Thermocrinis albus</i> type strain (HI 11/12). <i>Standards in Genomic Sciences</i> , 2010 , 2, 194-202		14
51	Complete genome sequence of <i>Meiothermus silvanus</i> type strain (VI-R2). <i>Standards in Genomic Sciences</i> , 2010 , 3, 37-46		16
50	Complete genome sequence of <i>Olsenella uli</i> type strain (VPI D76D-27C). <i>Standards in Genomic Sciences</i> , 2010 , 3, 76-84		27
49	Complete genome sequence of <i>Meiothermus ruber</i> type strain (21). <i>Standards in Genomic Sciences</i> , 2010 , 3, 26-36		28

48	Complete genome sequence of <i>Acetohalobium arabaticum</i> type strain (Z-7288). <i>Standards in Genomic Sciences</i> , 2010 , 3, 57-65	16
47	Complete genome sequence of <i>Ignisphaera aggregans</i> type strain (AQ1.S1). <i>Standards in Genomic Sciences</i> , 2010 , 3, 66-75	13
46	Complete genome sequence of <i>Vulcanisaeta distributa</i> type strain (IC-017). <i>Standards in Genomic Sciences</i> , 2010 , 3, 117-25	8
45	Complete genome sequence of <i>Arcanobacterium haemolyticum</i> type strain (11018). <i>Standards in Genomic Sciences</i> , 2010 , 3, 126-35	7
44	Complete genome sequence of <i>Thermosediminibacter oceani</i> type strain (JW/IW-1228P). <i>Standards in Genomic Sciences</i> , 2010 , 3, 108-16	10
43	Complete genome sequence of <i>Spirochaeta smaragdinae</i> type strain (SEBR 4228). <i>Standards in Genomic Sciences</i> , 2010 , 3, 136-44	15
42	Complete genome sequence of <i>Syntrophothermus lipocalidus</i> type strain (TGB-C1). <i>Standards in Genomic Sciences</i> , 2010 , 3, 268-75	10
41	Complete genome sequence of <i>Intrasporangium calvum</i> type strain (7 KIP). <i>Standards in Genomic Sciences</i> , 2010 , 3, 294-303	4
40	Complete genome sequence of <i>Methanothermus fervidus</i> type strain (V24S). <i>Standards in Genomic Sciences</i> , 2010 , 3, 315-24	14
39	Complete genome sequence of <i>Alicyclobacillus acidocaldarius</i> type strain (104-IA). <i>Standards in Genomic Sciences</i> , 2010 , 2, 9-18	20
38	Complete genome sequence of <i>Sphaerobacter thermophilus</i> type strain (S 6022). <i>Standards in Genomic Sciences</i> , 2010 , 2, 49-56	20
37	Complete genome sequence of <i>Streptosporangium roseum</i> type strain (NI 9100). <i>Standards in Genomic Sciences</i> , 2010 , 2, 29-37	25
36	Complete genome sequence of <i>Sulfurospirillum deleyianum</i> type strain (5175). <i>Standards in Genomic Sciences</i> , 2010 , 2, 149-57	24
35	Complete genome sequence of <i>Geodermatophilus obscurus</i> type strain (G-20). <i>Standards in Genomic Sciences</i> , 2010 , 2, 158-67	49
34	Complete genome sequence of <i>Spirosoma linguale</i> type strain (1). <i>Standards in Genomic Sciences</i> , 2010 , 2, 176-85	35
33	Complete genome sequence of <i>Segniliparus rotundus</i> type strain (CDC 1076). <i>Standards in Genomic Sciences</i> , 2010 , 2, 203-11	9
32	Complete genome sequence of <i>Brachyspira murdochii</i> type strain (56-150). <i>Standards in Genomic Sciences</i> , 2010 , 2, 260-9	18
31	Complete genome sequence of <i>Aminobacterium colombiense</i> type strain (ALA-1). <i>Standards in Genomic Sciences</i> , 2010 , 2, 280-9	27

30	Complete genome sequence of <i>Thermobispora bispora</i> type strain (R51). <i>Standards in Genomic Sciences</i> , 2010 , 2, 318-26		18
29	Complete genome sequence of <i>Gordonia bronchialis</i> type strain (3410). <i>Standards in Genomic Sciences</i> , 2010 , 2, 19-28		19
28	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	4.5	51
27	Complete genome sequence of <i>Sulfurimonas autotrophica</i> type strain (OK10). <i>Standards in Genomic Sciences</i> , 2010 , 3, 194-202		32
26	Complete genome sequence of <i>Methanoplanus petrolearius</i> type strain (SEBR 4847). <i>Standards in Genomic Sciences</i> , 2010 , 3, 203-11		12
25	Complete genome sequence of <i>Sanguibacter keddieii</i> type strain (ST-74). <i>Standards in Genomic Sciences</i> , 2009 , 1, 110-8		10
24	Complete genome sequence of <i>Saccharomonospora viridis</i> type strain (P101). <i>Standards in Genomic Sciences</i> , 2009 , 1, 141-9		21
23	Complete genome sequence of <i>Atopobium parvulum</i> type strain (IPP 1246). <i>Standards in Genomic Sciences</i> , 2009 , 1, 166-73		21
22	Complete genome sequence of <i>Kangiella koreensis</i> type strain (SW-125). <i>Standards in Genomic Sciences</i> , 2009 , 1, 226-33		10
21	Complete genome sequence of <i>Pirellula staleyii</i> type strain (ATCC 27377). <i>Standards in Genomic Sciences</i> , 2009 , 1, 308-16		26
20	Complete genome sequence of <i>Thermanaerovibrio acidaminovorans</i> type strain (Su883). <i>Standards in Genomic Sciences</i> , 2009 , 1, 254-61		19
19	Identifying the fundamental units of bacterial diversity: a paradigm shift to incorporate ecology into bacterial systematics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 2504-9	11.5	248
18	The temperature-adaptive fatty acid content in <i>Bacillus simplex</i> strains from Ævolution Canyon, Israel. <i>Microbiology (United Kingdom)</i> , 2008 , 154, 2416-2426	2.9	21
17	Populations under microevolutionary scrutiny: what will we gain?. <i>Archives of Microbiology</i> , 2008 , 189, 1-5	3	16
16	Carbon source utilization patterns of <i>Bacillus simplex</i> ecotypes do not reflect their adaptation to ecologically divergent slopes in Ævolution Canyon, Israel. <i>FEMS Microbiology Ecology</i> , 2008 , 66, 38-44	4.3	4
15	Patterns of thermal adaptation of <i>Bacillus simplex</i> to the microclimatically contrasting slopes of Ævolution Canyons I and II, Israel. <i>Environmental Microbiology</i> , 2007 , 9, 716-26	5.2	35
14	Adaptive Mutations In RNA-Based Regulatory Mechanisms: Computational and Experimental Investigations. <i>Israel Journal of Ecology and Evolution</i> , 2006 , 52, 263-279	0.8	8
13	On The Necessity to Study Natural Bacterial Populations-The Model of <i>Bacillus Simplex</i> From "Evolution Canyons" I and II, Israel. <i>Israel Journal of Ecology and Evolution</i> , 2006 , 52, 527-542	0.8	7

12	Identifying the Fundamental Units of Diversity Among Bacillus Isolates From "Evolution Canyon" III. <i>Israel Journal of Ecology and Evolution</i> , 2006 , 52, 543-552	0.8	4
11	Adaptation and incipient sympatric speciation of Bacillus simplex under microclimatic contrast at "Evolution Canyons" I and II, Israel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 15924-9	11.5	89
10	Genomovars 11 to 18 of Pseudomonas stutzeri, identified among isolates from soil and marine sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2005 , 55, 1767-1770	2.2	23
9	Identification of complex composition, strong strain diversity and directional selection in local Pseudomonas stutzeri populations from marine sediment and soils. <i>Environmental Microbiology</i> , 2002 , 4, 465-76	5.2	45
8	Highly different levels of natural transformation are associated with genomic subgroups within a local population of Pseudomonas stutzeri from soil. <i>Applied and Environmental Microbiology</i> , 2002 , 68, 865-73	4.8	59
7	The structure of a local population of phytopathogenic Pseudomonas brassicacearum from agricultural soil indicates development under purifying selection pressure. <i>Environmental Microbiology</i> , 2001 , 3, 176-86	5.2	25
6	The potential for intraspecific horizontal gene exchange by natural genetic transformation: sexual isolation among genomovars of Pseudomonas stutzeri. <i>Microbiology (United Kingdom)</i> , 2000 , 146 Pt 12, 3081-3090	2.9	25
5	Analysis of genotypic diversity and relationships among Pseudomonas stutzeri strains by PCR-based genomic fingerprinting and multilocus enzyme electrophoresis. <i>Systematic and Applied Microbiology</i> , 1999 , 22, 393-402	4.2	37
4	Natural genetic transformation of Pseudomonas stutzeri in a non-sterile soil. <i>Microbiology (United Kingdom)</i> , 1998 , 144 (Pt 2), 569-576	2.9	79
3	Microbial diversity-ecosystem function relationships across environmental gradients. <i>Research Ideas and Outcomes</i> , 6,	2.5	4
2	Phylogenomic analysis reveals the basis of adaptation of Pseudorhizobium species to extreme environments		1
1	Blind spots in global soil biodiversity and ecosystem function research		2