

# Heiko Liesegang

## List of Publications by Year in descending order

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63  
papers

8,851  
citations

101384

36  
h-index

114278

63  
g-index

66  
all docs

66  
docs citations

66  
times ranked

11072  
citing authors

#	ARTICLE	IF	CITATIONS
1	Complete Genome Sequence of <i>Kinneretia</i> sp. Strain DAIF2, Isolated from a Freshwater Pond. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	2
2	IDOPS, a Profile HMM-Based Tool to Detect Pesticidal Sequences and Compare Their Genetic Context. <i>Frontiers in Microbiology</i> , 2021, 12, 664476.	1.5	5
3	Closely Related <i>Vibrio alginolyticus</i> Strains Encode an Identical Repertoire of Caudovirales-Like Regions and Filamentous Phages. <i>Viruses</i> , 2020, 12, 1359.	1.5	13
4	Genomic variation among closely related <i>Vibrio alginolyticus</i> strains is located on mobile genetic elements. <i>BMC Genomics</i> , 2020, 21, 354.	1.2	19
5	Classifying the Unclassified: A Phage Classification Method. <i>Viruses</i> , 2019, 11, 195.	1.5	44
6	Draft Genome Sequence of the Endophyte <i>Bacillus mycoides</i> Strain GM6LP Isolated from <i>Lolium perenne</i> . <i>Genome Announcements</i> , 2018, 6, .	0.8	7
7	Draft Genome Sequence of the Endophyte <i>Bacillus mycoides</i> Strain GM5LP Isolated from <i>Lolium perenne</i> . <i>Genome Announcements</i> , 2018, 6, .	0.8	3
8	Comparative genome and phenotypic analysis of three <i>Clostridioides difficile</i> strains isolated from a single patient provide insight into multiple infection of <i>C. difficile</i> . <i>BMC Genomics</i> , 2018, 19, 1.	1.2	725
9	High metabolic versatility of different toxigenic and non-toxigenic <i>Clostridioides difficile</i> isolates. <i>International Journal of Medical Microbiology</i> , 2017, 307, 311-320.	1.5	67
10	Draft Genome Sequence of <i>Bacillus pumilus</i> Strain GM3FR, an Endophyte Isolated from Aerial Plant Tissues of <i>Festuca rubra</i> L. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
11	Complete genome sequence of the nematocidal <i>Bacillus thuringiensis</i> MYBT18247. <i>Journal of Biotechnology</i> , 2017, 260, 48-52.	1.9	8
12	Small RNA mediated repression of subtilisin production in <i>Bacillus licheniformis</i> . <i>Scientific Reports</i> , 2017, 7, 5699.	1.6	13
13	Tripartite species interaction: eukaryotic hosts suffer more from phage susceptible than from phage resistant bacteria. <i>BMC Evolutionary Biology</i> , 2017, 17, 98.	3.2	27
14	Complete Genome sequence of the nematocidal <i>Bacillus thuringiensis</i> MYBT18246. <i>Standards in Genomic Sciences</i> , 2017, 12, 48.	1.5	10
15	Draft Genome Sequence of <i>Vibrio splendidus</i> DSM 19640. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
16	Manual curation and reannotation of the genomes of <i>Clostridium difficile</i> 630 <sup>erm</sup> and <i>C. difficile</i> 630. <i>Journal of Medical Microbiology</i> , 2017, 66, 286-293.	0.7	117
17	Complete Genome Sequence of the <i>Clostridium difficile</i> Type Strain DSM 1296 T. <i>Genome Announcements</i> , 2015, 3, .	0.8	11
18	The two putative comS homologs of the biotechnologically important <i>Bacillus licheniformis</i> do not contribute to competence development. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 2255-2266.	1.7	4

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19	Genome Resequencing of the Virulent and Multidrug-Resistant Reference Strain <i>Clostridium difficile</i> 630. <i>Genome Announcements</i> , 2015, 3, .	0.8	36
20	Analysis and comparative genomics of ICEMh1, a novel integrative and conjugative element (ICE) of <i>Mannheimia haemolytica</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 93-97.	1.3	59
21	Conjugative reporter system for the use in <i>Bacillus licheniformis</i> and closely related <i>Bacilli</i> . <i>Letters in Applied Microbiology</i> , 2015, 60, 162-167.	1.0	5
22	Host-Pathogen Coevolution: The Selective Advantage of <i>Bacillus thuringiensis</i> Virulence and Its Cry Toxin Genes. <i>PLoS Biology</i> , 2015, 13, e1002169.	2.6	69
23	Genome-Based Identification of Active Prophage Regions by Next Generation Sequencing in <i>Bacillus licheniformis</i> DSM13. <i>PLoS ONE</i> , 2015, 10, e0120759.	1.1	22
24	How to Kill the Honey Bee Larva: Genomic Potential and Virulence Mechanisms of <i>Paenibacillus</i> larvae. <i>PLoS ONE</i> , 2014, 9, e90914.	1.1	84
25	Cell physiology of the biotechnological relevant bacterium <i>Bacillus pumilus</i> —An omics-based approach. <i>Journal of Biotechnology</i> , 2014, 192, 204-214.	1.9	13
26	Unravelling the genetic basis for competence development of auxotrophic <i>Bacillus licheniformis</i> 9945A strains. <i>Microbiology (United Kingdom)</i> , 2014, 160, 2136-2147.	0.7	9
27	TraV: A Genome Context Sensitive Transcriptome Browser. <i>PLoS ONE</i> , 2014, 9, e93677.	1.1	22
28	Size unlimited markerless deletions by a transconjugative plasmid-system in <i>Bacillus licheniformis</i> . <i>Journal of Biotechnology</i> , 2013, 167, 365-369.	1.9	23
29	Fermentation stage-dependent adaptations of <i>Bacillus licheniformis</i> during enzyme production. <i>Microbial Cell Factories</i> , 2013, 12, 120.	1.9	19
30	Complete Genome Sequence of <i>Bacillus thuringiensis</i> Strain 407 Cry-. <i>Genome Announcements</i> , 2013, 1, .	0.8	40
31	RNA-Seq of <i>Bacillus licheniformis</i> : active regulatory RNA features expressed within a productive fermentation. <i>BMC Genomics</i> , 2013, 14, 667.	1.2	40
32	First Insights into the Completely Annotated Genome Sequence of <i>Bacillus licheniformis</i> Strain 9945A. <i>Genome Announcements</i> , 2013, 1, .	0.8	18
33	ICEPmu1, an integrative conjugative element (ICE) of <i>Pasteurella multocida</i> : analysis of the regions that comprise 12 antimicrobial resistance genes. <i>Journal of Antimicrobial Chemotherapy</i> , 2012, 67, 84-90.	1.3	117
34	Genetic Analysis of the Upper Phenylacetate Catabolic Pathway in the Production of Tropodithietic Acid by <i>Phaeobacter gallaeciensis</i> . <i>Applied and Environmental Microbiology</i> , 2012, 78, 3539-3551.	1.4	48
35	ICEPmu1, an integrative conjugative element (ICE) of <i>Pasteurella multocida</i> : structure and transfer. <i>Journal of Antimicrobial Chemotherapy</i> , 2012, 67, 91-100.	1.3	108
36	<i>Phaeobacter gallaeciensis</i> genomes from globally opposite locations reveal high similarity of adaptation to surface life. <i>ISME Journal</i> , 2012, 6, 2229-2244.	4.4	143

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37	Physiological homogeneity among the endosymbionts of <i>Riftia pachyptila</i> and <i>Tevnia jerichonana</i> revealed by proteogenomics. <i>ISME Journal</i> , 2012, 6, 766-776.	4.4	80
38	Genome sequence analyses of two isolates from the recent <i>Escherichia coli</i> outbreak in Germany reveal the emergence of a new pathotype: Entero-Aggregative-Haemorrhagic <i>Escherichia coli</i> (EAHEC). <i>Archives of Microbiology</i> , 2011, 193, 883-891.	1.0	238
39	Comparative genome analysis and genome-guided physiological analysis of <i>Roseobacter litoralis</i> . <i>BMC Genomics</i> , 2011, 12, 324.	1.2	54
40	Deep sequencing-based identification of small non-coding RNAs in <i>Streptomyces coelicolor</i> . <i>RNA Biology</i> , 2011, 8, 468-477.	1.5	100
41	Genomic features and insights into the biology of <i>Mycoplasma fermentans</i> . <i>Microbiology (United Kingdom)</i> , 2011, 155, 1077-1088.	0.7	28
42	Molecular Basis of Macrolide, Triamidine, and Lincosamide Resistance in <i>Pasteurella multocida</i> from Bovine Respiratory Disease. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 2475-2477.	1.4	57
43	<i>Clostridium ljungdahlii</i> represents a microbial production platform based on syngas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 13087-13092.	3.3	594
44	The complete genome sequence of the algal symbiont <i>Dinoroseobacter shibae</i> : a hitchhiker's guide to life in the sea. <i>ISME Journal</i> , 2010, 4, 61-77.	4.4	244
45	Genome Sequence of the Polysaccharide-Degrading, Thermophilic Anaerobe <i>Spirochaeta thermophila</i> DSM 6192. <i>Journal of Bacteriology</i> , 2010, 192, 6492-6493.	1.0	19
46	Facilitation of Direct Conditional Knockout of Essential Genes in <i>Bacillus licheniformis</i> DSM13 by Comparative Genetic Analysis and Manipulation of Genetic Competence. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5046-5057.	1.4	37
47	Complete Genome Sequence of <i>Methanothermobacter marburgensis</i> , a Methanoarchaeon Model Organism. <i>Journal of Bacteriology</i> , 2010, 192, 5850-5851.	1.0	32
48	Host Imprints on Bacterial Genomes—Rapid, Divergent Evolution in Individual Patients. <i>PLoS Pathogens</i> , 2010, 6, e1001078.	2.1	130
49	The Genome of a <i>Bacillus</i> Isolate Causing Anthrax in Chimpanzees Combines Chromosomal Properties of <i>B. cereus</i> with <i>B. anthracis</i> Virulence Plasmids. <i>PLoS ONE</i> , 2010, 5, e10986.	1.1	157
50	<i>Rhizobium</i> sp. Strain NGR234 Possesses a Remarkable Number of Secretion Systems. <i>Applied and Environmental Microbiology</i> , 2009, 75, 4035-4045.	1.4	170
51	The third pillar of bacterial signal transduction: classification of the extracytoplasmic function (ECF) $\sigma$ factor protein family. <i>Molecular Microbiology</i> , 2009, 74, 557-581.	1.2	374
52	Genome sequence of <i>Desulfobacterium autotrophicum</i> HRM2, a marine sulfate reducer oxidizing organic carbon completely to carbon dioxide. <i>Environmental Microbiology</i> , 2009, 11, 1038-1055.	1.8	100
53	The genome of <i>Clostridium kluyveri</i> , a strict anaerobe with unique metabolic features. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 2128-2133.	3.3	409
54	Comparative analysis of the complete genome sequence of the plant growth-promoting bacterium <i>Bacillus amyloliquefaciens</i> FZB42. <i>Nature Biotechnology</i> , 2007, 25, 1007-1014.	9.4	703

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55	Genome sequence of the bioplastic-producing "Knallgas" bacterium <i>Ralstonia eutropha</i> H16. <i>Nature Biotechnology</i> , 2006, 24, 1257-1262.	9.4	527
56	The Genome Sequence of <i>Methanosphaera stadtmanae</i> Reveals Why This Human Intestinal Archaeon Is Restricted to Methanol and H <sub>2</sub> for Methane Formation and ATP Synthesis. <i>Journal of Bacteriology</i> , 2006, 188, 642-658.	1.0	245
57	How to become a uropathogen: Comparative genomic analysis of extraintestinal pathogenic <i>Escherichia coli</i> strains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 12879-12884.	3.3	320
58	Complete genome sequence of the acetic acid bacterium <i>Gluconobacter oxydans</i> . <i>Nature Biotechnology</i> , 2005, 23, 195-200.	9.4	371
59	Structural and Functional Characterization of Gene Clusters Directing Nonribosomal Synthesis of Bioactive Cyclic Lipopeptides in <i>Bacillus amyloliquefaciens</i> Strain FZB42. <i>Journal of Bacteriology</i> , 2004, 186, 1084-1096.	1.0	551
60	The genome sequence of the extreme thermophile <i>Thermus thermophilus</i> . <i>Nature Biotechnology</i> , 2004, 22, 547-553.	9.4	345
61	The Complete Genome Sequence of <i>Bacillus licheniformis</i> DSM13, an Organism with Great Industrial Potential. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2004, 7, 204-211.	1.0	284
62	The Complete Genome Sequence of <i>Propionibacterium Acnes</i> , a Commensal of Human Skin. <i>Science</i> , 2004, 305, 671-673.	6.0	400
63	The genome sequence of <i>Clostridium tetani</i> , the causative agent of tetanus disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 1316-1321.	3.3	324