

# Harald Kusch

## List of Publications by Year in descending order

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Version: 2024-02-01

29  
papers

1,774  
citations

361045

20  
h-index

525886

27  
g-index

32  
all docs

32  
docs citations

32  
times ranked

2591  
citing authors

#	ARTICLE	IF	CITATIONS
1	5.3 Kollaboratives Arbeiten mit Daten. , 2021, , 451-476.		1
2	<i>Pseudomonas</i> Strains Induce Transcriptional and Morphological Changes and Reduce Root Colonization of <i>Verticillium</i> spp.. <i>Frontiers in Microbiology</i> , 2021, 12, 652468.	1.5	6
3	A 20â€kb lineageâ€specific genomic region tames virulence in pathogenic amphidiploid <i>Verticillium longisporum</i> . <i>Molecular Plant Pathology</i> , 2021, 22, 939-953.	2.0	6
4	Management of Metadata Types in Basic Cardiological Research. <i>Studies in Health Technology and Informatics</i> , 2021, 283, 59-68.	0.2	0
5	<i>Verticillium longisporum</i> Elicits Media-Dependent Secretome Responses With Capacity to Distinguish Between Plant-Related Environments. <i>Frontiers in Microbiology</i> , 2020, 11, 1876.	1.5	18
6	Fluorescent pseudomonads pursue media-dependent strategies to inhibit growth of pathogenic <i>Verticillium</i> fungi. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 817-831.	1.7	6
7	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus <i>Aspergillus</i> . <i>Genome Biology</i> , 2017, 18, 28.	3.8	417
8	Opinion paper: Data provenance challenges in biomedical research. <i>IT - Information Technology</i> , 2017, 59, .	0.6	3
9	The effect of skin fatty acids on <i>Staphylococcus aureus</i> . <i>Archives of Microbiology</i> , 2015, 197, 245-267.	1.0	28
10	<i><scp>V</scp>erticillium</i> transcription activator of adhesion <scp>V</scp>ta2 suppresses microsclerotia formation and is required for systemic infection of plant roots. <i>New Phytologist</i> , 2014, 202, 565-581.	3.5	92
11	Secrets of the secretome in <i>Staphylococcus aureus</i> . <i>International Journal of Medical Microbiology</i> , 2014, 304, 133-141.	1.5	49
12	<i>Verticillium dahliae</i> VdTHI4, involved in thiazole biosynthesis, stress response and DNA repair functions, is required for vascular disease induction in tomato. <i>Environmental and Experimental Botany</i> , 2014, 108, 14-22.	2.0	40
13	Common versus noble <i>Bacillus subtilis</i> differentially responds to air and argon gas plasma. <i>Proteomics</i> , 2013, 13, 2608-2621.	1.3	21
14	Aureolib â€” A Proteome Signature Library: Towards an Understanding of <i>Staphylococcus aureus</i> Pathophysiology. <i>PLoS ONE</i> , 2013, 8, e70669.	1.1	28
15	Characterization of the global impact of low temperature gas plasma on vegetative microorganisms. <i>Proteomics</i> , 2011, 11, 3518-3530.	1.3	41
16	Genomic and proteomic characterization of <i>Staphylococcus aureus</i> mastitis isolates of bovine origin. <i>Proteomics</i> , 2011, 11, 2491-2502.	1.3	63
17	Distinctive patterns in the human antibody response to <i>Staphylococcus aureus</i> bacteremia in carriers and nonâ€carriers. <i>Proteomics</i> , 2011, 11, 3914-3927.	1.3	65
18	Proteomics uncovers extreme heterogeneity in the <i>Staphylococcus aureus</i> exoproteome due to genomic plasticity and variant gene regulation. <i>Proteomics</i> , 2010, 10, 1634-1644.	1.3	129

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19	Protecs, a comprehensive and powerful storage and analysis system for OMICS data, applied for profiling the anaerobiosis response of <i>Staphylococcus aureus</i> COL. <i>Proteomics</i> , 2010, 10, 2982-3000.	1.3	16
20	Human Immune Proteome in Experimental Colonization with <i>Staphylococcus aureus</i> . <i>Vaccine Journal</i> , 2009, 16, 1607-1614.	3.2	62
21	Proteomic analysis of the bacterial pathogen <i>Bartonella henselae</i> and identification of immunogenic proteins for serodiagnosis. <i>Proteomics</i> , 2009, 9, 1967-1981.	1.3	28
22	Proteomic analysis of Legionella-containing phagosomes isolated from Dictyostelium. <i>International Journal of Medical Microbiology</i> , 2009, 299, 489-508.	1.5	82
23	Proteomic analysis of antioxidant strategies of <i>Staphylococcus aureus</i> : Diverse responses to different oxidants. <i>Proteomics</i> , 2008, 8, 3139-3153.	1.3	109
24	A proteomic view of <i>Candida albicans</i> yeast cell metabolism in exponential and stationary growth phases. <i>International Journal of Medical Microbiology</i> , 2008, 298, 291-318.	1.5	59
25	Proteomic Characterization of the Whole Secretome of <i>Legionella pneumophila</i> and Functional Analysis of Outer Membrane Vesicles. <i>Infection and Immunity</i> , 2008, 76, 1825-1836.	1.0	175
26	“Gently Rough”: The Vaccine Potential of a <i>Salmonella enterica</i> Regulatory Lipopolysaccharide Mutant. <i>Journal of Infectious Diseases</i> , 2008, 198, 1699-1706.	1.9	30
27	Proteomic analysis of the oxidative stress response in <i>Candida albicans</i> . <i>Proteomics</i> , 2007, 7, 686-697.	1.3	82
28	Proteomic Analysis of Azole Resistance in <i>Candida albicans</i> Clinical Isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2004, 48, 2733-2735.	1.4	60
29	A proteomic approach to understanding the development of multidrug-resistant <i>Candida albicans</i> strains. <i>Molecular Genetics and Genomics</i> , 2004, 271, 554-565.	1.0	39