

Bernhard Krismer

List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

3,328
citations

218677

26
h-index

361022

35
g-index

38
all docs

38
docs citations

38
times ranked

4506
citing authors

#	ARTICLE	IF	CITATIONS
1	Sensitizing <i>Staphylococcus aureus</i> to antibacterial agents by decoding and blocking the lipid flippase MprF. <i>ELife</i> , 2022, 11, .	6.0	23
2	Distinct Lugdunins from a New Efficient Synthesis and Broad Exploitation of Its MRSA-Antimicrobial Structure. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 4034-4058.	6.4	2
3	<i>Staphylococcus epidermidis</i> clones express <i>Staphylococcus aureus</i> -type wall teichoic acid to shift from a commensal to pathogen lifestyle. <i>Nature Microbiology</i> , 2021, 6, 757-768.	13.3	37
4	The microbiome-shaping roles of bacteriocins. <i>Nature Reviews Microbiology</i> , 2021, 19, 726-739.	28.6	143
5	Secondary Metabolites Governing Microbiome Interaction of Staphylococcal Pathogens and Commensals. <i>Microbial Physiology</i> , 2021, 31, 198-216.	2.4	14
6	Secretion of and Self-Resistance to the Novel Fibupeptide Antimicrobial Lugdunin by Distinct ABC Transporters in <i>Staphylococcus lugdunensis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 65, .	3.2	10
7	Lugdunin amplifies innate immune responses in the skin in synergy with host- and microbiota-derived factors. <i>Nature Communications</i> , 2019, 10, 2730.	12.8	74
8	Synthetische Analoga zeigen die essentiellen Struktur motive von Lugdunin und seinen Protonentransport. <i>Angewandte Chemie</i> , 2019, 131, 9333-9338.	2.0	2
9	<i>Staphylococcus aureus</i> Colonization of the Human Nose and Interaction with Other Microbiome Members. <i>Microbiology Spectrum</i> , 2019, 7, .	3.0	60
10	Synthetic Lugdunin Analogues Reveal Essential Structural Motifs for Antimicrobial Action and Proton Translocation Capability. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 9234-9238.	13.8	44
11	Lantibiotic production is a burden for the producing staphylococci. <i>Scientific Reports</i> , 2018, 8, 7471.	3.3	18
12	Keratinocytes as sensors and central players in the immune defense against <i>Staphylococcus aureus</i> in the skin. <i>Journal of Dermatological Science</i> , 2017, 87, 215-220.	1.9	65
13	The commensal lifestyle of <i>Staphylococcus aureus</i> and its interactions with the nasal microbiota. <i>Nature Reviews Microbiology</i> , 2017, 15, 675-687.	28.6	222
14	High Frequency and Diversity of Antimicrobial Activities Produced by Nasal <i>Staphylococcus</i> Strains against Bacterial Competitors. <i>PLoS Pathogens</i> , 2016, 12, e1005812.	4.7	124
15	An essential role for the baseplate protein Gp45 in phage adsorption to <i>Staphylococcus aureus</i> . <i>Scientific Reports</i> , 2016, 6, 26455.	3.3	61
16	Human commensals producing a novel antibiotic impair pathogen colonization. <i>Nature</i> , 2016, 535, 511-516.	27.8	667
17	Secretome analysis revealed adaptive and non-adaptive responses of the <i>Staphylococcus carnosus</i> femB mutant. <i>Proteomics</i> , 2015, 15, 1268-1279.	2.2	29
18	The microbial community structure of the cotton rat nose. <i>Environmental Microbiology Reports</i> , 2015, 7, 929-935.	2.4	35

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19	The MazEF Toxin-Antitoxin System Alters the β -Lactam Susceptibility of <i>Staphylococcus aureus</i> . PLoS ONE, 2015, 10, e0126118.	2.5	39
20	The Lipid-Modifying Multiple Peptide Resistance Factor Is an Oligomer Consisting of Distinct Interacting Synthase and Flippase Subunits. MBio, 2015, 6, .	4.1	60
21	Transfer of Plasmid DNA to Clinical Coagulase-Negative Staphylococcal Pathogens by Using a Unique Bacteriophage. Applied and Environmental Microbiology, 2015, 81, 2481-2488.	3.1	28
22	Nutrient Limitation Governs <i>Staphylococcus aureus</i> Metabolism and Niche Adaptation in the Human Nose. PLoS Pathogens, 2014, 10, e1003862.	4.7	166
23	The Stringent Response of <i>Staphylococcus aureus</i> and Its Impact on Survival after Phagocytosis through the Induction of Intracellular PSMs Expression. PLoS Pathogens, 2012, 8, e1003016.	4.7	209
24	Highly Efficient <i>Staphylococcus carnosus</i> Mutant Selection System Based on Suicidal Bacteriocin Activation. Applied and Environmental Microbiology, 2012, 78, 1148-1156.	3.1	4
25	Exometabolome Analysis Identifies Pyruvate Dehydrogenase as a Target for the Antibiotic Triphenylbismuthdichloride in Multiresistant Bacterial Pathogens. Journal of Biological Chemistry, 2012, 287, 2887-2895.	3.4	55
26	Intracellular monitoring of target protein production in <i>Staphylococcus aureus</i> by peptide tag-induced reporter fluorescence. Microbial Biotechnology, 2012, 5, 129-134.	4.2	12
27	Does <i>Staphylococcus aureus</i> nasal colonization involve biofilm formation?. Future Microbiology, 2011, 6, 489-493.	2.0	39
28	Skin Commensals Amplify the Innate Immune Response to Pathogens by Activation of Distinct Signaling Pathways. Journal of Investigative Dermatology, 2011, 131, 382-390.	0.7	218
29	Role of staphylococcal wall teichoic acid in targeting the major autolysin Atl. Molecular Microbiology, 2010, 75, 864-873.	2.5	232
30	Temporal Expression of Adhesion Factors and Activity of Global Regulators during Establishment of <i>Staphylococcus aureus</i> Nasal Colonization. Journal of Infectious Diseases, 2010, 201, 1414-1421.	4.0	114
31	Relative contribution of <i>Prevotella intermedia</i> and <i>Pseudomonas aeruginosa</i> to lung pathology in airways of patients with cystic fibrosis. Thorax, 2010, 65, 978-984.	5.6	84
32	Marker Removal in Staphylococci via Cre Recombinase and Different <i>lox</i> Sites. Applied and Environmental Microbiology, 2008, 74, 1316-1323.	3.1	61
33	Abyssomicins, Inhibitors of the para-Aminobenzoic Acid Pathway Produced by the Marine <i>Verrucosipora</i> Strain AB-18-032. Journal of Antibiotics, 2004, 57, 271-279.	2.0	272
34	The Nitrate Reductase and Nitrite Reductase Operons and the narT Gene of <i>Staphylococcus carnosus</i> Are Positively Controlled by the Novel Two-Component System NreBC. Journal of Bacteriology, 2002, 184, 6624-6634.	2.2	86
35	<i>Staphylococcus aureus</i> Colonization of the Human Nose and Interaction with Other Microbiome Members. , 0, , 723-730.		5