

Jiri Doskar

List of Publications by Year in descending order

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65
papers

2,170
citations

218677

26
h-index

243625

44
g-index

66
all docs

66
docs citations

66
times ranked

2415
citing authors

#	ARTICLE	IF	CITATIONS
1	Staphylococcus ratti sp. nov. Isolated from a Lab Rat. Pathogens, 2022, 11, 51.	2.8	7
2	Global Transcriptomic Analysis of Bacteriophage-Host Interactions between a Kayvirus Therapeutic Phage and Staphylococcus aureus. Microbiology Spectrum, 2022, 10, e0012322.	3.0	3
3	Staphylococcus epidermidis Phages Transduce Antimicrobial Resistance Plasmids and Mobilize Chromosomal Islands. MSphere, 2021, 6, .	2.9	27
4	Characterization of Staphylococcus intermedius Group Isolates Associated with Animals from Antarctica and Emended Description of Staphylococcus delphini. Microorganisms, 2020, 8, 204.	3.6	19
5	Staphylococcus petrasii diagnostics and its pathogenic potential enhanced by mobile genetic elements. International Journal of Medical Microbiology, 2019, 309, 151355.	3.6	2
6	Lytic and genomic properties of spontaneous host-range Kayvirus mutants prove their suitability for upgrading phage therapeutics against staphylococci. Scientific Reports, 2019, 9, 5475.	3.3	33
7	Draft Genome Sequence of the Panton-Valentine Leucocidin-Producing Staphylococcus aureus Sequence Type 154 Strain NRL 08/001, Isolated from a Fatal Case of Necrotizing Pneumonia. Microbiology Resource Announcements, 2019, 8, .	0.6	1
8	New Genus Fibralongavirus in Siphoviridae Phages of Staphylococcus pseudintermedius. Viruses, 2019, 11, 1143.	3.3	6
9	Variability of resistance plasmids in coagulase-negative staphylococci and their importance as a reservoir of antimicrobial resistance. Research in Microbiology, 2019, 170, 105-111.	2.1	22
10	Staphylococcus edaphicus sp. nov., Isolated in Antarctica, Harbors the <i>mecC</i> Gene and Genomic Islands with a Suspected Role in Adaptation to Extreme Environments. Applied and Environmental Microbiology, 2018, 84, .	3.1	60
11	Role of SH3b binding domain in a natural deletion mutant of Kayvirus endolysin LysF1 with a broad range of lytic activity. Virus Genes, 2018, 54, 130-139.	1.6	40
12	Silk Route to the Acceptance and Re-Implementation of Bacteriophage Therapyâ€™ Part II. Antibiotics, 2018, 7, 35.	3.7	46
13	Description and Comparative Genomics of Macrocooccus caseolyticus subsp. hominis subsp. nov., Macrocooccus goetzii sp. nov., Macrocooccus epidermidis sp. nov., and Macrocooccus bohemicus sp. nov., Novel Macrococci From Human Clinical Material With Virulence Potential and Suspected Uptake of Foreign DNA by Natural Transformation. Frontiers in Microbiology, 2018, 9, 1178.	3.5	65
14	Rapid Identification of Intact Staphylococcal Bacteriophages Using Matrix-Assisted Laser Desorption Ionization-Time-of-Flight Mass Spectrometry. Viruses, 2018, 10, 176.	3.3	21
15	Staphylococcus sciuri bacteriophages double-convert for staphylokinase and phospholipase, mediate interspecies plasmid transduction, and package mecA gene. Scientific Reports, 2017, 7, 46319.	3.3	48
16	Characterisation of methicillin-susceptible Staphylococcus pseudintermedius isolates from canine infections and determination of virulence factors using multiplex PCR. Veterinarni Medicina, 2017, 62, 81-89.	0.6	6
17	Two highly divergent lineages of exfoliative toxin B-encoding plasmids revealed in impetigo strains of Staphylococcus aureus. International Journal of Medical Microbiology, 2017, 307, 291-296.	3.6	8
18	Genetically modified bacteriophages in applied microbiology. Journal of Applied Microbiology, 2016, 121, 618-633.	3.1	52

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19	The evolutionary pathway of the staphylococcal cassette chromosome element. <i>Biologia (Poland)</i> , 2016, 71, 1195-1203.	1.5	10
20	Silk route to the acceptance and reimplementation of bacteriophage therapy. <i>Biotechnology Journal</i> , 2016, 11, 595-600.	3.5	54
21	Efficient plasmid transduction to <i>Staphylococcus aureus</i> strains insensitive to the lytic action of transducing phage. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw211.	1.8	40
22	Structure and genome release of Twort-like Myoviridae phage with a double-layered baseplate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9351-9356.	7.1	77
23	Efficient non-enzymatic cleavage of <i>Staphylococcus aureus</i> plasmid DNAs mediated by neodymium ions. <i>Analytical Biochemistry</i> , 2016, 507, 66-70.	2.4	0
24	High intraspecies heterogeneity within <i>Staphylococcus sciuri</i> and rejection of its classification into <i>S. sciuri</i> subsp. <i>sciuri</i> , <i>S. sciuri</i> subsp. <i>carnaticus</i> and <i>S. sciuri</i> subsp. <i>rodentium</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 5181-5186.	1.7	18
25	Molecular characterization of a new efficiently transducing bacteriophage identified in methicillin-resistant <i>Staphylococcus aureus</i> . <i>Journal of General Virology</i> , 2016, 97, 258-268.	2.9	33
26	Characterization of <i>Staphylococcus aureus</i> strains isolated from Czech Cystic Fibrosis Patients: High Rate of Ribosomal Mutation Conferring Resistance to MLSB Antibiotics as a Result of Long-Term and Low-Dose Azithromycin Treatment. <i>Microbial Drug Resistance</i> , 2015, 21, 416-423.	2.0	12
27	Complete genome analysis of two new bacteriophages isolated from impetigo strains of <i>Staphylococcus aureus</i> . <i>Virus Genes</i> , 2015, 51, 122-131.	1.6	11
28	The Staphylococcal Cassette Chromosome mec type V from <i>Staphylococcus aureus</i> ST398 is packaged into bacteriophage capsids. <i>International Journal of Medical Microbiology</i> , 2014, 304, 764-774.	3.6	39
29	<i>Staphylococcus petrasii</i> sp. nov. including <i>S. petrasii</i> subsp. <i>petrasii</i> subsp. nov. and <i>S. petrasii</i> subsp. <i>croceilyticus</i> subsp. nov., isolated from human clinical specimens and human ear infections. <i>Systematic and Applied Microbiology</i> , 2013, 36, 90-95.	2.8	45
30	Bacteriophages of <i>Staphylococcus aureus</i> efficiently package various bacterial genes and mobile genetic elements including SCCmec with different frequencies. <i>Environmental Microbiology Reports</i> , 2013, 5, 66-73.	2.4	66
31	Major clonal lineages in impetigo <i>Staphylococcus aureus</i> strains isolated in Czech and Slovak maternity hospitals. <i>International Journal of Medical Microbiology</i> , 2012, 302, 237-241.	3.6	16
32	Characteristics and distribution of plasmids in a clonally diverse set of methicillin-resistant <i>Staphylococcus aureus</i> strains. <i>Archives of Microbiology</i> , 2012, 194, 607-614.	2.2	24
33	Efficient transfer of antibiotic resistance plasmids by transduction within methicillin-resistant <i>Staphylococcus aureus</i> USA300 clone. <i>FEMS Microbiology Letters</i> , 2012, 332, 146-152.	1.8	73
34	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.	2.2	129
35	Multilocus PCR typing strategy for differentiation of <i>Staphylococcus aureus</i> siphoviruses reflecting their modular genome structure. <i>Environmental Microbiology</i> , 2010, 12, 2527-2538.	3.8	67
36	Rapid detection and differentiation of the exfoliative toxin A-producing <i>Staphylococcus aureus</i> strains based on ϕ ETA prophage polymorphisms. <i>Diagnostic Microbiology and Infectious Disease</i> , 2010, 66, 248-252.	1.8	11

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37	Genomic diversity of two lineages of exfoliative toxin A-converting phages predominating in <i>Staphylococcus aureus</i> strains in the Czech Republic. <i>Research in Microbiology</i> , 2010, 161, 260-267.	2.1	6
38	Molecular Diagnostics of <i>Staphylococcus aureus</i> . NATO Science for Peace and Security Series A: Chemistry and Biology, 2010, , 139-184.	0.5	1
39	Diversity of Prophages in Dominant <i>Staphylococcus aureus</i> Clonal Lineages. <i>Journal of Bacteriology</i> , 2009, 191, 3462-3468.	2.2	257
40	Extraction of PCR-ready DNA from <i>Staphylococcus aureus</i> bacteriophages using carboxyl functionalized magnetic nonporous microspheres. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2009, 877, 599-602.	2.3	13
41	Genotype analysis of enterotoxin H-positive <i>Staphylococcus aureus</i> strains isolated from food samples in the Czech Republic. <i>International Journal of Food Microbiology</i> , 2008, 121, 60-65.	4.7	20
42	Structural protein analysis of the polyvalent staphylococcal bacteriophage 812. <i>Proteomics</i> , 2007, 7, 64-72.	2.2	33
43	Genome rearrangements in host-range mutants of the polyvalent staphylococcal bacteriophage 812. <i>Folia Microbiologica</i> , 2007, 52, 331-338.	2.3	13
44	Genotypic characterization of toxic shock syndrome toxin-1-producing strains of <i>Staphylococcus aureus</i> isolated in the Czech Republic. <i>International Journal of Medical Microbiology</i> , 2006, 296, 49-54.	3.6	7
45	Genotypic characterisation of vancomycin-resistant <i>Enterococcus faecium</i> isolates from haemato-oncological patients at Olomouc University Hospital, Czech Republic. <i>Clinical Microbiology and Infection</i> , 2006, 12, 353-360.	6.0	5
46	Multiplex PCR for detection of three exfoliative toxin serotype genes in <i>Staphylococcus aureus</i> . <i>Folia Microbiologica</i> , 2005, 50, 499-502.	2.3	25
47	<i>Staphylococcus simiae</i> sp. nov., isolated from South American squirrel monkeys. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2005, 55, 1953-1958.	1.7	47
48	Molecular diagnostics of clinically important staphylococci. <i>Folia Microbiologica</i> , 2004, 49, 353-386.	2.3	28
49	Identification of bacteriophage types and their carriage in <i>Staphylococcus aureus</i> . <i>Archives of Virology</i> , 2004, 149, 1689-1703.	2.1	76
50	Molecular typing of exfoliative toxin-producing <i>Staphylococcus aureus</i> strains involved in epidermolytic infections. <i>International Journal of Medical Microbiology</i> , 2003, 292, 541-545.	3.6	13
51	<i>Macrocooccus brunensis</i> sp. nov., <i>Macrocooccus hajekii</i> sp. nov. and <i>Macrocooccus lamae</i> sp. nov., from the skin of llamas. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2003, 53, 1647-1654.	1.7	55
52	Characterization of yellow-pigmented and motile enterococci isolated from intestines of the garden snail <i>Helix aspersa</i> . <i>Journal of Applied Microbiology</i> , 2002, 92, 951-957.	3.1	18
53	Occurrence of antibiotic-resistant bacterial strains isolated in poultry. <i>Veterinarni Medicina</i> , 2002, 47, 52-59.	0.6	27
54	Identification of <i>Staphylococcus aureus</i> based on PCR amplification of species specific genomic 826 bp sequence derived from a common 44-kb Sma I restriction fragment. <i>Molecular and Cellular Probes</i> , 2001, 15, 249-257.	2.1	18

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55	Evaluation of ribotyping for characterization and identification of <i>Enterococcus haemoperoxidus</i> and <i>Enterococcus moraviensis</i> strains. <i>FEMS Microbiology Letters</i> , 2001, 203, 23-27.	1.8	1
56	<i>Enterococcus haemoperoxidus</i> sp. nov. and <i>Enterococcus moraviensis</i> sp. nov., isolated from water.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2001, 51, 1567-1574.	1.7	64
57	Genomic relatedness of <i>Staphylococcus aureus</i> phages of the International Typing Set and detection of serogroup A, B, and F prophages in lysogenic strains. <i>Canadian Journal of Microbiology</i> , 2000, 46, 1066-1076.	1.7	20
58	Complex genomic and phenotypic characterization of the related species <i>Staphylococcus carnosus</i> and <i>Staphylococcus piscifermentans</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 1999, 49, 941-951.	1.7	10
59	The Polyvalent Staphylococcal Phage ϕ 812: Its Host-Range Mutants and Related Phages. <i>Virology</i> , 1998, 246, 241-252.	2.4	81
60	DNA cycle sequencing of a common restriction fragment of <i>Staphylococcus aureus</i> bacteriophages by capillary electrophoresis using replaceable linear polyacrylamide. <i>Electrophoresis</i> , 1998, 19, 695-700.	2.4	9
61	Physical and genetic map of the genome of <i>Staphylococcus carnosus</i> TM300. <i>Microbiology (United Kingdom)</i> , 1998, 154, 107-114.	1.8	20
62	Genomic Variability of <i>Staphylococcus aureus</i> and the Other Coagulase-Positive <i>Staphylococcus</i> Species Estimated by Macrorestriction Analysis Using Pulsed-Field Gel Electrophoresis. <i>International Journal of Systematic Bacteriology</i> , 1996, 46, 216-222.	2.8	67
63	Localization of prophages of serological group B and F on restriction fragments defined in the restriction map of <i>Staphylococcus aureus</i> NCTC 8325. <i>FEMS Microbiology Letters</i> , 1996, 143, 203-210.	1.8	0
64	An improvement of restriction analysis of bacteriophage DNA using capillary electrophoresis in agarose solution. <i>Electrophoresis</i> , 1995, 16, 366-376.	2.4	24
65	Pulsed-field gel electrophoresis of the genomic restriction fragments of coagulase-negative staphylococci. <i>FEMS Microbiology Letters</i> , 1994, 124, 131-139.	1.8	21