

Philippe Glaser

List of Publications by Year in descending order

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149
papers

18,550
citations

19636

61
h-index

12585

132
g-index

160
all docs

160
docs citations

160
times ranked

14725
citing authors

#	ARTICLE	IF	CITATIONS
1	The complete genome sequence of the Gram-positive bacterium <i>Bacillus subtilis</i> . <i>Nature</i> , 1997, 390, 249-256.	13.7	3,519
2	Lysergic acid diethylamide- and mescaline-induced attenuation of the effect of punishment in the rat. <i>Science</i> , 1976, 192, 801-803.	6.0	1,415
3	Differentiation of the Major <i>Listeria monocytogenes</i> Serovars by Multiplex PCR. <i>Journal of Clinical Microbiology</i> , 2004, 42, 3819-3822.	1.8	915
4	Evidence in the <i>Legionella pneumophila</i> genome for exploitation of host cell functions and high genome plasticity. <i>Nature Genetics</i> , 2004, 36, 1165-1173.	9.4	573
5	The genome sequence of the entomopathogenic bacterium <i>Photorhabdus luminescens</i> . <i>Nature Biotechnology</i> , 2003, 21, 1307-1313.	9.4	538
6	Multilocus Sequence Typing System for Group B <i>Streptococcus</i> . <i>Journal of Clinical Microbiology</i> , 2003, 41, 2530-2536.	1.8	509
7	Genome sequence of <i>Streptococcus agalactiae</i> , a pathogen causing invasive neonatal disease. <i>Molecular Microbiology</i> , 2002, 45, 1499-1513.	1.2	439
8	Towards the sustainable discovery and development of new antibiotics. <i>Nature Reviews Chemistry</i> , 2021, 5, 726-749.	13.8	439
9	The virulence plasmid pWR100 and the repertoire of proteins secreted by the type III secretion apparatus of <i>Shigella flexneri</i> . <i>Molecular Microbiology</i> , 2000, 38, 760-771.	1.2	357
10	<i>Listeria monocytogenes</i> bile salt hydrolase is a PrfA-regulated virulence factor involved in the intestinal and hepatic phases of listeriosis. <i>Molecular Microbiology</i> , 2002, 45, 1095-1106.	1.2	307
11	New Aspects Regarding Evolution and Virulence of <i>Listeria monocytogenes</i> Revealed by Comparative Genomics and DNA Arrays. <i>Infection and Immunity</i> , 2004, 72, 1072-1083.	1.0	307
12	Dynamic, mitotic-like behavior of a bacterial protein required for accurate chromosome partitioning.. <i>Genes and Development</i> , 1997, 11, 1160-1168.	2.7	304
13	Multiple protein-aspartate phosphatases provide a mechanism for the integration of diverse signals in the control of development in <i>B. subtilis</i> . <i>Cell</i> , 1994, 79, 1047-1055.	13.5	302
14	Transcriptome analysis of <i>Listeria monocytogenes</i> identifies three groups of genes differently regulated by PrfA. <i>Molecular Microbiology</i> , 2003, 47, 1613-1625.	1.2	290
15	Group B <i>Streptococcus</i> : global incidence and vaccine development. <i>Nature Reviews Microbiology</i> , 2006, 4, 932-942.	13.6	272
16	Incorporation of D-Alanine into Lipoteichoic Acid and Wall Teichoic Acid in <i>Bacillus subtilis</i> . <i>Journal of Biological Chemistry</i> , 1995, 270, 15598-15606.	1.6	265
17	Fermentative Metabolism of <i>Bacillus subtilis</i> : Physiology and Regulation of Gene Expression. <i>Journal of Bacteriology</i> , 2000, 182, 3072-3080.	1.0	219
18	<i>Streptococcus agalactiae</i> clones infecting humans were selected and fixed through the extensive use of tetracycline. <i>Nature Communications</i> , 2014, 5, 4544.	5.8	208

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19	Genomic diversity and evolution within the species <i>Streptococcus agalactiae</i> . <i>Microbes and Infection</i> , 2006, 8, 1227-1243.	1.0	188
20	<i>Bacillus subtilis</i> genome project: cloning and sequencing of the 97 kb region from 325° to 333deg;. <i>Molecular Microbiology</i> , 1993, 10, 371-384.	1.2	187
21	Comparison of the genome sequences of <i>Listeria monocytogenes</i> and <i>Listeria innocua</i> : clues for evolution and pathogenicity. <i>FEMS Immunology and Medical Microbiology</i> , 2003, 35, 207-213.	2.7	187
22	CovS/CovR of group B streptococcus: a two-component global regulatory system involved in virulence. <i>Molecular Microbiology</i> , 2004, 54, 1250-1268.	1.2	185
23	Control of cell shape and elongation by the rodA gene in <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 1998, 28, 235-247.	1.2	173
24	Macro-array and bioinformatic analyses reveal mycobacterial "core" genes, variation in the ESAT-6 gene family and new phylogenetic markers for the <i>Mycobacterium tuberculosis</i> complex. <i>Microbiology (United Kingdom)</i> , 2004, 150, 483-496.	0.7	159
25	Multigenome analysis identifies a worldwide distributed epidemic <i>Legionella pneumophila</i> clone that emerged within a highly diverse species. <i>Genome Research</i> , 2008, 18, 431-441.	2.4	155
26	Antibiotic resistance: turning evolutionary principles into clinical reality. <i>FEMS Microbiology Reviews</i> , 2020, 44, 171-188.	3.9	154
27	The highly dynamic CRISPR1 system of <i>Streptococcus agalactiae</i> controls the diversity of its mobilome. <i>Molecular Microbiology</i> , 2012, 85, 1057-1071.	1.2	153
28	Characterization of transposon Tn1549, conferring VanB-type resistance in <i>Enterococcus</i> spp. The GenBank accession number for the 33803bp sequence of Tn1549 is AJ192329.. <i>Microbiology (United Kingdom)</i> , 2000, 144, 107-114.	0.7	150
29	Identification of a gene, spoII _R , that links the activation of sigma E to the transcriptional activity of sigma F during sporulation in <i>Bacillus subtilis</i> .. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 2012-2016.	3.3	147
30	Salt Stress Proteins Induced in <i>Listeria monocytogenes</i> . <i>Applied and Environmental Microbiology</i> , 2002, 68, 1491-1498.	1.4	140
31	Novel Clues on the Specific Association of <i>Streptococcus gallolyticus</i> subsp. <i>gallolyticus</i> With Colorectal Cancer. <i>Journal of Infectious Diseases</i> , 2011, 203, 1101-1109.	1.9	137
32	Aspartyl-phosphate phosphatases deactivate the response regulator components of the sporulation signal transduction system in <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 1996, 19, 1151-1157.	1.2	134
33	Shaping a bacterial genome by large chromosomal replacements, the evolutionary history of <i>Streptococcus agalactiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 15961-15966.	3.3	131
34	The 102-Kilobase <i>pgm</i> Locus of <i>Yersinia pestis</i> : Sequence Analysis and Comparison of Selected Regions among Different <i>Yersinia pestis</i> and <i>Yersinia pseudotuberculosis</i> Strains. <i>Infection and Immunity</i> , 1999, 67, 4851-4861.	1.0	128
35	RocR, a novel regulatory protein controlling arginine utilization in <i>Bacillus subtilis</i> , belongs to the NtrC/NifA family of transcriptional activators. <i>Journal of Bacteriology</i> , 1994, 176, 1234-1241.	1.0	121
36	Two-component regulatory proteins ResD-ResE are required for transcriptional activation of <i>fnr</i> upon oxygen limitation in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 1996, 178, 3796-3802.	1.0	121

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37	Bacillus subtilis FOF1 ATPase: DNA sequence of the atp operon and characterization of atp mutants. Journal of Bacteriology, 1994, 176, 6802-6811.	1.0	120
38	Genome Sequence of <i>Streptococcus gallolyticus</i> : Insights into Its Adaptation to the Bovine Rumen and Its Ability To Cause Endocarditis. Journal of Bacteriology, 2010, 192, 2266-2276.	1.0	120
39	Transcriptomic analysis of the exit from dormancy of Aspergillus fumigatus conidia. BMC Genomics, 2008, 9, 417.	1.2	118
40	Capsular Switching in Group B Streptococcus CC17 Hypervirulent Clone: A Future Challenge for Polysaccharide Vaccine Development. Journal of Infectious Diseases, 2012, 206, 1745-1752.	1.9	117
41	Rapid detection of the "highly virulent" group B streptococcus ST-17 clone. Microbes and Infection, 2006, 8, 1714-1722.	1.0	113
42	Catabolite Regulation of the pta Gene as Part of Carbon Flow Pathways in Bacillus subtilis. Journal of Bacteriology, 1999, 181, 6889-6897.	1.0	111
43	The SrtA Sortase of Streptococcus agalactiae Is Required for Cell Wall Anchoring of Proteins Containing the LPXTG Motif, for Adhesion to Epithelial Cells, and for Colonization of the Mouse Intestine. Infection and Immunity, 2005, 73, 3342-3350.	1.0	107
44	A Xanthomonas campestris pv. campestris protein similar to catabolite activation factor is involved in regulation of phytopathogenicity. Journal of Bacteriology, 1990, 172, 5877-5883.	1.0	96
45	High-level synthesis of active adenylate cyclase toxin of Bordetella pertussis in a reconstructed Escherichia coli system. Gene, 1991, 104, 19-24.	1.0	96
46	Demography and Intercontinental Spread of the USA300 Community-Acquired Methicillin-Resistant Staphylococcus aureus Lineage. MBio, 2016, 7, e02183-15.	1.8	96
47	Assessment of the rind microbial diversity in a farmhouse-produced vs a pasteurized industrially produced soft red-smear cheese using both cultivation and rDNA-based methods. Journal of Applied Microbiology, 2004, 97, 546-556.	1.4	94
48	Cloning and expression of the calmodulin-sensitive Bacillus anthracis adenylate cyclase in Escherichia coli. Gene, 1988, 64, 277-284.	1.0	90
49	The LE1 Bacteriophage Replicates as a Plasmid within Leptospira biflexa: Construction of an L. biflexa-Escherichia coli Shuttle Vector. Journal of Bacteriology, 2000, 182, 5700-5705.	1.0	88
50	Comparative genomics and transcriptomics of lineages I, II, and III strains of Listeria monocytogenes. BMC Genomics, 2012, 13, 144.	1.2	88
51	NeMeSys: a biological resource for narrowing the gap between sequence and function in the human pathogen Neisseria meningitidis. Genome Biology, 2009, 10, R110.	13.9	86
52	Pathogenomics of Listeria spp.. International Journal of Medical Microbiology, 2007, 297, 541-557.	1.5	84
53	Global analysis of gene expression in an rpoN mutant of Listeria monocytogenes. Microbiology (United Kingdom), 2004, 150, 1581-1590.	0.7	83
54	Reductive evolution in Streptococcus agalactiae and the emergence of a host adapted lineage. BMC Genomics, 2013, 14, 252.	1.2	81

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55	Molecular Characterization of a <i>Streptococcus gallolyticus</i> Genomic Island Encoding a Pilus Involved in Endocarditis. <i>Journal of Infectious Diseases</i> , 2011, 204, 1960-1970.	1.9	78
56	Integrative Conjugative Elements and Related Elements Are Major Contributors to the Genome Diversity of <i>Streptococcus agalactiae</i> . <i>Journal of Bacteriology</i> , 2008, 190, 6913-6917.	1.0	74
57	<i>ICEA</i> of <i>Mycoplasma agalactiae</i> : a new family of self-transmissible integrative elements that confers conjugative properties to the recipient strain. <i>Molecular Microbiology</i> , 2013, 89, 1226-1239.	1.2	72
58	Multiple major disease-associated clones of <i>Legionella pneumophila</i> have emerged recently and independently. <i>Genome Research</i> , 2016, 26, 1555-1564.	2.4	72
59	Isolation and characterization of catalytic and calmodulin-binding domains of <i>Bordetella pertussis</i> adenylate cyclase. <i>FEBS Journal</i> , 1991, 196, 469-474.	0.2	71
60	Identification and characterization of a new beta-glucoside utilization system in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 1997, 179, 496-506.	1.0	69
61	Growth inhibition of <i>Listeria monocytogenes</i> by a nonbacteriocinogenic <i>Carnobacterium piscicola</i> . <i>Journal of Applied Microbiology</i> , 2005, 98, 172-183.	1.4	67
62	Comparative Transcriptome Analysis of <i>Listeria monocytogenes</i> Strains of the Two Major Lineages Reveals Differences in Virulence, Cell Wall, and Stress Response. <i>Applied and Environmental Microbiology</i> , 2007, 73, 6078-6088.	1.4	66
63	Structural and functional genomics and evolutionary relationships in the cluster of genes encoding murine 2,5-oligoadenylate synthetases. <i>Genomics</i> , 2003, 82, 537-552.	1.3	63
64	Zinc, a novel structural element found in the family of bacterial adenylate kinases. <i>Biochemistry</i> , 1992, 31, 3038-3043.	1.2	62
65	Identification and isolation of a gene required for nitrate assimilation and anaerobic growth of <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 1995, 177, 1112-1115.	1.0	62
66	How Seryl-Phosphorylated HPr Inhibits PrfA, a Transcription Activator of <i>Listeria monocytogenes</i> Virulence Genes. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2005, 9, 224-234.	1.0	59
67	Cloning and assembly strategies in microbial genome projects. <i>Microbiology (United Kingdom)</i> , 1999, 145, 2625-2634.	0.7	56
68	Modular Evolution of Tn <i>GBS</i> s, a New Family of Integrative and Conjugative Elements Associating Insertion Sequence Transposition, Plasmid Replication, and Conjugation for Their Spreading. <i>Journal of Bacteriology</i> , 2013, 195, 1979-1990.	1.0	54
69	A 4.5-Year Within-Patient Evolution of a Colistin-Resistant <i>Klebsiella pneumoniae</i> Carbapenemase-Producing <i>K. pneumoniae</i> Sequence Type 258. <i>Clinical Infectious Diseases</i> , 2018, 67, 1388-1394.	2.9	54
70	Single nucleotide resolution RNA-seq uncovers new regulatory mechanisms in the opportunistic pathogen <i>Streptococcus agalactiae</i> . <i>BMC Genomics</i> , 2015, 16, 419.	1.2	53
71	Insertional mutagenesis of <i>Bordetella pertussis</i> adenylate cyclase. <i>Journal of Biological Chemistry</i> , 1992, 267, 2244-50.	1.6	53
72	Gene expression profiles in normal and <i>Otx2</i> ^{-/-} early gastrulating mouse embryos. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 14388-14393.	3.3	51

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73	The Diversity of Prokaryotic DDE Transposases of the Mutator Superfamily, Insertion Specificity, and Association with Conjugation Machineries. <i>Genome Biology and Evolution</i> , 2014, 6, 260-272.	1.1	51
74	The <i>Bacillus subtilis</i> ureABC operon. <i>Journal of Bacteriology</i> , 1997, 179, 3371-3373.	1.0	50
75	A Naturally Occurring Gene Amplification Leading to Sulfonamide and Trimethoprim Resistance in <i>Streptococcus agalactiae</i> . <i>Journal of Bacteriology</i> , 2008, 190, 672-680.	1.0	50
76	Equilibrium dissociation and unfolding of nucleoside diphosphate kinase from <i>Dictyostelium discoideum</i> . Role of proline 100 in the stability of the hexameric enzyme. <i>Journal of Biological Chemistry</i> , 1993, 268, 20268-75.	1.6	49
77	The Abi-domain Protein Abx1 Interacts with the CovS Histidine Kinase to Control Virulence Gene Expression in Group B <i>Streptococcus</i> . <i>PLoS Pathogens</i> , 2013, 9, e1003179.	2.1	47
78	Exploring the <i>Penicillium marneffei</i> genome. <i>Archives of Microbiology</i> , 2003, 179, 339-353.	1.0	45
79	Taxonomic characterization of nine strains isolated from clinical and environmental specimens, and proposal of <i>Corynebacterium tuberculostearicum</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004, 54, 1055-1061.	0.8	45
80	Characterization of the flexible genome complement of the commensal <i>Escherichia coli</i> strain AO 34/86 (O83:H24:H31). <i>Microbiology (United Kingdom)</i> , 2005, 151, 385-398.	0.7	45
81	Atypical association of DDE transposition with conjugation specifies a new family of mobile elements. <i>Molecular Microbiology</i> , 2009, 71, 948-959.	1.2	45
82	Analysis of the type II-A CRISPR-Cas system of <i>Streptococcus agalactiae</i> reveals distinctive features according to genetic lineages. <i>Frontiers in Genetics</i> , 2015, 6, 214.	1.1	45
83	Increased exposure to bacterial antigen Rpl7/L12 in early stage colorectal cancer patients. <i>Cancer</i> , 2010, 116, 4014-4022.	2.0	44
84	A gene encoding a tyrosine tRNA synthetase is located near Sacs in <i>Bacillus subtilis</i> . <i>DNA Sequence</i> , 1991, 1, 251-261.	0.7	43
85	Two genes encoding uracil phosphoribosyltransferase are present in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 1995, 177, 271-274.	1.0	42
86	Zinc Chelation and Structural Stability of Adenylate Kinase from <i>Bacillus subtilis</i> . <i>Biochemistry</i> , 1994, 33, 9960-9967.	1.2	41
87	DNA Macroarray for Identification and Typing of <i>Staphylococcus aureus</i> Isolates. <i>Journal of Clinical Microbiology</i> , 2004, 42, 2054-2064.	1.8	41
88	OXA-244-Producing <i>Escherichia coli</i> Isolates, a Challenge for Clinical Microbiology Laboratories. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	41
89	Surface-Exposed Histone-Like Protein A Modulates Adherence of <i>Streptococcus gallolyticus</i> to Colon Adenocarcinoma Cells. <i>Infection and Immunity</i> , 2009, 77, 5519-5527.	1.0	40
90	Stepwise evolution and convergent recombination underlie the global dissemination of carbapenemase-producing <i>Escherichia coli</i> . <i>Genome Medicine</i> , 2020, 12, 10.	3.6	40

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91	Long-lasting successful dissemination of resistance to oxazolidinones in MDR <i>Staphylococcus epidermidis</i> clinical isolates in a tertiary care hospital in France. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 41-51.	1.3	39
92	Emergence of New Non-Clonal Group 258 High-Risk Clones among <i>Klebsiella pneumoniae</i> Carbapenemase-Producing <i>K. pneumoniae</i> Isolates, France. <i>Emerging Infectious Diseases</i> , 2020, 26, 1212-1220.	2.0	39
93	Persistence of a dominant bovine lineage of group B <i>Streptococcus</i> reveals genomic signatures of host adaptation. <i>Environmental Microbiology</i> , 2016, 18, 4216-4229.	1.8	38
94	Chromosomal Amplification of the bla OXA-58 Carbapenemase Gene in a <i>Proteus mirabilis</i> Clinical Isolate. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	38
95	Genetic diversity of <i>Listeria monocytogenes</i> recovered from infected persons and pork, seafood and dairy products on retail sale in France during 2000 and 2001. <i>International Journal of Food Microbiology</i> , 2007, 114, 187-194.	2.1	37
96	Complete Nucleotide Sequence of the LE1 Prophage from the Spirochete <i>Leptospira biflexa</i> and Characterization of Its Replication and Partition Functions. <i>Journal of Bacteriology</i> , 2005, 187, 3931-3940.	1.0	34
97	Sequence and Binding Activity of the Autolysin-Adhesin Ami from Epidemic <i>Listeria monocytogenes</i> 4b. <i>Infection and Immunity</i> , 2004, 72, 4401-4409.	1.0	31
98	Parallel Evolution of Group B <i>Streptococcus</i> Hypervirulent Clonal Complex 17 Unveils New Pathoadaptive Mutations. <i>MSystems</i> , 2017, 2, .	1.7	31
99	Conserved and specific features of <i>Streptococcus pyogenes</i> and <i>Streptococcus agalactiae</i> transcriptional landscapes. <i>BMC Genomics</i> , 2019, 20, 236.	1.2	30
100	Cloning and expression of mouse-brain calmodulin as an activator of <i>Bordetella pertussis</i> adenylate cyclase in <i>Escherichia coli</i> . <i>Gene</i> , 1989, 80, 145-149.	1.0	27
101	Modulation of Anaerobic Energy Metabolism of <i>Bacillus subtilis</i> by arfM (<i>ywiD</i>). <i>Journal of Bacteriology</i> , 2001, 183, 6815-6821.	1.0	26
102	Whole-Genome Comparison Uncovers Genomic Mutations between Group B <i>Streptococci</i> Sampled from Infected Newborns and Their Mothers. <i>Journal of Bacteriology</i> , 2015, 197, 3354-3366.	1.0	25
103	Mapping of repetitive and non-repetitive DNA probes to chromosomes of the microsporidian <i>Encephalitozoon cuniculi</i> . <i>Gene</i> , 1997, 191, 39-45.	1.0	24
104	High third-generation cephalosporin resistant <i>Enterobacteriaceae</i> prevalence rate among neonatal infections in Dakar, Senegal. <i>BMC Infectious Diseases</i> , 2016, 16, 587.	1.3	24
105	Diversity of mucoid to non-mucoid switch among carbapenemase-producing <i>Klebsiella pneumoniae</i> . <i>BMC Microbiology</i> , 2020, 20, 325.	1.3	24
106	Functional analysis of subunits III and IV of <i>Bacillus subtilis</i> aa3-600 quinol oxidase by in vitro mutagenesis and gene replacement. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 1995, 1232, 67-74.	0.5	23
107	Population Structure of Human Isolates of <i>Streptococcus agalactiae</i> from Dakar and Bangui. <i>Journal of Clinical Microbiology</i> , 2009, 47, 800-803.	1.8	23
108	CTX-M-15-Producing <i>Shewanella</i> Species Clinical Isolate Expressing OXA-535, a Chromosome-Encoded OXA-48 Variant, Putative Progenitor of the Plasmid-Encoded OXA-436. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	22

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109	Inference of Significant Microbial Interactions From Longitudinal Metagenomics Data. <i>Frontiers in Microbiology</i> , 2018, 9, 2319.	1.5	22
110	Intrinsic fluorescence of a truncated <i>Bordetella pertussis</i> adenylate cyclase expressed in <i>Escherichia coli</i> . <i>Biochemistry</i> , 1990, 29, 8126-8130.	1.2	20
111	Construction of isogenic mutants in <i>Streptococcus gallolyticus</i> based on the development of new mobilizable vectors. <i>Research in Microbiology</i> , 2013, 164, 973-978.	1.0	20
112	Molecular epidemiology of invasive and non-invasive group B <i>Streptococcus</i> circulating in Serbia. <i>International Journal of Medical Microbiology</i> , 2019, 309, 19-25.	1.5	20
113	FindTarget: software for subtractive genome analysis. <i>Microbiology (United Kingdom)</i> , 2001, 147, 2643-2649.	0.7	18
114	A single <i>Proteus mirabilis</i> lineage from human and animal sources: a hidden reservoir of OXA-23 or OXA-58 carbapenemases in Enterobacterales. <i>Scientific Reports</i> , 2020, 10, 9160.	1.6	17
115	Rga, a RofA-Like Regulator, Is the Major Transcriptional Activator of the PI-2a Pilus in <i>Streptococcus agalactiae</i> . <i>Microbial Drug Resistance</i> , 2012, 18, 286-297.	0.9	15
116	Host specificity in the diversity and transfer of <i>isaA</i> resistance genes in group B <i>Streptococcus</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, dkv277.	1.3	14
117	The <i>fnr</i> Gene of <i>Bacillus licheniformis</i> and the Cysteine Ligands of the C-Terminal FeS Cluster. <i>Journal of Bacteriology</i> , 1998, 180, 3483-3485.	1.0	14
118	The CovR regulatory network drives the evolution of Group B <i>Streptococcus</i> virulence. <i>PLoS Genetics</i> , 2021, 17, e1009761.	1.5	13
119	Transcriptional Landscape of a blaKPC-2 Plasmid and Response to Imipenem Exposure in <i>Escherichia coli</i> TOP10. <i>Frontiers in Microbiology</i> , 2018, 9, 2929.	1.5	12
120	<i>Streptococcus Gallolyticus</i> Subsp. <i>Pasteurianus</i> Infection In A Neonatal Intensive Care Unit. <i>Pediatric Infectious Disease Journal</i> , 2016, 35, 1272-1275.	1.1	11
121	Demographic fluctuation of community-acquired antibiotic-resistant <i>Staphylococcus aureus</i> lineages: potential role of flimsy antibiotic exposure. <i>ISME Journal</i> , 2018, 12, 1879-1894.	4.4	11
122	A clone of the emergent <i>Streptococcus pyogenes</i> emm89 clade responsible for a large outbreak in a post-surgery oncology unit in France. <i>Medical Microbiology and Immunology</i> , 2018, 207, 287-296.	2.6	10
123	Dynamics of livestock-associated methicillin resistant <i>Staphylococcus aureus</i> in pig movement networks: Insight from mathematical modeling and French data. <i>Epidemics</i> , 2020, 31, 100389.	1.5	10
124	Complete Genome Sequence of <i>Streptococcus pyogenes</i> emm28 Clinical Isolate M28PF1, Responsible for a Puerperal Fever. <i>Genome Announcements</i> , 2015, 3, .	0.8	9
125	<i>Streptococcal</i> group B integrative and mobilizable element IMESag- <i>rpsI</i> encodes a functional relaxase involved in its transfer. <i>Open Biology</i> , 2016, 6, 160084.	1.5	9
126	SME-4-producing <i>Serratia marcescens</i> from Argentina belonging to clade 2 of the <i>S. marcescens</i> phylogeny. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1836-1841.	1.3	9

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127	Concomitant carriage of KPC-producing and non-KPC-producing <i>Klebsiella pneumoniae</i> ST512 within a single patient. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 2087-2092.	1.3	9
128	Pathogenomics: An updated European Research Agenda. <i>Infection, Genetics and Evolution</i> , 2008, 8, 386-393.	1.0	8
129	Serum resistance and phase variation of a nasopharyngeal non-typeable <i>Haemophilus influenzae</i> isolate. <i>International Journal of Medical Microbiology</i> , 2017, 307, 139-146.	1.5	8
130	Structural flexibility of the calmodulin-binding locus in <i>Bordetella pertussis</i> adenylate cyclase. Reconstitution of catalytically active species from fragments or inactive forms of the enzyme. <i>FEBS Journal</i> , 1993, 217, 581-586.	0.2	7
131	DiffTool: building, visualizing and querying protein clusters. <i>Bioinformatics</i> , 2002, 18, 1143-1144.	1.8	7
132	Specific regions of genome plasticity and genetic diversity of the commensal <i>Escherichia coli</i> A0 34/86. <i>International Journal of Medical Microbiology</i> , 2006, 296, 541-546.	1.5	7
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