

Ian Paulsen

List of Publications by Year in descending order

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333
papers

78,749
citations

807

118
h-index

470

271
g-index

347
all docs

347
docs citations

347
times ranked

64602
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysis of the genome sequence of the flowering plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 796-815.	13.7	8,336
2	Complete genome sequence of <i>Pseudomonas aeruginosa</i> PAO1, an opportunistic pathogen. <i>Nature</i> , 2000, 406, 959-964.	13.7	3,943
3	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002, 419, 498-511.	13.7	3,881
4	Environmental Genome Shotgun Sequencing of the Sargasso Sea. <i>Science</i> , 2004, 304, 66-74.	6.0	3,776
5	The <i>Chlamydomonas</i> Genome Reveals the Evolution of Key Animal and Plant Functions. <i>Science</i> , 2007, 318, 245-250.	6.0	2,354
6	Major Facilitator Superfamily. <i>Microbiology and Molecular Biology Reviews</i> , 1998, 62, 1-34.	2.9	1,760
7	The genome sequence of the filamentous fungus <i>Neurospora crassa</i> . <i>Nature</i> , 2003, 422, 859-868.	13.7	1,528
8	The genome sequence of <i>Schizosaccharomyces pombe</i> . <i>Nature</i> , 2002, 415, 871-880.	13.7	1,508
9	Complete Genome Sequence of a Virulent Isolate of <i>Streptococcus pneumoniae</i> . <i>Science</i> , 2001, 293, 498-506.	6.0	1,281
10	Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>Nature</i> , 2005, 438, 1151-1156.	13.7	1,272
11	Complete genome sequence and comparative analysis of the metabolically versatile <i>Pseudomonas putida</i> KT2440. <i>Environmental Microbiology</i> , 2002, 4, 799-808.	1.8	1,218
12	Genome sequencing and analysis of <i>Aspergillus oryzae</i> . <i>Nature</i> , 2005, 438, 1157-1161.	13.7	1,128
13	Genome Sequence of <i>Aedes aegypti</i> , a Major Arbovirus Vector. <i>Science</i> , 2007, 316, 1718-1723.	6.0	1,025
14	Proton-dependent multidrug efflux systems. <i>Microbiological Reviews</i> , 1996, 60, 575-608.	10.1	993
15	Insights on Evolution of Virulence and Resistance from the Complete Genome Analysis of an Early Methicillin-Resistant <i>Staphylococcus aureus</i> Strain and a Biofilm-Producing Methicillin-Resistant <i>Staphylococcus epidermidis</i> Strain. <i>Journal of Bacteriology</i> , 2005, 187, 2426-2438.	1.0	940
16	Role of Mobile DNA in the Evolution of Vancomycin-Resistant <i>Enterococcus faecalis</i> . <i>Science</i> , 2003, 299, 2071-2074.	6.0	849
17	Three Genomes from the Phylum <i>Acidobacteria</i> Provide Insight into the Lifestyles of These Microorganisms in Soils. <i>Applied and Environmental Microbiology</i> , 2009, 75, 2046-2056.	1.4	804
18	The complete genome sequence of the <i>Arabidopsis</i> and tomato pathogen <i>Pseudomonas syringae</i> pv. tomato DC3000. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10181-10186.	3.3	785

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19	Genome sequence of the dissimilatory metal ion-reducing bacterium <i>Shewanella oneidensis</i> . <i>Nature Biotechnology</i> , 2002, 20, 1118-1123.	9.4	771
20	The genome sequence of <i>Bacillus anthracis</i> Ames and comparison to closely related bacteria. <i>Nature</i> , 2003, 423, 81-86.	13.7	760
21	Comparative genomics of the neglected human malaria parasite <i>Plasmodium vivax</i> . <i>Nature</i> , 2008, 455, 757-763.	13.7	756
22	The Genome of the Natural Genetic Engineer <i>Agrobacterium tumefaciens</i> C58. <i>Science</i> , 2001, 294, 2317-2323.	6.0	741
23	Draft Genome Sequence of the Sexually Transmitted Pathogen <i>Trichomonas vaginalis</i> . <i>Science</i> , 2007, 315, 207-212.	6.0	731
24	Phylogenomics of the Reproductive Parasite <i>Wolbachia pipientis</i> wMel: A Streamlined Genome Overrun by Mobile Genetic Elements. <i>PLoS Biology</i> , 2004, 2, e69.	2.6	713
25	Genome of <i>Geobacter sulfurreducens</i> : Metal Reduction in Subsurface Environments. <i>Science</i> , 2003, 302, 1967-1969.	6.0	648
26	Proton-dependent multidrug efflux systems.. <i>Microbiological Reviews</i> , 1996, 60, 575-608.	10.1	644
27	Ecological Genomics of Marine Picocyanobacteria. <i>Microbiology and Molecular Biology Reviews</i> , 2009, 73, 249-299.	2.9	642
28	Complete genome sequence of the plant commensal <i>Pseudomonas fluorescens</i> Pf-5. <i>Nature Biotechnology</i> , 2005, 23, 873-878.	9.4	615
29	The genome of a motile marine <i>Synechococcus</i> . <i>Nature</i> , 2003, 424, 1037-1042.	13.7	611
30	EcoCyc: a comprehensive database resource for <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2004, 33, D334-D337.	6.5	597
31	Green Evolution and Dynamic Adaptations Revealed by Genomes of the Marine Picoeukaryotes <i>Micromonas</i> . <i>Science</i> , 2009, 324, 268-272.	6.0	591
32	Comparative Genomics of Plant-Associated <i>Pseudomonas</i> spp.: Insights into Diversity and Inheritance of Traits Involved in Multitrophic Interactions. <i>PLoS Genetics</i> , 2012, 8, e1002784.	1.5	578
33	The Genome of <i>M. acetivorans</i> Reveals Extensive Metabolic and Physiological Diversity. <i>Genome Research</i> , 2002, 12, 532-542.	2.4	573
34	Lessons from the Genome Sequence of <i>Neurospora crassa</i> : Tracing the Path from Genomic Blueprint to Multicellular Organism. <i>Microbiology and Molecular Biology Reviews</i> , 2004, 68, 1-108.	2.9	572
35	The tiny eukaryote <i>Ostreococcus</i> provides genomic insights into the paradox of plankton speciation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7705-7710.	3.3	563
36	The genome sequence of the anaerobic, sulfate-reducing bacterium <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Nature Biotechnology</i> , 2004, 22, 554-559.	9.4	559

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37	Pathway Tools version 13.0: integrated software for pathway/genome informatics and systems biology. <i>Briefings in Bioinformatics</i> , 2010, 11, 40-79.	3.2	551
38	The EcoCyc database: reflecting new knowledge about <i>Escherichia coli</i> K-12. <i>Nucleic Acids Research</i> , 2017, 45, D543-D550.	6.5	541
39	Complete genome sequence of the Q-fever pathogen <i>Coxiella burnetii</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5455-5460.	3.3	506
40	EcoCyc: fusing model organism databases with systems biology. <i>Nucleic Acids Research</i> , 2013, 41, D605-D612.	6.5	505
41	Complete genome sequence of <i>Caulobacter crescentus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 4136-4141.	3.3	489
42	Whole genome comparisons of serotype 4b and 1/2a strains of the food-borne pathogen <i>Listeria monocytogenes</i> reveal new insights into the core genome components of this species. <i>Nucleic Acids Research</i> , 2004, 32, 2386-2395.	6.5	460
43	Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V <i>Streptococcus agalactiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12391-12396.	3.3	447
44	TIGRFAMs: a protein family resource for the functional identification of proteins. <i>Nucleic Acids Research</i> , 2001, 29, 41-43.	6.5	445
45	EcoCyc: a comprehensive database of <i>Escherichia coli</i> biology. <i>Nucleic Acids Research</i> , 2011, 39, D583-D590.	6.5	444
46	Comparative genomic analysis of the thermophilic biomass-degrading fungi <i>Myceliophthora thermophila</i> and <i>Thielavia terrestris</i> . <i>Nature Biotechnology</i> , 2011, 29, 922-927.	9.4	428
47	The <i>Brucella suis</i> genome reveals fundamental similarities between animal and plant pathogens and symbionts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 13148-13153.	3.3	422
48	Genome sequence of <i>Silicibacter pomeroyi</i> reveals adaptations to the marine environment. <i>Nature</i> , 2004, 432, 910-913.	13.7	415
49	The EcoCyc Database. <i>Nucleic Acids Research</i> , 2002, 30, 56-58.	6.5	386
50	The complete genome sequence of <i>Chlorobium tepidum</i> TLS, a photosynthetic, anaerobic, green-sulfur bacterium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 9509-9514.	3.3	362
51	Complete Genome Sequence of the Oral Pathogenic Bacterium <i>Porphyromonas gingivalis</i> Strain W83. <i>Journal of Bacteriology</i> , 2003, 185, 5591-5601.	1.0	362
52	TransportDB: a comprehensive database resource for cytoplasmic membrane transport systems and outer membrane channels. <i>Nucleic Acids Research</i> , 2007, 35, D274-D279.	6.5	352
53	A Novel Family of Ubiquitous Heavy Metal Ion Transport Proteins. <i>Journal of Membrane Biology</i> , 1997, 156, 99-103.	1.0	347
54	Genome Sequence of <i>Babesia bovis</i> and Comparative Analysis of Apicomplexan Hemoprotozoa. <i>PLoS Pathogens</i> , 2007, 3, e148.	2.1	335

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55	Membrane transport proteins: implications of sequence comparisons. <i>Current Opinion in Cell Biology</i> , 1992, 4, 684-695.	2.6	333
56	The multidrug efflux protein NorM is a prototype of a new family of transporters. <i>Molecular Microbiology</i> , 1999, 31, 394-395.	1.2	329
57	Ecological Genomics of Marine Roseobacters. <i>Applied and Environmental Microbiology</i> , 2007, 73, 4559-4569.	1.4	327
58	A family of extracytoplasmic proteins that allow transport of large molecules across the outer membranes of gram-negative bacteria. <i>Journal of Bacteriology</i> , 1994, 176, 3825-3831.	1.0	325
59	EcoCyc: A comprehensive view of <i>Escherichia coli</i> biology. <i>Nucleic Acids Research</i> , 2009, 37, D464-D470.	6.5	320
60	Genome Sequence of <i>Theileria parva</i> , a Bovine Pathogen That Transforms Lymphocytes. <i>Science</i> , 2005, 309, 134-137.	6.0	309
61	TransportDB 2.0: a database for exploring membrane transporters in sequenced genomes from all domains of life. <i>Nucleic Acids Research</i> , 2017, 45, D320-D324.	6.5	306
62	The 3' conserved segment of integrons contains a gene associated with multidrug resistance to antiseptics and disinfectants. <i>Antimicrobial Agents and Chemotherapy</i> , 1993, 37, 761-768.	1.4	295
63	Microbial genome analyses: global comparisons of transport capabilities based on phylogenies, bioenergetics and substrate specificities 1 Edited by G. Von Heijne. <i>Journal of Molecular Biology</i> , 1998, 277, 573-592.	2.0	289
64	Phylogeny of multidrug transporters. <i>Seminars in Cell and Developmental Biology</i> , 2001, 12, 205-213.	2.3	288
65	Unravelling the genomic mosaic of a ubiquitous genus of marine cyanobacteria. <i>Genome Biology</i> , 2008, 9, R90.	13.9	288
66	Multidrug resistance proteins QacA and QacB from <i>Staphylococcus aureus</i> : membrane topology and identification of residues involved in substrate specificity.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 3630-3635.	3.3	281
67	Skewed genomic variability in strains of the toxigenic bacterial pathogen, <i>Clostridium perfringens</i> . <i>Genome Research</i> , 2006, 16, 1031-1040.	2.4	281
68	Antibiotic Discovery: Combatting Bacterial Resistance in Cells and in Biofilm Communities. <i>Molecules</i> , 2015, 20, 5286-5298.	1.7	276
69	The SMR family: a novel family of multidrug efflux proteins involved with the efflux of lipophilic drugs. <i>Molecular Microbiology</i> , 1996, 19, 1167-1175.	1.2	275
70	Genomic Insights into Methanotrophy: The Complete Genome Sequence of <i>Methylococcus capsulatus</i> (Bath). <i>PLoS Biology</i> , 2004, 2, e303.	2.6	275
71	The major facilitator superfamily. <i>Journal of Molecular Microbiology and Biotechnology</i> , 1999, 1, 257-79.	1.0	267
72	Genome sequence of <i>Chlamydomonada caviae</i> (<i>Chlamydia psittaci</i> GPIC): examining the role of niche-specific genes in the evolution of the Chlamydiaceae. <i>Nucleic Acids Research</i> , 2003, 31, 2134-2147.	6.5	266

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73	Microbial genome analyses: comparative transport capabilities in eighteen prokaryotes 1 Edited by G. von Heijne. Journal of Molecular Biology, 2000, 301, 75-100.	2.0	265
74	Genome Sequence of <i>Azotobacter vinelandii</i> , an Obligate Aerobe Specialized To Support Diverse Anaerobic Metabolic Processes. Journal of Bacteriology, 2009, 191, 4534-4545.	1.0	265
75	Niche of harmful alga <i>Aureococcus anophagefferens</i> revealed through ecogenomics. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4352-4357.	3.3	256
76	The amino acid/polyamine/organocation (APC) superfamily of transporters specific for amino acids, polyamines and organocations. Microbiology (United Kingdom), 2000, 146, 1797-1814.	0.7	251
77	Comparison of the genome of the oral pathogen <i>Treponema denticola</i> with other spirochete genomes. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 5646-5651.	3.3	251
78	Complete Genome Sequence of the Multiresistant Taxonomic Outlier <i>Pseudomonas aeruginosa</i> PA7. PLoS ONE, 2010, 5, e8842.	1.1	236
79	The EcoCyc and MetaCyc databases. Nucleic Acids Research, 2000, 28, 56-59.	6.5	234
80	Genome analysis of the proteorhodopsin-containing marine bacterium <i>Polaribacter</i> sp. MED152 (Flavobacteria). Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8724-8729.	3.3	231
81	Genome sequence of <i>Synechococcus</i> CC9311: Insights into adaptation to a coastal environment. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 13555-13559.	3.3	230
82	Genome of the Epsilonproteobacterial Chemolithoautotroph <i>Sulfurimonas denitrificans</i> . Applied and Environmental Microbiology, 2008, 74, 1145-1156.	1.4	228
83	A decade of advances in transposon-insertion sequencing. Nature Reviews Genetics, 2020, 21, 526-540.	7.7	228
84	Catabolite repression and inducer control in Gram-positive bacteria. Microbiology (United Kingdom), 1996, 142, 217-230.	0.7	222
85	Genome Sequences of Three <i>Agrobacterium</i> Biovars Help Elucidate the Evolution of Multichromosome Genomes in Bacteria. Journal of Bacteriology, 2009, 191, 2501-2511.	1.0	220
86	A family of Gram-negative bacterial outer membrane factors that function in the export of proteins, carbohydrates, drugs and heavy metals from Gram-negative bacteria. FEMS Microbiology Letters, 1997, 156, 1-8.	0.7	215
87	Investigation of the human pathogen <i>Acinetobacter baumannii</i> under iron limiting conditions. BMC Genomics, 2011, 12, 126.	1.2	215
88	Complete Genome Sequence of the Broad-Host-Range <i>Vibriophage</i> KVP40: Comparative Genomics of a T4-Related Bacteriophage. Journal of Bacteriology, 2003, 185, 5220-5233.	1.0	214
89	Evolutionary origins of multidrug and drug-specific efflux pumps in bacteria. FASEB Journal, 1998, 12, 265-274.	0.2	210
90	Phylogenetic characterization of novel transport protein families revealed by genome analyses. BBA - Biomembranes, 1999, 1422, 1-56.	7.9	207

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91	Unified inventory of established and putative transporters encoded within the complete genome of <i>Saccharomyces cerevisiae</i> . <i>FEBS Letters</i> , 1998, 430, 116-125.	1.3	203
92	Multidrug efflux pumps and resistance: regulation and evolution. <i>Current Opinion in Microbiology</i> , 2003, 6, 446-451.	2.3	191
93	Evolutionary origins of multidrug and drug-specific efflux pumps in bacteria. <i>FASEB Journal</i> , 1998, 12, 265-274.	0.2	184
94	TransportDB: a relational database of cellular membrane transport systems. <i>Nucleic Acids Research</i> , 2004, 32, 284D-288.	6.5	175
95	Genome-based evolutionary history of <i>Pseudomonas</i> spp. <i>Environmental Microbiology</i> , 2018, 20, 2142-2159.	1.8	172
96	ToxoDB: accessing the <i>Toxoplasma gondii</i> genome. <i>Nucleic Acids Research</i> , 2003, 31, 234-236.	6.5	171
97	Multidimensional annotation of the <i>Escherichia coli</i> K-12 genome. <i>Nucleic Acids Research</i> , 2007, 35, 7577-7590.	6.5	168
98	Adherence and motility characteristics of clinical <i>Acinetobacter baumannii</i> isolates. <i>FEMS Microbiology Letters</i> , 2011, 323, 44-51.	0.7	168
99	Substrate specificity and energetics of antiseptic and disinfectant resistance in <i>Staphylococcus aureus</i> . <i>FEMS Microbiology Letters</i> , 1992, 95, 259-265.	0.7	164
100	QacR Is a Repressor Protein That Regulates Expression of the <i>Staphylococcus aureus</i> Multidrug Efflux Pump QacA. <i>Journal of Biological Chemistry</i> , 1998, 273, 18665-18673.	1.6	163
101	New Glycoprotein-Associated Amino Acid Transporters. <i>Journal of Membrane Biology</i> , 1999, 172, 181-192.	1.0	161
102	Genome Sequences of the Biotechnologically Important <i>Bacillus megaterium</i> Strains QM B1551 and DSM319. <i>Journal of Bacteriology</i> , 2011, 193, 4199-4213.	1.0	155
103	Computer-based analyses of the protein constituents of transport systems catalysing export of complex carbohydrates in bacteria. <i>Microbiology (United Kingdom)</i> , 1997, 143, 2685-2699.	0.7	152
104	Community-acquired <i>Acinetobacter baumannii</i> : clinical characteristics, epidemiology and pathogenesis. <i>Expert Review of Anti-Infective Therapy</i> , 2015, 13, 567-573.	2.0	150
105	Comparative analysis of surface-exposed virulence factors of <i>Acinetobacter baumannii</i> . <i>BMC Genomics</i> , 2014, 15, 1020.	1.2	149
106	Multidrug resistance to antiseptics and disinfectants in coagulase-negative staphylococci. <i>Journal of Medical Microbiology</i> , 1994, 40, 214-220.	0.7	147
107	Composite genome map and recombination parameters derived from three archetypal lineages of <i>Toxoplasma gondii</i> . <i>Nucleic Acids Research</i> , 2005, 33, 2980-2992.	6.5	147
108	The Genome of Deep-Sea Vent Chemolithoautotroph <i>Thiomicrospira crunogena</i> XCL-2. <i>PLoS Biology</i> , 2006, 4, e383.	2.6	144

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109	Comparative Analyses of Fundamental Differences in Membrane Transport Capabilities in Prokaryotes and Eukaryotes. <i>PLoS Computational Biology</i> , 2005, 1, e27.	1.5	141
110	The ergosterol biosynthesis pathway, transporter genes, and azole resistance in <i>Aspergillus fumigatus</i> . <i>Medical Mycology</i> , 2005, 43, 313-319.	0.3	140
111	Transcriptomic and biochemical analyses identify a family of chlorhexidine efflux proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20254-20259.	3.3	138
112	Homologs of the <i>Acinetobacter baumannii</i> Acet Transporter Represent a New Family of Bacterial Multidrug Efflux Systems. <i>MBio</i> , 2015, 6, .	1.8	138
113	Multidrug-Resistant Transport Proteins in Yeast: Complete Inventory and Phylogenetic Characterization of Yeast Open Reading Frames within the Major Facilitator Superfamily. , 1997, 13, 43-54.		137
114	Contribution of Target Gene Mutations and Efflux to Decreased Susceptibility of <i>Salmonella enterica</i> Serovar Typhimurium to Fluoroquinolones and Other Antimicrobials. <i>Antimicrobial Agents and Chemotherapy</i> , 2007, 51, 535-542.	1.4	137
115	Inactivation of the GacA response regulator in <i>Pseudomonas fluorescens</i> Pf-5 has far-reaching transcriptomic consequences. <i>Environmental Microbiology</i> , 2010, 12, 899-915.	1.8	137
116	Topology, structure and evolution of two families of proteins involved in antibiotic and antiseptic resistance in eukaryotes and prokaryotes – an analysis. <i>Gene</i> , 1993, 124, 1-11.	1.0	133
117	The POT family of transport proteins. <i>Trends in Biochemical Sciences</i> , 1994, 19, 404.	3.7	131
118	Microarray analysis of phosphate regulation in the marine cyanobacterium <i>Synechococcus</i> sp. WH8102. <i>ISME Journal</i> , 2009, 3, 835-849.	4.4	131
119	A family of Gram-negative bacterial outer membrane factors that function in the export of proteins, carbohydrates, drugs and heavy metals from Gram-negative bacteria. <i>FEMS Microbiology Letters</i> , 2006, 156, 1-8.	0.7	125
120	Molecular characterization of the staphylococcal multidrug resistance export protein QacC. <i>Journal of Bacteriology</i> , 1995, 177, 2827-2833.	1.0	124
121	The EcoCyc Database in 2021. <i>Frontiers in Microbiology</i> , 2021, 12, 711077.	1.5	122
122	Influence of nutrients and currents on the genomic composition of microbes across an upwelling mosaic. <i>ISME Journal</i> , 2012, 6, 1403-1414.	4.4	120
123	RamA Confers Multidrug Resistance in <i>Salmonella enterica</i> via Increased Expression of <i>acrB</i> , Which Is Inhibited by Chlorpromazine. <i>Antimicrobial Agents and Chemotherapy</i> , 2008, 52, 3604-3611.	1.4	118
124	The Genomic Sequence of <i>Pseudomonas fluorescens</i> Pf-5: Insights Into Biological Control. <i>Phytopathology</i> , 2007, 97, 233-238.	1.1	115
125	Yeast's balancing act between ethanol and glycerol production in low-alcohol wines. <i>Microbial Biotechnology</i> , 2017, 10, 264-278.	2.0	113
126	Just one cross appears capable of dramatically altering the population biology of a eukaryotic pathogen like <i>Toxoplasma gondii</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 10514-10519.	3.3	112

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127	Genome Degradation in <i>Brucella ovis</i> Corresponds with Narrowing of Its Host Range and Tissue Tropism. <i>PLoS ONE</i> , 2009, 4, e5519.	1.1	110
128	Substrate specificity and energetics of antiseptic and disinfectant resistance in <i>Staphylococcus aureus</i> . <i>FEMS Microbiology Letters</i> , 1992, 74, 259-65.	0.7	110
129	The Value of Complete Microbial Genome Sequencing (You Get What You Pay For). <i>Journal of Bacteriology</i> , 2002, 184, 6403-6405.	1.0	101
130	The EcoCyc Database. <i>EcoSal Plus</i> , 2014, 6, .	2.1	101
131	Tiny Microbes with a Big Impact: The Role of Cyanobacteria and Their Metabolites in Shaping Our Future. <i>Marine Drugs</i> , 2016, 14, 97.	2.2	101
132	H-NS Plays a Role in Expression of <i>Acinetobacter baumannii</i> Virulence Features. <i>Infection and Immunity</i> , 2013, 81, 2574-2583.	1.0	100
133	The 2008 update of the <i>Aspergillus nidulans</i> genome annotation: A community effort. <i>Fungal Genetics and Biology</i> , 2009, 46, S2-S13.	0.9	99
134	Blueprints for Biosensors: Design, Limitations, and Applications. <i>Genes</i> , 2018, 9, 375.	1.0	99
135	Enzyme INtr from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 1999, 274, 26185-26191.	1.6	97
136	Rapid microevolution of biofilm cells in response to antibiotics. <i>Npj Biofilms and Microbiomes</i> , 2019, 5, 34.	2.9	96
137	Bioenergetics of the Staphylococcal Multidrug Export Protein QacA. <i>Journal of Biological Chemistry</i> , 1999, 274, 3541-3548.	1.6	95
138	A Broad-Specificity Multidrug Efflux Pump Requiring a Pair of Homologous SMR-Type Proteins. <i>Journal of Bacteriology</i> , 2000, 182, 2311-2313.	1.0	94
139	Three faces of biofilms: a microbial lifestyle, a nascent multicellular organism, and an incubator for diversity. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 80.	2.9	94
140	Status of genome projects for nonpathogenic bacteria and archaea. <i>Nature Biotechnology</i> , 2000, 18, 1049-1054.	9.4	93
141	The Complete Genome and Phenome of a Community-Acquired <i>Acinetobacter baumannii</i> . <i>PLoS ONE</i> , 2013, 8, e58628.	1.1	93
142	Mobile genetic elements in the genome of the beneficial rhizobacterium <i>Pseudomonas fluorescens</i> Pf-5. <i>BMC Microbiology</i> , 2009, 9, 8.	1.3	91
143	Synthetic Evolution of Metabolic Productivity Using Biosensors. <i>Trends in Biotechnology</i> , 2016, 34, 371-381.	4.9	90
144	Microbial Drug Efflux Proteins of the Major Facilitator Superfamily. <i>Current Drug Targets</i> , 2006, 7, 793-811.	1.0	87

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145	Exopolysaccharide-associated protein sorting in environmental organisms: the PEP-CTERM/EpsH system. Application of a novel phylogenetic profiling heuristic. <i>BMC Biology</i> , 2006, 4, 29.	1.7	86
146	Coastal <i>Synechococcus</i> metagenome reveals major roles for horizontal gene transfer and plasmids in population diversity. <i>Environmental Microbiology</i> , 2009, 11, 349-359.	1.8	86
147	Microbiology of the Anthropocene. <i>Anthropocene</i> , 2014, 5, 1-8.	1.6	83
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