

# Ian Paulsen

## List of Publications by Citations

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327  
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347  
ext. papers

72,865  
ext. citations

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7.53  
L-index

#	Paper	IF	Citations
327	Analysis of the genome sequence of the flowering plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , <b>2000</b> , 408, 796-815	50.4	7262
326	Complete genome sequence of <i>Pseudomonas aeruginosa</i> PAO1, an opportunistic pathogen. <i>Nature</i> , <b>2000</b> , 406, 959-64	50.4	3373
325	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , <b>2002</b> , 419, 498-511	50.4	3336
324	Environmental genome shotgun sequencing of the Sargasso Sea. <i>Science</i> , <b>2004</b> , 304, 66-74	33.3	3231
323	The <i>Chlamydomonas</i> genome reveals the evolution of key animal and plant functions. <i>Science</i> , <b>2007</b> , 318, 245-50	33.3	1969
322	Major facilitator superfamily. <i>Microbiology and Molecular Biology Reviews</i> , <b>1998</b> , 62, 1-34	13.2	1423
321	The genome sequence of the filamentous fungus <i>Neurospora crassa</i> . <i>Nature</i> , <b>2003</b> , 422, 859-68	50.4	1323
320	The genome sequence of <i>Schizosaccharomyces pombe</i> . <i>Nature</i> , <b>2002</b> , 415, 871-80	50.4	1281
319	Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>Nature</i> , <b>2005</b> , 438, 1151-6	50.4	1114
318	Complete genome sequence of a virulent isolate of <i>Streptococcus pneumoniae</i> . <i>Science</i> , <b>2001</b> , 293, 498-506	39.6	1112
317	Complete genome sequence and comparative analysis of the metabolically versatile <i>Pseudomonas putida</i> KT2440. <i>Environmental Microbiology</i> , <b>2002</b> , 4, 799-808	5.2	1069
316	Genome sequencing and analysis of <i>Aspergillus oryzae</i> . <i>Nature</i> , <b>2005</b> , 438, 1157-61	50.4	962
315	Genome sequence of <i>Aedes aegypti</i> , a major arbovirus vector. <i>Science</i> , <b>2007</b> , 316, 1718-23	33.3	867
314	Proton-dependent multidrug efflux systems. <i>Microbiological Reviews</i> , <b>1996</b> , 60, 575-608		848
313	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> , <b>2005</b> , 187, 2426-38	3.5	814
312	Role of mobile DNA in the evolution of vancomycin-resistant <i>Enterococcus faecalis</i> . <i>Science</i> , <b>2003</b> , 299, 2071-4	33.3	725
311	The complete genome sequence of the <i>Arabidopsis</i> and tomato pathogen <i>Pseudomonas syringae</i> pv. <i>tomato</i> DC3000. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2003</b> , 100, 10181-6	11.5	695

310	The genome sequence of <i>Bacillus anthracis</i> Ames and comparison to closely related bacteria. <i>Nature</i> , <b>2003</b> , 423, 81-6	50.4	692
309	Genome sequence of the dissimilatory metal ion-reducing bacterium <i>Shewanella oneidensis</i> . <i>Nature Biotechnology</i> , <b>2002</b> , 20, 1118-23	44.5	680
308	The genome of the natural genetic engineer <i>Agrobacterium tumefaciens</i> C58. <i>Science</i> , <b>2001</b> , 294, 2317-23	33.3	659
307	Comparative genomics of the neglected human malaria parasite <i>Plasmodium vivax</i> . <i>Nature</i> , <b>2008</b> , 455, 757-63	50.4	633
306	Draft genome sequence of the sexually transmitted pathogen <i>Trichomonas vaginalis</i> . <i>Science</i> , <b>2007</b> , 315, 207-12	33.3	622
305	Proton-dependent multidrug efflux systems.. <i>Microbiological Reviews</i> , <b>1996</b> , 60, 575-608		620
304	Phylogenomics of the reproductive parasite <i>Wolbachia pipientis</i> wMel: a streamlined genome overrun by mobile genetic elements. <i>PLoS Biology</i> , <b>2004</b> , 2, E69	9.7	613
303	Three genomes from the phylum Acidobacteria provide insight into the lifestyles of these microorganisms in soils. <i>Applied and Environmental Microbiology</i> , <b>2009</b> , 75, 2046-56	4.8	590
302	Genome of <i>Geobacter sulfurreducens</i> : metal reduction in subsurface environments. <i>Science</i> , <b>2003</b> , 302, 1967-9	33.3	573
301	The genome of a motile marine <i>Synechococcus</i> . <i>Nature</i> , <b>2003</b> , 424, 1037-42	50.4	534
300	Complete genome sequence of the plant commensal <i>Pseudomonas fluorescens</i> Pf-5. <i>Nature Biotechnology</i> , <b>2005</b> , 23, 873-8	44.5	522
299	EcoCyc: a comprehensive database resource for <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D334-7	20.1	514
298	Green evolution and dynamic adaptations revealed by genomes of the marine picoeukaryotes <i>Micromonas</i> . <i>Science</i> , <b>2009</b> , 324, 268-72	33.3	503
297	Ecological genomics of marine picocyanobacteria. <i>Microbiology and Molecular Biology Reviews</i> , <b>2009</b> , 73, 249-99	13.2	499
296	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> , <b>2004</b> , 68, 1-108	13.2	492
295	The genome of <i>M. acetivorans</i> reveals extensive metabolic and physiological diversity. <i>Genome Research</i> , <b>2002</b> , 12, 532-42	9.7	487
294	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> , <b>2007</b> , 104, 7705-10	11.5	482
293	The genome sequence of the anaerobic, sulfate-reducing bacterium <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Nature Biotechnology</i> , <b>2004</b> , 22, 554-9	44.5	477

292	EcoCyc: fusing model organism databases with systems biology. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D605-120.1	20.1	436
291	Complete genome sequence of <i>Caulobacter crescentus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2001</b> , 98, 4136-41	11.5	436
290	Comparative genomics of plant-associated <i>Pseudomonas</i> spp.: insights into diversity and inheritance of traits involved in multitrophic interactions. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002784	6	432
289	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> , <b>2003</b> , 100, 5455-60	11.5	428
288	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> , <b>2002</b> , 99, 12391-6	11.5	405
287	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> , <b>2004</b> , 32, 2386-95	20.1	404
286	Pathway Tools version 13.0: integrated software for pathway/genome informatics and systems biology. <i>Briefings in Bioinformatics</i> , <b>2010</b> , 11, 40-79	13.4	378
285	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> , <b>2002</b> , 99, 13148-53	11.5	372
284	EcoCyc: a comprehensive database of <i>Escherichia coli</i> biology. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D583-90	20.1	362
283	Genome sequence of <i>Silicibacter pomeroyi</i> reveals adaptations to the marine environment. <i>Nature</i> , <b>2004</b> , 432, 910-3	50.4	345
282	The EcoCyc database: reflecting new knowledge about <i>Escherichia coli</i> K-12. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D543-D550	20.1	333
281	Comparative genomic analysis of the thermophilic biomass-degrading fungi <i>Myceliophthora thermophila</i> and <i>Thielavia terrestris</i> . <i>Nature Biotechnology</i> , <b>2011</b> , 29, 922-7	44.5	324
280	Complete genome sequence of the oral pathogenic <i>Bacterium porphyromonas gingivalis</i> strain W83. <i>Journal of Bacteriology</i> , <b>2003</b> , 185, 5591-601	3.5	321
279	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> , <b>2002</b> , 99, 9509-14	11.5	321
278	A novel family of ubiquitous heavy metal ion transport proteins. <i>Journal of Membrane Biology</i> , <b>1997</b> , 156, 99-103	2.3	297
277	TransportDB: a comprehensive database resource for cytoplasmic membrane transport systems and outer membrane channels. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D274-9	20.1	296
276	The EcoCyc Database. <i>Nucleic Acids Research</i> , <b>2002</b> , 30, 56-8	20.1	296
275	TIGRFAMs: a protein family resource for the functional identification of proteins. <i>Nucleic Acids Research</i> , <b>2001</b> , 29, 41-3	20.1	295

274	The multidrug efflux protein NorM is a prototype of a new family of transporters. <i>Molecular Microbiology</i> , <b>1999</b> , 31, 394-5	4.1	293
273	Membrane transport proteins: implications of sequence comparisons. <i>Current Opinion in Cell Biology</i> , <b>1992</b> , 4, 684-95	9	292
272	A family of extracytoplasmic proteins that allow transport of large molecules across the outer membranes of gram-negative bacteria. <i>Journal of Bacteriology</i> , <b>1994</b> , 176, 3825-31	3.5	289
271	EcoCyc: a comprehensive view of Escherichia coli biology. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D464-70	20.1	288
270	Genome sequence of Babesia bovis and comparative analysis of apicomplexan hemoprotozoa. <i>PLoS Pathogens</i> , <b>2007</b> , 3, 1401-13	7.6	279
269	Ecological genomics of marine Roseobacters. <i>Applied and Environmental Microbiology</i> , <b>2007</b> , 73, 4559-69	4.8	269
268	Microbial genome analyses: global comparisons of transport capabilities based on phylogenies, bioenergetics and substrate specificities. <i>Journal of Molecular Biology</i> , <b>1998</b> , 277, 573-92	6.5	262
267	Genome sequence of Theileria parva, a bovine pathogen that transforms lymphocytes. <i>Science</i> , <b>2005</b> , 309, 134-7	33.3	259
266	The major facilitator superfamily. <i>Journal of Molecular Microbiology and Biotechnology</i> , <b>1999</b> , 1, 257-79	0.9	258
265	Phylogeny of multidrug transporters. <i>Seminars in Cell and Developmental Biology</i> , <b>2001</b> , 12, 205-13	7.5	254
264	Skewed genomic variability in strains of the toxigenic bacterial pathogen, Clostridium perfringens. <i>Genome Research</i> , <b>2006</b> , 16, 1031-40	9.7	250
263	Microbial genome analyses: comparative transport capabilities in eighteen prokaryotes. <i>Journal of Molecular Biology</i> , <b>2000</b> , 301, 75-100	6.5	243
262	Unraveling the genomic mosaic of a ubiquitous genus of marine cyanobacteria. <i>Genome Biology</i> , <b>2008</b> , 9, R90	18.3	242
261	The 3' conserved segment of integrons contains a gene associated with multidrug resistance to antiseptics and disinfectants. <i>Antimicrobial Agents and Chemotherapy</i> , <b>1993</b> , 37, 761-8	5.9	241
260	Genomic insights into methanotrophy: the complete genome sequence of Methylococcus capsulatus (Bath). <i>PLoS Biology</i> , <b>2004</b> , 2, e303	9.7	236
259	Genome sequence of Chlamydophila caviae (Chlamydia psittaci GPIC): examining the role of niche-specific genes in the evolution of the Chlamydiaceae. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 2134-47	20.1	233
258	Multidrug resistance proteins QacA and QacB from Staphylococcus aureus: 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> , <b>1996</b> , 93, 3630-5	11.5	233
257	The SMR family: a novel family of multidrug efflux proteins involved with the efflux of lipophilic drugs. <i>Molecular Microbiology</i> , <b>1996</b> , 19, 1167-75	4.1	232

256	The amino acid/polyamine/organocation (APC) superfamily of transporters specific for amino acids, polyamines and organocations. <i>Microbiology (United Kingdom)</i> , <b>2000</b> , 146 ( Pt 8), 1797-1814	2.9	220
255	Comparison of the genome of the oral pathogen <i>Treponema denticola</i> with other spirochete genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2004</b> , 101, 5646-51	11.5	215
254	Antibiotic discovery: combatting bacterial resistance in cells and in biofilm communities. <i>Molecules</i> , <b>2015</b> , 20, 5286-98	4.8	208
253	Niche of harmful alga <i>Aureococcus anophagefferens</i> revealed through ecogenomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 4352-7	11.5	205
252	Genome sequence of <i>Azotobacter vinelandii</i> , an obligate aerobe specialized to support diverse anaerobic metabolic processes. <i>Journal of Bacteriology</i> , <b>2009</b> , 191, 4534-45	3.5	202
251	Genome sequence of <i>Synechococcus</i> CC9311: Insights into adaptation to a coastal environment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2006</b> , 103, 13555-9	11.5	200
250	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> , <b>1997</b> , 156, 1-8	2.9	198
249	Genome analysis of the proteorhodopsin-containing marine bacterium <i>Polaribacter</i> sp. MED152 (Flavobacteria). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 8724-9	11.5	195
248	Complete genome sequence of the broad-host-range vibriophage KVP40: comparative genomics of a T4-related bacteriophage. <i>Journal of Bacteriology</i> , <b>2003</b> , 185, 5220-33	3.5	194
247	Genome of the epsilonproteobacterial chemolithoautotroph <i>Sulfurimonas denitrificans</i> . <i>Applied and Environmental Microbiology</i> , <b>2008</b> , 74, 1145-56	4.8	191
246	Phylogenetic characterization of novel transport protein families revealed by genome analyses. <i>BBA - Biomembranes</i> , <b>1999</b> , 1422, 1-56		189
245	Genome sequences of three agrobacterium biovars help elucidate the evolution of multichromosome genomes in bacteria. <i>Journal of Bacteriology</i> , <b>2009</b> , 191, 2501-11	3.5	184
244	Unified inventory of established and putative transporters encoded within the complete genome of <i>Saccharomyces cerevisiae</i> . <i>FEBS Letters</i> , <b>1998</b> , 430, 116-25	3.8	180
243	The EcoCyc and MetaCyc databases. <i>Nucleic Acids Research</i> , <b>2000</b> , 28, 56-9	20.1	177
242	Complete genome sequence of the multiresistant taxonomic outlier <i>Pseudomonas aeruginosa</i> PA7. <i>PLoS ONE</i> , <b>2010</b> , 5, e8842	3.7	176
241	Evolutionary origins of multidrug and drug-specific efflux pumps in bacteria. <i>FASEB Journal</i> , <b>1998</b> , 12, 265-274	0.9	174
240	Catabolite repression and inducer control in Gram-positive bacteria. <i>Microbiology (United Kingdom)</i> , <b>1996</b> , 142 ( Pt 2), 217-230	2.9	170
239	Evolutionary origins of multidrug and drug-specific efflux pumps in bacteria. <i>FASEB Journal</i> , <b>1998</b> , 12, 265-74	0.9	169

238	Multidrug efflux pumps and resistance: regulation and evolution. <i>Current Opinion in Microbiology</i> , <b>2003</b> , 6, 446-51	7.9	167
237	TransportDB: a relational database of cellular membrane transport systems. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, D284-8	20.1	157
236	TransportDB 2.0: a database for exploring membrane transporters in sequenced genomes from all domains of life. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D320-D324	20.1	156
235	Multidimensional annotation of the Escherichia coli K-12 genome. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, 7577-7601	20.1	151
234	ToxoDB: accessing the Toxoplasma gondii genome. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 234-6	20.1	149
233	Substrate specificity and energetics of antiseptic and disinfectant resistance in Staphylococcus aureus. <i>FEMS Microbiology Letters</i> , <b>1992</b> , 95, 259-265	2.9	148
232	Investigation of the human pathogen Acinetobacter baumannii under iron limiting conditions. <i>BMC Genomics</i> , <b>2011</b> , 12, 126	4.5	146
231	QacR is a repressor protein that regulates expression of the Staphylococcus aureus multidrug efflux pump QacA. <i>Journal of Biological Chemistry</i> , <b>1998</b> , 273, 18665-73	5.4	146
230	Computer-based analyses of the protein constituents of transport systems catalysing export of complex carbohydrates in bacteria. <i>Microbiology (United Kingdom)</i> , <b>1997</b> , 143 ( Pt 8), 2685-2699	2.9	139
229	New glycoprotein-associated amino acid transporters. <i>Journal of Membrane Biology</i> , <b>1999</b> , 172, 181-92	2.3	137
228	Composite genome map and recombination parameters derived from three archetypal lineages of Toxoplasma gondii. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, 2980-92	20.1	133
227	Genome sequences of the biotechnologically important Bacillus megaterium strains QM B1551 and DSM319. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 4199-213	3.5	128
226	Comparative analyses of fundamental differences in membrane transport capabilities in prokaryotes and eukaryotes. <i>PLoS Computational Biology</i> , <b>2005</b> , 1, e27	5	124
225	Multidrug resistance to antiseptics and disinfectants in coagulase-negative staphylococci. <i>Journal of Medical Microbiology</i> , <b>1994</b> , 40, 214-20	3.2	119
224	Inactivation of the GacA response regulator in Pseudomonas fluorescens Pf-5 has far-reaching transcriptomic consequences. <i>Environmental Microbiology</i> , <b>2010</b> , 12, 899-915	5.2	118
223	Multidrug-resistant transport proteins in yeast: complete inventory and phylogenetic characterization of yeast open reading frames with the major facilitator superfamily. <i>Yeast</i> , <b>1997</b> , 13, 43-54	3.4	113
222	The genome of deep-sea vent chemolithoautotroph Thiomicrospira crunogena XCL-2. <i>PLoS Biology</i> , <b>2006</b> , 4, e383	9.7	112
221	The ergosterol biosynthesis pathway, transporter genes, and azole resistance in Aspergillus fumigatus. <i>Medical Mycology</i> , <b>2005</b> , 43 Suppl 1, S313-9	3.9	111

220	Topology, structure and evolution of two families of proteins involved in antibiotic and antiseptic resistance in eukaryotes and prokaryotes--an analysis. <i>Gene</i> , <b>1993</b> , 124, 1-11	3.8	111
219	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> , <b>2013</b> , 110, 20254-9	11.5	110
218	Adherence and motility characteristics of clinical <i>Acinetobacter baumannii</i> isolates. <i>FEMS Microbiology Letters</i> , <b>2011</b> , 323, 44-51	2.9	110
217	Molecular characterization of the staphylococcal multidrug resistance export protein QacC. <i>Journal of Bacteriology</i> , <b>1995</b> , 177, 2827-33	3.5	109
216	The POT family of transport proteins. <i>Trends in Biochemical Sciences</i> , <b>1994</b> , 19, 404	10.3	108
215	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> , <b>2007</b> , 51, 535-42	5.9	106
214	Homologs of the <i>Acinetobacter baumannii</i> Acel transporter represent a new family of bacterial multidrug efflux systems. <i>MBio</i> , <b>2015</b> , 6,	7.8	103
213	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> , <b>2006</b> , 103, 10514-10519	11.5	102
212	The Genomic Sequence of <i>Pseudomonas fluorescens</i> Pf-5: Insights Into Biological Control. <i>Phytopathology</i> , <b>2007</b> , 97, 233-8	3.8	98
211	Microarray analysis of phosphate regulation in the marine cyanobacterium <i>Synechococcus</i> sp. WH8102. <i>ISME Journal</i> , <b>2009</b> , 3, 835-49	11.9	97
210	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> , <b>1997</b> , 156, 1-8	2.9	95
209	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> , <b>2008</b> , 52, 3604-11	5.9	94
208	Community-acquired <i>Acinetobacter baumannii</i> : clinical characteristics, epidemiology and pathogenesis. <i>Expert Review of Anti-Infective Therapy</i> , <b>2015</b> , 13, 567-73	5.5	93
207	The value of complete microbial genome sequencing (you get what you pay for). <i>Journal of Bacteriology</i> , <b>2002</b> , 184, 6403-5; discussion 6405	3.5	93
206	Enzyme I(Ntr) from <i>Escherichia coli</i> . A novel enzyme of the phosphoenolpyruvate-dependent phosphotransferase system exhibiting strict specificity for its phosphoryl acceptor, NPr. <i>Journal of Biological Chemistry</i> , <b>1999</b> , 274, 26185-91	5.4	88
205	Influence of nutrients and currents on the genomic composition of microbes across an upwelling mosaic. <i>ISME Journal</i> , <b>2012</b> , 6, 1403-14	11.9	87
204	Genome degradation in <i>Brucella ovis</i> corresponds with narrowing of its host range and tissue tropism. <i>PLoS ONE</i> , <b>2009</b> , 4, e5519	3.7	84
203	The 2008 update of the <i>Aspergillus nidulans</i> genome annotation: a community effort. <i>Fungal Genetics and Biology</i> , <b>2009</b> , 46 Suppl 1, S2-13	3.9	82

202	Yeast's balancing act between ethanol and glycerol production in low-alcohol wines. <i>Microbial Biotechnology</i> , <b>2017</b> , 10, 264-278	6.3	81
201	Genome-based evolutionary history of <i>Pseudomonas</i> spp. <i>Environmental Microbiology</i> , <b>2018</b> , 20, 2142-2159	5.9	81
200	A decade of advances in transposon-insertion sequencing. <i>Nature Reviews Genetics</i> , <b>2020</b> , 21, 526-540	30.1	78
199	Status of genome projects for nonpathogenic bacteria and archaea. <i>Nature Biotechnology</i> , <b>2000</b> , 18, 1049-54	4.5	78
198	A broad-specificity multidrug efflux pump requiring a pair of homologous SMR-type proteins. <i>Journal of Bacteriology</i> , <b>2000</b> , 182, 2311-3	3.5	78
197	Bioenergetics of the staphylococcal multidrug export protein QacA. Identification of distinct binding sites for monovalent and divalent cations. <i>Journal of Biological Chemistry</i> , <b>1999</b> , 274, 3541-8	5.4	78
196	Coastal <i>Synechococcus</i> metagenome reveals major roles for horizontal gene transfer and plasmids in population diversity. <i>Environmental Microbiology</i> , <b>2009</b> , 11, 349-59	5.2	77
195	Comparative analysis of surface-exposed virulence factors of <i>Acinetobacter baumannii</i> . <i>BMC Genomics</i> , <b>2014</b> , 15, 1020	4.5	76
194	Microbial drug efflux proteins of the major facilitator superfamily. <i>Current Drug Targets</i> , <b>2006</b> , 7, 793-813	3.5	75
193	Synthetic Evolution of Metabolic Productivity Using Biosensors. <i>Trends in Biotechnology</i> , <b>2016</b> , 34, 371-383	3.1	73
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191	Substrate specificity and energetics of antiseptic and disinfectant resistance in <i>Staphylococcus aureus</i> . <i>FEMS Microbiology Letters</i> , <b>1992</b> , 74, 259-65	2.9	72
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