

# Ian Paulsen

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

327  
papers

65,204  
citations

110  
h-index

254  
g-index

347  
ext. papers

72,865  
ext. citations

9.7  
avg, IF

7.53  
L-index

#	Paper	IF	Citations
327	Fluorescence-Based Biosensors for the Detection of the Unfolded Protein Response.. <i>Methods in Molecular Biology</i> , <b>2022</b> , 2378, 19-30	1.4	
326	Novel functional insights into a modified sugar-binding protein from <i>Synechococcus</i> MITS9220.. <i>Scientific Reports</i> , <b>2022</b> , 12, 4805	4.9	0
325	Delving into defence: identifying the Pf-5 gene suite involved in defence against secreted products of fungal, oomycete and bacterial rhizosphere competitors. <i>Microbial Genomics</i> , <b>2021</b> , 7,	4.4	1
324	Homecoming: rewinding the reductive evolution of the chloroplast genome for increasing crop yields. <i>Nature Communications</i> , <b>2021</b> , 12, 6734	17.4	2
323	Three faces of biofilms: a microbial lifestyle, a nascent multicellular organism, and an incubator for diversity. <i>Npj Biofilms and Microbiomes</i> , <b>2021</b> , 7, 80	8.2	19
322	Microbial Community Shifts on Organic Rocks of Different Maturities Reveal potential Catabolisers of Organic Matter in Coal. <i>Microbial Ecology</i> , <b>2021</b> , 1	4.4	
321	Benzalkonium chloride antagonises aminoglycoside antibiotics and promotes evolution of resistance. <i>EBioMedicine</i> , <b>2021</b> , 73, 103653	8.8	2
320	Physiological Functions of Bacterial "Multidrug" Efflux Pumps. <i>Chemical Reviews</i> , <b>2021</b> , 121, 5417-5478	68.1	22
319	Aromatic compound-degrading taxa in an anoxic coal seam microbiome from the Surat Basin, Australia. <i>FEMS Microbiology Ecology</i> , <b>2021</b> , 97,	4.3	1
318	Seeding the idea of encapsulating a representative synthetic metagenome in a single yeast cell. <i>Nature Communications</i> , <b>2021</b> , 12, 1599	17.4	3
317	Elucidating Essential Genes in Plant-Associated <i>Pseudomonas protegens</i> Pf-5 Using Transposon Insertion Sequencing. <i>Journal of Bacteriology</i> , <b>2021</b> , 203,	3.5	3
316	Cell size, genome size, and maximum growth rate are near-independent dimensions of ecological variation across bacteria and archaea. <i>Ecology and Evolution</i> , <b>2021</b> , 11, 3956-3976	2.8	12
315	Root Exudates Alter the Expression of Diverse Metabolic, Transport, Regulatory, and Stress Response Genes in Rhizosphere. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 651282	5.7	13
314	Trait dimensions in bacteria and archaea compared to vascular plants. <i>Ecology Letters</i> , <b>2021</b> , 24, 1487-1506	15.2	3
313	Identification of a Novel Ciprofloxacin Tolerance Gene, , Which Contributes to Filamentation in <i>Acinetobacter baumannii</i> . <i>Antimicrobial Agents and Chemotherapy</i> , <b>2021</b> , 65,	5.9	2
312	Fatty Acid Desaturases Facilitate Survival in Distinct Environments. <i>ACS Infectious Diseases</i> , <b>2021</b> , 7, 2221-2228	15.2	2
311	The Membrane Composition Defines the Spatial Organization and Function of a Major <i>Acinetobacter baumannii</i> Drug Efflux System. <i>MBio</i> , <b>2021</b> , 12, e0107021	7.8	7

310	Yeast Synthetic Minimal Biosensors for Evaluating Protein Production. <i>ACS Synthetic Biology</i> , <b>2021</b> , 10, 1640-1650	5.7	6
309	The EcoCyc Database in 2021. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 711077	5.7	16
308	Microdroplet enabled cultivation of single yeast cells correlates with bulk growth and reveals subpopulation phenomena. <i>Biotechnology and Bioengineering</i> , <b>2021</b> , 118, 647-658	4.9	5
307	Adherent microbes in coal seam environments prefer mineral-rich and crack-associated microhabitats. <i>International Journal of Coal Geology</i> , <b>2021</b> , 234, 103652	5.5	4
306	Aerobic bacteria and archaea tend to have larger and more versatile genomes. <i>Oikos</i> , <b>2021</b> , 130, 501-514		6
305	The Molecular Basis of <i>Acinetobacter baumannii</i> Cadmium Toxicity and Resistance. <i>Applied and Environmental Microbiology</i> , <b>2021</b> , 87, e0171821	4.8	1
304	The <i>Acinetobacter baumannii</i> disinfectant resistance protein, AmvA, is a spermidine and spermine efflux pump. <i>Communications Biology</i> , <b>2021</b> , 4, 1114	6.7	2
303	Increasing the PACE of characterising novel transporters by functional genomics. <i>Current Opinion in Microbiology</i> , <b>2021</b> , 64, 1-8	7.9	0
302	Draft Genome Sequence of sp. Strain CSMB_222, Isolated from Coal Seam Formation Water. <i>Microbiology Resource Announcements</i> , <b>2021</b> , 10, e0056421	1.3	
301	Adaptive laboratory evolution of native methanol assimilation in <i>Saccharomyces cerevisiae</i> . <i>Nature Communications</i> , <b>2020</b> , 11, 5564	17.4	19
300	A decade of advances in transposon-insertion sequencing. <i>Nature Reviews Genetics</i> , <b>2020</b> , 21, 526-540	30.1	78
299	A synthesis of bacterial and archaeal phenotypic trait data. <i>Scientific Data</i> , <b>2020</b> , 7, 170	8.2	20
298	Characterizing the Mechanism of Action of an Ancient Antimicrobial, Manuka Honey, against <i>Pseudomonas aeruginosa</i> Using Modern Transcriptomics. <i>MSystems</i> , <b>2020</b> , 5,	7.6	10
297	The Sensory Significance of Apocarotenoids in Wine: Importance of Carotenoid Cleavage Dioxygenase 1 (CCD1) in the Production of $\beta$ -ionone. <i>Molecules</i> , <b>2020</b> , 25,	4.8	9
296	Changes in dietary fiber intake in mice reveal associations between colonic mucin -glycosylation and specific gut bacteria. <i>Gut Microbes</i> , <b>2020</b> , 12, 1802209	8.8	10
295	The Role of Zinc Efflux during Infection. <i>ACS Infectious Diseases</i> , <b>2020</b> , 6, 150-158	5.5	11
294	Subsurface <i>Stappia</i> : Success Through Defence, Specialisation and Putative Pressure-Dependent Carbon Fixation. <i>Microbial Ecology</i> , <b>2020</b> , 80, 34-46	4.4	6
293	Comparative membrane proteomics reveal contrasting adaptation strategies for coastal and oceanic marine <i>Synechococcus</i> cyanobacteria. <i>Environmental Microbiology</i> , <b>2020</b> , 22, 1816-1828	5.2	1

292	Rapid optimisation of cellulolytic enzymes ratios in <i>Saccharomyces cerevisiae</i> using in vitro SCRaMBLE. <i>Biotechnology for Biofuels</i> , <b>2020</b> , 13, 182	7.8	6
291	The Transcriptomic Signature of Tigecycline in. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 565438	5.7	5
290	Secondary Effects of Antibiotics on Microbial Biofilms. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 2109	5.7	12
289	Rapid Colorimetric Detection of Genome Evolution in SCRaMBLEd Synthetic Strains. <i>Microorganisms</i> , <b>2020</b> , 8,	4.9	1
288	Application of Transposon Insertion Sequencing to Agricultural Science. <i>Frontiers in Plant Science</i> , <b>2020</b> , 11, 291	6.2	6
287	The Role of the CopA Copper Efflux System in Virulence. <i>International Journal of Molecular Sciences</i> , <b>2019</b> , 20,	6.3	23
286	Who eats what? Unravelling microbial conversion of coal to methane. <i>FEMS Microbiology Ecology</i> , <b>2019</b> , 95,	4.3	10
285	Catabolism of Nucleic Acids by a Cystic Fibrosis Isolate: An Adaptive Pathway to Cystic Fibrosis Sputum Environment. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 1199	5.7	8
284	Evolutionary engineering in reveals a -dependent potassium influx mechanism for propionic acid tolerance. <i>Biotechnology for Biofuels</i> , <b>2019</b> , 12, 97	7.8	15
283	Interactions of an Emerging Fungal Pathogen <i>Scedosporium aurantiacum</i> with Human Lung Epithelial Cells. <i>Scientific Reports</i> , <b>2019</b> , 9, 5035	4.9	7
282	Identification of Novel Host Fatty Acid Stress Adaptation Strategies. <i>MBio</i> , <b>2019</b> , 10,	7.8	25
281	Microbial communities are sensitive indicators for freshwater sediment copper contamination. <i>Environmental Pollution</i> , <b>2019</b> , 247, 1028-1038	9.3	18
280	Microbial Solute Transporters <b>2019</b> , 157-157		
279	QTL analysis of natural <i>Saccharomyces cerevisiae</i> isolates reveals unique alleles involved in lignocellulosic inhibitor tolerance. <i>FEMS Yeast Research</i> , <b>2019</b> , 19,	3.1	5
278	Benchmarking two laboratory strains for growth and transcriptional response to methanol. <i>Synthetic and Systems Biotechnology</i> , <b>2019</b> , 4, 180-188	4.2	8
277	Rapid microevolution of biofilm cells in response to antibiotics. <i>Npj Biofilms and Microbiomes</i> , <b>2019</b> , 5, 34	8.2	49
276	Succession Patterns and Physical Niche Partitioning in Microbial Communities from Subsurface Coal Seams. <i>IScience</i> , <b>2019</b> , 12, 152-167	6.1	15
275	Genomic and phenotypic insights point to diverse ecological strategies by facultative anaerobes obtained from subsurface coal seams. <i>Scientific Reports</i> , <b>2019</b> , 9, 16186	4.9	5

274	Short-chain diamines are the physiological substrates of PACE family efflux pumps. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2019</b> , 116, 18015-18020	11.5	15
273	Pacing across the membrane: the novel PACE family of efflux pumps is widespread in Gram-negative pathogens. <i>Research in Microbiology</i> , <b>2018</b> , 169, 450-454	4	50
272	Regulation of the aceI multidrug efflux pump gene in <i>Acinetobacter baumannii</i> . <i>Journal of Antimicrobial Chemotherapy</i> , <b>2018</b> , 73, 1492-1500	5.1	18
271	Genome-based evolutionary history of <i>Pseudomonas</i> spp. <i>Environmental Microbiology</i> , <b>2018</b> , 20, 2142-2159	5.9	81
270	The Coal Seam Microbiome (CSMB) reference set, a lingua franca for the microbial coal-to-methane community. <i>International Journal of Coal Geology</i> , <b>2018</b> , 186, 41-50	5.5	23
269	Fiber Supplements Derived From Sugarcane Stem, Wheat Dextrin and Psyllium Husk Have Different Effects on the Human Gut Microbiota. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 1618	5.7	15
268	Long-Term Irrigation Affects the Dynamics and Activity of the Wheat Rhizosphere Microbiome. <i>Frontiers in Plant Science</i> , <b>2018</b> , 9, 345	6.2	45
267	Blueprints for Biosensors: Design, Limitations, and Applications. <i>Genes</i> , <b>2018</b> , 9,	4.2	66
266	Diverse fungal lineages in subtropical ponds are altered by sediment-bound copper. <i>Fungal Ecology</i> , <b>2018</b> , 34, 28-42	4.1	15
265	Crystal structure of a UDP-GlcNAc epimerase for surface polysaccharide biosynthesis in <i>Acinetobacter baumannii</i> . <i>PLoS ONE</i> , <b>2018</b> , 13, e0191610	3.7	1
264	Screening of candidate substrates and coupling ions of transporters by thermostability shift assays. <i>ELife</i> , <b>2018</b> , 7,	8.9	26
263	Systematic, continental scale temporal monitoring of marine pelagic microbiota by the Australian Marine Microbial Biodiversity Initiative. <i>Scientific Data</i> , <b>2018</b> , 5, 180130	8.2	17
262	A Transcriptomic Approach to Identify Novel Drug Efflux Pumps in Bacteria. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1700, 221-235	1.4	7
261	Insights from the Genomes of Microbes Thriving in Uranium-Enriched Sediments. <i>Microbial Ecology</i> , <b>2018</b> , 75, 970-984	4.4	9
260	Ecological effects of cefepime use during antibiotic cycling on the Gram-negative enteric flora of ICU patients. <i>Intensive Care Medicine Experimental</i> , <b>2018</b> , 6, 19	3.7	4
259	The EcoCyc Database. <i>EcoSal Plus</i> , <b>2018</b> , 8,	7.7	29
258	Stormwater influences phytoplankton assemblages within the diverse, but impacted Sydney Harbour estuary. <i>PLoS ONE</i> , <b>2018</b> , 13, e0209857	3.7	4
257	Dual Transcriptomics of Host-Pathogen Interaction of Cystic Fibrosis Isolate PASS1 With Zebrafish. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2018</b> , 8, 406	5.9	13

256	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
255	Effects of uranium concentration on microbial community structure and functional potential. <i>Environmental Microbiology</i> , <b>2017</b> , 19, 3323-3341	5.2	25
254	Physical enrichment of transposon mutants from saturation mutant libraries using the TraDISort approach. <i>Mobile Genetic Elements</i> , <b>2017</b> , 7, 1-7		6
253	Characterization and Vaccine Potential of Membrane Vesicles Produced by <i>Francisella noatunensis</i> subsp. <i>orientalis</i> in an Adult Zebrafish Model. <i>Vaccine Journal</i> , <b>2017</b> , 24,		23
252	Global Gene Expression Profile of <i>Acinetobacter baumannii</i> During Bacteremia. <i>Journal of Infectious Diseases</i> , <b>2017</b> , 215, S52-S57	7	26
251	Positive-feedback, ratiometric biosensor expression improves high-throughput metabolite-producer screening efficiency in yeast. <i>Synthetic Biology</i> , <b>2017</b> , 2, ysw002	3.3	21
250	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
249	Zinc stress induces copper depletion in <i>Acinetobacter baumannii</i> . <i>BMC Microbiology</i> , <b>2017</b> , 17, 59	4.5	28
248	Genomics and the evolution of antibiotic resistance. <i>Annals of the New York Academy of Sciences</i> , <b>2017</b> , 1388, 92-107	6.5	39
247	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
246	The putative drug efflux systems of the <i>Bacillus cereus</i> group. <i>PLoS ONE</i> , <b>2017</b> , 12, e0176188	3.7	9
245	Revealing colonisation and biofilm formation of an adherent coal seam associated microbial community on a coal surface. <i>International Journal of Coal Geology</i> , <b>2016</b> , 160-161, 42-50	5.5	22
244	Fluorescence-Based Flow Sorting in Parallel with Transposon Insertion Site Sequencing Identifies Multidrug Efflux Systems in <i>Acinetobacter baumannii</i> . <i>MBio</i> , <b>2016</b> , 7,	7.8	20
243	<i>Pseudomonas aeruginosa</i> Cell Membrane Protein Expression from Phenotypically Diverse Cystic Fibrosis Isolates Demonstrates Host-Specific Adaptations. <i>Journal of Proteome Research</i> , <b>2016</b> , 15, 2152-63	5.6	25
242	Rapid multiplexed phenotypic screening identifies drug resistance functions for three novel efflux pumps in <i>Acinetobacter baumannii</i> . <i>Journal of Antimicrobial Chemotherapy</i> , <b>2016</b> , 71, 1223-32	5.1	19
241	Synthetic Evolution of Metabolic Productivity Using Biosensors. <i>Trends in Biotechnology</i> , <b>2016</b> , 34, 371-381	3.1	73
240	Effects of low temperature on tropical and temperate isolates of marine <i>Synechococcus</i> . <i>ISME Journal</i> , <b>2016</b> , 10, 1252-63	11.9	17
239	Comparative Analysis of Membrane Vesicles from Three <i>Piscirickettsia salmonis</i> Isolates Reveals Differences in Vesicle Characteristics. <i>PLoS ONE</i> , <b>2016</b> , 11, e0165099	3.7	17

238	A Sample-to-Sequence Protocol for Genus Targeted Transcriptomic Profiling: Application to Marine. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 1592	5.7	1
237	Tiny Microbes with a Big Impact: The Role of Cyanobacteria and Their Metabolites in Shaping Our Future. <i>Marine Drugs</i> , <b>2016</b> , 14,	6	71
236	Disruption of Transporters Affiliated with Enantio-Pyochelin Biosynthesis Gene Cluster of <i>Pseudomonas protegens</i> Pf-5 Has Pleiotropic Effects. <i>PLoS ONE</i> , <b>2016</b> , 11, e0159884	3.7	3
235	Defining the microbial effluxome in the content of the host-microbiome interaction. <i>Frontiers in Pharmacology</i> , <b>2015</b> , 6, 31	5.6	4
234	Antibiotic discovery: combatting bacterial resistance in cells and in biofilm communities. <i>Molecules</i> , <b>2015</b> , 20, 5286-98	4.8	208
233	An ace up their sleeve: a transcriptomic approach exposes the Acel efflux protein of <i>Acinetobacter baumannii</i> and reveals the drug efflux potential hidden in many microbial pathogens. <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 333	5.7	23
232	A novel family of integrases associated with prophages and genomic islands integrated within the tRNA-dihydrouridine synthase A ( <i>dusA</i> ) gene. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, 4547-57	20.1	19
231	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
230	One-Step Protein Conjugation to Upconversion Nanoparticles. <i>Analytical Chemistry</i> , <b>2015</b> , 87, 10406-13	7.8	42
229	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
228	The Rsm regulon of plant growth-promoting <i>Pseudomonas fluorescens</i> SS101: role of small RNAs in regulation of lipopeptide biosynthesis. <i>Microbial Biotechnology</i> , <b>2015</b> , 8, 296-310	6.3	15
227	Genomic analyses of <i>Clostridium perfringens</i> isolates from five toxinotypes. <i>Research in Microbiology</i> , <b>2015</b> , 166, 255-63	4	45
226	Proteomics of hosts and pathogens in cystic fibrosis. <i>Proteomics - Clinical Applications</i> , <b>2015</b> , 9, 134-46	3.1	14
225	Spatially extensive microbial biogeography of the Indian Ocean provides insights into the unique community structure of a pristine coral atoll. <i>Scientific Reports</i> , <b>2015</b> , 5, 15383	4.9	19
224	Draft Genome of Australian Environmental Strain WM 09.24 of the Opportunistic Human Pathogen <i>Scedosporium aurantiacum</i> . <i>Genome Announcements</i> , <b>2015</b> , 3,		18
223	Ecology and Evolution of the Human Microbiota: Fire, Farming and Antibiotics. <i>Genes</i> , <b>2015</b> , 6, 841-57	4.2	48
222	<i>Pseudomonas aeruginosa</i> inhibits the growth of <i>Scedosporium aurantiacum</i> , an opportunistic fungal pathogen isolated from the lungs of cystic fibrosis patients. <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 866	5.7	30
221	Insights on virulence from the complete genome of <i>Staphylococcus capitis</i> . <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 980	5.7	29

220	Bacillus cereus eDx protein BC3310 - a multidrug transporter of the unknown major facilitator family, UMF-2. <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 1063	5.7	8
219	Phenotypic profiling of <i>Scenedosporium aurantiacum</i> , an opportunistic pathogen colonizing human lungs. <i>PLoS ONE</i> , <b>2015</b> , 10, e0122354	3.7	18
218	Genetically and Phenotypically Distinct <i>Pseudomonas aeruginosa</i> Cystic Fibrosis Isolates Share a Core Proteomic Signature. <i>PLoS ONE</i> , <b>2015</b> , 10, e0138527	3.7	20
217	Addition of <i>Escherichia coli</i> K-12 growth observation and gene essentiality data to the EcoCyc database. <i>Journal of Bacteriology</i> , <b>2014</b> , 196, 982-8	3.5	8
216	The EcoCyc Database. <i>EcoSal Plus</i> , <b>2014</b> , 6,	7.7	47
215	Overall Transport Capabilities of <i>Bacillus subtilis</i> <b>2014</b> , 111-128		6
214	Comparative analysis of surface-exposed virulence factors of <i>Acinetobacter baumannii</i> . <i>BMC Genomics</i> , <b>2014</b> , 15, 1020	4.5	76
213	The common oceanographer: crowdsourcing the collection of oceanographic data. <i>PLoS Biology</i> , <b>2014</b> , 12, e1001947	9.7	27
212	Draft Genome Sequence of <i>Bacillus alcalophilus</i> AV1934, a Classic Alkaliphile Isolated from Human Feces in 1934. <i>Genome Announcements</i> , <b>2014</b> , 2,		4
211	Microbiology of the Anthropocene. <i>Anthropocene</i> , <b>2014</b> , 5, 1-8	3.9	53
210	A genome-scale metabolic flux model of <i>Escherichia coli</i> K-12 derived from the EcoCyc database. <i>BMC Systems Biology</i> , <b>2014</b> , 8, 79	3.5	34
209	Structure of a short-chain dehydrogenase/reductase (SDR) within a genomic island from a clinical strain of <i>Acinetobacter baumannii</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2014</b> , 70, 1318-23	1.1	4
208	SecDF as part of the Sec-translocase facilitates efficient secretion of <i>Bacillus cereus</i> toxins and cell wall-associated proteins. <i>PLoS ONE</i> , <b>2014</b> , 9, e103326	3.7	17
207	Biolog Phenotype Microarrays for phenotypic characterization of microbial cells. <i>Methods in Molecular Biology</i> , <b>2014</b> , 1096, 123-30	1.4	18
206	Application of exonuclease III-aided target recycling in flow cytometry: DNA detection sensitivity enhanced by orders of magnitude. <i>Analytical Chemistry</i> , <b>2013</b> , 85, 8240-5	7.8	23
205	The effect of zinc limitation on the transcriptome of <i>Pseudomonas protegens</i> Pf-5. <i>Environmental Microbiology</i> , <b>2013</b> , 15, 702-15	5.2	45
204	A novel family of genomic resistance islands, AbGRI2, contributing to aminoglycoside resistance in <i>Acinetobacter baumannii</i> isolates belonging to global clone 2. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2013</b> , 68, 554-7	5.1	50
203	Genes expressed by the biological control bacterium <i>Pseudomonas protegens</i> Pf-5 on seed surfaces under the control of the global regulators GacA and RpoS. <i>Environmental Microbiology</i> , <b>2013</b> , 15, 716-35	5.2	32

202	pA506, a conjugative plasmid of the plant epiphyte <i>Pseudomonas fluorescens</i> A506. <i>Applied and Environmental Microbiology</i> , <b>2013</b> , 79, 5272-82	4.8	10
201	Stress effects caused by the expression of a mutant cellobiohydrolase I and proteasome inhibition in <i>Trichoderma reesei</i> Rut-C30. <i>New Biotechnology</i> , <b>2013</b> , 30, 183-91	6.4	13
200	Life in the dark: metagenomic evidence that a microbial slime community is driven by inorganic nitrogen metabolism. <i>ISME Journal</i> , <b>2013</b> , 7, 1227-36	11.9	40
199	Maintenance of essential amino acid synthesis pathways in the <i>Blattabacterium cuenoti</i> symbiont of a wood-feeding cockroach. <i>Biology Letters</i> , <b>2013</b> , 9, 20121153	3.6	33
198	Effect of tannic acid on the transcriptome of the soil bacterium <i>Pseudomonas protegens</i> Pf-5. <i>Applied and Environmental Microbiology</i> , <b>2013</b> , 79, 3141-5	4.8	14
197	H-NS plays a role in expression of <i>Acinetobacter baumannii</i> virulence features. <i>Infection and Immunity</i> , <b>2013</b> , 81, 2574-83	3.7	71
196	EcoCyc: fusing model organism databases with systems biology. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D605-12	12.1	436
195	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
194	Single-step selection of drug resistant <i>Acinetobacter baylyi</i> ADP1 mutants reveals a functional redundancy in the recruitment of multidrug efflux systems. <i>PLoS ONE</i> , <b>2013</b> , 8, e56090	3.7	15
193	Dead end metabolites--defining the known unknowns of the <i>E. coli</i> metabolic network. <i>PLoS ONE</i> , <b>2013</b> , 8, e75210	3.7	19
192	Impact of DNA damaging agents on genome-wide transcriptional profiles in two marine <i>Synechococcus</i> species. <i>Frontiers in Microbiology</i> , <b>2013</b> , 4, 232	5.7	12
191	The complete genome and phenome of a community-acquired <i>Acinetobacter baumannii</i> . <i>PLoS ONE</i> , <b>2013</b> , 8, e58628	3.7	61
190	Sequences of two related multiple antibiotic resistance virulence plasmids sharing a unique IS26-related molecular signature isolated from different <i>Escherichia coli</i> pathotypes from different hosts. <i>PLoS ONE</i> , <b>2013</b> , 8, e78862	3.7	37
189	Analysis of two marine metagenomes reveals the diversity of plasmids in oceanic environments. <i>Environmental Microbiology</i> , <b>2012</b> , 14, 453-66	5.2	32
188	Genomic analysis reveals multiple [FeFe] hydrogenases and hydrogen sensors encoded by treponemes from the H <sub>2</sub> -rich termite gut. <i>Microbial Ecology</i> , <b>2012</b> , 63, 282-94	4.4	19
187	Resolving low-expression cell surface antigens by time-gated orthogonal scanning automated microscopy. <i>Analytical Chemistry</i> , <b>2012</b> , 84, 9674-8	7.8	13
186	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
185	Genetic identification of a high-affinity Ni transporter and the transcriptional response to Ni deprivation in <i>Synechococcus</i> sp. strain WH8102. <i>Applied and Environmental Microbiology</i> , <b>2012</b> , 78, 7822-32	4.8	18

184	pEI1573 Carrying blaIMP-4, from Sydney, Australia, is closely related to other IncL/M plasmids. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2012</b> , 56, 6029-32	5.9	55
183	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
182	pJIE137 carrying blaCTX-M-62 is closely related to p271A carrying blaNDM-1. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2012</b> , 56, 2166-8	5.9	25
181	The effect of iron limitation on the transcriptome and proteome of <i>Pseudomonas fluorescens</i> Pf-5. <i>PLoS ONE</i> , <b>2012</b> , 7, e39139	3.7	50
180	Development of a high-throughput cloning strategy for characterization of <i>Acinetobacter baumannii</i> drug transporter proteins. <i>Journal of Molecular Microbiology and Biotechnology</i> , <b>2011</b> , 20, 211-9	0.9	7
179	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
178	Crystal structure of an integron gene cassette-associated protein from <i>Vibrio cholerae</i> identifies a cationic drug-binding module. <i>PLoS ONE</i> , <b>2011</b> , 6, e16934	3.7	9
177	Genome of alkaliphilic <i>Bacillus pseudofirmus</i> OF4 reveals adaptations that support the ability to grow in an external pH range from 7.5 to 11.4. <i>Environmental Microbiology</i> , <b>2011</b> , 13, 3289-309	5.2	63
176	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
175	Investigation of the human pathogen <i>Acinetobacter baumannii</i> under iron limiting conditions. <i>BMC Genomics</i> , <b>2011</b> , 12, 126	4.5	146
174	Structural and functional analysis of the type III secretion system from <i>Pseudomonas fluorescens</i> Q8r1-96. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 177-89	3.5	43
173	Bacterial subfamily of LuxR regulators that respond to plant compounds. <i>Applied and Environmental Microbiology</i> , <b>2011</b> , 77, 4579-88	4.8	63
172	The MFS efflux proteins of gram-positive and gram-negative bacteria. <i>Advances in Enzymology and Related Areas of Molecular Biology</i> , <b>2011</b> , 77, 147-66		10
171	Genome sequence of <i>Vibrio rotiferianus</i> strain DAT722. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 3381-2	3.5	13
170	Complete sequence of pJIE143, a pir-type plasmid carrying ISEcp1-blaCTX-M-15 from an <i>Escherichia coli</i> ST131 isolate. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2011</b> , 55, 5933-5	5.9	37
169	Roles of DHA2 family transporters in drug resistance and iron homeostasis in <i>Acinetobacter</i> spp. <i>Journal of Molecular Microbiology and Biotechnology</i> , <b>2011</b> , 20, 116-24	0.9	26
168	Genome sequences of the biotechnologically important <i>Bacillus megaterium</i> strains QM B1551 and DSM319. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 4199-213	3.5	128
167	EcoCyc: a comprehensive database of <i>Escherichia coli</i> biology. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D583-90	20.1	362

166	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
165	Selection in coastal <i>Synechococcus</i> (cyanobacteria) populations evaluated from environmental metagenomes. <i>PLoS ONE</i> , <b>2011</b> , 6, e24249	3.7	15
164	PtrA is required for coordinate regulation of gene expression during phosphate stress in a marine <i>Synechococcus</i> . <i>ISME Journal</i> , <b>2010</b> , 4, 908-21	11.9	34
163	Inactivation of the GacA response regulator in <i>Pseudomonas fluorescens</i> Pf-5 has far-reaching transcriptomic consequences. <i>Environmental Microbiology</i> , <b>2010</b> , 12, 899-915	5.2	118
162	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
161	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
160	Computational prediction of the osmoregulation network in <i>Synechococcus</i> sp. WH8102. <i>BMC Genomics</i> , <b>2010</b> , 11, 291	4.5	12
159	Transport, Solute <b>2009</b> , 529-544		0
158	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
157	Ecological genomics of marine picocyanobacteria. <i>Microbiology and Molecular Biology Reviews</i> , <b>2009</b> , 73, 249-99	13.2	499
156	EcoCyc: a comprehensive view of <i>Escherichia coli</i> biology. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D464-70	20.1	288
155	Statistical analysis of microarray data with replicated spots: a case study with <i>Synechococcus</i> WH8102. <i>Comparative and Functional Genomics</i> , <b>2009</b> , 950171		3
154	Coastal strains of marine <i>Synechococcus</i> species exhibit increased tolerance to copper shock and a distinctive transcriptional response relative to those of open-ocean strains. <i>Applied and Environmental Microbiology</i> , <b>2009</b> , 75, 5047-57	4.8	53
153	Genome sequences of three <i>Agrobacterium</i> biovars help elucidate the evolution of multichromosome genomes in bacteria. <i>Journal of Bacteriology</i> , <b>2009</b> , 191, 2501-11	3.5	184
152	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
151	Mobile genetic elements in the genome of the beneficial rhizobacterium <i>Pseudomonas fluorescens</i> Pf-5. <i>BMC Microbiology</i> , <b>2009</b> , 9, 8	4.5	72
150	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
149	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

148	Whole-genome microarray analyses of Synechococcus-Vibrio interactions. <i>Environmental Microbiology</i> , <b>2009</b> , 11, 2698-709	5.2	34
147	Green evolution and dynamic adaptations revealed by genomes of the marine picoeukaryotes Micromonas. <i>Science</i> , <b>2009</b> , 324, 268-72	33.3	503
146	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
145	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
144	Comparative genomics of the neglected human malaria parasite <i>Plasmodium vivax</i> . <i>Nature</i> , <b>2008</b> , 455, 757-63	50.4	633
143	Unraveling the genomic mosaic of a ubiquitous genus of marine cyanobacteria. <i>Genome Biology</i> , <b>2008</b> , 9, R90	18.3	242
142	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
141	Annotation-based inference of transporter function. <i>Bioinformatics</i> , <b>2008</b> , 24, i259-67	7.2	28
140	Genome of the epsilonproteobacterial chemolithoautotroph <i>Sulfurimonas denitrificans</i> . <i>Applied and Environmental Microbiology</i> , <b>2008</b> , 74, 1145-56	4.8	191
139	High-throughput phenotypic characterization of <i>Pseudomonas aeruginosa</i> membrane transport genes. <i>PLoS Genetics</i> , <b>2008</b> , 4, e1000211	6	42
138	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
137	Genome sequence of <i>Aedes aegypti</i> , a major arbovirus vector. <i>Science</i> , <b>2007</b> , 316, 1718-23	33.3	867
136	Genome sequence and identification of candidate vaccine antigens from the animal pathogen <i>Dichelobacter nodosus</i> . <i>Nature Biotechnology</i> , <b>2007</b> , 25, 569-75	44.5	58
135	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
134	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
133	Genome sequence of <i>Babesia bovis</i> and comparative analysis of apicomplexan hemoprotozoa. <i>PLoS Pathogens</i> , <b>2007</b> , 3, 1401-13	7.6	279
132	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
131	Ecological genomics of marine Roseobacters. <i>Applied and Environmental Microbiology</i> , <b>2007</b> , 73, 4559-69	4.8	269

130	Multidimensional annotation of the Escherichia coli K-12 genome. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, 7577-801	20.1	151
129	Contribution of target gene mutations and efflux to decreased susceptibility of Salmonella enterica serovar typhimurium to fluoroquinolones and other antimicrobials. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2007</b> , 51, 535-42	5.9	106
128	Large-scale comparative genomic analyses of cytoplasmic membrane transport systems in prokaryotes. <i>Journal of Molecular Microbiology and Biotechnology</i> , <b>2007</b> , 12, 165-79	0.9	56
127	The Genomic Sequence of Pseudomonas fluorescens Pf-5: Insights Into Biological Control. <i>Phytopathology</i> , <b>2007</b> , 97, 233-8	3.8	98
126	Draft genome sequence of the sexually transmitted pathogen Trichomonas vaginalis. <i>Science</i> , <b>2007</b> , 315, 207-12	33.3	622
125	Genomics of Pseudomonas fluorescens Pf-5 <b>2007</b> , 3-30		3
124	Microbial drug efflux proteins of the major facilitator superfamily. <i>Current Drug Targets</i> , <b>2006</b> , 7, 793-813	3	75
123	The genome of deep-sea vent chemolithoautotroph Thiomicrospira crunogena XCL-2. <i>PLoS Biology</i> , <b>2006</b> , 4, e383	9.7	112
122	Genome sequence of Synechococcus 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
121	Just one cross appears capable of dramatically altering the population biology of a eukaryotic pathogen like Toxoplasma gondii. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2006</b> , 103, 10514-10519	11.5	102
120	Regulation of type IV fimbrial biogenesis in Dichelobacter nodosus. <i>Journal of Bacteriology</i> , <b>2006</b> , 188, 4801-11	3.5	22
119	Comparative genomic evidence for a close relationship between the dimorphic prosthecate bacteria Hyphomonas neptunium and Caulobacter crescentus. <i>Journal of Bacteriology</i> , <b>2006</b> , 188, 6841-50	5.5	52
118	Common inheritance of chromosome Ia associated with clonal expansion of Toxoplasma gondii. <i>Genome Research</i> , <b>2006</b> , 16, 1119-25	9.7	49
117	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
116	Computational inference and experimental validation of the nitrogen assimilation regulatory network in cyanobacterium Synechococcus sp. WH 8102. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, 1050-65	20.1	54
115	Exopolysaccharide-associated protein sorting in environmental organisms: the PEP-CTERM/EpsH system. Application of a novel phylogenetic profiling heuristic. <i>BMC Biology</i> , <b>2006</b> , 4, 29	7.3	65
114	A high efficiency cloning and expression system for proteomic analysis. <i>Proteomics</i> , <b>2006</b> , 6, 4038-46	4.8	4
113	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

112	Genome sequence of <i>Theileria parva</i> , a bovine pathogen that transforms lymphocytes. <i>Science</i> , <b>2005</b> , 309, 134-7	33.3	259
111	Composite genome map and recombination parameters derived from three archetypal lineages of <i>Toxoplasma gondii</i> . <i>Nucleic Acids Research</i> , <b>2005</b> , 33, 2980-92	20.1	133
110	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
109	The ergosterol biosynthesis pathway, transporter genes, and azole resistance in <i>Aspergillus fumigatus</i> . <i>Medical Mycology</i> , <b>2005</b> , 43 Suppl 1, S313-9	3.9	111
108	Cloning, expression, and purification of <i>Brucella suis</i> outer membrane proteins. <i>Protein Expression and Purification</i> , <b>2005</b> , 40, 134-41	2	6
107	EcoCyc: a comprehensive database resource for <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D334-7	20.1	514
106	Genomic Efforts With Biodefense Pathogens <b>2005</b> , 417-433		
105	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
104	Genome sequencing and analysis of <i>Aspergillus oryzae</i> . <i>Nature</i> , <b>2005</b> , 438, 1157-61	50.4	962
103	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
102	Reciprocal regulation of pyoluteorin production with membrane transporter gene expression in <i>Pseudomonas fluorescens</i> Pf-5. <i>Applied and Environmental Microbiology</i> , <b>2005</b> , 71, 6900-9	4.8	30
101	Identification of a <i>Dichelobacter nodosus</i> ferric uptake regulator and determination of its regulatory targets. <i>Journal of Bacteriology</i> , <b>2005</b> , 187, 366-75	3.5	17
100	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
99	TransportDB: a relational database of cellular membrane transport systems. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, D284-8	20.1	157
98	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
97	Genomic insights into methanotrophy: the complete genome sequence of <i>Methylococcus capsulatus</i> (Bath). <i>PLoS Biology</i> , <b>2004</b> , 2, e303	9.7	236
96	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
95	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

94	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
93	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
92	Environmental genome shotgun sequencing of the Sargasso Sea. <i>Science</i> , <b>2004</b> , 304, 66-74	33.3	3231
91	Complete genome sequence and comparative analysis of the metabolically versatile <i>Pseudomonas putida</i> KT2440. <i>Environmental Microbiology</i> , <b>2003</b> , 5, 630-630	5.2	8
90	The genome sequence of the filamentous fungus <i>Neurospora crassa</i> . <i>Nature</i> , <b>2003</b> , 422, 859-68	50.4	1323
89	The genome of a motile marine <i>Synechococcus</i> . <i>Nature</i> , <b>2003</b> , 424, 1037-42	50.4	534
88	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
87	Multidrug efflux pumps and resistance: regulation and evolution. <i>Current Opinion in Microbiology</i> , <b>2003</b> , 6, 446-51	7.9	167
86	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
85	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
84	The complete genome sequence of the Arabidopsis 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> , <b>2003</b> , 100, 10181-6	11.5	695
83	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
82	ToxoDB: accessing the <i>Toxoplasma gondii</i> genome. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 234-6	20.1	149
81	Genome sequence of <i>Chlamydomonas reinhardtii</i> (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
80	Complete genome sequence of the oral pathogenic bacterium <i>Porphyromonas gingivalis</i> strain W83. <i>Journal of Bacteriology</i> , <b>2003</b> , 185, 5591-601	3.5	321
79	Genome of <i>Geobacter sulfurreducens</i> : metal reduction in subsurface environments. <i>Science</i> , <b>2003</b> , 302, 1967-9	33.3	573
78	Sugar metabolism by <i>Brucellae</i> . <i>Veterinary Microbiology</i> , <b>2002</b> , 90, 249-61	3.3	35
77	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

76	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , <b>2002</b> , 419, 498-511	50.4	3336
75	The genome sequence of <i>Schizosaccharomyces pombe</i> . <i>Nature</i> , <b>2002</b> , 415, 871-80	50.4	1281
74	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
73	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
72	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
71	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
70	The EcoCyc Database. <i>Nucleic Acids Research</i> , <b>2002</b> , 30, 56-8	20.1	296
69	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
68	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
67	Regulation of carbon utilization by sulfur availability in <i>Escherichia coli</i> and <i>Salmonella typhimurium</i> . <i>Microbiology (United Kingdom)</i> , <b>2002</b> , 148, 123-131	2.9	19
66	Microbial Genomics <b>2001</b> , 1196-1203		
65	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
64	The genome of the natural genetic engineer <i>Agrobacterium tumefaciens</i> C58. <i>Science</i> , <b>2001</b> , 294, 2317-23	33.3	659
63	Microbial Genomics <b>2001</b> , 399-404		
62	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
61	Phylogeny of multidrug transporters. <i>Seminars in Cell and Developmental Biology</i> , <b>2001</b> , 12, 205-13	7.5	254
60	Complete genome sequence of a virulent isolate of <i>Streptococcus pneumoniae</i> . <i>Science</i> , <b>2001</b> , 293, 498-506	39.6	1112
59	Microbial multidrug efflux: introduction. <i>Journal of Molecular Microbiology and Biotechnology</i> , <b>2001</b> , 3, 143-4	0.9	5

58	Comparative genomics of microbial drug efflux systems. <i>Journal of Molecular Microbiology and Biotechnology</i> , <b>2001</b> , 3, 145-50	0.9	57
57	Status of genome projects for nonpathogenic bacteria and archaea. <i>Nature Biotechnology</i> , <b>2000</b> , 18, 1049-54	4.4	78
56	Complete genome sequence of <i>Pseudomonas aeruginosa</i> PAO1, an opportunistic pathogen. <i>Nature</i> , <b>2000</b> , 406, 959-64	50.4	3373
55	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
54	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
53	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
52	The EcoCyc and MetaCyc databases. <i>Nucleic Acids Research</i> , <b>2000</b> , 28, 56-9	20.1	177
51	Microbial genome analyses: comparative transport capabilities in eighteen prokaryotes. <i>Journal of Molecular Biology</i> , <b>2000</b> , 301, 75-100	6.5	243
50	Functional genomic studies of dihydroxyacetone utilization in <i>Escherichia coli</i> . <i>Microbiology (United Kingdom)</i> , <b>2000</b> , 146 ( Pt 10), 2343-2344	2.9	18
49	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
48	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
47	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
46	The <i>Escherichia coli</i> ABC transporters: an update. <i>Molecular Microbiology</i> , <b>1999</b> , 32, 887-9	4.1	34
45	New glycoprotein-associated amino acid transporters. <i>Journal of Membrane Biology</i> , <b>1999</b> , 172, 181-92	2.3	137
44	Phylogenetic characterization of novel transport protein families revealed by genome analyses. <i>BBA - Biomembranes</i> , <b>1999</b> , 1422, 1-56		189
43	Paralogous genes encoding transport proteins in microbial genomes. <i>Research in Microbiology</i> , <b>1999</b> , 150, 689-99	4	11
42	The major facilitator superfamily. <i>Journal of Molecular Microbiology and Biotechnology</i> , <b>1999</b> , 1, 257-79	0.9	258
41	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

40	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
39	QacR is a repressor protein that regulates expression of the <i>Staphylococcus aureus</i> multidrug efflux pump QacA. <i>Journal of Biological Chemistry</i> , <b>1998</b> , 273, 18665-73	5.4	146
38	Evolutionary origins of multidrug and drug-specific efflux pumps in bacteria. <i>FASEB Journal</i> , <b>1998</b> , 12, 265-74	0.9	169
37	Evolutionary origins of multidrug and drug-specific efflux pumps in bacteria. <i>FASEB Journal</i> , <b>1998</b> , 12, 265-274	0.9	174
36	Major facilitator superfamily. <i>Microbiology and Molecular Biology Reviews</i> , <b>1998</b> , 62, 1-34	13.2	1423
35	Characterization of the earliest known <i>Staphylococcus aureus</i> plasmid encoding a multidrug efflux system. <i>Journal of Bacteriology</i> , <b>1998</b> , 180, 3477-9	3.5	51
34	Characterization of glucose-specific catabolite repression-resistant mutants of <i>Bacillus subtilis</i> : identification of a novel hexose:H <sup>+</sup> symporter. <i>Journal of Bacteriology</i> , <b>1998</b> , 180, 498-504	3.5	44
33	A bacterial model system for understanding multi-drug resistance. <i>Microbial Drug Resistance</i> , <b>1997</b> , 3, 289-95	2.9	14
32	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
31	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
30	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
29	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
28	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
27	Carbon metabolism and its regulation in <i>Streptomyces</i> and other high GC gram-positive bacteria. <i>Research in Microbiology</i> , <b>1996</b> , 147, 535-41	4	16
26	IS257-mediated cointegration in the evolution of a family of staphylococcal trimethoprim resistance plasmids. <i>Journal of Bacteriology</i> , <b>1996</b> , 178, 6070-3	3.5	45
25	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> , <b>1996</b> , 93, 3630-5	11.5	233
24	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
23	Proton-dependent multidrug efflux systems.. <i>Microbiological Reviews</i> , <b>1996</b> , 60, 575-608		620

22	Proton-dependent multidrug efflux systems. <i>Microbiological Reviews</i> , <b>1996</b> , 60, 575-608		848
21	Phylogenetic analyses of the homologous transmembrane channel-forming proteins of the F0F1-ATPases of bacteria, chloroplasts and mitochondria. <i>Microbiology (United Kingdom)</i> , <b>1996</b> , 142 (Pt 1), 17-32	2.9	21
20	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
19	Multidrug resistance plasmid pSK108 from coagulase-negative staphylococci; relationships to <i>Staphylococcus aureus</i> qacC plasmids. <i>Plasmid</i> , <b>1995</b> , 34, 62-7	3.3	42
18	Molecular characterization of the staphylococcal multidrug resistance export protein QacC. <i>Journal of Bacteriology</i> , <b>1995</b> , 177, 2827-33	3.5	109
17	The DAG family of glycosyl hydrolases combines two previously identified protein families. <i>Biochemical Journal</i> , <b>1995</b> , 311 (Pt 1), 349-50	3.8	18
16	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
15	The POT family of transport proteins. <i>Trends in Biochemical Sciences</i> , <b>1994</b> , 19, 404	10.3	108
14	Characterisation of sin, a potential recombinase-encoding gene from <i>Staphylococcus aureus</i> . <i>Gene</i> , <b>1994</b> , 141, 109-14	3.8	46
13	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
12	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
11	Analysis of a transfer region from the staphylococcal conjugative plasmid pSK41. <i>Gene</i> , <b>1993</b> , 136, 13-25	3.8	49
10	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> , 132, 155	3.8	2
9	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
8	Membrane transport proteins: implications of sequence comparisons. <i>Current Opinion in Cell Biology</i> , <b>1992</b> , 4, 684-95	9	292
7	Substrate specificity and energetics of antiseptic and disinfectant resistance in <i>Staphylococcus aureus</i> . <i>FEMS Microbiology Letters</i> , <b>1992</b> , 95, 259-265	2.9	148
6	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
5	<i>Clostridium perfringens</i> 213-221		1

4	Elucidating essential genes in plant-associated <i>Pseudomonas protegens</i> PF-5 using transposon insertion sequencing	1
3	Spermidine and spermine are the natural substrates of the <i>Acinetobacter baumannii</i> AmvA multidrug efflux pump	1
2	The effect of root exudates on the transcriptome of rhizosphere <i>Pseudomonas</i> spp	1
1	Unravelling Stratified Microbial Assemblages in Australia's Only Deep Anchialine System, The Bundera Sinkhole. <i>Frontiers in Marine Science</i> ,9,	4.5 2