

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	Microbial Community Shifts on Organic Rocks of Different Maturities Reveal potential Catabolisers of Organic Matter in Coal. <i>Microbial Ecology</i> , 2022, 84, 780-793.	1.4	2
2	Picochlorum sp. SENEW3. <i>Trends in Genetics</i> , 2022, 38, 209-210.	2.9	3
3	Fluorescence-Based for the Detection of the Unfolded Protein. <i>Methods in Molecular Biology</i> , 2022, 2378, 19-30.	0.4	1
4	Novel functional insights into a modified sugar-binding protein from <i>Synechococcus</i> MITS9220. <i>Scientific Reports</i> , 2022, 12, 4805.	1.6	3
5	Genomic and phenotypic analyses of diverse non-clinical <i>Acinetobacter baumannii</i> strains reveals strain-specific virulence and resistance capacity. <i>Microbial Genomics</i> , 2022, 8, .	1.0	7
6	Construction of a synthetic <i>Saccharomyces cerevisiae</i> pan-genome neo-chromosome. <i>Nature Communications</i> , 2022, 13, .	5.8	22
7	Toward Methanol-Based Biomanufacturing: Emerging Strategies for Engineering Synthetic Methylo-trophy in <i>Saccharomyces cerevisiae</i> . <i>ACS Synthetic Biology</i> , 2022, 11, 2548-2563.	1.9	6
8	Microdroplet enabled cultivation of single yeast cells correlates with bulk growth and reveals subpopulation phenomena. <i>Biotechnology and Bioengineering</i> , 2021, 118, 647-658.	1.7	16
9	Adherent microbes in coal seam environments prefer mineral-rich and crack-associated microhabitats. <i>International Journal of Coal Geology</i> , 2021, 234, 103652.	1.9	13
10	Aerobic bacteria and archaea tend to have larger and more versatile genomes. <i>Oikos</i> , 2021, 130, 501-511.	1.2	19
11	Physiological Functions of Bacterial Multidrug Efflux Pumps. <i>Chemical Reviews</i> , 2021, 121, 5417-5478.	23.0	78
12	Aromatic compound-degrading taxa in an anoxic coal seam microbiome from the Surat Basin, Australia. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	7
13	Draft Genome Sequence of <i>Dietzia</i> sp. Strain SYD-A1, Isolated from Coal Seam Formation Water. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	1
14	Seeding the idea of encapsulating a representative synthetic metagenome in a single yeast cell. <i>Nature Communications</i> , 2021, 12, 1599.	5.8	11
15	Elucidating Essential Genes in Plant-Associated <i>Pseudomonas protegens</i> Pf-5 Using Transposon Insertion Sequencing. <i>Journal of Bacteriology</i> , 2021, 203, .	1.0	11
16	Cell size, genome size, and maximum growth rate are near-independent dimensions of ecological variation across bacteria and archaea. <i>Ecology and Evolution</i> , 2021, 11, 3956-3976.	0.8	43
17	Root Exudates Alter the Expression of Diverse Metabolic, Transport, Regulatory, and Stress Response Genes in Rhizosphere <i>Pseudomonas</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 651282.	1.5	58
18	Trait dimensions in bacteria and archaea compared to vascular plants. <i>Ecology Letters</i> , 2021, 24, 1487-1504.	3.0	21

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19	Identification of a Novel Ciprofloxacin Tolerance Gene, <i>aciT</i> , Which Contributes to Filamentation in <i>Acinetobacter baumannii</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	1.4	7
20	<i>Acinetobacter baumannii</i> Fatty Acid Desaturases Facilitate Survival in Distinct Environments. <i>ACS Infectious Diseases</i> , 2021, 7, 2221-2228.	1.8	9
21	The Membrane Composition Defines the Spatial Organization and Function of a Major <i>Acinetobacter baumannii</i> Drug Efflux System. <i>MBio</i> , 2021, 12, e0107021.	1.8	14
22	Yeast Synthetic Minimal Biosensors for Evaluating Protein Production. <i>ACS Synthetic Biology</i> , 2021, 10, 1640-1650.	1.9	12
23	The EcoCyc Database in 2021. <i>Frontiers in Microbiology</i> , 2021, 12, 711077.	1.5	122
24	The Molecular Basis of <i>Acinetobacter baumannii</i> Cadmium Toxicity and Resistance. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0171821.	1.4	9
25	The <i>Acinetobacter baumannii</i> disinfectant resistance protein, AmvA, is a spermidine and spermine efflux pump. <i>Communications Biology</i> , 2021, 4, 1114.	2.0	17
26	Increasing the PACE of characterising novel transporters by functional genomics. <i>Current Opinion in Microbiology</i> , 2021, 64, 1-8.	2.3	5
27	Strategic traits of bacteria and archaea vary widely within substrate-use groups. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	8
28	Benzalkonium chloride antagonises aminoglycoside antibiotics and promotes evolution of resistance. <i>EBioMedicine</i> , 2021, 73, 103653.	2.7	29
29	Delving into defence: identifying the <i>Pseudomonas protegens</i> Pf-5 gene suite involved in defence against secreted products of fungal, oomycete and bacterial rhizosphere competitors. <i>Microbial Genomics</i> , 2021, 7, .	1.0	4
30	Homecoming: rewinding the reductive evolution of the chloroplast genome for increasing crop yields. <i>Nature Communications</i> , 2021, 12, 6734.	5.8	7
31	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
32	Functional characterisation of substrate-binding proteins to address nutrient uptake in marine picocyanobacteria. <i>Biochemical Society Transactions</i> , 2021, 49, 2465-2481.	1.6	6
33	Draft Genome Sequence of <i>Desulfovibrio</i> sp. Strain CSMB_222, Isolated from Coal Seam Formation Water. <i>Microbiology Resource Announcements</i> , 2021, 10, e0056421.	0.3	2
34	The Role of Zinc Efflux during <i>Acinetobacter baumannii</i> Infection. <i>ACS Infectious Diseases</i> , 2020, 6, 150-158.	1.8	21
35	Subsurface <i>Stappia</i> : Success Through Defence, Specialisation and Putative Pressure-Dependent Carbon Fixation. <i>Microbial Ecology</i> , 2020, 80, 34-46.	1.4	9
36	Comparative membrane proteomics reveal contrasting adaptation strategies for coastal and oceanic marine <i>Synechococcus</i> cyanobacteria. <i>Environmental Microbiology</i> , 2020, 22, 1816-1828.	1.8	6

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37	Rapid optimisation of cellulolytic enzymes ratios in <i>Saccharomyces cerevisiae</i> using in vitro SCRaMbLE. <i>Biotechnology for Biofuels</i> , 2020, 13, 182.	6.2	6
38	The Transcriptomic Signature of Tigecycline in <i>Acinetobacter baumannii</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 565438.	1.5	10
39	Secondary Effects of Antibiotics on Microbial Biofilms. <i>Frontiers in Microbiology</i> , 2020, 11, 2109.	1.5	61
40	Rapid Colorimetric Detection of Genome Evolution in SCRaMbLEd Synthetic <i>Saccharomyces cerevisiae</i> Strains. <i>Microorganisms</i> , 2020, 8, 1914.	1.6	5
41	Adaptive laboratory evolution of native methanol assimilation in <i>Saccharomyces cerevisiae</i> . <i>Nature Communications</i> , 2020, 11, 5564.	5.8	64
42	A decade of advances in transposon-insertion sequencing. <i>Nature Reviews Genetics</i> , 2020, 21, 526-540.	7.7	228
43	A synthesis of bacterial and archaeal phenotypic trait data. <i>Scientific Data</i> , 2020, 7, 170.	2.4	59
44	Characterizing the Mechanism of Action of an Ancient Antimicrobial, Manuka Honey, against <i>Pseudomonas aeruginosa</i> Using Modern Transcriptomics. <i>MSystems</i> , 2020, 5, .	1.7	30
45	The Sensory Significance of Apocarotenoids in Wine: Importance of Carotenoid Cleavage Dioxygenase 1 (CCD1) in the Production of Î²-Ionone. <i>Molecules</i> , 2020, 25, 2779.	1.7	19
46	Application of Transposon Insertion Sequencing to Agricultural Science. <i>Frontiers in Plant Science</i> , 2020, 11, 291.	1.7	16
47	Changes in dietary fiber intake in mice reveal associations between colonic mucin O-glycosylation and specific gut bacteria. <i>Gut Microbes</i> , 2020, 12, 1802209.	4.3	25
48	Microbial Solute Transporters. , 2019, , 157-157.		0
49	QTL analysis of natural <i>Saccharomyces cerevisiae</i> isolates reveals unique alleles involved in lignocellulosic inhibitor tolerance. <i>FEMS Yeast Research</i> , 2019, 19, .	1.1	10
50	Benchmarking two <i>Saccharomyces cerevisiae</i> laboratory strains for growth and transcriptional response to methanol. <i>Synthetic and Systems Biotechnology</i> , 2019, 4, 180-188.	1.8	16
51	Rapid microevolution of biofilm cells in response to antibiotics. <i>Npj Biofilms and Microbiomes</i> , 2019, 5, 34.	2.9	96
52	The Role of the CopA Copper Efflux System in <i>Acinetobacter baumannii</i> Virulence. <i>International Journal of Molecular Sciences</i> , 2019, 20, 575.	1.8	35
53	Who eats what? Unravelling microbial conversion of coal to methane. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	29
54	Catabolism of Nucleic Acids by a Cystic Fibrosis <i>Pseudomonas aeruginosa</i> Isolate: An Adaptive Pathway to Cystic Fibrosis Sputum Environment. <i>Frontiers in Microbiology</i> , 2019, 10, 1199.	1.5	11

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55	Evolutionary engineering in <i>Saccharomyces cerevisiae</i> reveals a TRK1-dependent potassium influx mechanism for propionic acid tolerance. <i>Biotechnology for Biofuels</i> , 2019, 12, 97.	6.2	25
56	Interactions of an Emerging Fungal Pathogen <i>Scedosporium aurantiacum</i> with Human Lung Epithelial Cells. <i>Scientific Reports</i> , 2019, 9, 5035.	1.6	11
57	Identification of Novel <i>Acinetobacter baumannii</i> Host Fatty Acid Stress Adaptation Strategies. <i>MBio</i> , 2019, 10, .	1.8	43
58	Microbial communities are sensitive indicators for freshwater sediment copper contamination. <i>Environmental Pollution</i> , 2019, 247, 1028-1038.	3.7	38
59	Genomic and phenotypic insights point to diverse ecological strategies by facultative anaerobes obtained from subsurface coal seams. <i>Scientific Reports</i> , 2019, 9, 16186.	1.6	19
60	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> , 2019, 116, 18015-18020.	3.3	21
61	Succession Patterns and Physical Niche Partitioning in Microbial Communities from Subsurface Coal Seams. <i>IScience</i> , 2019, 12, 152-167.	1.9	32
62	Pacing across the membrane: the novel PACE family of efflux pumps is widespread in Gram-negative pathogens. <i>Research in Microbiology</i> , 2018, 169, 450-454.	1.0	77
63	Regulation of the <i>aceL</i> multidrug efflux pump gene in <i>Acinetobacter baumannii</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 1492-1500.	1.3	25
64	Genome-based evolutionary history of <i>Pseudomonas</i> spp. <i>Environmental Microbiology</i> , 2018, 20, 2142-2159.	1.8	172
65	The Coal Seam Microbiome (CSMB) reference set, a lingua franca for the microbial coal-to-methane community. <i>International Journal of Coal Geology</i> , 2018, 186, 41-50.	1.9	46
66	A Transcriptomic Approach to Identify Novel Drug Efflux Pumps in Bacteria. <i>Methods in Molecular Biology</i> , 2018, 1700, 221-235.	0.4	7
67	Insights from the Genomes of Microbes Thriving in Uranium-Enriched Sediments. <i>Microbial Ecology</i> , 2018, 75, 970-984.	1.4	17
68	Ecological effects of cefepime use during antibiotic cycling on the Gram-negative enteric flora of ICU patients. <i>Intensive Care Medicine Experimental</i> , 2018, 6, 19.	0.9	6
69	The EcoCyc Database. <i>EcoSal Plus</i> , 2018, 8, .	2.1	75
70	Stormwater influences phytoplankton assemblages within the diverse, but impacted Sydney Harbour estuary. <i>PLoS ONE</i> , 2018, 13, e0209857.	1.1	12
71	Dual Transcriptomics of Host-Pathogen Interaction of Cystic Fibrosis Isolate <i>Pseudomonas aeruginosa</i> PASS1 With Zebrafish. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 406.	1.8	21
72	Fiber Supplements Derived From Sugarcane Stem, Wheat Dextrin and Psyllium Husk Have Different In Vitro Effects on the Human Gut Microbiota. <i>Frontiers in Microbiology</i> , 2018, 9, 1618.	1.5	25

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73	Long-Term Irrigation Affects the Dynamics and Activity of the Wheat Rhizosphere Microbiome. <i>Frontiers in Plant Science</i> , 2018, 9, 345.	1.7	73
74	Blueprints for Biosensors: Design, Limitations, and Applications. <i>Genes</i> , 2018, 9, 375.	1.0	99
75	Diverse fungal lineages in subtropical ponds are altered by sediment-bound copper. <i>Fungal Ecology</i> , 2018, 34, 28-42.	0.7	26
76	Systematic, continental scale temporal monitoring of marine pelagic microbiota by the Australian Marine Microbial Biodiversity Initiative. <i>Scientific Data</i> , 2018, 5, 180130.	2.4	41
77	Crystal structure of a UDP-GlcNAc epimerase for surface polysaccharide biosynthesis in <i>Acinetobacter baumannii</i> . <i>PLoS ONE</i> , 2018, 13, e0191610.	1.1	1
78	Screening of candidate substrates and coupling ions of transporters by thermostability shift assays. <i>ELife</i> , 2018, 7, .	2.8	45
79	Yeast's balancing act between ethanol and glycerol production in low alcohol wines. <i>Microbial Biotechnology</i> , 2017, 10, 264-278.	2.0	113
80	Effects of uranium concentration on microbial community structure and functional potential. <i>Environmental Microbiology</i> , 2017, 19, 3323-3341.	1.8	38
81	Physical enrichment of transposon mutants from saturation mutant libraries using the TraDISort approach. <i>Mobile Genetic Elements</i> , 2017, 7, 1-7.	1.8	14
82	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> , 2017, 24, .	3.2	34
83	Global Gene Expression Profile of <i>Acinetobacter baumannii</i> During Bacteremia. <i>Journal of Infectious Diseases</i> , 2017, 215, S52-S57.	1.9	38
84	Zinc stress induces copper depletion in <i>Acinetobacter baumannii</i> . <i>BMC Microbiology</i> , 2017, 17, 59.	1.3	55
85	Genomics and the evolution of antibiotic resistance. <i>Annals of the New York Academy of Sciences</i> , 2017, 1388, 92-107.	1.8	50
86	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
87	Positive-feedback, ratiometric biosensor expression improves high-throughput metabolite-producer screening efficiency in yeast. <i>Synthetic Biology</i> , 2017, 2, ysw002.	1.2	32
88	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
89	The putative drug efflux systems of the <i>Bacillus cereus</i> group. <i>PLoS ONE</i> , 2017, 12, e0176188.	1.1	11
90	A Sample-to-Sequence Protocol for Genus Targeted Transcriptomic Profiling: Application to Marine <i>Synechococcus</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 1592.	1.5	1

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91	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
92	Disruption of Transporters Affiliated with Enantio-Pyochelin Biosynthesis Gene Cluster of <i>Pseudomonas protegens</i> Pf-5 Has Pleiotropic Effects. <i>PLoS ONE</i> , 2016, 11, e0159884.	1.1	4
93	Revealing colonisation and biofilm formation of an adherent coal seam associated microbial community on a coal surface. <i>International Journal of Coal Geology</i> , 2016, 160-161, 42-50.	1.9	27
94	Fluorescence-Based Flow Sorting in Parallel with Transposon Insertion Site Sequencing Identifies Multidrug Efflux Systems in <i>Acinetobacter baumannii</i> . <i>MBio</i> , 2016, 7, .	1.8	27
95	<i>Pseudomonas aeruginosa</i> Cell Membrane Protein Expression from Phenotypically Diverse Cystic Fibrosis Isolates Demonstrates Host-Specific Adaptations. <i>Journal of Proteome Research</i> , 2016, 15, 2152-2163.	1.8	28
96	Rapid multiplexed phenotypic screening identifies drug resistance functions for three novel efflux pumps in <i>Acinetobacter baumannii</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 1223-1232.	1.3	26
97	Synthetic Evolution of Metabolic Productivity Using Biosensors. <i>Trends in Biotechnology</i> , 2016, 34, 371-381.	4.9	90
98	Effects of low temperature on tropical and temperate isolates of marine <i>Synechococcus</i> . <i>ISME Journal</i> , 2016, 10, 1252-1263.	4.4	36
99	Comparative Analysis of Membrane Vesicles from Three <i>Piscirickettsia salmonis</i> Isolates Reveals Differences in Vesicle Characteristics. <i>PLoS ONE</i> , 2016, 11, e0165099.	1.1	22
100	Spatially extensive microbial biogeography of the Indian Ocean provides insights into the unique community structure of a pristine coral atoll. <i>Scientific Reports</i> , 2015, 5, 15383.	1.6	28
101	Draft Genome of Australian Environmental Strain WM 09.24 of the Opportunistic Human Pathogen <i>Scedosporium aurantiacum</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	21
102	Ecology and Evolution of the Human Microbiota: Fire, Farming and Antibiotics. <i>Genes</i> , 2015, 6, 841-857.	1.0	61
103	<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> , 2015, 6, 866.	1.5	52
104	Insights on virulence from the complete genome of <i>Staphylococcus capitis</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 980.	1.5	56
105	<i>Bacillus cereus</i> efflux protein BC3310 is a multidrug transporter of the unknown major facilitator family, UMF-2. <i>Frontiers in Microbiology</i> , 2015, 6, 1063.	1.5	10
106	Phenotypic Profiling of <i>Scedosporium aurantiacum</i> , an Opportunistic Pathogen Colonizing Human Lungs. <i>PLoS ONE</i> , 2015, 10, e0122354.	1.1	22
107	6. Microbial Slime Curtain Communities of the Nullarbor Caves. , 2015, , 125-136.		0
108	Defining the microbial effluxome in the context of the host-microbiome interaction. <i>Frontiers in Pharmacology</i> , 2015, 6, 31.	1.6	5

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109	Antibiotic Discovery: Combatting Bacterial Resistance in Cells and in Biofilm Communities. <i>Molecules</i> , 2015, 20, 5286-5298.	1.7	276
110	An ace up their sleeve: a transcriptomic approach exposes the AceI efflux protein of <i>Acinetobacter baumannii</i> and reveals the drug efflux potential hidden in many microbial pathogens. <i>Frontiers in Microbiology</i> , 2015, 6, 333.	1.5	35
111	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> , 2015, 43, 4547-4557.	6.5	34
112	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
113	One-Step Protein Conjugation to Upconversion Nanoparticles. <i>Analytical Chemistry</i> , 2015, 87, 10406-10413.	3.2	54
114	Homologs of the <i>Acinetobacter baumannii</i> AceI Transporter Represent a New Family of Bacterial Multidrug Efflux Systems. <i>MBio</i> , 2015, 6, .	1.8	138
115	The <i>Rsm</i> regulon of plant growth-promoting <i>Pseudomonas fluorescens</i> SS101: role of small RNAs in regulation of lipopeptide biosynthesis. <i>Microbial Biotechnology</i> , 2015, 8, 296-310.	2.0	31
116	Genomic analyses of <i>Clostridium perfringens</i> isolates from five toxinotypes. <i>Research in Microbiology</i> , 2015, 166, 255-263.	1.0	71
117	Proteomics of hosts and pathogens in cystic fibrosis. <i>Proteomics - Clinical Applications</i> , 2015, 9, 134-146.	0.8	16
118	Genetically and Phenotypically Distinct <i>Pseudomonas aeruginosa</i> Cystic Fibrosis Isolates Share a Core Proteomic Signature. <i>PLoS ONE</i> , 2015, 10, e0138527.	1.1	37
119	Overall Transport Capabilities of <i>Bacillus subtilis</i> . , 2014, , 111-128.		7
120	Comparative analysis of surface-exposed virulence factors of <i>Acinetobacter baumannii</i> . <i>BMC Genomics</i> , 2014, 15, 1020.	1.2	149
121	The Common Oceanographer: Crowdsourcing the Collection of Oceanographic Data. <i>PLoS Biology</i> , 2014, 12, e1001947.	2.6	41
122	Draft Genome Sequence of <i>Bacillus alcalophilus</i> AV1934, a Classic Alkaliphile Isolated from Human Feces in 1934. <i>Genome Announcements</i> , 2014, 2, .	0.8	5
123	Microbiology of the Anthropocene. <i>Anthropocene</i> , 2014, 5, 1-8.	1.6	83
124	A genome-scale metabolic flux model of <i>Escherichia coli</i> K12 derived from the EcoCyc database. <i>BMC Systems Biology</i> , 2014, 8, 79.	3.0	42
125	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> , 2014, 70, 1318-1323.	0.4	5
126	Addition of <i>Escherichia coli</i> K-12 Growth Observation and Gene Essentiality Data to the EcoCyc Database. <i>Journal of Bacteriology</i> , 2014, 196, 982-988.	1.0	9

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127	The EcoCyc Database. EcoSal Plus, 2014, 6, .	2.1	101
128	Biolog Phenotype MicroArrays for Phenotypic Characterization of Microbial Cells. Methods in Molecular Biology, 2014, 1096, 123-130.	0.4	35
129	SecDF as Part of the Sec-Translocase Facilitates Efficient Secretion of Bacillus cereus Toxins and Cell Wall-Associated Proteins. PLoS ONE, 2014, 9, e103326.	1.1	21
130	Microbial Solute Transporters, 2014, .		0
131	Application of Exonuclease III-Aided Target Recycling in Flow Cytometry: DNA Detection Sensitivity Enhanced by Orders of Magnitude. Analytical Chemistry, 2013, 85, 8240-8245.	3.2	24
132	The effect of zinc limitation on the transcriptome of <i>Pseudomonas protegens</i> Pf-5. Environmental Microbiology, 2013, 15, 702-715.	1.8	53
133	A novel family of genomic resistance islands, AbGRI2, contributing to aminoglycoside resistance in Acinetobacter baumannii isolates belonging to global clone 2. Journal of Antimicrobial Chemotherapy, 2013, 68, 554-557.	1.3	77
134	Genes expressed by the biological control bacterium <i>Pseudomonas protegens</i> Pf-5 on seed surfaces under the control of the global regulators <i>GacA</i> and <i>RpoS</i> . Environmental Microbiology, 2013, 15, 716-735.	1.8	41
135	pA506, a Conjugative Plasmid of the Plant Epiphyte Pseudomonas fluorescens A506. Applied and Environmental Microbiology, 2013, 79, 5272-5282.	1.4	12
136	Stress effects caused by the expression of a mutant cellobiohydrolase I and proteasome inhibition in Trichoderma reesei Rut-C30. New Biotechnology, 2013, 30, 183-191.	2.4	14
137	Life in the dark: metagenomic evidence that a microbial slime community is driven by inorganic nitrogen metabolism. ISME Journal, 2013, 7, 1227-1236.	4.4	63
138	Maintenance of essential amino acid synthesis pathways in the <i>Blattabacterium cuenoti</i> symbiont of a wood-feeding cockroach. Biology Letters, 2013, 9, 20121153.	1.0	45
139	Effect of Tannic Acid on the Transcriptome of the Soil Bacterium Pseudomonas protegens Pf-5. Applied and Environmental Microbiology, 2013, 79, 3141-3145.	1.4	23
140	H-NS Plays a Role in Expression of Acinetobacter baumannii Virulence Features. Infection and Immunity, 2013, 81, 2574-2583.	1.0	100
141	EcoCyc: fusing model organism databases with systems biology. Nucleic Acids Research, 2013, 41, D605-D612.	6.5	505
142	Transcriptomic and biochemical analyses identify a family of chlorhexidine efflux proteins. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20254-20259.	3.3	138
143	Single-Step Selection of Drug Resistant Acinetobacter baylyi ADP1 Mutants Reveals a Functional Redundancy in the Recruitment of Multidrug Efflux Systems. PLoS ONE, 2013, 8, e56090.	1.1	20
144	Dead End Metabolites - Defining the Known Unknowns of the E. coli Metabolic Network. PLoS ONE, 2013, 8, e75210.	1.1	23

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145	Impact of DNA damaging agents on genome-wide transcriptional profiles in two marine <i>Synechococcus</i> species. <i>Frontiers in Microbiology</i> , 2013, 4, 232.	1.5	25
146	The Complete Genome and Phenome of a Community-Acquired <i>Acinetobacter baumannii</i> . <i>PLoS ONE</i> , 2013, 8, e58628.	1.1	93
147	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> , 2013, 8, e78862.	1.1	80
148	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> , 2012, 78, 7822-7832.	1.4	23
149	pEI1573 Carrying <i>bla</i> _{IMP-4} , from Sydney, Australia, Is Closely Related to Other IncL/M Plasmids. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 6029-6032.	1.4	82
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