

# Antoine Danchin

## List of Publications by Year in descending order

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480  
papers

31,144  
citations

5896

81  
h-index

6653

156  
g-index

516  
all docs

516  
docs citations

516  
times ranked

22812  
citing authors

#	ARTICLE	IF	CITATIONS
1	The complete genome sequence of the Gram-positive bacterium <i>Bacillus subtilis</i> . <i>Nature</i> , 1997, 390, 249-256.	27.8	3,519
2	Selective stabilisation of developing synapses as a mechanism for the specification of neuronal networks. <i>Nature</i> , 1976, 264, 705-712.	27.8	1,559
3	Essential <i>Bacillus subtilis</i> genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 4678-4683.	7.1	1,261
4	Organised Genome Dynamics in the <i>Escherichia coli</i> Species Results in Highly Diverse Adaptive Paths. <i>PLoS Genetics</i> , 2009, 5, e1000344.	3.5	1,005
5	Cross-host evolution of severe acute respiratory syndrome coronavirus in palm civet and human. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 2430-2435.	7.1	602
6	The genome sequence of the entomopathogenic bacterium <i>Photobacterium luminescens</i> . <i>Nature Biotechnology</i> , 2003, 21, 1307-1313.	17.5	538
7	Unique physiological and pathogenic features of <i>Leptospira interrogans</i> revealed by whole-genome sequencing. <i>Nature</i> , 2003, 422, 888-893.	27.8	513
8	Base composition bias might result from competition for metabolic resources. <i>Trends in Genetics</i> , 2002, 18, 291-294.	6.7	447
9	Open-Source Genomic Analysis of Shiga-Toxin-Producing <i>E. coli</i> O104:H4. <i>New England Journal of Medicine</i> , 2011, 365, 718-724.	27.0	392
10	Genome-based analysis of virulence genes in a non-biofilm-forming <i>Staphylococcus epidermidis</i> strain (ATCC 12228). <i>Molecular Microbiology</i> , 2003, 49, 1577-1593.	2.5	387
11	Secretion of cyclolysin, the calmodulin-sensitive adenylate cyclase-haemolysin bifunctional protein of <i>Bordetella pertussis</i> . <i>EMBO Journal</i> , 1988, 7, 3997-4004.	7.8	377
12	Large-scale monitoring of pleiotropic regulation of gene expression by the prokaryotic nucleoid-associated protein, H-NS. <i>Molecular Microbiology</i> , 2001, 40, 20-36.	2.5	376
13	CotA of <i>Bacillus subtilis</i> Is a Copper-Dependent Laccase. <i>Journal of Bacteriology</i> , 2001, 183, 5426-5430.	2.2	369
14	Coping with cold: The genome of the versatile marine Antarctica bacterium <i>Pseudoalteromonas haloplanktis</i> TAC125. <i>Genome Research</i> , 2005, 15, 1325-1335.	5.5	367
15	Evidence for horizontal gene transfer in <i>Escherichia coli</i> speciation. <i>Journal of Molecular Biology</i> , 1991, 222, 851-856.	4.2	364
16	From a consortium sequence to a unified sequence: the <i>Bacillus subtilis</i> 168 reference genome a decade later. <i>Microbiology (United Kingdom)</i> , 2009, 155, 1758-1775.	1.8	317
17	The calmodulin-sensitive adenylate cyclase of <i>Bordetella pertussis</i> : cloning and expression in <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 1988, 2, 19-30.	2.5	297
18	The revisited genome of <i>Pseudomonas putida</i> KT2440 enlightens its value as a robust metabolic chassis. <i>Environmental Microbiology</i> , 2016, 18, 3403-3424.	3.8	270

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19	Multiple Control of Flagellum Biosynthesis in <i>Escherichia coli</i> : Role of H-NS Protein and the Cyclic AMP-Catabolite Activator Protein Complex in Transcription of the <i>flhDC</i> Master Operon. <i>Journal of Bacteriology</i> , 1999, 181, 7500-7508.	2.2	246
20	An Analysis of Determinants of Amino Acids Substitution Rates in Bacterial Proteins. <i>Molecular Biology and Evolution</i> , 2004, 21, 108-116.	8.9	240
21	Generation of mutation hotspots in ageing bacterial colonies. <i>Scientific Reports</i> , 2016, 6, 2.	3.3	231
22	A Theory of the Epigenesis of Neuronal Networks by Selective Stabilization of Synapses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1973, 70, 2974-2978.	7.1	230
23	Secretion of cyclolysin, the calmodulin-sensitive adenylate cyclase-haemolysin bifunctional protein of <i>Bordetella pertussis</i> . <i>EMBO Journal</i> , 1988, 7, 3997-4004.	7.8	213
24	From dirt to industrial applications: <i>Pseudomonas putida</i> as a Synthetic Biology chassis for hosting harsh biochemical reactions. <i>Current Opinion in Chemical Biology</i> , 2016, 34, 20-29.	6.1	199
25	Essentiality, not expressiveness, drives gene-strand bias in bacteria. <i>Nature Genetics</i> , 2003, 34, 377-378.	21.4	198
26	Subtilist: a relational database for the <i>Bacillus subtilis</i> genome. <i>Microbiology (United Kingdom)</i> , 1995, 141, 261-268.	1.8	194
27	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. <i>PLoS Biology</i> , 2014, 12, e1001920.	5.6	190
28	<i>Bacillus subtilis</i> genome project: cloning and sequencing of the 97 kb region from 325° to 333deg;. <i>Molecular Microbiology</i> , 1993, 10, 371-384.	2.5	187
29	The H-NS protein is involved in the biogenesis of flagella in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 1994, 176, 5537-5540.	2.2	174
30	Universal replication biases in bacteria. <i>Molecular Microbiology</i> , 1999, 32, 11-16.	2.5	170
31	GadE (YhiE): a novel activator involved in the response to acid environment in <i>Escherichia coli</i> . <i>Microbiology (United Kingdom)</i> , 2004, 150, 61-72.	1.8	166
32	A Tale of Two Oxidation States: Bacterial Colonization of Arsenic-Rich Environments. <i>PLoS Genetics</i> , 2007, 3, e53.	3.5	166
33	Synthetic biology: discovering new worlds and new words. <i>EMBO Reports</i> , 2008, 9, 822-827.	4.5	148
34	Sulfur metabolism in <i>Escherichia coli</i> and related bacteria: facts and fiction. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2000, 2, 145-77.	1.0	146
35	Gene essentiality determines chromosome organisation in bacteria. <i>Nucleic Acids Research</i> , 2003, 31, 6570-6577.	14.5	145
36	S-box and T-box riboswitches and antisense RNA control a sulfur metabolic operon of <i>Clostridium acetobutylicum</i> . <i>Nucleic Acids Research</i> , 2008, 36, 5955-5969.	14.5	144

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37	Bacterial variations on the methionine salvage pathway. <i>BMC Microbiology</i> , 2004, 4, 9.	3.3	142
38	The ptsH, ptsI, and crr genes of the Escherichia coli phosphoenolpyruvate-dependent phosphotransferase system: a complex operon with several modes of transcription. <i>Journal of Bacteriology</i> , 1988, 170, 3827-3837.	2.2	137
39	How Essential Are Nonessential Genes?. <i>Molecular Biology and Evolution</i> , 2005, 22, 2147-2156.	8.9	135
40	Detection of new genes in a bacterial genome using Markov models for three gene classes. <i>Nucleic Acids Research</i> , 1995, 23, 3554-3562.	14.5	132
41	The calmodulin-sensitive adenylate cyclase of Bordetella pertussis: cloning and expression in Escherichia coli. <i>Molecular Microbiology</i> , 1988, 2, 19-30.	2.5	125
42	Two-component regulatory proteins ResD-ResE are required for transcriptional activation of fnr upon oxygen limitation in Bacillus subtilis. <i>Journal of Bacteriology</i> , 1996, 178, 3796-3802.	2.2	121
43	The viral transmembrane superfamily: possible divergence of Arenavirus and Filovirus glycoproteins from a common RNA virus ancestor. <i>BMC Microbiology</i> , 2001, 1, 1.	3.3	121
44	Bacillus subtilis FOF1 ATPase: DNA sequence of the atp operon and characterization of atp mutants. <i>Journal of Bacteriology</i> , 1994, 176, 6802-6811.	2.2	120
45	Proton magnetic relaxation studies of manganous complexes of transfer RNA and related compounds. <i>Journal of Molecular Biology</i> , 1969, 39, 199-217.	4.2	119
46	Identification, Characterization, and Regulation of a Cluster of Genes Involved in Carbapenem Biosynthesis in Photorhabdus luminescens. <i>Applied and Environmental Microbiology</i> , 2002, 68, 3780-3789.	3.1	116
47	Genomics of an extreme psychrophile, Psychromonas ingrahamii. <i>BMC Genomics</i> , 2008, 9, 210.	2.8	114
48	Bacteria as computers making computers. <i>FEMS Microbiology Reviews</i> , 2009, 33, 3-26.	8.6	113
49	A double epidemic model for the SARS propagation. <i>BMC Infectious Diseases</i> , 2003, 3, 19.	2.9	111
50	Catabolite Regulation of the pta Gene as Part of Carbon Flow Pathways in Bacillus subtilis. <i>Journal of Bacteriology</i> , 1999, 181, 6889-6897.	2.2	111
51	YtqI from Bacillus subtilis has both oligoribonuclease and pAp-phosphatase activity. <i>Nucleic Acids Research</i> , 2007, 35, 4552-4561.	14.5	109
52	Molecular cloning, sequencing, and physiological characterization of the qox operon from Bacillus subtilis encoding the aa3-600 quinol oxidase.. <i>Journal of Biological Chemistry</i> , 1992, 267, 10225-10231.	3.4	107
53	From essential to persistent genes: a functional approach to constructing synthetic life. <i>Trends in Genetics</i> , 2013, 29, 273-279.	6.7	106
54	SubtiList: the reference database for the Bacillus subtilis genome. <i>Nucleic Acids Research</i> , 2002, 30, 62-65.	14.5	105

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55	Persistence drives gene clustering in bacterial genomes. <i>BMC Genomics</i> , 2008, 9, 4.	2.8	104
56	A rapid test for the relA mutation in <i>E. coli</i> . <i>Biochemical and Biophysical Research Communications</i> , 1976, 69, 751-758.	2.1	103
57	Cyclic AMP as a modulator of polarity in polycistronic transcriptional units.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1979, 76, 3194-3197.	7.1	101
58	Codon usage and lateral gene transfer in <i>Bacillus subtilis</i> . <i>Current Opinion in Microbiology</i> , 1999, 2, 524-528.	5.1	101
59	Evolutionary Role of Restriction/Modification Systems as Revealed by Comparative Genome Analysis. <i>Genome Research</i> , 2001, 11, 946-958.	5.5	101
60	Structural homology between virulence-associated bacterial adenylate cyclases. <i>Gene</i> , 1988, 71, 293-298.	2.2	100
61	The urgent need for microbiology literacy in society. <i>Environmental Microbiology</i> , 2019, 21, 1513-1528.	3.8	99
62	Identification of residues essential for catalysis and binding of calmodulin in <i>Bordetella pertussis</i> adenylate cyclase by site-directed mutagenesis.. <i>EMBO Journal</i> , 1989, 8, 967-972.	7.8	98
63	The Trw Type IV Secretion System of <i>Bartonella</i> Mediates Host-Specific Adhesion to Erythrocytes. <i>PLoS Pathogens</i> , 2010, 6, e1000946.	4.7	98
64	A <i>Xanthomonas campestris</i> pv. <i>campestris</i> protein similar to catabolite activation factor is involved in regulation of phytopathogenicity. <i>Journal of Bacteriology</i> , 1990, 172, 5877-5883.	2.2	96
65	Conversion of Methionine to Cysteine in <i>Bacillus subtilis</i> and Its Regulation. <i>Journal of Bacteriology</i> , 2007, 189, 187-197.	2.2	96
66	Cooperative Binding of Manganese (II) to Transfer RNA. <i>FEBS Journal</i> , 1970, 16, 532-536.	0.2	95
67	Structure-based discovery of inhibitors of the YycG histidine kinase: new chemical leads to combat <i>Staphylococcus epidermidis</i> infections. <i>BMC Microbiology</i> , 2006, 6, 96.	3.3	95
68	Global Control of Cysteine Metabolism by CymR in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2006, 188, 2184-2197.	2.2	95
69	<i>Bacillus subtilis</i> , the model Gram-positive bacterium: 20 years of annotation refinement. <i>Microbial Biotechnology</i> , 2018, 11, 3-17.	4.2	95
70	Translation in <i>Bacillus subtilis</i> : roles and trends of initiation and termination, insights from a genome analysis. <i>Nucleic Acids Research</i> , 1999, 27, 3567-3576.	14.5	94
71	The PhoP-PhoQ Two-Component Regulatory System of <i>Photobacterium luminescens</i> Is Essential for Virulence in Insects. <i>Journal of Bacteriology</i> , 2004, 186, 1270-1279.	2.2	94
72	<i>Escherichia coli</i> UMP kinase, a Member of the Aspartokinase Family, Is a Hexamer Regulated by Guanine Nucleotides and UTP. <i>Biochemistry</i> , 1995, 34, 5066-5074.	2.5	93

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73	Anaerobic transcription activation in <i>Bacillus subtilis</i> : identification of distinct FNR-dependent and -independent regulatory mechanisms.. <i>EMBO Journal</i> , 1995, 14, 5984-5994.	7.8	93
74	The structural and functional organization of H-NS-like proteins is evolutionarily conserved in Gram-negative bacteria. <i>Molecular Microbiology</i> , 1999, 31, 319-329.	2.5	92
75	Proteomics of life at low temperatures: trigger factor is the primary chaperone in the Antarctic bacterium <i>Pseudoalteromonas haloplanktis</i> TAC125. <i>Molecular Microbiology</i> , 2010, 76, 120-132.	2.5	91
76	The <i>cya</i> locus of <i>Escherichia coli</i> K12: Organization and gene products. <i>Molecular Genetics and Genomics</i> , 1982, 188, 465-471.	2.4	90
77	Cloning and expression of the calmodulin-sensitive <i>Bacillus anthracis</i> adenylate cyclase in <i>Escherichia coli</i> . <i>Gene</i> , 1988, 64, 277-284.	2.2	90
78	Cyclic AMP synthesis in <i>Escherichia coli</i> strains bearing known deletions in the <i>pts</i> phosphotransferase operon. <i>Gene</i> , 1990, 86, 27-33.	2.2	89
79	Oligonucleotide bias in <i>Bacillus subtilis</i> : General trends and taxonomic comparisons. <i>Nucleic Acids Research</i> , 1998, 26, 2971-2980.	14.5	87
80	Life in the Cold: a Proteomic Study of Cold-Repressed Proteins in the Antarctic Bacterium <i>Pseudoalteromonas haloplanktis</i> TAC125. <i>Applied and Environmental Microbiology</i> , 2011, 77, 3881-3883.	3.1	87
81	Three Different Systems Participate in l-Cystine Uptake in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2004, 186, 4875-4884.	2.2	86
82	Regulation of adenylate cyclase synthesis in <i>Escherichia coli</i> : nucleotide sequence of the control region.. <i>EMBO Journal</i> , 1983, 2, 791-797.	7.8	85
83	Was photosynthetic RuBisCO recruited by acquisitive evolution from RuBisCO-like proteins involved in sulfur metabolism?. <i>Research in Microbiology</i> , 2005, 156, 611-618.	2.1	85
84	The complete nucleotide sequence of the adenylate cyclase gene of <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 1984, 12, 9427-9440.	14.5	84
85	The methionine salvage pathway in <i>Bacillus subtilis</i> . <i>BMC Microbiology</i> , 2002, 2, 8.	3.3	83
86	Molecular cloning, sequencing, and physiological characterization of the <i>qox</i> operon from <i>Bacillus subtilis</i> encoding the <i>aa3-600</i> quinol oxidase. <i>Journal of Biological Chemistry</i> , 1992, 267, 10225-31.	3.4	82
87	Correlation between the serine sensitivity and the derepressibility of the <i>ilv</i> genes in <i>Escherichia coli</i> <i>relA</i> mutants. <i>Molecular Genetics and Genomics</i> , 1978, 165, 21-30.	2.4	81
88	Mapping of sequenced genes (700 kbp) in the restriction map of the <i>Escherichia coli</i> chromosome. <i>Molecular Microbiology</i> , 1990, 4, 169-187.	2.5	81
89	The CymR Regulator in Complex with the Enzyme CysK Controls Cysteine Metabolism in <i>Bacillus subtilis</i> . <i>Journal of Biological Chemistry</i> , 2008, 283, 35551-35560.	3.4	81
90	Mutations in the <i>bglY</i> gene increase the frequency of spontaneous deletions in <i>Escherichia coli</i> K-12.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1990, 87, 360-363.	7.1	80

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91	<i>Aeromonas hydrophila</i> Adenylyl Cyclase 2: a New Class of Adenylyl Cyclases with Thermophilic Properties and Sequence Similarities to Proteins from Hyperthermophilic Archaeobacteria. Journal of Bacteriology, 1998, 180, 3339-3344.	2.2	79
92	Colibri: a functional data base for the Escherichia coli genome. Microbiological Reviews, 1993, 57, 623-654.	10.1	79
93	tRNA structure and binding sites for cations. Biopolymers, 1972, 11, 1317-1333.	2.4	78
94	Analysis of long repeats in bacterial genomes reveals alternative evolutionary mechanisms in Bacillus subtilis and other competent prokaryotes. Molecular Biology and Evolution, 1999, 16, 1219-1230.	8.9	78
95	CymR, the master regulator of cysteine metabolism in <i>Staphylococcus aureus</i> , controls host sulphur source utilization and plays a role in biofilm formation. Molecular Microbiology, 2009, 73, 194-211.	2.5	76
96	Structural and catalytic characteristics of Escherichia coli adenylate kinase.. Journal of Biological Chemistry, 1987, 262, 622-629.	3.4	75
97	MvaT proteins in Pseudomonas spp.: a novel class of H-NS-like proteins. Microbiology (United Kingdom), 2013, 153, 187-194.	1.8	74
98	Role of Escherichia Coli Histone-Like Nucleoid-Structuring Protein in Bacterial Metabolism and Stress Response. Identification of Targets by Two-Dimensional Electrophoresis. FEBS Journal, 1997, 244, 767-773.	0.2	73
99	Small noncoding RNA GcvB is a novel regulator of acid resistance in Escherichia coli. BMC Genomics, 2009, 10, 165.	2.8	73
100	The contribution of microbial biotechnology to sustainable development goals. Microbial Biotechnology, 2017, 10, 984-987.	4.2	73
101	An updated metabolic view of the Bacillus subtilis 168 genome. Microbiology (United Kingdom), 2013, 153, 757-770.	1.8	72
102	Homeotopic transformation and the origin of translation. Progress in Biophysics and Molecular Biology, 1989, 54, 81-86.	2.9	71
103	Isolation and characterization of catalytic and calmodulin-binding domains of Bordetella pertussis adenylate cyclase. FEBS Journal, 1991, 196, 469-474.	0.2	71
104	Scaling up synthetic biology: Do not forget the chassis. FEBS Letters, 2012, 586, 2129-2137.	2.8	69
105	Mutations in bglY, the structural gene for the DNA-binding protein H1, affect expression of several Escherichia coli genes. Biochimie, 1990, 72, 889-891.	2.6	68
106	Degradation of nanoRNA is performed by multiple redundant RNases in Bacillus subtilis. Nucleic Acids Research, 2009, 37, 5114-5125.	14.5	68
107	Unknown unknowns: essential genes in quest for function. Microbial Biotechnology, 2016, 9, 530-540.	4.2	68
108	Chemical reactivity drives spatiotemporal organisation of bacterial metabolism. FEMS Microbiology Reviews, 2014, 39, n/a-n/a.	8.6	67

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109	Uneven Distribution of GATC Motifs in the Escherichia coli Chromosome, its Plasmids and its Phages. Journal of Molecular Biology, 1996, 257, 574-585.	4.2	66
110	Adenylyl Cyclases: A Heterogeneous Class of ATP-Utilizing Enzymes. Progress in Molecular Biology and Translational Science, 1994, 49, 241-283.	1.9	65
111	Phylogenomics of expanding uncultured environmental Tenericutes provides insights into their pathogenicity and evolutionary relationship with Bacilli. BMC Genomics, 2020, 21, 408.	2.8	65
112	CMP Kinase from Escherichia coli Is Structurally Related to Other Nucleoside Monophosphate Kinases. Journal of Biological Chemistry, 1996, 271, 2856-2862.	3.4	64
113	Characterization of polyamine synthesis pathway in Bacillus subtilis 168. Molecular Microbiology, 1998, 29, 851-858.	2.5	64
114	Catabolite repression in Escherichia coli mutants lacking cyclic AMP receptor protein. Proceedings of the National Academy of Sciences of the United States of America, 1980, 77, 5799-5801.	7.1	63
115	Identification and isolation of a gene required for nitrate assimilation and anaerobic growth of Bacillus subtilis. Journal of Bacteriology, 1995, 177, 1112-1115.	2.2	62
116	On proteins of the microsporidian invasive apparatus: complete sequence of a polar tube protein of Encephalitozoon cuniculi. Molecular Microbiology, 1998, 29, 825-834.	2.5	62
117	Mta, a global MerR-type regulator of the Bacillus subtilis multidrug-efflux transporters. Molecular Microbiology, 1999, 31, 1549-1559.	2.5	62
118	Ongoing Evolution of Strand Composition in Bacterial Genomes. Molecular Biology and Evolution, 2001, 18, 1789-1799.	8.9	62
119	Nucleotide Sequence Database Policies. Science, 2002, 298, 1333b-1333.	12.6	62
120	Oligoribonuclease is a common downstream target of lithium-induced pAp accumulation in Escherichia coli and human cells. Nucleic Acids Research, 2006, 34, 2364-2373.	14.5	62
121	Extracting biological information from DNA arrays: an unexpected link between arginine and methionine metabolism in Bacillus subtilis. Genome Biology, 2001, 2, research0019.1.	9.6	61
122	Pleiotropic Role of Quorum-Sensing Autoinducer 2 in Photobacterium luminescens. Applied and Environmental Microbiology, 2006, 72, 6439-6451.	3.1	59
123	Phylogeny of related functions: the case of polyamine biosynthetic enzymes. Microbiology (United Kingdom), 2002, 148, 1543-1551.	1.8	59
124	Regulation of bacterial motility in response to low pH in Escherichia coli: the role of H-NS protein. Microbiology (United Kingdom), 2002, 148, 1543-1551.	1.8	59
125	Anaerobic transcription activation in Bacillus subtilis: identification of distinct FNR-dependent and -independent regulatory mechanisms. EMBO Journal, 1995, 14, 5984-94.	7.8	59
126	Escherichia coli molecular genetic map (1500 kbp): update II. Molecular Microbiology, 1991, 5, 2629-2640.	2.5	58



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127	Decrypting the H-NS-dependent regulatory cascade of acid stress resistance in <i>Escherichia coli</i> . <i>BMC Microbiology</i> , 2010, 10, 273.	3.3	58
128	Structural and catalytic characteristics of <i>Escherichia coli</i> adenylate kinase. <i>Journal of Biological Chemistry</i> , 1987, 262, 622-9.	3.4	58
129	Cloning and assembly strategies in microbial genome projects. <i>Microbiology (United Kingdom)</i> , 1999, 145, 2625-2634.	1.8	56
130	Evolutionary Role of Restriction/Modification Systems as Revealed by Comparative Genome Analysis. <i>Genome Research</i> , 2001, 11, 946-958.	5.5	56
131	Analysis of the ptsH-ptsI-crr region in <i>Escherichia coli</i> K-12: nucleotide sequence of the ptsH gene. <i>Gene</i> , 1985, 35, 199-207.	2.2	55
132	Testing the hypothesis of a recombinant origin of the SARS-associated coronavirus. <i>Archives of Virology</i> , 2005, 150, 1-20.	2.1	54
133	The ten grand challenges of synthetic life. <i>Systems and Synthetic Biology</i> , 2011, 5, 1-9.	1.0	54
134	Coenzyme B12 synthesis as a baseline to study metabolite contribution of animal microbiota. <i>Microbial Biotechnology</i> , 2017, 10, 688-701.	4.2	54
135	<scp>The importance of naturally attenuated SARSâ€CoV</scp>â€2<scp> in the fight against COVID</scp>â€19. <i>Environmental Microbiology</i> , 2020, 22, 1997-2000.	3.8	54
136	H-NS and H-NS-like proteins in Gram-negative bacteria and their multiple role in the regulation of bacterial metabolism. <i>Biochimie</i> , 2001, 83, 235-241.	2.6	53
137	Molecular diagnosis of human cancer type by gene expression profiles and independent component analysis. <i>European Journal of Human Genetics</i> , 2005, 13, 1303-1311.	2.8	53
138	Imagene: an integrated computer environment for sequence annotation and analysis. <i>Bioinformatics</i> , 1999, 15, 2-15.	4.1	51
139	Identification of <i>Bacillus subtilis</i> CysL, a Regulator of the <i>cysJI</i> Operon, Which Encodes Sulfite Reductase. <i>Journal of Bacteriology</i> , 2002, 184, 4681-4689.	2.2	51
140	The PatB protein of <i>Bacillus subtilis</i> is a C-S-lyase. <i>Biochimie</i> , 2005, 87, 231-238.	2.6	51
141	RcsB plays a central role in H-NS-dependent regulation of motility and acid stress resistance in <i>Escherichia coli</i> . <i>Research in Microbiology</i> , 2010, 161, 363-371.	2.1	51
142	Two functional domains in adenylate cyclase of <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 1983, 165, 197-202.	4.2	50
143	Metabolic alterations mediated by 2-ketobutyrate in <i>Escherichia coli</i> K12. <i>Molecular Genetics and Genomics</i> , 1984, 193, 473-478.	2.4	50
144	<i>Rhizobium meliloti</i> adenylate cyclase is related to eucaryotic adenylate and guanylate cyclases. <i>Journal of Bacteriology</i> , 1990, 172, 2614-2621.	2.2	50

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145	Functional and evolutionary roles of long repeats in prokaryotes. <i>Research in Microbiology</i> , 1999, 150, 725-733.	2.1	50
146	The metNPQ operon of <i>Bacillus subtilis</i> encodes an ABC permease transporting methionine sulfoxide, d- and l-methionine. <i>Research in Microbiology</i> , 2004, 155, 80-86.	2.1	50
147	Control of Bacterial Motility by Environmental Factors in Polarly Flagellated and Peritrichous Bacteria Isolated from Lake Baikal. <i>Applied and Environmental Microbiology</i> , 2001, 67, 3852-3859.	3.1	49
148	Global Expression Profile of <i>Bacillus subtilis</i> Grown in the Presence of Sulfate or Methionine. <i>Journal of Bacteriology</i> , 2002, 184, 5179-5186.	2.2	49
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150	Genomic characterization of symbiotic mycoplasmas from the stomach of deep-sea isopod <i>Bathynomus</i> sp. <i>Environmental Microbiology</i> , 2016, 18, 2646-2659.	3.8	49
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