

Antoine Danchin

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456
papers

26,286
citations

77
h-index

146
g-index

516
ext. papers

28,968
ext. citations

6.5
avg, IF

6.73
L-index

#	Paper	IF	Citations
456	The complete genome sequence of the gram-positive bacterium <i>Bacillus subtilis</i> . <i>Nature</i> , 1997 , 390, 249-564	50.4	3107
455	Selective stabilisation of developing synapses as a mechanism for the specification of neuronal networks. <i>Nature</i> , 1976 , 264, 705-12	50.4	1323
454	Essential <i>Bacillus subtilis</i> genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 4678-83	11.5	1115
453	Organised genome dynamics in the <i>Escherichia coli</i> species results in highly diverse adaptive paths. <i>PLoS Genetics</i> , 2009 , 5, e1000344	6	802
452	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, 2430-5	11.5	508
451	The genome sequence of the entomopathogenic bacterium <i>Photobacterium luminescens</i> . <i>Nature Biotechnology</i> , 2003 , 21, 1307-13	44.5	485
450	Unique physiological and pathogenic features of <i>Leptospira interrogans</i> revealed by whole-genome sequencing. <i>Nature</i> , 2003 , 422, 888-93	50.4	446
449	Base composition bias might result from competition for metabolic resources. <i>Trends in Genetics</i> , 2002 , 18, 291-4	8.5	354
448	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	4.1	346
447	Open-source genomic analysis of Shiga-toxin-producing <i>E. coli</i> O104:H4. <i>New England Journal of Medicine</i> , 2011 , 365, 718-24	59.2	340
446	Evidence for horizontal gene transfer in <i>Escherichia coli</i> speciation. <i>Journal of Molecular Biology</i> , 1991 , 222, 851-6	6.5	331
445	Secretion of cyclolysin, the calmodulin-sensitive adenylate cyclase-haemolysin bifunctional protein of <i>Bordetella pertussis</i> . <i>EMBO Journal</i> , 1988 , 7, 3997-4004	13	326
444	Genome-based analysis of virulence genes in a non-biofilm-forming <i>Staphylococcus epidermidis</i> strain (ATCC 12228). <i>Molecular Microbiology</i> , 2003 , 49, 1577-93	4.1	323
443	Coping with cold: the genome of the versatile marine Antarctica bacterium <i>Pseudoalteromonas haloplanktis</i> TAC125. <i>Genome Research</i> , 2005 , 15, 1325-35	9.7	309
442	CotA of <i>Bacillus subtilis</i> is a copper-dependent laccase. <i>Journal of Bacteriology</i> , 2001 , 183, 5426-30	3.5	300
441	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	2.9	257
440	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	4.1	250

439	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, 7500-8	3.5	222
438	An analysis of determinants of amino acids substitution rates in bacterial proteins. <i>Molecular Biology and Evolution</i> , 2004 , 21, 108-16	8.3	204
437	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	5.2	194
436	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, 2974-8	11.5	193
435	SubtiList: a relational database for the <i>Bacillus subtilis</i> genome. <i>Microbiology (United Kingdom)</i> , 1995 , 141 (Pt 2), 261-8	2.9	168
434	Essentiality, not expressiveness, drives gene-strand bias in bacteria. <i>Nature Genetics</i> , 2003 , 34, 377-8	36.3	167
433	Secretion of cyclolysin, the calmodulin-sensitive adenylate cyclase-haemolysin bifunctional protein of <i>Bordetella pertussis</i> . <i>EMBO Journal</i> , 1988 , 7, 3997-4004	13	163
432	The H-NS protein is involved in the biogenesis of flagella in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 1994 , 176, 5537-40	3.5	160
431	Generation of mutation hotspots in ageing bacterial colonies. <i>Scientific Reports</i> , 2016 , 6, 2	4.9	155
430	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	9.7	151
429	Universal replication biases in bacteria. <i>Molecular Microbiology</i> , 1999 , 32, 11-6	4.1	149
428	A tale of two oxidation states: bacterial colonization of arsenic-rich environments. <i>PLoS Genetics</i> , 2007 , 3, e53	6	148
427	Genomic encyclopedia of bacteria and archaea: sequencing a myriad of type strains. <i>PLoS Biology</i> , 2014 , 12, e1001920	9.7	146
426	<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	4.1	143
425	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	2.9	141
424	Synthetic biology: discovering new worlds and new words. <i>EMBO Reports</i> , 2008 , 9, 822-7	6.5	126
423	Bacterial variations on the methionine salvage pathway. <i>BMC Microbiology</i> , 2004 , 4, 9	4.5	126
422	Detection of new genes in a bacterial genome using Markov models for three gene classes. <i>Nucleic Acids Research</i> , 1995 , 23, 3554-62	20.1	123

421	Gene essentiality determines chromosome organisation in bacteria. <i>Nucleic Acids Research</i> , 2003 , 31, 6570-7	20.1	122
420	How essential are nonessential genes?. <i>Molecular Biology and Evolution</i> , 2005 , 22, 2147-56	8.3	120
419	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, 3827-37	3.5	118
418	Sulfur metabolism in Escherichia coli and related bacteria: facts and fiction. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2000 , 2, 145-77	0.9	117
417	S-box and T-box riboswitches and antisense RNA control a sulfur metabolic operon of Clostridium acetobutylicum. <i>Nucleic Acids Research</i> , 2008 , 36, 5955-69	20.1	110
416	The viral transmembrane superfamily: possible divergence of Arenavirus and Filovirus glycoproteins from a common RNA virus ancestor. <i>BMC Microbiology</i> , 2001 , 1, 1	4.5	105
415	Bacillus subtilis F0F1 ATPase: DNA sequence of the atp operon and characterization of atp mutants. <i>Journal of Bacteriology</i> , 1994 , 176, 6802-11	3.5	105
414	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, 3796-802	3.5	104
413	Genomics of an extreme psychrophile, Psychromonas ingrahamii. <i>BMC Genomics</i> , 2008 , 9, 210	4.5	101
412	Identification, characterization, and regulation of a cluster of genes involved in carbapenem biosynthesis in Photobacterium luminescens. <i>Applied and Environmental Microbiology</i> , 2002 , 68, 3780-9	4.8	100
411	Catabolite regulation of the pta gene as part of carbon flow pathways in Bacillus subtilis. <i>Journal of Bacteriology</i> , 1999 , 181, 6889-97	3.5	99
410	Proton magnetic relaxation studies of manganese complexes of transfer RNA and related compounds. <i>Journal of Molecular Biology</i> , 1969 , 39, 199-217	6.5	98
409	Bacteria as computers making computers. <i>FEMS Microbiology Reviews</i> , 2009 , 33, 3-26	15.1	97
408	The calmodulin-sensitive adenylate cyclase of Bordetella pertussis: cloning and expression in Escherichia coli. <i>Molecular Microbiology</i> , 1988 , 2, 19-30	4.1	96
407	SubtiList: the reference database for the Bacillus subtilis genome. <i>Nucleic Acids Research</i> , 2002 , 30, 62-5	20.1	94
406	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	5.4	91
405	The structural and functional organization of H-NS-like proteins is evolutionarily conserved in gram-negative bacteria. <i>Molecular Microbiology</i> , 1999 , 31, 319-29	4.1	90
404	The PhoP-PhoQ two-component regulatory system of Photobacterium luminescens is essential for virulence in insects. <i>Journal of Bacteriology</i> , 2004 , 186, 1270-9	3.5	89

403	Evolutionary role of restriction/modification systems as revealed by comparative genome analysis. <i>Genome Research</i> , 2001 , 11, 946-58	9.7	89
402	Codon usage and lateral gene transfer in <i>Bacillus subtilis</i> . <i>Current Opinion in Microbiology</i> , 1999 , 2, 524-87.9	87.9	89
401	A rapid test for the rel A mutation in <i>E. coli</i> . <i>Biochemical and Biophysical Research Communications</i> , 1976 , 69, 751-8	3.4	88
400	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, 5877-83	3.5	87
399	Structural homology between virulence-associated bacterial adenylate cyclases. <i>Gene</i> , 1988 , 71, 293-8	3.8	86
398	Cooperative binding of manganese (II) to transfer RNA. <i>FEBS Journal</i> , 1970 , 16, 532-6		86
397	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, 3567-76	20.1	85
396	The Trw type IV secretion system of <i>Bartonella</i> mediates host-specific adhesion to erythrocytes. <i>PLoS Pathogens</i> , 2010 , 6, e1000946	7.6	84
395	Global control of cysteine metabolism by CymR in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2006 , 188, 2184-97	3.5	84
394	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	13	84
393	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, 3194-7	11.5	84
392	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	4.5	83
391	Cyclic AMP synthesis in <i>Escherichia coli</i> strains bearing known deletions in the pts phosphotransferase operon. <i>Gene</i> , 1990 , 86, 27-33	3.8	83
390	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, 120-32	4.1	81
389	The methionine salvage pathway in <i>Bacillus subtilis</i> . <i>BMC Microbiology</i> , 2002 , 2, 8	4.5	81
388	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	13	81
387	Persistence drives gene clustering in bacterial genomes. <i>BMC Genomics</i> , 2008 , 9, 4	4.5	79
386	From essential to persistent genes: a functional approach to constructing synthetic life. <i>Trends in Genetics</i> , 2013 , 29, 273-9	8.5	78

385	Beneficial biological warfare. <i>EMBO Reports</i> , 2006 , 7, 767-767	6.5	78
384	Three different systems participate in L-cystine uptake in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2004 , 186, 4875-84	3.5	78
383	Conserved transcription factor binding sites of cancer markers derived from primary lung adenocarcinoma microarrays. <i>Nucleic Acids Research</i> , 2005 , 33, 2764-2764	20.1	78
382	On our tiniest foes. <i>EMBO Reports</i> , 2001 , 2, 468-469	6.5	78
381	The natural war. <i>EMBO Reports</i> , 2000 , 1, 216-216	6.5	78
380	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	5.4	78
379	YtqI from <i>Bacillus subtilis</i> has both oligoribonuclease and pAp-phosphatase activity. <i>Nucleic Acids Research</i> , 2007 , 35, 4552-61	20.1	76
378	<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, 5066-74	3.2	75
377	Was photosynthetic RuBisCO recruited by acquisitive evolution from RuBisCO-like proteins involved in sulfur metabolism?. <i>Research in Microbiology</i> , 2005 , 156, 611-8	4	74
376	Cloning and expression of the calmodulin-sensitive <i>Bacillus anthracis</i> adenylate cyclase in <i>Escherichia coli</i> . <i>Gene</i> , 1988 , 64, 277-84	3.8	74
375	Conversion of methionine to cysteine in <i>Bacillus subtilis</i> and its regulation. <i>Journal of Bacteriology</i> , 2007 , 189, 187-97	3.5	73
374	Mapping of sequenced genes (700 kbp) in the restriction map of the <i>Escherichia coli</i> chromosome. <i>Molecular Microbiology</i> , 1990 , 4, 169-87	4.1	73
373	tRNA structure and binding sites for cations. <i>Biopolymers</i> , 1972 , 11, 1317-33	2.2	73
372	The <i>cya</i> locus of <i>Escherichia coli</i> K12: organization and gene products. <i>Molecular Genetics and Genomics</i> , 1982 , 188, 465-71		72
371	Oligonucleotide bias in <i>Bacillus subtilis</i> : general trends and taxonomic comparisons. <i>Nucleic Acids Research</i> , 1998 , 26, 2971-80	20.1	71
370	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, 360-3	11.5	70
369	Colibri: a functional data base for the <i>Escherichia coli</i> genome. <i>Microbiological Reviews</i> , 1993 , 57, 623-54		69
368	A double epidemic model for the SARS propagation. <i>BMC Infectious Diseases</i> , 2003 , 3, 19	4	68

367	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		68
366	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, 35551-60	5.4	67
365	MvaT proteins in <i>Pseudomonas</i> spp.: a novel class of H-NS-like proteins. <i>Microbiology (United Kingdom)</i> , 2003 , 149, 3047-3050	2.9	67
364	The complete nucleotide sequence of the adenylate cyclase gene of <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 1984 , 12, 9427-40	20.1	67
363	Regulation of adenylate cyclase synthesis in <i>Escherichia coli</i> : nucleotide sequence of the control region.. <i>EMBO Journal</i> , 1983 , 2, 791-797	13	66
362	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, 3881-3	4.8	64
361	Homeotopic transformation and the origin of translation. <i>Progress in Biophysics and Molecular Biology</i> , 1989 , 54, 81-6	4.7	64
360	Analysis of long repeats in bacterial genomes reveals alternative evolutionary mechanisms in <i>Bacillus subtilis</i> and other competent prokaryotes. <i>Molecular Biology and Evolution</i> , 1999 , 16, 1219-30	8.3	62
359	Mutations in <i>bglY</i> , the structural gene for the DNA-binding protein H1, affect expression of several <i>Escherichia coli</i> genes. <i>Biochimie</i> , 1990 , 72, 889-91	4.6	62
358	<i>Aeromonas hydrophila</i> adenyl cyclase 2: a new class of adenyl cyclases with thermophilic properties and sequence similarities to proteins from hyperthermophilic archaeobacteria. <i>Journal of Bacteriology</i> , 1998 , 180, 3339-44	3.5	62
357	Isolation and characterization of catalytic and calmodulin-binding domains of <i>Bordetella pertussis</i> adenylate cyclase. <i>FEBS Journal</i> , 1991 , 196, 469-74		60
356	An updated metabolic view of the <i>Bacillus subtilis</i> 168 genome. <i>Microbiology (United Kingdom)</i> , 2013 , 159, 757-770	2.9	59
355	Degradation of nanoRNA is performed by multiple redundant RNases in <i>Bacillus subtilis</i> . <i>Nucleic Acids Research</i> , 2009 , 37, 5114-25	20.1	58
354	CymR, the master regulator of cysteine metabolism in <i>Staphylococcus aureus</i> , controls host sulphur source utilization and plays a role in biofilm formation. <i>Molecular Microbiology</i> , 2009 , 73, 194-211	4.1	58
353	Role of <i>Escherichia coli</i> histone-like nucleoid-structuring protein in bacterial metabolism and stress response—identification of targets by two-dimensional electrophoresis. <i>FEBS Journal</i> , 1997 , 244, 767-73		58
352	Characterization of polyamine synthesis pathway in <i>Bacillus subtilis</i> 168. <i>Molecular Microbiology</i> , 1998 , 29, 851-8	4.1	58
351	Structural and catalytic characteristics of <i>Escherichia coli</i> adenylate kinase.. <i>Journal of Biological Chemistry</i> , 1987 , 262, 622-629	5.4	58
350	Scaling up synthetic biology: Do not forget the chassis. <i>FEBS Letters</i> , 2012 , 586, 2129-37	3.8	57

349	On proteins of the microsporidian invasive apparatus: complete sequence of a polar tube protein of <i>Encephalitozoon cuniculi</i> . <i>Molecular Microbiology</i> , 1998 , 29, 825-34	4.1	57
348	Unknown unknowns: essential genes in quest for function. <i>Microbial Biotechnology</i> , 2016 , 9, 530-40	6.3	56
347	Small noncoding RNA GcvB is a novel regulator of acid resistance in <i>Escherichia coli</i> . <i>BMC Genomics</i> , 2009 , 10, 165	4.5	55
346	Ongoing evolution of strand composition in bacterial genomes. <i>Molecular Biology and Evolution</i> , 2001 , 18, 1789-99	8.3	55
345	Mta, a global MerR-type regulator of the <i>Bacillus subtilis</i> multidrug-efflux transporters. <i>Molecular Microbiology</i> , 1999 , 31, 1549-59	4.1	55
344	Uneven distribution of GATC motifs in the <i>Escherichia coli</i> chromosome, its plasmids and its phages. <i>Journal of Molecular Biology</i> , 1996 , 257, 574-85	6.5	55
343	Regulation of bacterial motility in response to low pH in <i>Escherichia coli</i> : the role of H-NS protein. <i>Microbiology (United Kingdom)</i> , 2002 , 148, 1543-1551	2.9	54
342	Pleiotropic role of quorum-sensing autoinducer 2 in <i>Photobacterium luminescens</i> . <i>Applied and Environmental Microbiology</i> , 2006 , 72, 6439-51	4.8	53
341	Structural and catalytic characteristics of <i>Escherichia coli</i> adenylate kinase. <i>Journal of Biological Chemistry</i> , 1987 , 262, 622-9	5.4	53
340	Oligoribonuclease is a common downstream target of lithium-induced pAp accumulation in <i>Escherichia coli</i> and human cells. <i>Nucleic Acids Research</i> , 2006 , 34, 2364-73	20.1	52
339	CMP kinase from <i>Escherichia coli</i> is structurally related to other nucleoside monophosphate kinases. <i>Journal of Biological Chemistry</i> , 1996 , 271, 2856-62	5.4	52
338	Extracting biological information from DNA arrays: an unexpected link between arginine and methionine metabolism in <i>Bacillus subtilis</i> . <i>Genome Biology</i> , 2001 , 2, RESEARCH0019	18.3	50
337	Identification and isolation of a gene required for nitrate assimilation and anaerobic growth of <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 1995 , 177, 1112-5	3.5	50
336	Phylogeny of related functions: the case of polyamine biosynthetic enzymes. <i>Microbiology (United Kingdom)</i> , 2000 , 146 (Pt 8), 1815-1828	2.9	50
335	Chemical reactivity drives spatiotemporal organisation of bacterial metabolism. <i>FEMS Microbiology Reviews</i> , 2015 , 39, 96-119	15.1	49
334	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, 235-41	4.6	49
333	Anaerobic transcription activation in <i>Bacillus subtilis</i> : identification of distinct FNR-dependent and -independent regulatory mechanisms. <i>EMBO Journal</i> , 1995 , 14, 5984-94	13	49
332	Molecular diagnosis of human cancer type by gene expression profiles and independent component analysis. <i>European Journal of Human Genetics</i> , 2005 , 13, 1303-11	5.3	48

331	Nucleotide sequence database policies. <i>Science</i> , 2002 , 298, 1333	33.3	48
330	Cloning and assembly strategies in microbial genome projects. <i>Microbiology (United Kingdom)</i> , 1999 , 145 (Pt 10), 2625-34	2.9	48
329	Imagene: an integrated computer environment for sequence annotation and analysis. <i>Bioinformatics</i> , 1999 , 15, 2-15	7.2	48
328	Adenylyl cyclases: a heterogeneous class of ATP-utilizing enzymes. <i>Progress in Molecular Biology and Translational Science</i> , 1994 , 49, 241-83		48
327	Catabolite repression in Escherichia coli mutants lacking cyclic AMP receptor protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1980 , 77, 5799-801	11.5	48
326	Decrypting the H-NS-dependent regulatory cascade of acid stress resistance in Escherichia coli. <i>BMC Microbiology</i> , 2010 , 10, 273	4.5	47
325	RcsB plays a central role in H-NS-dependent regulation of motility and acid stress resistance in Escherichia coli. <i>Research in Microbiology</i> , 2010 , 161, 363-71	4	46
324	Global expression profile of Bacillus subtilis grown in the presence of sulfate or methionine. <i>Journal of Bacteriology</i> , 2002 , 184, 5179-86	3.5	46
323	Analysis of the ptsH-ptsI-crr region in Escherichia coli K-12: nucleotide sequence of the ptsH gene. <i>Gene</i> , 1985 , 35, 199-207	3.8	46
322	Testing the hypothesis of a recombinant origin of the SARS-associated coronavirus. <i>Archives of Virology</i> , 2005 , 150, 1-20	2.6	45
321	Identification of Bacillus subtilis CysL, a regulator of the cysJI operon, which encodes sulfite reductase. <i>Journal of Bacteriology</i> , 2002 , 184, 4681-9	3.5	45
320	Functional and evolutionary roles of long repeats in prokaryotes. <i>Research in Microbiology</i> , 1999 , 150, 725-33	4	45
319	Escherichia coli molecular genetic map (1500 kbp): update II. <i>Molecular Microbiology</i> , 1991 , 5, 2629-40	4.1	45
318	The extant core bacterial proteome is an archive of the origin of life. <i>Proteomics</i> , 2007 , 7, 875-89	4.8	44
317	The PatB protein of Bacillus subtilis is a C-S-lyase. <i>Biochimie</i> , 2005 , 87, 231-8	4.6	44
316	Rhizobium meliloti adenylate cyclase is related to eucaryotic adenylate and guanylate cyclases. <i>Journal of Bacteriology</i> , 1990 , 172, 2614-21	3.5	43
315	Proton magnetic relaxation study of the manganese-transfer-RNA complex. <i>Journal of Chemical Physics</i> , 1970 , 53, 3599-609	3.9	43
314	The ten grand challenges of synthetic life. <i>Systems and Synthetic Biology</i> , 2011 , 5, 1-9		42

313	Exploring the <i>Penicillium marneffeii</i> genome. <i>Archives of Microbiology</i> , 2003 , 179, 339-53	3	42
312	Phylogeny of metabolic pathways: O-acetylserine sulphhydrylase A is homologous to the tryptophan synthase beta subunit. <i>Molecular Microbiology</i> , 1988 , 2, 777-83	4.1	42
311	The metIC operon involved in methionine biosynthesis in <i>Bacillus subtilis</i> is controlled by transcription antitermination. <i>Microbiology (United Kingdom)</i> , 2002 , 148, 507-518	2.9	42
310	<i>Bacillus subtilis</i> , the model Gram-positive bacterium: 20 years of annotation refinement. <i>Microbial Biotechnology</i> , 2018 , 11, 3-17	6.3	41
309	Toward an understanding of the formylation of initiator tRNA methionine in prokaryotic protein synthesis. I. In vitro studies of the 30S and 70S ribosomal-tRNA complex. <i>Biochemistry</i> , 1976 , 15, 1357-62 ^{3.2}		41
308	RuBisCO-like proteins as the enolase enzyme in the methionine salvage pathway: functional and evolutionary relationships between RuBisCO-like proteins and photosynthetic RuBisCO. <i>Journal of Experimental Botany</i> , 2008 , 59, 1543-54	7	39
307	Positive regulation of the pts operon of <i>Escherichia coli</i> : genetic evidence for a signal transduction mechanism. <i>Journal of Bacteriology</i> , 1991 , 173, 727-33	3.5	39
306	Metabolic alterations mediated by 2-ketobutyrate in <i>Escherichia coli</i> K12. <i>Molecular Genetics and Genomics</i> , 1984 , 193, 473-8		39
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