Antoine Danchin

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.

26,286 456 146 77 h-index g-index citations papers 28,968 6.73 516 6.5 avg, IF L-index ext. citations ext. papers

#	Paper	IF	Citations
456	Computation of Antigenicity Predicts SARS-CoV-2 Vaccine Breakthrough Variants <i>Frontiers in Immunology</i> , 2022 , 13, 861050	8.4	O
455	Temporal evolution of master regulator Crp identifies pyrimidines as catabolite modulator factors. <i>Nature Communications</i> , 2021 , 12, 5880	17.4	2
454	A Strong Seasonality Pattern for Covid-19 Incidence Rates Modulated by UV Radiation Levels. <i>Viruses</i> , 2021 , 13,	6.2	3
453	Immunity after COVID-19: Protection or sensitization?. <i>Mathematical Biosciences</i> , 2021 , 331, 108499	3.9	7
452	Three overlooked key functional classes for building up minimal synthetic cells <i>Synthetic Biology</i> , 2021 , 6, ysab010	3.3	Ο
451	Escherichia coli segments its controls on carbon-dependent gene expression into global and specific regulations. <i>Microbial Biotechnology</i> , 2021 , 14, 1084-1106	6.3	1
450	Queuine, a bacterial-derived hypermodified nucleobase, shows protection in in vitro models of neurodegeneration. <i>PLoS ONE</i> , 2021 , 16, e0253216	3.7	1
449	SARS-CoV-2 variants: Relevance for symptom granularity, epidemiology, immunity (herd, vaccines), virus origin and containment?. <i>Environmental Microbiology</i> , 2020 , 22, 2001-2006	5.2	12
448	Interpretable and accurate prediction models for metagenomics data. <i>GigaScience</i> , 2020 , 9,	7.6	16
447	Zinc, an unexpected integrator of metabolism?. <i>Microbial Biotechnology</i> , 2020 , 13, 895-898	6.3	4
446	One-carbon metabolism, folate, zinc and translation. <i>Microbial Biotechnology</i> , 2020 , 13, 899-925	6.3	7
445	Isobiology: A Variational Principle for Exploring Synthetic Life. <i>ChemBioChem</i> , 2020 , 21, 1781-1792	3.8	2
444	Phylogenomics of expanding uncultured environmental Tenericutes provides insights into their pathogenicity and evolutionary relationship with Bacilli. <i>BMC Genomics</i> , 2020 , 21, 408	4.5	19
443	The importance of naturally attenuated SARS-CoV-2in the fight against COVID-19. <i>Environmental Microbiology</i> , 2020 , 22, 1997-2000	5.2	35
442	A New Transmission Route for the Propagation of the SARS-CoV-2 Coronavirus. <i>Biology</i> , 2020 , 10,	4.9	6
441	From Minimal to Minimized Genomes: Functional Design of Microbial Cell Factories 2020 , 177-210		
440	A Path toward SARS-CoV-2 Attenuation: Metabolic Pressure on CTP Synthesis Rules the Virus Evolution. <i>Genome Biology and Evolution</i> , 2020 , 12, 2467-2485	3.9	9

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439	Evaluating the probability of CRISPR-based gene drive contaminating another species. <i>Evolutionary Applications</i> , 2020 , 13, 1888-1905	4.8	9
438	Cytosine drives evolution of SARS-CoV-2. Environmental Microbiology, 2020 , 22, 1977-1985	5.2	13
437	Why Nature Chose Potassium. <i>Journal of Molecular Evolution</i> , 2019 , 87, 271-288	3.1	18
436	Toward unrestricted use of public genomic data. <i>Science</i> , 2019 , 363, 350-352	33.3	25
435	Consent insufficient for data release-Response. <i>Science</i> , 2019 , 364, 446	33.3	4
434	Deciphering global gene expression and regulation strategy in Escherichia coli during carbon limitation. <i>Microbial Biotechnology</i> , 2019 , 12, 360-376	6.3	5
433	Omnipresent Maxwell's demons orchestrate information management in living cells. <i>Microbial Biotechnology</i> , 2019 , 12, 210-242	6.3	17
432	Mutations in the Global Transcription Factor CRP/CAP: Insights from Experimental Evolution and Deep Sequencing. <i>Computational and Structural Biotechnology Journal</i> , 2019 , 17, 730-736	6.8	8
431	Genomic Characterization of a Novel Gut Symbiont From the Hadal Snailfish. <i>Frontiers in Microbiology</i> , 2019 , 10, 2978	5.7	11
430	Hypothesis, analysis and synthesis, it's all Greek to me. <i>ELife</i> , 2019 , 8,	8.9	3
429	Conceptual sequel to biological expeditions at the time of global changes. <i>Environmental Microbiology Reports</i> , 2019 , 11, 38-40	3.7	
428	Revisiting the methionine salvage pathway and its paralogues. <i>Microbial Biotechnology</i> , 2019 , 12, 77-97	6.3	21
427	Unique tRNA gene profile suggests paucity of nucleotide modifications in anticodons of a deep-sea symbiotic Spiroplasma. <i>Nucleic Acids Research</i> , 2018 , 46, 2197-2203	20.1	4
426	Bacillus subtilis, the model Gram-positive bacterium: 20 years of annotation refinement. <i>Microbial Biotechnology</i> , 2018 , 11, 3-17	6.3	41
425	Functional Requirements in the Program and the Cell Chassis for Next-Generation Synthetic Biology 2018 , 81-106		1
424	The Enigmatic Genome of an Obligate Ancient Spiroplasma Symbiont in a Hadal Holothurian. <i>Applied and Environmental Microbiology</i> , 2018 , 84,	4.8	19
423	Multiple Clocks in the Evolution of Living Organisms. <i>Grand Challenges in Biology and Biotechnology</i> , 2018 , 101-118	2.4	
422	No wisdom in the crowd: genome annotation in the era of big data - current status and future prospects. <i>Microbial Biotechnology</i> , 2018 , 11, 588-605	6.3	28

421	Coenzyme B12 synthesis as a baseline to study metabolite contribution of animal microbiota. <i>Microbial Biotechnology</i> , 2017 , 10, 688-701	6.3	20
420	Coping with inevitable accidents in metabolism. <i>Microbial Biotechnology</i> , 2017 , 10, 57-72	6.3	21
419	From chemical metabolism to life: the origin of the genetic coding process. <i>Beilstein Journal of Organic Chemistry</i> , 2017 , 13, 1119-1135	2.5	12
418	The contribution of microbial biotechnology to economic growth and employment creation. <i>Microbial Biotechnology</i> , 2017 , 10, 1137-1144	6.3	21
417	Parallel evolution of non-homologous isofunctional enzymes in methionine biosynthesis. <i>Nature Chemical Biology</i> , 2017 , 13, 858-866	11.7	19
416	Unknown unknowns: essential genes in quest for function. <i>Microbial Biotechnology</i> , 2016 , 9, 530-40	6.3	56
415	Generation of mutation hotspots in ageing bacterial colonies. Scientific Reports, 2016, 6, 2	4.9	155
414	The revisited genome of Pseudomonas putida KT2440 enlightens its value as a robust metabolic chassis. <i>Environmental Microbiology</i> , 2016 , 18, 3403-3424	5.2	194
413	Genomic characterization of symbiotic mycoplasmas from the stomach of deep-sea isopod bathynomus sp. <i>Environmental Microbiology</i> , 2016 , 18, 2646-59	5.2	23
412	From function to structure take the archaeal TRAM. Environmental Microbiology, 2016, 18, 2776-8	5.2	1
411	From dirt to industrial applications: Pseudomonas putida as a Synthetic Biology chassis for hosting harsh biochemical reactions. <i>Current Opinion in Chemical Biology</i> , 2016 , 34, 20-29	9.7	151
410	Reminder to deposit DNA sequences. <i>Science</i> , 2016 , 352, 780	33.3	18
409	Nature or manufacture: What should we fear most?. Comptes Rendus - Biologies, 2016, 339, 329-35	1.4	0
408	The Cellular Chassis as the Basis for New Functionalities: Shortcomings and Requirements. <i>Risk Engineering</i> , 2015 , 155-172	1	O
407	The logic of metabolism. <i>Perspectives in Science</i> , 2015 , 6, 15-26	0.8	6
406	Confidence, tolerance, and allowance in biological engineering: the nuts and bolts of living things. <i>BioEssays</i> , 2015 , 37, 95-102	4.1	16
405	Chemical reactivity drives spatiotemporal organisation of bacterial metabolism. <i>FEMS Microbiology Reviews</i> , 2015 , 39, 96-119	15.1	49
404	Paralogous metabolism: S-alkyl-cysteine degradation in Bacillus subtilis. <i>Environmental Microbiology</i> , 2014 , 16, 101-17	5.2	24

403	The Emergence of the First Cells 2014 , 1-25		3
402	Genomic encyclopedia of bacteria and archaea: sequencing a myriad of type strains. <i>PLoS Biology</i> , 2014 , 12, e1001920	9.7	146
401	The logic of metabolism and its fuzzy consequences. <i>Environmental Microbiology</i> , 2014 , 16, 19-28	5.2	18
400	From essential to persistent genes: a functional approach to constructing synthetic life. <i>Trends in Genetics</i> , 2013 , 29, 273-9	8.5	78
399	An updated metabolic view of the Bacillus subtilis 168 genome. <i>Microbiology (United Kingdom)</i> , 2013 , 159, 757-770	2.9	59
398	Constraints in the Design of the Synthetic Bacterial Chassis. <i>Methods in Microbiology</i> , 2013 , 40, 39-67	2.8	3
397	Linking selenium biogeochemistry to the sulfur-dependent biological detoxification of arsenic. <i>Environmental Microbiology</i> , 2012 , 14, 1612-23	5.2	19
396	3'-5' phosphoadenosine phosphate is an inhibitor of PARP-1 and a potential mediator of the lithium-dependent inhibition of PARP-1 in vivo. <i>Biochemical Journal</i> , 2012 , 443, 485-90	3.8	19
395	Distinct co-evolution patterns of genes associated to DNA polymerase III DnaE and PolC. <i>BMC Genomics</i> , 2012 , 13, 69	4.5	16
394	Biomaterials 2012 , 103-143		
393	Scaling up synthetic biology: Do not forget the chassis. <i>FEBS Letters</i> , 2012 , 586, 2129-37	3.8	57
392	Characterization of NrnA homologs from Mycobacterium tuberculosis and Mycoplasma pneumoniae. <i>Rna</i> , 2012 , 18, 155-65	5.8	34
391	Identification of a novel nanoRNase in Bartonella. <i>Microbiology (United Kingdom)</i> , 2012 , 158, 886-895	2.9	29
390	Synthetic biology's flywheel. <i>EMBO Reports</i> , 2012 , 13, 92	6.5	
389	Open-source genomic analysis of Shiga-toxin-producing E. coli O104:H4. <i>New England Journal of Medicine</i> , 2011 , 365, 718-24	59.2	340
388	Antifragility and Tinkering in Biology (and in Business) Flexibility Provides an Efficient Epigenetic Way to Manage Risk. <i>Genes</i> , 2011 , 2, 998-1016	4.2	27
387	Life's demons: information and order in biology. What subcellular machines gather and process the information necessary to sustain life?. <i>EMBO Reports</i> , 2011 , 12, 495-9	6.5	32
386	Hydrothermally generated aromatic compounds are consumed by bacteria colonizing in Atlantis II Deep of the Red Sea. <i>ISME Journal</i> , 2011 , 5, 1652-9	11.9	30

385	The ten grand challenges of synthetic life. Systems and Synthetic Biology, 2011, 5, 1-9		42
384	Les gfies du dfinon de Maxwell´: est-il possible de construire une usine cellulaire ?. <i>Comptes Rendus Chimie</i> , 2011 , 14, 413-419	2.7	0
383	Cytoplasmic and periplasmic proteomic signatures of exponentially growing cells of the psychrophilic bacterium Pseudoalteromonas haloplanktis TAC125. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 1276-83	4.8	21
382	Life in the cold: a proteomic study of cold-repressed proteins in the antarctic bacterium pseudoalteromonas haloplanktis TAC125. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 3881-3	4.8	64
381	Bacterial niche-specific genome expansion is coupled with highly frequent gene disruptions in deep-sea sediments. <i>PLoS ONE</i> , 2011 , 6, e29149	3.7	10
380	Proteomics of life at low temperatures: trigger factor is the primary chaperone in the Antarctic bacterium Pseudoalteromonas haloplanktis TAC125. <i>Molecular Microbiology</i> , 2010 , 76, 120-32	4.1	81
379	A path from predation to mutualism. <i>Molecular Microbiology</i> , 2010 , 77, 1346-50	4.1	
378	Perfect time or perfect crime?. EMBO Reports, 2010, 11, 74	6.5	1
377	Motivated research. EMBO Reports, 2010, 11, 488	6.5	2
376	PssA is required for alpha-amylase secretion in Antarctic Pseudoalteromonas haloplanktis. <i>Microbiology (United Kingdom)</i> , 2010 , 156, 211-219	2.9	7
375	The Trw type IV secretion system of Bartonella mediates host-specific adhesion to erythrocytes. <i>PLoS Pathogens</i> , 2010 , 6, e1000946	7.6	84
374	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
373	Decrypting the H-NS-dependent regulatory cascade of acid stress resistance in Escherichia coli. <i>BMC Microbiology</i> , 2010 , 10, 273	4.5	47
372	The Role of Information in Evolutionary Genomics of Bacteria 2010 , 81-94		1
371	Structural and functional similarities between a ribulose-1,5-bisphosphate carboxylase/oxygenase (RuBisCO)-like protein from Bacillus subtilis and photosynthetic RuBisCO. <i>Journal of Biological Chemistry</i> , 2009 , 284, 13256-64	5.4	22
370	From a consortium sequence to a unified sequence: the Bacillus subtilis 168 reference genome a decade later. <i>Microbiology (United Kingdom)</i> , 2009 , 155, 1758-1775	2.9	257
369	Organised genome dynamics in the Escherichia coli species results in highly diverse adaptive paths. <i>PLoS Genetics</i> , 2009 , 5, e1000344	6	802
368	Degradation of nanoRNA is performed by multiple redundant RNases in Bacillus subtilis. <i>Nucleic Acids Research</i> , 2009 , 37, 5114-25	20.1	58

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367	Use of a riboswitch-controlled conditional hypomorphic mutation to uncover a role for the essential csrA gene in bacterial autoaggregation. <i>Journal of Biological Chemistry</i> , 2009 , 284, 28738-45	5.4	22
366	Small noncoding RNA GcvB is a novel regulator of acid resistance in Escherichia coli. <i>BMC Genomics</i> , 2009 , 10, 165	4.5	55
365	Cells need safety valves. <i>BioEssays</i> , 2009 , 31, 769-73	4.1	28
364	Natural selection and immortality. <i>Biogerontology</i> , 2009 , 10, 503-16	4.5	28
363	Myopic selection of novel information drives evolution. Current Opinion in Biotechnology, 2009, 20, 504	-811.4	8
362	Information of the chassis and information of the program in synthetic cells. <i>Systems and Synthetic Biology</i> , 2009 , 3, 125-34		22
361	CymR, the master regulator of cysteine metabolism in Staphylococcus aureus, controls host sulphur source utilization and plays a role in biofilm formation. <i>Molecular Microbiology</i> , 2009 , 73, 194-211	4.1	58
360	Nature, artifice and emerging diseases. <i>EMBO Reports</i> , 2009 , 10, 418-9	6.5	1
359	Bacteria as computers making computers. FEMS Microbiology Reviews, 2009, 33, 3-26	15.1	97
358	A challenge to vaccinology: living organisms trap information. <i>Vaccine</i> , 2009 , 27 Suppl 6, G13-6	4.1	
357	Repulsion and metabolic switches in the collective behavior of bacterial colonies. <i>Biophysical Journal</i> , 2009 , 97, 688-98	2.9	11
356	A phylogenetic view of bacterial ribonucleases. <i>Progress in Molecular Biology and Translational Science</i> , 2009 , 85, 1-41	4	28
355	Synthetic biology: discovering new worlds and new words. <i>EMBO Reports</i> , 2008 , 9, 822-7	6.5	126
354	Regulatory role of UvrY in adaptation of Photorhabdus luminescens growth inside the insect. <i>Environmental Microbiology</i> , 2008 , 10, 1118-34	5.2	24
353	Genomics of an extreme psychrophile, Psychromonas ingrahamii. BMC Genomics, 2008, 9, 210	4.5	101
352	Persistence drives gene clustering in bacterial genomes. <i>BMC Genomics</i> , 2008 , 9, 4	4.5	79
351	Spx mediates oxidative stress regulation of the methionine sulfoxide reductases operon in Bacillus subtilis. <i>BMC Microbiology</i> , 2008 , 8, 128	4.5	33
350	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

349	The CymR regulator in complex with the enzyme CysK controls cysteine metabolism in Bacillus subtilis. <i>Journal of Biological Chemistry</i> , 2008 , 283, 35551-60	5.4	67
348	A variable gene in a conserved region of the Helicobacter pylori genome: isotopic gene replacement or rapid evolution?. <i>DNA Research</i> , 2008 , 15, 163-8	4.5	3
347	Cinnamic acid, an autoinducer of its own biosynthesis, is processed via Hca enzymes in Photorhabdus luminescens. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 1717-25	4.8	24
346	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
345	Evolutionary Potential of Rubisco-Like Protein in Bacillus subtilis: Interaction with Transition-State Analog of Rubisco 2008 , 875-879		
344	Annotating bacterial genomes 2008 , 165-190		1
343	The extant core bacterial proteome is an archive of the origin of life. <i>Proteomics</i> , 2007 , 7, 875-89	4.8	44
342	The HcaR regulatory protein of Photorhabdus luminescens affects the production of proteins involved in oxidative stress and toxemia. <i>Proteomics</i> , 2007 , 7, 4499-510	4.8	16
341	Hon-yaku: a biology-driven Bayesian methodology for identifying translation initiation sites in prokaryotes. <i>BMC Bioinformatics</i> , 2007 , 8, 47	3.6	18
340	Conversion of methionine to cysteine in Bacillus subtilis and its regulation. <i>Journal of Bacteriology</i> , 2007 , 189, 187-97	3.5	73
339	A tale of two oxidation states: bacterial colonization of arsenic-rich environments. <i>PLoS Genetics</i> , 2007 , 3, e53	6	148
338	YtqI from Bacillus subtilis has both oligoribonuclease and pAp-phosphatase activity. <i>Nucleic Acids Research</i> , 2007 , 35, 4552-61	20.1	76
337	Potent and selective inhibitors of Staphylococcus epidermidis tryptophanyl-tRNA synthetase. <i>Journal of Antimicrobial Chemotherapy</i> , 2007 , 60, 502-9	5.1	19
336	Visualizing the proteome of Escherichia coli: an efficient and versatile method for labeling chromosomal coding DNA sequences (CDSs) with fluorescent protein genes. <i>Nucleic Acids Research</i> , 2007 , 35, e37	20.1	10
335	Archives or Palimpsests? Bacterial Genomes Unveil a Scenario for the Origin of Life. <i>Biological Theory</i> , 2007 , 2, 52-61	1.7	14
334	A parasite vector-host epidemic model for TSE propagation. <i>Medical Science Monitor</i> , 2007 , 13, BR59-66	5 3.2	1
333	Conserved genes in a path from commensalism to pathogenicity: comparative phylogenetic profiles of Staphylococcus epidermidis RP62A and ATCC12228. <i>BMC Genomics</i> , 2006 , 7, 112	4.5	25
332	Structure-based discovery of inhibitors of the YycG histidine kinase: new chemical leads to combat Staphylococcus epidermidis infections. <i>BMC Microbiology</i> , 2006 , 6, 96	4.5	83

331	Persistent biases in the amino acid composition of prokaryotic proteins. <i>BioEssays</i> , 2006 , 28, 726-38	4.1	21
330	Re: request from the International Advisory Committee to DDBJ/EMBL/GenBank. <i>Journal of Medical Virology</i> , 2006 , 78, 995	19.7	
329	Oligoribonuclease is a common downstream target of lithium-induced pAp accumulation in Escherichia coli and human cells. <i>Nucleic Acids Research</i> , 2006 , 34, 2364-73	20.1	52
328	Pleiotropic role of quorum-sensing autoinducer 2 in Photorhabdus luminescens. <i>Applied and Environmental Microbiology</i> , 2006 , 72, 6439-51	4.8	53
327	Codon usage domains over bacterial chromosomes. <i>PLoS Computational Biology</i> , 2006 , 2, e37	5	36
326	Global control of cysteine metabolism by CymR in Bacillus subtilis. <i>Journal of Bacteriology</i> , 2006 , 188, 2184-97	3.5	84
325	Identification of genes and proteins involved in the pleiotropic response to arsenic stress in Caenibacter arsenoxydans, a metalloresistant beta-proteobacterium with an unsequenced genome. <i>Biochimie</i> , 2006 , 88, 595-606	4.6	37
324	Proteome analysis of the phenotypic variation process in Photorhabdus luminescens. <i>Proteomics</i> , 2006 , 6, 2705-25	4.8	28
323	Beneficial biological warfare. <i>EMBO Reports</i> , 2006 , 7, 767-767	6.5	78
322	Proteomic identification of a two-component regulatory system in Pseudoalteromonas haloplanktis TAC125. <i>Extremophiles</i> , 2006 , 10, 483-91	3	19
322		4.6	19
	haloplanktis TAC125. Extremophiles, 2006 , 10, 483-91		
321	haloplanktis TAC125. Extremophiles, 2006 , 10, 483-91 The PatB protein of Bacillus subtilis is a C-S-lyase. Biochimie, 2005 , 87, 231-8 3-phenylpropionate catabolism and the Escherichia coli oxidative stress response. Research in		44
321	haloplanktis TAC125. Extremophiles, 2006, 10, 483-91 The PatB protein of Bacillus subtilis is a C-S-lyase. Biochimie, 2005, 87, 231-8 3-phenylpropionate catabolism and the Escherichia coli oxidative stress response. Research in Microbiology, 2005, 156, 312-21 Was photosynthetic RuBisCO recruited by acquisitive evolution from RuBisCO-like proteins	4.6	44 20 74
321 320 319	haloplanktis TAC125. Extremophiles, 2006, 10, 483-91 The PatB protein of Bacillus subtilis is a C-S-lyase. Biochimie, 2005, 87, 231-8 3-phenylpropionate catabolism and the Escherichia coli oxidative stress response. Research in Microbiology, 2005, 156, 312-21 Was photosynthetic RuBisCO recruited by acquisitive evolution from RuBisCO-like proteins involved in sulfur metabolism?. Research in Microbiology, 2005, 156, 611-8 Conserved transcription factor binding sites of cancer markers derived from primary lung	4.6	44 20 74
321 320 319 318	The PatB protein of Bacillus subtilis is a C-S-lyase. <i>Biochimie</i> , 2005 , 87, 231-8 3-phenylpropionate catabolism and the Escherichia coli oxidative stress response. <i>Research in Microbiology</i> , 2005 , 156, 312-21 Was photosynthetic RuBisCO recruited by acquisitive evolution from RuBisCO-like proteins involved in sulfur metabolism?. <i>Research in Microbiology</i> , 2005 , 156, 611-8 Conserved transcription factor binding sites of cancer markers derived from primary lung adenocarcinoma microarrays. <i>Nucleic Acids Research</i> , 2005 , 33, 409-21 Molecular diagnosis of human cancer type by gene expression profiles and independent	4.6 4 20.1	44207425
321 320 319 318 317	The PatB protein of Bacillus subtilis is a C-S-lyase. <i>Biochimie</i> , 2005, 87, 231-8 3-phenylpropionate catabolism and the Escherichia coli oxidative stress response. <i>Research in Microbiology</i> , 2005, 156, 312-21 Was photosynthetic RuBisCO recruited by acquisitive evolution from RuBisCO-like proteins involved in sulfur metabolism?. <i>Research in Microbiology</i> , 2005, 156, 611-8 Conserved transcription factor binding sites of cancer markers derived from primary lung adenocarcinoma microarrays. <i>Nucleic Acids Research</i> , 2005, 33, 409-21 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 Genomes are covered with ubiquitous 11 bp periodic patterns, the "class A flexible patterns". <i>BMC</i>	4.6 4 20.1 5.3	4420742548

313	Testing the hypothesis of a recombinant origin of the SARS-associated coronavirus. <i>Archives of Virology</i> , 2005 , 150, 1-20	2.6	45
312	Universal biases in protein composition of model prokaryotes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 60, 27-35	4.2	27
311	Regulation of the Bacillus subtilis ytml operon, involved in sulfur metabolism. <i>Journal of Bacteriology</i> , 2005 , 187, 6019-30	3.5	24
310	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
309	Coping with cold: the genome of the versatile marine Antarctica bacterium Pseudoalteromonas haloplanktis TAC125. <i>Genome Research</i> , 2005 , 15, 1325-35	9.7	309
308	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
307	How essential are nonessential genes?. <i>Molecular Biology and Evolution</i> , 2005 , 22, 2147-56	8.3	120
306	Genome Diversity: A Grammar of Microbial Genomes. <i>Complexus</i> , 2004 , 2, 61-70		2
305	GadE (YhiE): a novel activator involved in the response to acid environment in Escherichia coli. <i>Microbiology (United Kingdom)</i> , 2004 , 150, 61-72	2.9	141
304	AstR-AstS, a new two-component signal transduction system, mediates swarming, adaptation to stationary phase and phenotypic variation in Photorhabdus luminescens. <i>Microbiology (United Kingdom)</i> , 2004 , 150, 897-910	2.9	25
303	Three different systems participate in L-cystine uptake in Bacillus subtilis. <i>Journal of Bacteriology</i> , 2004 , 186, 4875-84	3.5	78
302	The PhoP-PhoQ two-component regulatory system of Photorhabdus luminescens is essential for virulence in insects. <i>Journal of Bacteriology</i> , 2004 , 186, 1270-9	3.5	89
301	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
300	Bacterial variations on the methionine salvage pathway. <i>BMC Microbiology</i> , 2004 , 4, 9	4.5	126
299	Classification between normal and tumor tissues based on the pair-wise gene expression ratio. <i>BMC Cancer</i> , 2004 , 4, 72	4.8	20
298	Cytosine methylation is not the major factor inducing CpG dinucleotide deficiency in bacterial genomes. <i>Journal of Molecular Evolution</i> , 2004 , 58, 692-700	3.1	10
297	The bag or the spindle: the cell factory at the time of systems' biology. <i>Microbial Cell Factories</i> , 2004 , 3, 13	6.4	7
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