

Eduardo Rocha

List of Publications by Year in descending order

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Version: 2024-02-01

179
papers

24,511
citations

10986

71
h-index

8866

145
g-index

220
all docs

220
docs citations

220
times ranked

21002
citing authors

#	ARTICLE	IF	CITATIONS
1	To catch a hijacker: abundance, evolution and genetic diversity of P4-like bacteriophage satellites. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, 20200475.	4.0	21
2	Microbial defenses against mobile genetic elements and viruses: Who defends whom from what?. <i>PLoS Biology</i> , 2022, 20, e3001514.	5.6	83
3	Phages and their satellites encode hotspots of antiviral systems. <i>Cell Host and Microbe</i> , 2022, 30, 740-753.e5.	11.0	129
4	IntegronFinder 2.0: Identification and Analysis of Integrons across Bacteria, with a Focus on Antibiotic Resistance in <i>Klebsiella</i> . <i>Microorganisms</i> , 2022, 10, 700.	3.6	61
5	Evolution of Plasmid Mobility: Origin and Fate of Conjugative and Nonconjugative Plasmids. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	44
6	Phage-host coevolution in natural populations. <i>Nature Microbiology</i> , 2022, 7, 1075-1086.	13.3	58
7	Causes and Consequences of Bacteriophage Diversification via Genetic Exchanges across Lifestyles and Bacterial Taxa. <i>Molecular Biology and Evolution</i> , 2021, 38, 2497-2512.	8.9	48
8	Bacteria have numerous distinctive groups of phage-plasmids with conserved phage and variable plasmid gene repertoires. <i>Nucleic Acids Research</i> , 2021, 49, 2655-2673.	14.5	91
9	Nutrient conditions are primary drivers of bacterial capsule maintenance in <i>Klebsiella</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20202876.	2.6	21
10	Interplay between the cell envelope and mobile genetic elements shapes gene flow in populations of the nosocomial pathogen <i>Klebsiella pneumoniae</i> . <i>PLoS Biology</i> , 2021, 19, e3001276.	5.6	44
11	Human commensal gut Proteobacteria withstand type VI secretion attacks through immunity protein-independent mechanisms. <i>Nature Communications</i> , 2021, 12, 5751.	12.8	34
12	The impact of genetic diversity on gene essentiality within the <i>Escherichia coli</i> species. <i>Nature Microbiology</i> , 2021, 6, 301-312.	13.3	76
13	PanACoTA: a modular tool for massive microbial comparative genomics. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqaa106.	3.2	26
14	Evolution of ColE1-like plasmids across β -Proteobacteria: From bacteriocin production to antimicrobial resistance. <i>PLoS Genetics</i> , 2021, 17, e1009919.	3.5	8
15	Atypical organizations and epistatic interactions of CRISPRs and cas clusters in genomes and their mobile genetic elements. <i>Nucleic Acids Research</i> , 2020, 48, 748-760.	14.5	32
16	Unlinked rRNA genes are widespread among bacteria and archaea. <i>ISME Journal</i> , 2020, 14, 597-608.	9.8	30
17	Pathways for horizontal gene transfer in bacteria revealed by a global map of their plasmids. <i>Nature Communications</i> , 2020, 11, 3602.	12.8	211
18	Modular prophage interactions driven by capsule serotype select for capsule loss under phage predation. <i>ISME Journal</i> , 2020, 14, 2980-2996.	9.8	43

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19	Phylogenetic background and habitat drive the genetic diversification of Escherichia coli. PLoS Genetics, 2020, 16, e1008866.	3.5	131
20	A synthesis of bacterial and archaeal phenotypic trait data. Scientific Data, 2020, 7, 170.	5.3	59
21	PPanGGOLiN: Depicting microbial diversity via a partitioned pangenome graph. PLoS Computational Biology, 2020, 16, e1007732.	3.2	102
22	Macromolecular crowding links ribosomal protein gene dosage to growth rate in Vibrio cholerae. BMC Biology, 2020, 18, 43.	3.8	10
23	Community diversity and habitat structure shape the repertoire of extracellular proteins in bacteria. Nature Communications, 2020, 11, 758.	12.8	26
24	The Evolution of Protein Secretion Systems by Co-option and Tinkering of Cellular Machineries. Trends in Microbiology, 2020, 28, 372-386.	7.7	43
25	Intracellular Positioning Systems Limit the Entropic Eviction of Secondary Replicons Toward the Nucleoid Edges in Bacterial Cells. Journal of Molecular Biology, 2020, 432, 745-761.	4.2	21
26	The major subunit of widespread competence pili exhibits a novel and conserved type IV pilin fold. Journal of Biological Chemistry, 2020, 295, 6594-6604.	3.4	19
27	Identifying Conjugative Plasmids and Integrative Conjugative Elements with CONJscan. Methods in Molecular Biology, 2020, 2075, 265-283.	0.9	51
28	PPanGGOLiN: Depicting microbial diversity via a partitioned pangenome graph. , 2020, 16, e1007732.		0
29	PPanGGOLiN: Depicting microbial diversity via a partitioned pangenome graph. , 2020, 16, e1007732.		0
30	PPanGGOLiN: Depicting microbial diversity via a partitioned pangenome graph. , 2020, 16, e1007732.		0
31	PPanGGOLiN: Depicting microbial diversity via a partitioned pangenome graph. , 2020, 16, e1007732.		0
32	Phylogenetic background and habitat drive the genetic diversification of Escherichia coli. , 2020, 16, e1008866.		0
33	Phylogenetic background and habitat drive the genetic diversification of Escherichia coli. , 2020, 16, e1008866.		0
34	Phylogenetic background and habitat drive the genetic diversification of Escherichia coli. , 2020, 16, e1008866.		0
35	Phylogenetic background and habitat drive the genetic diversification of Escherichia coli. , 2020, 16, e1008866.		0
36	A simple, reproducible and cost-effective procedure to analyse gut phageome: from phage isolation to bioinformatic approach. Scientific Reports, 2019, 9, 11331.	3.3	30

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37	Diversification of the type IV filament superfamily into machines for adhesion, protein secretion, DNA uptake, and motility. <i>PLoS Biology</i> , 2019, 17, e3000390.	5.6	121
38	Bacteriophages benefit from generalized transduction. <i>PLoS Pathogens</i> , 2019, 15, e1007888.	4.7	69
39	Experimental Evolution as a Tool to Investigate Natural Processes and Molecular Functions. <i>Trends in Microbiology</i> , 2019, 27, 623-634.	7.7	32
40	A matter of background: DNA repair pathways as a possible cause for the sparse distribution of CRISPR-Cas systems in bacteria. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180088.	4.0	30
41	Environmental structure drives resistance to phages and antibiotics during phage therapy and to invading lysogens during colonisation. <i>Scientific Reports</i> , 2019, 9, 3149.	3.3	36
42	Ultrafast search of all deposited bacterial and viral genomic data. <i>Nature Biotechnology</i> , 2019, 37, 152-159.	17.5	123
43	Neutral Theory, Microbial Practice: Challenges in Bacterial Population Genetics. <i>Molecular Biology and Evolution</i> , 2018, 35, 1338-1347.	8.9	93
44	<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
45	Genetic exchanges are more frequent in bacteria encoding capsules. <i>PLoS Genetics</i> , 2018, 14, e1007862.	3.5	31
46	HflXr, a homolog of a ribosome-splitting factor, mediates antibiotic resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 13359-13364.	7.1	41
47	CRISPRCasFinder, an update of CRISPRFinder, includes a portable version, enhanced performance and integrates search for Cas proteins. <i>Nucleic Acids Research</i> , 2018, 46, W246-W251.	14.5	985
48	Host Range and Genetic Plasticity Explain the Coexistence of Integrative and Extrachromosomal Mobile Genetic Elements. <i>Molecular Biology and Evolution</i> , 2018, 35, 2230-2239.	8.9	57
49	Parallels between experimental and natural evolution of legume symbionts. <i>Nature Communications</i> , 2018, 9, 2264.	12.8	11
50	Metabolic diversity of the emerging pathogenic lineages of <i>Klebsiella pneumoniae</i> . <i>Environmental Microbiology</i> , 2017, 19, 1881-1898.	3.8	79
51	Differences in Integron Cassette Excision Dynamics Shape a Trade-Off between Evolvability and Genetic Capacitance. <i>MBio</i> , 2017, 8, .	4.1	27
52	Embracing the enemy: the diversification of microbial gene repertoires by phage-mediated horizontal gene transfer. <i>Current Opinion in Microbiology</i> , 2017, 38, 66-73.	5.1	238
53	Evolutionary dynamics and genomic features of the <i>Elizabethkingia anophelis</i> 2015 to 2016 Wisconsin outbreak strain. <i>Nature Communications</i> , 2017, 8, 15483.	12.8	132
54	Recruitment of a Lineage-Specific Virulence Regulatory Pathway Promotes Intracellular Infection by a Plant Pathogen Experimentally Evolved into a Legume Symbiont. <i>Molecular Biology and Evolution</i> , 2017, 34, 2503-2521.	8.9	40

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55	Metagenomic assessment of the interplay between the environment and the genetic diversification of <i>Acinetobacter</i> . <i>Environmental Microbiology</i> , 2017, 19, 5010-5024.	3.8	24
56	The chromosomal organization of horizontal gene transfer in bacteria. <i>Nature Communications</i> , 2017, 8, 841.	12.8	184
57	Inhibition of NHEJ repair by type II-A CRISPR-Cas systems in bacteria. <i>Nature Communications</i> , 2017, 8, 2094.	12.8	77
58	Identification of Protein Secretion Systems in Bacterial Genomes Using MacSyFinder. <i>Methods in Molecular Biology</i> , 2017, 1615, 1-21.	0.9	92
59	Whole genome-based population biology and epidemiological surveillance of <i>Listeria monocytogenes</i> . <i>Nature Microbiology</i> , 2017, 2, 16185.	13.3	562
60	Experimental evolution of rhizobia may lead to either extra- or intracellular symbiotic adaptation depending on the selection regime. <i>Molecular Ecology</i> , 2017, 26, 1818-1831.	3.9	21
61	Integrative and conjugative elements and their hosts: composition, distribution and organization. <i>Nucleic Acids Research</i> , 2017, 45, 8943-8956.	14.5	129
62	A widespread family of polymorphic toxins encoded by temperate phages. <i>BMC Biology</i> , 2017, 15, 75.	3.8	33
63	Comparative genomic analysis of <i>Acinetobacter</i> strains isolated from murine colonic crypts. <i>BMC Genomics</i> , 2017, 18, 525.	2.8	14
64	Abundance and co-occurrence of extracellular capsules increase environmental breadth: Implications for the emergence of pathogens. <i>PLoS Pathogens</i> , 2017, 13, e1006525.	4.7	62
65	Using Sex to Cure the Genome. <i>PLoS Biology</i> , 2016, 14, e1002417.	5.6	16
66	Identification of protein secretion systems in bacterial genomes. <i>Scientific Reports</i> , 2016, 6, 23080.	3.3	315
67	Regulation of genetic flux between bacteria by restriction-modification systems. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 5658-5663.	7.1	161
68	Identification and analysis of integrons and cassette arrays in bacterial genomes. <i>Nucleic Acids Research</i> , 2016, 44, 4539-4550.	14.5	235
69	Genomic epidemiology and global diversity of the emerging bacterial pathogen <i>Elizabethkingia anophelis</i> . <i>Scientific Reports</i> , 2016, 6, 30379.	3.3	65
70	The Impact of Selection, Gene Conversion, and Biased Sampling on the Assessment of Microbial Demography. <i>Molecular Biology and Evolution</i> , 2016, 33, 1711-1725.	8.9	62
71	Genetic and life-history traits associated with the distribution of prophages in bacteria. <i>ISME Journal</i> , 2016, 10, 2744-2754.	9.8	314
72	Uncovering <i>Listeria monocytogenes</i> hypervirulence by harnessing its biodiversity. <i>Nature Genetics</i> , 2016, 48, 308-313.	21.4	541

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73	Coevolution of the Organization and Structure of Prokaryotic Genomes. Cold Spring Harbor Perspectives in Biology, 2016, 8, a018168.	5.5	55
74	Eco-Evolutionary Dynamics of Episomes among Ecologically Cohesive Bacterial Populations. MBio, 2015, 6, e00552-15.	4.1	25
75	Insights on the Emergence of Mycobacterium tuberculosis from the Analysis of Mycobacterium kansasii. Genome Biology and Evolution, 2015, 7, 856-870.	2.5	79
76	Common Cell Shape Evolution of Two Nasopharyngeal Pathogens. PLoS Genetics, 2015, 11, e1005338.	3.5	26
77	MacSyFinder: A Program to Mine Genomes for Molecular Systems with an Application to CRISPR-Cas Systems. PLoS ONE, 2014, 9, e110726.	2.5	315
78	Pervasive domestication of defective prophages by bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 12127-12132.	7.1	304
79	TLR9 Activation Is Triggered by the Excess of Stimulatory versus Inhibitory Motifs Present in Trypanosomatidae DNA. PLoS Neglected Tropical Diseases, 2014, 8, e3308.	3.0	8
80	A PNPase Dependent CRISPR System in Listeria. PLoS Genetics, 2014, 10, e1004065.	3.5	76
81	Transient Hypermutagenesis Accelerates the Evolution of Legume Endosymbionts following Horizontal Gene Transfer. PLoS Biology, 2014, 12, e1001942.	5.6	50
82	The Genomic Diversification of the Whole Acinetobacter Genus: Origins, Mechanisms, and Consequences. Genome Biology and Evolution, 2014, 6, 2866-2882.	2.5	269
83	The interplay of restriction-modification systems with mobile genetic elements and their prokaryotic hosts. Nucleic Acids Research, 2014, 42, 10618-10631.	14.5	246
84	The chromosomal accommodation and domestication of mobile genetic elements. Current Opinion in Microbiology, 2014, 22, 22-29.	5.1	73
85	Key components of the eight classes of type IV secretion systems involved in bacterial conjugation or protein secretion. Nucleic Acids Research, 2014, 42, 5715-5727.	14.5	200
86	Natural Genome Diversity of AI-2 Quorum Sensing in Escherichia coli: Conserved Signal Production but Labile Signal Reception. Genome Biology and Evolution, 2013, 5, 16-30.	2.5	26
87	With a Little Help from Prokaryotes. Science, 2013, 339, 1154-1155.	12.6	13
88	Manipulating or Superseding Host Recombination Functions: A Dilemma That Shapes Phage Evolvability. PLoS Genetics, 2013, 9, e1003825.	3.5	41
89	Natural Selection for Operons Depends on Genome Size. Genome Biology and Evolution, 2013, 5, 2242-2254.	2.5	19
90	The Adaptation of Temperate Bacteriophages to Their Host Genomes. Molecular Biology and Evolution, 2013, 30, 737-751.	8.9	196

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91	Evolution of Conjugation and Type IV Secretion Systems. <i>Molecular Biology and Evolution</i> , 2013, 30, 315-331.	8.9	193
92	Immune Subversion and Quorum-Sensing Shape the Variation in Infectious Dose among Bacterial Pathogens. <i>PLoS Pathogens</i> , 2012, 8, e1002503.	4.7	36
93	The Non-Flagellar Type III Secretion System Evolved from the Bacterial Flagellum and Diversified into Host-Cell Adapted Systems. <i>PLoS Genetics</i> , 2012, 8, e1002983.	3.5	254
94	After the bottleneck: Genome-wide diversification of the <i>Mycobacterium tuberculosis</i> complex by mutation, recombination, and natural selection. <i>Genome Research</i> , 2012, 22, 721-734.	5.5	141
95	A Single Amino Acid Substitution Changes the Self-Assembly Status of a Type IV Piliation Secretin. <i>Journal of Bacteriology</i> , 2012, 194, 4951-4958.	2.2	14
96	Characterization of Novel Phages Isolated in Coagulase-Negative Staphylococci Reveals Evolutionary Relationships with <i>Staphylococcus aureus</i> Phages. <i>Journal of Bacteriology</i> , 2012, 194, 5829-5839.	2.2	50
97	Antibiotic resistance plasmids spread among natural isolates of <i>Escherichia coli</i> in spite of CRISPR elements. <i>Microbiology (United Kingdom)</i> , 2012, 158, 2997-3004.	1.8	67
98	Rapid Evolution of the Sequences and Gene Repertoires of Secreted Proteins in Bacteria. <i>PLoS ONE</i> , 2012, 7, e49403.	2.5	37
99	CRISPR Distribution within the <i>Escherichia coli</i> Species Is Not Suggestive of Immunity-Associated Diversifying Selection. <i>Journal of Bacteriology</i> , 2011, 193, 2460-2467.	2.2	139
100	What traits are carried on mobile genetic elements, and why?. <i>Heredity</i> , 2011, 106, 1-10.	2.6	266
101	Function-Specific Accelerations in Rates of Sequence Evolution Suggest Predictable Epistatic Responses to Reduced Effective Population Size. <i>Molecular Biology and Evolution</i> , 2011, 28, 2339-2349.	8.9	11
102	Investment in rapid growth shapes the evolutionary rates of essential proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 20030-20035.	7.1	7
103	Complete Genome Sequence of the Fish Pathogen <i>Flavobacterium branchiophilum</i> . <i>Applied and Environmental Microbiology</i> , 2011, 77, 7656-7662.	3.1	64
104	Bacterial cooperation controlled by mobile elements: kin selection and infectivity are part of the same process. <i>Heredity</i> , 2011, 107, 279-281.	2.6	11
105	The Repertoire of ICE in Prokaryotes Underscores the Unity, Diversity, and Ubiquity of Conjugation. <i>PLoS Genetics</i> , 2011, 7, e1002222.	3.5	329
106	Horizontal Transfer, Not Duplication, Drives the Expansion of Protein Families in Prokaryotes. <i>PLoS Genetics</i> , 2011, 7, e1001284.	3.5	426
107	Mutational Patterns Cannot Explain Genome Composition: Are There Any Neutral Sites in the Genomes of Bacteria?. <i>PLoS Genetics</i> , 2010, 6, e1001104.	3.5	92
108	The Systemic Imprint of Growth and Its Uses in Ecological (Meta)Genomics. <i>PLoS Genetics</i> , 2010, 6, e1000808.	3.5	286

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109	The Small, Slow and Specialized CRISPR and Anti-CRISPR of Escherichia and Salmonella. PLoS ONE, 2010, 5, e11126.	2.5	198
110	Mobility of Plasmids. Microbiology and Molecular Biology Reviews, 2010, 74, 434-452.	6.6	919
111	No evidence for elemental-based streamlining of prokaryotic genomes. Trends in Ecology and Evolution, 2010, 25, 319-320.	8.7	25
112	Genome-wide analysis of DNA repeats in Burkholderia cenocepacia J2315 identifies a novel adhesin-like gene unique to epidemic-associated strains of the ET-12 lineage. Microbiology (United Kingdom), 2010, 156, 1084-1096.	1.8	32
113	A Module Located at a Chromosomal Integration Hot Spot Is Responsible for the Multidrug Resistance of a Reference Strain from <i>Escherichia coli</i> Clonal Group A. Antimicrobial Agents and Chemotherapy, 2009, 53, 2283-2288.	3.2	33
114	Organised Genome Dynamics in the Escherichia coli Species Results in Highly Diverse Adaptive Paths. PLoS Genetics, 2009, 5, e1000344.	3.5	1,005
115	The Genome of <i>Burkholderia cenocepacia</i> J2315, an Epidemic Pathogen of Cystic Fibrosis Patients. Journal of Bacteriology, 2009, 191, 261-277.	2.2	329
116	Horizontal Gene Transfer of the Secretome Drives the Evolution of Bacterial Cooperation and Virulence. Current Biology, 2009, 19, 1683-1691.	3.9	217
117	Genesis, effects and fates of repeats in prokaryotic genomes. FEMS Microbiology Reviews, 2009, 33, 539-571.	8.6	137
118	Microbial DNA metabolism, genome dynamics and human disease. FEMS Microbiology Reviews, 2009, 33, 451-452.	8.6	0
119	The Temporal Dynamics of Slightly Deleterious Mutations in Escherichia coli and Shigella spp.. Molecular Biology and Evolution, 2009, 26, 345-355.	8.9	67
120	Alternative to Homo-oligomerisation: The Creation of Local Symmetry in Proteins by Internal Amplification. Journal of Molecular Biology, 2009, 394, 522-534.	4.2	19
121	A Novel Heuristic for Local Multiple Alignment of Interspersed DNA Repeats. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 180-189.	3.0	14
122	Protein evolution driven by symmetric structural repeats. BMC Bioinformatics, 2008, 9, .	2.6	1
123	Persistence drives gene clustering in bacterial genomes. BMC Genomics, 2008, 9, 4.	2.8	104
124	The impact of the neisserial DNA uptake sequences on genome evolution and stability. Genome Biology, 2008, 9, R60.	9.6	73
125	Evolutionary patterns in prokaryotic genomes. Current Opinion in Microbiology, 2008, 11, 454-460.	5.1	43
126	The Organization of the Bacterial Genome. Annual Review of Genetics, 2008, 42, 211-233.	7.6	266

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127	From GC skews to wavelets: A gentle guide to the analysis of compositional asymmetries in genomic data. <i>Biochimie</i> , 2008, 90, 648-659.	2.6	34
128	Swelife: a detector of internal repeats in sequences and structures. <i>Bioinformatics</i> , 2008, 24, 1536-1537.	4.1	53
129	An Assessment of the Impacts of Molecular Oxygen on the Evolution of Proteomes. <i>Molecular Biology and Evolution</i> , 2008, 25, 1931-1942.	8.9	37
130	Reconstructing the ancestor of <i>Mycobacterium leprae</i> : The dynamics of gene loss and genome reduction. <i>Genome Research</i> , 2007, 17, 1178-1185.	5.5	110
131	Repseek, a tool to retrieve approximate repeats from large DNA sequences. <i>Bioinformatics</i> , 2007, 23, 119-121.	4.1	69
132	Causes for the intriguing presence of tRNAs in phages. <i>Genome Research</i> , 2007, 17, 1486-1495.	5.5	312
133	Causes of Insertion Sequences Abundance in Prokaryotic Genomes. <i>Molecular Biology and Evolution</i> , 2007, 24, 969-981.	8.9	202
134	Editorial: microbial genomics. <i>Research in Microbiology</i> , 2007, 158, 721-723.	2.1	0
135	Erosion of interaction networks in reduced and degraded genomes. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2007, 308B, 97-103.	1.3	11
136	Intrastrain Heterogeneity of the <i>mgpB</i> Gene in <i>Mycoplasma genitalium</i> Is Extensive In Vitro and In Vivo and Suggests that Variation Is Generated via Recombination with Repetitive Chromosomal Sequences. <i>Infection and Immunity</i> , 2006, 74, 3715-3726.	2.2	68
137	Replication-associated gene dosage effects shape the genomes of fast-growing bacteria but only for transcription and translation genes. <i>Molecular Microbiology</i> , 2006, 59, 1506-1518.	2.5	182
138	Causes of trends in amino-acid gain and loss. <i>Nature</i> , 2006, 442, E11-E12.	27.8	47
139	Comparisons of dN/dS are time dependent for closely related bacterial genomes. <i>Journal of Theoretical Biology</i> , 2006, 239, 226-235.	1.7	400
140	The quest for the universals of protein evolution. <i>Trends in Genetics</i> , 2006, 22, 412-416.	6.7	76
141	Inference and Analysis of the Relative Stability of Bacterial Chromosomes. <i>Molecular Biology and Evolution</i> , 2006, 23, 513-522.	8.9	99
142	Highly Variable Rates of Genome Rearrangements between Hemiascomycetous Yeast Lineages. <i>PLoS Genetics</i> , 2006, 2, e32.	3.5	94
143	An Integrative Method for Accurate Comparative Genome Mapping. <i>PLoS Computational Biology</i> , 2006, 2, e75.	3.2	25
144	Similar compositional biases are caused by very different mutational effects. <i>Genome Research</i> , 2006, 16, 1537-1547.	5.5	87

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145	The unusually large Plasmodium telomerase reverse-transcriptase localizes in a discrete compartment associated with the nucleolus. <i>Nucleic Acids Research</i> , 2005, 33, 1111-1122.	14.5	65
146	Comparative and Evolutionary Analysis of the Bacterial Homologous Recombination Systems. <i>PLoS Genetics</i> , 2005, 1, e15.	3.5	275
147	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
148	How Essential Are Nonessential Genes?. <i>Molecular Biology and Evolution</i> , 2005, 22, 2147-2156.	8.9	135
149	The replication-related organization of bacterial genomes. <i>Microbiology (United Kingdom)</i> , 2004, 150, 1609-1627.	1.8	235
150	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
151	Cytosine Methylation Is Not the Major Factor Inducing CpG Dinucleotide Deficiency in Bacterial Genomes. <i>Journal of Molecular Evolution</i> , 2004, 58, 692-700.	1.8	10
152	Codon usage bias from tRNA's point of view: Redundancy, specialization, and efficient decoding for translation optimization. <i>Genome Research</i> , 2004, 14, 2279-2286.	5.5	339
153	Order and disorder in bacterial genomes. <i>Current Opinion in Microbiology</i> , 2004, 7, 519-527.	5.1	92
154	DNA repeats lead to the accelerated loss of gene order in bacteria. <i>Trends in Genetics</i> , 2003, 19, 600-603.	6.7	64
155	A strand-specific model for chromosome segregation in bacteria. <i>Molecular Microbiology</i> , 2003, 49, 895-903.	2.5	44
156	Essentiality, not expressiveness, drives gene-strand bias in bacteria. <i>Nature Genetics</i> , 2003, 34, 377-378.	21.4	198
157	Gene essentiality determines chromosome organisation in bacteria. <i>Nucleic Acids Research</i> , 2003, 31, 6570-6577.	14.5	145
158	An Appraisal of the Potential for Illegitimate Recombination in Bacterial Genomes and Its Consequences: From Duplications to Genome Reduction. <i>Genome Research</i> , 2003, 13, 1123-1132.	5.5	65
159	Associations Between Inverted Repeats and the Structural Evolution of Bacterial Genomes. <i>Genetics</i> , 2003, 164, 1279-1289.	2.9	70
160	Over-representation of repeats in stress response genes: a strategy to increase versatility under stressful conditions?. <i>Nucleic Acids Research</i> , 2002, 30, 1886-1894.	14.5	97
161	A new family of highly variable proteins in the <i>Chlamydomonas reinhardtii</i> genome. <i>Nucleic Acids Research</i> , 2002, 30, 4351-4360.	14.5	21
162	Origin and fate of repeats in bacteria. <i>Nucleic Acids Research</i> , 2002, 30, 2987-2994.	14.5	75

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163	Genomic repeats, genome plasticity and the dynamics of Mycoplasma evolution. Nucleic Acids Research, 2002, 30, 2031-2042.	14.5	155
164	Is there a role for replication fork asymmetry in the distribution of genes in bacterial genomes?. Trends in Microbiology, 2002, 10, 393-395.	7.7	84
165	Base composition bias might result from competition for metabolic resources. Trends in Genetics, 2002, 18, 291-294.	6.7	447
166	Evolutionary Role of Restriction/Modification Systems as Revealed by Comparative Genome Analysis. Genome Research, 2001, 11, 946-958.	5.5	101
167	Ongoing Evolution of Strand Composition in Bacterial Genomes. Molecular Biology and Evolution, 2001, 18, 1789-1799.	8.9	62
168	The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis. Nucleic Acids Research, 2001, 29, 2145-2153.	14.5	241
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