

Eduardo Rocha

List of Publications by Year in descending order

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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	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	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
3	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
4	Mobility of Plasmids. <i>Microbiology and Molecular Biology Reviews</i> , 2010, 74, 434-452.	6.6	919
5	Whole genome-based population biology and epidemiological surveillance of <i>Listeria monocytogenes</i> . <i>Nature Microbiology</i> , 2017, 2, 16185.	13.3	562
6	Uncovering <i>Listeria monocytogenes</i> hypervirulence by harnessing its biodiversity. <i>Nature Genetics</i> , 2016, 48, 308-313.	21.4	541
7	Base composition bias might result from competition for metabolic resources. <i>Trends in Genetics</i> , 2002, 18, 291-294.	6.7	447
8	Horizontal Transfer, Not Duplication, Drives the Expansion of Protein Families in Prokaryotes. <i>PLoS Genetics</i> , 2011, 7, e1001284.	3.5	426
9	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
10	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
11	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
12	The Genome of <i>Burkholderia cenocepacia</i> J2315, an Epidemic Pathogen of Cystic Fibrosis Patients. <i>Journal of Bacteriology</i> , 2009, 191, 261-277.	2.2	329
13	The Repertoire of ICE in Prokaryotes Underscores the Unity, Diversity, and Ubiquity of Conjugation. <i>PLoS Genetics</i> , 2011, 7, e1002222.	3.5	329
14	MacSyFinder: A Program to Mine Genomes for Molecular Systems with an Application to CRISPR-Cas Systems. <i>PLoS ONE</i> , 2014, 9, e110726.	2.5	315
15	Identification of protein secretion systems in bacterial genomes. <i>Scientific Reports</i> , 2016, 6, 23080.	3.3	315
16	Genetic and life-history traits associated with the distribution of prophages in bacteria. <i>ISME Journal</i> , 2016, 10, 2744-2754.	9.8	314
17	Causes for the intriguing presence of tRNAs in phages. <i>Genome Research</i> , 2007, 17, 1486-1495.	5.5	312
18	Pervasive domestication of defective prophages by bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 12127-12132.	7.1	304

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19	The Systemic Imprint of Growth and Its Uses in Ecological (Meta)Genomics. <i>PLoS Genetics</i> , 2010, 6, e1000808.	3.5	286
20	Comparative and Evolutionary Analysis of the Bacterial Homologous Recombination Systems. <i>PLoS Genetics</i> , 2005, 1, e15.	3.5	275
21	The Genomic Diversification of the Whole <i>Acinetobacter</i> Genus: Origins, Mechanisms, and Consequences. <i>Genome Biology and Evolution</i> , 2014, 6, 2866-2882.	2.5	269
22	The Organization of the Bacterial Genome. <i>Annual Review of Genetics</i> , 2008, 42, 211-233.	7.6	266
23	What traits are carried on mobile genetic elements, and why?. <i>Heredity</i> , 2011, 106, 1-10.	2.6	266
24	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
25	The interplay of restriction-modification systems with mobile genetic elements and their prokaryotic hosts. <i>Nucleic Acids Research</i> , 2014, 42, 10618-10631.	14.5	246
26	The complete genome sequence of the murine respiratory pathogen <i>Mycoplasma pulmonis</i> . <i>Nucleic Acids Research</i> , 2001, 29, 2145-2153.	14.5	241
27	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
28	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
29	The replication-related organization of bacterial genomes. <i>Microbiology (United Kingdom)</i> , 2004, 150, 1609-1627.	1.8	235
30	Identification and analysis of integrons and cassette arrays in bacterial genomes. <i>Nucleic Acids Research</i> , 2016, 44, 4539-4550.	14.5	235
31	Horizontal Gene Transfer of the Secretome Drives the Evolution of Bacterial Cooperation and Virulence. <i>Current Biology</i> , 2009, 19, 1683-1691.	3.9	217
32	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
33	Causes of Insertion Sequences Abundance in Prokaryotic Genomes. <i>Molecular Biology and Evolution</i> , 2007, 24, 969-981.	8.9	202
34	Key components of the eight classes of type IV secretion systems involved in bacterial conjugation or protein secretion. <i>Nucleic Acids Research</i> , 2014, 42, 5715-5727.	14.5	200
35	Essentiality, not expressiveness, drives gene-strand bias in bacteria. <i>Nature Genetics</i> , 2003, 34, 377-378.	21.4	198
36	The Small, Slow and Specialized CRISPR and Anti-CRISPR of <i>Escherichia</i> and <i>Salmonella</i> . <i>PLoS ONE</i> , 2010, 5, e11126.	2.5	198

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37	The Adaptation of Temperate Bacteriophages to Their Host Genomes. <i>Molecular Biology and Evolution</i> , 2013, 30, 737-751.	8.9	196
38	Evolution of Conjugation and Type IV Secretion Systems. <i>Molecular Biology and Evolution</i> , 2013, 30, 315-331.	8.9	193
39	The chromosomal organization of horizontal gene transfer in bacteria. <i>Nature Communications</i> , 2017, 8, 841.	12.8	184
40	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
41	Universal replication biases in bacteria. <i>Molecular Microbiology</i> , 1999, 32, 11-16.	2.5	170
42	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
43	Genomic repeats, genome plasticity and the dynamics of <i>Mycoplasma</i> evolution. <i>Nucleic Acids Research</i> , 2002, 30, 2031-2042.	14.5	155
44	Gene essentiality determines chromosome organisation in bacteria. <i>Nucleic Acids Research</i> , 2003, 31, 6570-6577.	14.5	145
45	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
46	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
47	Genesis, effects and fates of repeats in prokaryotic genomes. <i>FEMS Microbiology Reviews</i> , 2009, 33, 539-571.	8.6	137
48	How Essential Are Nonessential Genes?. <i>Molecular Biology and Evolution</i> , 2005, 22, 2147-2156.	8.9	135
49	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
50	Phylogenetic background and habitat drive the genetic diversification of <i>Escherichia coli</i> . <i>PLoS Genetics</i> , 2020, 16, e1008866.	3.5	131
51	Integrative and conjugative elements and their hosts: composition, distribution and organization. <i>Nucleic Acids Research</i> , 2017, 45, 8943-8956.	14.5	129
52	Phages and their satellites encode hotspots of antiviral systems. <i>Cell Host and Microbe</i> , 2022, 30, 740-753.e5.	11.0	129
53	Ultrafast search of all deposited bacterial and viral genomic data. <i>Nature Biotechnology</i> , 2019, 37, 152-159.	17.5	123
54	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

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55	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
56	Persistence drives gene clustering in bacterial genomes. <i>BMC Genomics</i> , 2008, 9, 4.	2.8	104
57	PPanGGOLiN: Depicting microbial diversity via a partitioned pangenome graph. <i>PLoS Computational Biology</i> , 2020, 16, e1007732.	3.2	102
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	Inference and Analysis of the Relative Stability of Bacterial Chromosomes. <i>Molecular Biology and Evolution</i> , 2006, 23, 513-522.	8.9	99
61	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
62	<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
63	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
64	Highly Variable Rates of Genome Rearrangements between Hemiascomycetous Yeast Lineages. <i>PLoS Genetics</i> , 2006, 2, e32.	3.5	94
65	Neutral Theory, Microbial Practice: Challenges in Bacterial Population Genetics. <i>Molecular Biology and Evolution</i> , 2018, 35, 1338-1347.	8.9	93
66	Order and disorder in bacterial genomes. <i>Current Opinion in Microbiology</i> , 2004, 7, 519-527.	5.1	92
67	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
68	Identification of Protein Secretion Systems in Bacterial Genomes Using MacSyFinder. <i>Methods in Molecular Biology</i> , 2017, 1615, 1-21.	0.9	92
69	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
70	Oligonucleotide bias in <i>Bacillus subtilis</i> : General trends and taxonomic comparisons. <i>Nucleic Acids Research</i> , 1998, 26, 2971-2980.	14.5	87
71	Similar compositional biases are caused by very different mutational effects. <i>Genome Research</i> , 2006, 16, 1537-1547.	5.5	87
72	Is there a role for replication fork asymmetry in the distribution of genes in bacterial genomes?. <i>Trends in Microbiology</i> , 2002, 10, 393-395.	7.7	84

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73	Microbial defenses against mobile genetic elements and viruses: Who defends whom from what?. PLoS Biology, 2022, 20, e3001514.	5.6	83
74	Insights on the Emergence of Mycobacterium tuberculosis from the Analysis of Mycobacterium kansasii. Genome Biology and Evolution, 2015, 7, 856-870.	2.5	79
75	Metabolic diversity of the emerging pathogenic lineages of <i>Klebsiella pneumoniae</i> . Environmental Microbiology, 2017, 19, 1881-1898.	3.8	79
76	Analysis of long repeats in bacterial genomes reveals alternative evolutionary mechanisms in <i>Bacillus subtilis</i> and other competent prokaryotes. Molecular Biology and Evolution, 1999, 16, 1219-1230.	8.9	78
77	Inhibition of NHEJ repair by type II-A CRISPR-Cas systems in bacteria. Nature Communications, 2017, 8, 2094.	12.8	77
78	The quest for the universals of protein evolution. Trends in Genetics, 2006, 22, 412-416.	6.7	76
79	A PNPase Dependent CRISPR System in <i>Listeria</i> . PLoS Genetics, 2014, 10, e1004065.	3.5	76
80	The impact of genetic diversity on gene essentiality within the <i>Escherichia coli</i> species. Nature Microbiology, 2021, 6, 301-312.	13.3	76
81	Origin and fate of repeats in bacteria. Nucleic Acids Research, 2002, 30, 2987-2994.	14.5	75
82	The impact of the neisserial DNA uptake sequences on genome evolution and stability. Genome Biology, 2008, 9, R60.	9.6	73
83	The chromosomal accommodation and domestication of mobile genetic elements. Current Opinion in Microbiology, 2014, 22, 22-29.	5.1	73
84	Associations Between Inverted Repeats and the Structural Evolution of Bacterial Genomes. Genetics, 2003, 164, 1279-1289.	2.9	70
85	Repseek, a tool to retrieve approximate repeats from large DNA sequences. Bioinformatics, 2007, 23, 119-121.	4.1	69
86	Bacteriophages benefit from generalized transduction. PLoS Pathogens, 2019, 15, e1007888.	4.7	69
87	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. Infection and Immunity, 2006, 74, 3715-3726.	2.2	68
88	The Temporal Dynamics of Slightly Deleterious Mutations in <i>Escherichia coli</i> and <i>Shigella</i> spp.. Molecular Biology and Evolution, 2009, 26, 345-355.	8.9	67
89	Antibiotic resistance plasmids spread among natural isolates of <i>Escherichia coli</i> in spite of CRISPR elements. Microbiology (United Kingdom), 2012, 158, 2997-3004.	1.8	67
90	An Appraisal of the Potential for Illegitimate Recombination in Bacterial Genomes and Its Consequences: From Duplications to Genome Reduction. Genome Research, 2003, 13, 1123-1132.	5.5	65

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91	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
92	Genomic epidemiology and global diversity of the emerging bacterial pathogen <i>Elizabethkingia anophelis</i> . <i>Scientific Reports</i> , 2016, 6, 30379.	3.3	65
93	DNA repeats lead to the accelerated loss of gene order in bacteria. <i>Trends in Genetics</i> , 2003, 19, 600-603.	6.7	64
94	Complete Genome Sequence of the Fish Pathogen <i>Flavobacterium branchiophilum</i> . <i>Applied and Environmental Microbiology</i> , 2011, 77, 7656-7662.	3.1	64
95	Ongoing Evolution of Strand Composition in Bacterial Genomes. <i>Molecular Biology and Evolution</i> , 2001, 18, 1789-1799.	8.9	62
96	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
97	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
98	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
99	A synthesis of bacterial and archaeal phenotypic trait data. <i>Scientific Data</i> , 2020, 7, 170.	5.3	59
100	Phage-host coevolution in natural populations. <i>Nature Microbiology</i> , 2022, 7, 1075-1086.	13.3	58
101	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
102	Coevolution of the Organization and Structure of Prokaryotic Genomes. <i>Cold Spring Harbor Perspectives in Biology</i> , 2016, 8, a018168.	5.5	55
103	Swelife: a detector of internal repeats in sequences and structures. <i>Bioinformatics</i> , 2008, 24, 1536-1537.	4.1	53
104	Identifying Conjugative Plasmids and Integrative Conjugative Elements with CONJscan. <i>Methods in Molecular Biology</i> , 2020, 2075, 265-283.	0.9	51
105	Functional and evolutionary roles of long repeats in prokaryotes. <i>Research in Microbiology</i> , 1999, 150, 725-733.	2.1	50
106	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
107	Transient Hypermutagenesis Accelerates the Evolution of Legume Endosymbionts following Horizontal Gene Transfer. <i>PLoS Biology</i> , 2014, 12, e1001942.	5.6	50
108	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

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109	Causes of trends in amino-acid gain and loss. <i>Nature</i> , 2006, 442, E11-E12.	27.8	47
110	A strand-specific model for chromosome segregation in bacteria. <i>Molecular Microbiology</i> , 2003, 49, 895-903.	2.5	44
111	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
112	Evolution of Plasmid Mobility: Origin and Fate of Conjugative and Nonconjugative Plasmids. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	44
113	Evolutionary patterns in prokaryotic genomes. <i>Current Opinion in Microbiology</i> , 2008, 11, 454-460.	5.1	43
114	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
115	The Evolution of Protein Secretion Systems by Co-option and Tinkering of Cellular Machineries. <i>Trends in Microbiology</i> , 2020, 28, 372-386.	7.7	43
116	Manipulating or Superseding Host Recombination Functions: A Dilemma That Shapes Phage Evolvability. <i>PLoS Genetics</i> , 2013, 9, e1003825.	3.5	41
117	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
118	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
119	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
120	Rapid Evolution of the Sequences and Gene Repertoires of Secreted Proteins in Bacteria. <i>PLoS ONE</i> , 2012, 7, e49403.	2.5	37
121	Implication of gene distribution in the bacterial chromosome for the bacterial cell factory. <i>Journal of Biotechnology</i> , 2000, 78, 209-219.	3.8	36
122	Immune Subversion and Quorum-Sensing Shape the Variation in Infectious Dose among Bacterial Pathogens. <i>PLoS Pathogens</i> , 2012, 8, e1002503.	4.7	36
123	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
124	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
125	Human commensal gut Proteobacteria withstand type VI secretion attacks through immunity protein-independent mechanisms. <i>Nature Communications</i> , 2021, 12, 5751.	12.8	34
126	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. <i>Antimicrobial Agents and Chemotherapy</i> , 2009, 53, 2283-2288.	3.2	33

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127	A widespread family of polymorphic toxins encoded by temperate phages. BMC Biology, 2017, 15, 75.	3.8	33
128	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
129	Experimental Evolution as a Tool to Investigate Natural Processes and Molecular Functions. Trends in Microbiology, 2019, 27, 623-634.	7.7	32
130	Atypical organizations and epistatic interactions of CRISPRs and cas clusters in genomes and their mobile genetic elements. Nucleic Acids Research, 2020, 48, 748-760.	14.5	32
131	Genetic exchanges are more frequent in bacteria encoding capsules. PLoS Genetics, 2018, 14, e1007862.	3.5	31
132	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
133	A matter of background: DNA repair pathways as a possible cause for the sparse distribution of CRISPR-Cas systems in bacteria. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20180088.	4.0	30
134	Unlinked rRNA genes are widespread among bacteria and archaea. ISME Journal, 2020, 14, 597-608.	9.8	30
135	Sulphur islands in the <i>Escherichia coli</i> genome: markers of the cell's architecture?. FEBS Letters, 2000, 476, 8-11.	2.8	29
136	Differences in Integron Cassette Excision Dynamics Shape a Trade-Off between Evolvability and Genetic Capacitance. MBio, 2017, 8, .	4.1	27
137	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
138	Community diversity and habitat structure shape the repertoire of extracellular proteins in bacteria. Nature Communications, 2020, 11, 758.	12.8	26
139	PanACoTA: a modular tool for massive microbial comparative genomics. NAR Genomics and Bioinformatics, 2021, 3, lqaa106.	3.2	26
140	Common Cell Shape Evolution of Two Nasopharyngeal Pathogens. PLoS Genetics, 2015, 11, e1005338.	3.5	26
141	An Integrative Method for Accurate Comparative Genome Mapping. PLoS Computational Biology, 2006, 2, e75.	3.2	25
142	No evidence for elemental-based streamlining of prokaryotic genomes. Trends in Ecology and Evolution, 2010, 25, 319-320.	8.7	25
143	Eco-Evolutionary Dynamics of Episomes among Ecologically Cohesive Bacterial Populations. MBio, 2015, 6, e00552-15.	4.1	25
144	Metagenomic assessment of the interplay between the environment and the genetic diversification of <i>Acinetobacter</i> . Environmental Microbiology, 2017, 19, 5010-5024.	3.8	24

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145	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
146	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
147	Intracellular Positioning Systems Limit the Entropic Eviction of Secondary Replicons Toward the Nucleoid Edges in Bacterial Cells. <i>Journal of Molecular Biology</i> , 2020, 432, 745-761.	4.2	21
148	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
149	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
150	Alternative to Homo-oligomerisation: The Creation of Local Symmetry in Proteins by Internal Amplification. <i>Journal of Molecular Biology</i> , 2009, 394, 522-534.	4.2	19
151	Natural Selection for Operons Depends on Genome Size. <i>Genome Biology and Evolution</i> , 2013, 5, 2242-2254.	2.5	19
152	The major subunit of widespread competence pili exhibits a novel and conserved type IV pilin fold. <i>Journal of Biological Chemistry</i> , 2020, 295, 6594-6604.	3.4	19
153	Using Sex to Cure the Genome. <i>PLoS Biology</i> , 2016, 14, e1002417.	5.6	16
154	A Novel Heuristic for Local Multiple Alignment of Interspersed DNA Repeats. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009, 6, 180-189.	3.0	14
155	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
156	Comparative genomic analysis of <i>Acinetobacter</i> strains isolated from murine colonic crypts. <i>BMC Genomics</i> , 2017, 18, 525.	2.8	14
157	With a Little Help from Prokaryotes. <i>Science</i> , 2013, 339, 1154-1155.	12.6	13
158	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
159	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
160	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
161	Parallels between experimental and natural evolution of legume symbionts. <i>Nature Communications</i> , 2018, 9, 2264.	12.8	11
162	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

#	ARTICLE	IF	CITATIONS
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