

Marie Touchon

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

5,606
citations

304743

22
h-index

610901

24
g-index

31
all docs

31
docs citations

31
times ranked

6563
citing authors

#	ARTICLE	IF	CITATIONS
1	Systematic and quantitative view of the antiviral arsenal of prokaryotes. <i>Nature Communications</i> , 2022, 13, 2561.	12.8	208
2	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
3	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
4	Phylogenetic background and habitat drive the genetic diversification of <i>Escherichia coli</i> . <i>PLoS Genetics</i> , 2020, 16, e1008866.	3.5	131
5	Phylogenetic background and habitat drive the genetic diversification of <i>Escherichia coli</i> . , 2020, 16, e1008866.		0
6	Phylogenetic background and habitat drive the genetic diversification of <i>Escherichia coli</i> . , 2020, 16, e1008866.		0
7	Phylogenetic background and habitat drive the genetic diversification of <i>Escherichia coli</i> . , 2020, 16, e1008866.		0
8	Phylogenetic background and habitat drive the genetic diversification of <i>Escherichia coli</i> . , 2020, 16, e1008866.		0
9	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
10	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
11	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
12	The chromosomal organization of horizontal gene transfer in bacteria. <i>Nature Communications</i> , 2017, 8, 841.	12.8	184
13	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
14	Identification of protein secretion systems in bacterial genomes. <i>Scientific Reports</i> , 2016, 6, 23080.	3.3	315
15	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
16	Identification and analysis of integrons and cassette arrays in bacterial genomes. <i>Nucleic Acids Research</i> , 2016, 44, 4539-4550.	14.5	235
17	Genetic and life-history traits associated with the distribution of prophages in bacteria. <i>ISME Journal</i> , 2016, 10, 2744-2754.	9.8	314
18	Coevolution of the Organization and Structure of Prokaryotic Genomes. <i>Cold Spring Harbor Perspectives in Biology</i> , 2016, 8, a018168.	5.5	55

#	ARTICLE	IF	CITATIONS
19	MacSyFinder: A Program to Mine Genomes for Molecular Systems with an Application to CRISPR-Cas Systems. PLoS ONE, 2014, 9, e110726.	2.5	315
20	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
21	The interplay of restriction-modification systems with mobile genetic elements and their prokaryotic hosts. Nucleic Acids Research, 2014, 42, 10618-10631.	14.5	246
22	The chromosomal accommodation and domestication of mobile genetic elements. Current Opinion in Microbiology, 2014, 22, 22-29.	5.1	73
23	Manipulating or Superseding Host Recombination Functions: A Dilemma That Shapes Phage Evolvability. PLoS Genetics, 2013, 9, e1003825.	3.5	41
24	The Adaptation of Temperate Bacteriophages to Their Host Genomes. Molecular Biology and Evolution, 2013, 30, 737-751.	8.9	196
25	The Small, Slow and Specialized CRISPR and Anti-CRISPR of Escherichia and Salmonella. PLoS ONE, 2010, 5, e11126.	2.5	198
26	Organised Genome Dynamics in the Escherichia coli Species Results in Highly Diverse Adaptive Paths. PLoS Genetics, 2009, 5, e1000344.	3.5	1,005
27	Causes of Insertion Sequences Abundance in Prokaryotic Genomes. Molecular Biology and Evolution, 2007, 24, 969-981.	8.9	202