

Francisco Juan Martínez Mojica

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

11,259
citations

304743

22
h-index

501196

28
g-index

32
all docs

32
docs citations

32
times ranked

9142
citing authors

#	ARTICLE	IF	CITATIONS
1	Digging into the lesser-known aspects of CRISPR biology. <i>International Microbiology</i> , 2021, 24, 473-498.	2.4	10
2	Evolutionary classification of CRISPR-Cas systems: a burst of class 2 and derived variants. <i>Nature Reviews Microbiology</i> , 2020, 18, 67-83.	28.6	1,427
3	The CRISPR conundrum: evolve and maybe die, or survive and risk stagnation. <i>Microbial Cell</i> , 2018, 5, 262-268.	3.2	21
4	<i>Leuconostoc mesenteroides</i> and <i>Leuconostoc pseudomesenteroides</i> bacteriophages: Genomics and cross-species host ranges. <i>International Journal of Food Microbiology</i> , 2017, 257, 128-137.	4.7	19
5	Next-generation precision antimicrobials: towards personalized treatment of infectious diseases. <i>Current Opinion in Microbiology</i> , 2017, 37, 95-102.	5.1	100
6	The discovery of CRISPR in archaea and bacteria. <i>FEBS Journal</i> , 2016, 283, 3162-3169.	4.7	130
7	On the Origin of CRISPR-Cas Technology: From Prokaryotes to Mammals. <i>Trends in Microbiology</i> , 2016, 24, 811-820.	7.7	143
8	Anti-cas spacers in orphan CRISPR4 arrays prevent uptake of active CRISPR-Cas I-F systems. <i>Nature Microbiology</i> , 2016, 1, 16081.	13.3	40
9	CRISPR Content Correlates with the Pathogenic Potential of <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2015, 10, e0131935.	2.5	47
10	An updated evolutionary classification of CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2015, 13, 722-736.	28.6	2,081
11	Exploring CRISPR Interference by Transformation with Plasmid Mixtures: Identification of Target Interference Motifs in <i>Escherichia coli</i> . <i>Methods in Molecular Biology</i> , 2015, 1311, 161-170.	0.9	3
12	CRISPR-Cas Functional Module Exchange in <i>Escherichia coli</i> . <i>MBio</i> , 2014, 5, e00767-13.	4.1	31
13	Right of admission reserved, no matter the path. <i>Trends in Microbiology</i> , 2013, 21, 446-448.	7.7	2
14	Discovery and Seminal Developments in the CRISPR Field. , 2013, , 1-31.		9
15	CRISPR-spacer integration reporter plasmids reveal distinct genuine acquisition specificities among CRISPR-Cas I-E variants of <i>Escherichia coli</i> . <i>RNA Biology</i> , 2013, 10, 792-802.	3.1	123
16	Protospacer recognition motifs. <i>RNA Biology</i> , 2013, 10, 891-899.	3.1	309
17	Discovery and Seminal Developments in the CRISPR Field. , 2013, , 1-31.		8
18	Target Motifs Affecting Natural Immunity by a Constitutive CRISPR-Cas System in <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2012, 7, e50797.	2.5	54

#	ARTICLE	IF	CITATIONS
19	Reconstructing Viral Genomes from the Environment Using Fosmid Clones: The Case of Haloviruses. PLoS ONE, 2012, 7, e33802.	2.5	78
20	Evolution and classification of the CRISPR-Cas systems. Nature Reviews Microbiology, 2011, 9, 467-477.	28.6	2,078
21	The on-off switch of CRISPR immunity against phages in <i>Escherichia coli</i> . Molecular Microbiology, 2010, 77, 1341-1345.	2.5	31
22	Diversity of CRISPR loci in <i>Escherichia coli</i> . Microbiology (United Kingdom), 2010, 156, 1351-1361.	1.8	170
23	Complete Genome Sequence of Crohn's Disease-Associated Adherent-Invasive <i>E. coli</i> Strain LF82. PLoS ONE, 2010, 5, e12714.	2.5	180
24	Short motif sequences determine the targets of the prokaryotic CRISPR defence system. Microbiology (United Kingdom), 2009, 155, 733-740.	1.8	1,267
25	Intervening Sequences of Regularly Spaced Prokaryotic Repeats Derive from Foreign Genetic Elements. Journal of Molecular Evolution, 2005, 60, 174-182.	1.8	1,706
26	Biological significance of a family of regularly spaced repeats in the genomes of Archaea, Bacteria and mitochondria. Molecular Microbiology, 2000, 36, 244-246.	2.5	627
27	Localized domains of DNA supercoiling: topological coupling between promoters. Molecular Microbiology, 1996, 22, 919-928.	2.5	33
28	Long stretches of short tandem repeats are present in the largest replicons of the Archaea <i>Haloferax mediterranei</i> and <i>Haloferax volcanii</i> and could be involved in replicon partitioning. Molecular Microbiology, 1995, 17, 85-93.	2.5	266
29	Transcription at different salinities of <i>Haloferax mediterranei</i> sequences adjacent to partially modified PstI sites. Molecular Microbiology, 1993, 9, 613-621.	2.5	263
30	Response to Osmotic Stress in a Haloarchaeal Genome: a Role for General Stress Proteins and Global Regulatory Mechanisms. , 0, , 232-239.		0