

# Loris Mularoni

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/982872/publications.pdf>

Version: 2024-02-01

20  
papers

5,892  
citations

361413

20  
h-index

752698

20  
g-index

24  
all docs

24  
docs citations

24  
times ranked

13087  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.	28.9	1,670
2	Whole-genome landscapes of major melanoma subtypes. <i>Nature</i> , 2017, 545, 175-180.	27.8	1,068
3	A compendium of mutational cancer driver genes. <i>Nature Reviews Cancer</i> , 2020, 20, 555-572.	28.4	605
4	Pancreatic islet enhancer clusters enriched in type 2 diabetes risk-associated variants. <i>Nature Genetics</i> , 2014, 46, 136-143.	21.4	475
5	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020, 578, 102-111.	27.8	424
6	Nucleotide excision repair is impaired by binding of transcription factors to DNA. <i>Nature</i> , 2016, 532, 264-267.	27.8	274
7	OncodriveFML: a general framework to identify coding and non-coding regions with cancer driver mutations. <i>Genome Biology</i> , 2016, 17, 128.	8.8	251
8	Exploring Massive, Genome Scale Datasets with the GenometriCorr Package. <i>PLoS Computational Biology</i> , 2012, 8, e1002529.	3.2	167
9	Reduced mutation rate in exons due to differential mismatch repair. <i>Nature Genetics</i> , 2017, 49, 1684-1692.	21.4	139
10	Genome-Wide Analysis of Histidine Repeats Reveals Their Role in the Localization of Human Proteins to the Nuclear Speckles Compartment. <i>PLoS Genetics</i> , 2009, 5, e1000397.	3.5	118
11	DNA transposon <i>Hermes</i> inserts into DNA in nucleosome-free regions in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 21966-21972.	7.1	99
12	Discovery of Cancer Driver Long Noncoding RNAs across 1112 Tumour Genomes: New Candidates and Distinguishing Features. <i>Scientific Reports</i> , 2017, 7, 41544.	3.3	98
13	Natural selection drives the accumulation of amino acid tandem repeats in human proteins. <i>Genome Research</i> , 2010, 20, 745-754.	5.5	88
14	Retrotransposon Ty1 integration targets specifically positioned asymmetric nucleosomal DNA segments in tRNA hotspots. <i>Genome Research</i> , 2012, 22, 693-703.	5.5	70
15	A <i>Sleeping Beauty</i> mutagenesis screen reveals a tumor suppressor role for <i>Ncoa2/Src-2</i> in liver cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E1377-86.	7.1	67
16	Housekeeping genes tend to show reduced upstream sequence conservation. <i>Genome Biology</i> , 2007, 8, R140.	9.6	64
17	Highly constrained proteins contain an unexpectedly large number of amino acid tandem repeats. <i>Genomics</i> , 2007, 89, 316-325.	2.9	44
18	OncodriveCLUSTL: a sequence-based clustering method to identify cancer drivers. <i>Bioinformatics</i> , 2019, 35, 4788-4790.	4.1	41

#	ARTICLE	IF	CITATIONS
19	The Pancreatic Islet Regulome Browser. <i>Frontiers in Genetics</i> , 2017, 8, 13.	2.3	33
20	Mutation patterns of amino acid tandem repeats in the human proteome. <i>Genome Biology</i> , 2006, 7, R33.	9.6	27