Loris Mularoni

List of Publications by Year
in descending order

20	5,892	361413	752698
papers	citations	20	20
		h-index	g-index

24	24	24	13087
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A compendium of mutational cancer driver genes. Nature Reviews Cancer, 2020, 20, 555-572.	28.4	605
2	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. Nature, 2020, 578, 102-111.	27.8	424
3	OncodriveCLUSTL: a sequence-based clustering method to identify cancer drivers. Bioinformatics, 2019, 35, 4788-4790.	4.1	41
4	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	28.9	1,670
5	Discovery of Cancer Driver Long Noncoding RNAs across 1112 Tumour Genomes: New Candidates and Distinguishing Features. Scientific Reports, 2017, 7, 41544.	3.3	98
6	Whole-genome landscapes of major melanoma subtypes. Nature, 2017, 545, 175-180.	27.8	1,068
7	Reduced mutation rate in exons due to differential mismatch repair. Nature Genetics, 2017, 49, 1684-1692.	21.4	139
8	The Pancreatic Islet Regulome Browser. Frontiers in Genetics, 2017, 8, 13.	2.3	33
9	Nucleotide excision repair is impaired by binding of transcription factors to DNA. Nature, 2016, 532, 264-267.	27.8	274
10	OncodriveFML: a general framework to identify coding and non-coding regions with cancer driver mutations. Genome Biology, 2016, 17, 128.	8.8	251
11	Pancreatic islet enhancer clusters enriched in type 2 diabetes risk-associated variants. Nature Genetics, 2014, 46, 136-143.	21.4	475
12	Exploring Massive, Genome Scale Datasets with the GenometriCorr Package. PLoS Computational Biology, 2012, 8, e1002529.	3.2	167
13	A *Sleeping Beauty* mutagenesis screen reveals a tumor suppressor role for *Ncoa2/Src-2* in liver cancer. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1377-86.	7.1	67
14	Retrotransposon Ty1 integration targets specifically positioned asymmetric nucleosomal DNA segments in tRNA hotspots. Genome Research, 2012, 22, 693-703.	5.5	70
15	Natural selection drives the accumulation of amino acid tandem repeats in human proteins. Genome Research, 2010, 20, 745-754.	5.5	88
16	DNA transposon *Hermes* inserts into DNA in nucleosome-free regions in vivo. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 21966-21972.	7.1	99
17	Genome-Wide Analysis of Histidine Repeats Reveals Their Role in the Localization of Human Proteins to the Nuclear Speckles Compartment. PLoS Genetics, 2009, 5, e1000397.	3.5	118
18	Highly constrained proteins contain an unexpectedly large number of amino acid tandem repeats. Genomics, 2007, 89, 316-325.	2.9	44

#	Article	IF	Citations
19	Housekeeping genes tend to show reduced upstream sequence conservation. Genome Biology, 2007, 8, R140.	9.6	64
20	Mutation patterns of amino acid tandem repeats in the human proteome. Genome Biology, 2006, 7, R33.	9.6	27