

Daniel Rico

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

3,577
citations

331259

21
h-index

476904

29
g-index

37
all docs

37
docs citations

37
times ranked

9645
citing authors

#	ARTICLE	IF	CITATIONS
1	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. <i>Leukemia</i> , 2021, 35, 2002-2016.	3.3	34
2	Resolution of R-loops by INO80 promotes DNA replication and maintains cancer cell proliferation and viability. <i>Nature Communications</i> , 2020, 11, 4534.	5.8	63
3	Intronic CNVs and gene expression variation in human populations. <i>PLoS Genetics</i> , 2019, 15, e1007902.	1.5	61
4	Protection against gamma-radiation injury by protein tyrosine phosphatase 1B. <i>Redox Biology</i> , 2018, 17, 213-223.	3.9	9
5	Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. <i>Cell Reports</i> , 2018, 24, 2784-2794.	2.9	104
6	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. <i>Genome Biology</i> , 2017, 18, 18.	3.8	97
7	Automatic identification of informative regions with epigenomic changes associated to hematopoiesis. <i>Nucleic Acids Research</i> , 2017, 45, 9244-9259.	6.5	19
8	Integrating epigenomic data and 3D genomic structure with a new measure of chromatin assortativity. <i>Genome Biology</i> , 2016, 17, 152.	3.8	46
9	The BLUEPRINT Data Analysis Portal. <i>Cell Systems</i> , 2016, 3, 491-495.e5.	2.9	123
10	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	13.5	404
11	Epigenomic Co-localization and Co-evolution Reveal a Key Role for 5hmC as a Communication Hub in the Chromatin Network of ESCs. <i>Cell Reports</i> , 2016, 14, 1246-1257.	2.9	38
12	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. <i>Nature Genetics</i> , 2015, 47, 746-756.	9.4	278
13	Higher gene expression variability in the more aggressive subtype of chronic lymphocytic leukemia. <i>Genome Medicine</i> , 2015, 7, 8.	3.6	57
14	The UBC-40 Urothelial Bladder Cancer cell line index: a genomic resource for functional studies. <i>BMC Genomics</i> , 2015, 16, 403.	1.2	86
15	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. <i>Genome Research</i> , 2014, 24, 212-226.	2.4	175
16	Transcriptional dissection of pancreatic tumors engrafted in mice. <i>Genome Medicine</i> , 2014, 6, 27.	3.6	41
17	Subfunctionalization via Adaptive Evolution Influenced by Genomic Context: The Case of Histone Chaperones ASF1a and ASF1b. <i>Molecular Biology and Evolution</i> , 2013, 30, 1853-1866.	3.5	60
18	Recurrent inactivation of STAG2 in bladder cancer is not associated with aneuploidy. <i>Nature Genetics</i> , 2013, 45, 1464-1469.	9.4	224

#	ARTICLE	IF	CITATIONS
19	Late-replicating CNVs as a source of new genes. <i>Biology Open</i> , 2013, 2, 1402-1411.	0.6	9
20	Epigenomic analysis detects widespread gene-body DNA hypomethylation in chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2012, 44, 1236-1242.	9.4	525
21	Assessment of copy number variation using the Illumina Infinium 1M SNP-array: a comparison of methodological approaches in the Spanish Bladder Cancer/EPICURO study. <i>Human Mutation</i> , 2011, 32, 240-248.	1.1	57
22	Mosaic Uniparental Disomies and Aneuploidies as Large Structural Variants of the Human Genome. <i>American Journal of Human Genetics</i> , 2010, 87, 129-138.	2.6	111
23	waviCGH: a web application for the analysis and visualization of genomic copy number alterations. <i>Nucleic Acids Research</i> , 2010, 38, W182-W187.	6.5	18
24	Substrate Fate in Activated Macrophages: A Comparison between Innate, Classic, and Alternative Activation. <i>Journal of Immunology</i> , 2010, 185, 605-614.	0.4	820
25	<i>Tetrahymena</i> Metallothioneins Fall into Two Discrete Subfamilies. <i>PLoS ONE</i> , 2007, 2, e291.	1.1	76
26	Identification of conserved domains in the promoter regions of nitric oxide synthase 2: implications for the species-specific transcription and evolutionary differences. <i>BMC Genomics</i> , 2007, 8, 271.	1.2	17