Daniel Rico

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5535534/publications.pdf

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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	Substrate Fate in Activated Macrophages: A Comparison between Innate, Classic, and Alternative Activation. Journal of Immunology, 2010, 185, 605-614.	0.4	820
2	Epigenomic analysis detects widespread gene-body DNA hypomethylation in chronic lymphocytic leukemia. Nature Genetics, 2012, 44, 1236-1242.	9.4	525
3	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	13.5	404
4	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. Nature Genetics, 2015, 47, 746-756.	9.4	278
5	Recurrent inactivation of STAG2 in bladder cancer is not associated with aneuploidy. Nature Genetics, 2013, 45, 1464-1469.	9.4	224
6	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. Genome Research, 2014, 24, 212-226.	2.4	175
7	The BLUEPRINT Data Analysis Portal. Cell Systems, 2016, 3, 491-495.e5.	2.9	123
8	Mosaic Uniparental Disomies and Aneuploidies as Large Structural Variants of the Human Genome. American Journal of Human Genetics, 2010, 87, 129-138.	2.6	111
9	Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. Cell Reports, 2018, 24, 2784-2794.	2.9	104
10	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. Genome Biology, 2017, 18, 18.	3.8	97
11	The UBC-40 Urothelial Bladder Cancer cell line index: a genomic resource for functional studies. BMC Genomics, 2015, 16, 403.	1.2	86
12	Tetrahymena Metallothioneins Fall into Two Discrete Subfamilies. PLoS ONE, 2007, 2, e291.	1.1	76
13	Resolution of R-loops by INO80 promotes DNA replication and maintains cancer cell proliferation and viability. Nature Communications, 2020, 11, 4534.	5.8	63
14	Intronic CNVs and gene expression variation in human populations. PLoS Genetics, 2019, 15, e1007902.	1.5	61
15	Subfunctionalization via Adaptive Evolution Influenced by Genomic Context: The Case of Histone Chaperones ASF1a and ASF1b. Molecular Biology and Evolution, 2013, 30, 1853-1866.	3.5	60
16	Assessment of copy number variation using the Illumina Infinium 1M SNP-array: a comparison of methodological approaches in the Spanish Bladder Cancer/EPICURO study. Human Mutation, 2011, 32, 240-248.	1.1	57
17	Higher gene expression variability in the more aggressive subtype of chronic lymphocytic leukemia. Genome Medicine, 2015, 7, 8.	3.6	57
18	Integrating epigenomic data and 3D genomic structure with a new measure of chromatin assortativity. Genome Biology, 2016, 17, 152.	3.8	46

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19	Transcriptional dissection of pancreatic tumors engrafted in mice. Genome Medicine, 2014, 6, 27.	3.6	41
20	Epigenomic Co-localization and Co-evolution Reveal a Key Role for 5hmC as a Communication Hub in the Chromatin Network of ESCs. Cell Reports, 2016, 14, 1246-1257.	2.9	38
21	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. Leukemia, 2021, 35, 2002-2016.	3.3	34
22	Automatic identification of informative regions with epigenomic changes associated to hematopoiesis. Nucleic Acids Research, 2017, 45, 9244-9259.	6.5	19
23	waviCGH: a web application for the analysis and visualization of genomic copy number alterations. Nucleic Acids Research, 2010, 38, W182-W187.	6.5	18
24	Identification of conserved domains in the promoter regions of nitric oxide synthase 2: implications for the species-specific transcription and evolutionary differences. BMC Genomics, 2007, 8, 271.	1.2	17
25	Late-replicating CNVs as a source of new genes. Biology Open, 2013, 2, 1402-1411.	0.6	9
26	Protection against gamma-radiation injury by protein tyrosine phosphatase 1B. Redox Biology, 2018, 17, 213-223.	3.9	9