

Antonio Rausell

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

2,405
citations

394421

19
h-index

414414

32
g-index

40
all docs

40
docs citations

40
times ranked

5375
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrative genetic and immune cell analysis of plasma proteins in healthy donors identifies novel associations involving primary immune deficiency genes. <i>Genome Medicine</i> , 2022, 14, 28.	8.2	8
2	Gene signature extraction and cell identity recognition at the single-cell level with Cell-ID. <i>Nature Biotechnology</i> , 2021, 39, 1095-1102.	17.5	75
3	CNVxplorer: a web tool to assist clinical interpretation of CNVs in rare disease patients. <i>Nucleic Acids Research</i> , 2021, 49, W93-W103.	14.5	14
4	A DL-4- and TNF α -based culture system to generate high numbers of nonmodified or genetically modified immunotherapeutic human T-lymphoid progenitors. <i>Cellular and Molecular Immunology</i> , 2021, 18, 1662-1676.	10.5	6
5	Common homozygosity for predicted loss-of-function variants reveals both redundant and advantageous effects of dispensable human genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 13626-13636.	7.1	18
6	NCBoost classifies pathogenic non-coding variants in Mendelian diseases through supervised learning on purifying selection signals in humans. <i>Genome Biology</i> , 2019, 20, 32.	8.8	47
7	Distinctive roles of age, sex, and genetics in shaping transcriptional variation of human immune responses to microbial challenges. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E488-E497.	7.1	181
8	What do primary immunodeficiencies tell us about the essentiality/redundancy of immune responses?. <i>Seminars in Immunology</i> , 2018, 36, 13-16.	5.6	14
9	Generation of adult human T-cell progenitors for immunotherapeutic applications. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 1491-1494.e4.	2.9	15
10	Single-cell analysis identifies cellular markers of the HIV permissive cell. <i>PLoS Pathogens</i> , 2017, 13, e1006678.	4.7	44
11	Innate immune defects in HIV permissive cell lines. <i>Retrovirology</i> , 2016, 13, 43.	2.0	17
12	Primary immunodeficiencies suggest redundancy within the human immune system. <i>Science Immunology</i> , 2016, 1, .	11.9	33
13	The SIB Swiss Institute of Bioinformatics's™ resources: focus on curated databases. <i>Nucleic Acids Research</i> , 2016, 44, D27-D37.	14.5	64
14	The Characteristics of Heterozygous Protein Truncating Variants in the Human Genome. <i>PLoS Computational Biology</i> , 2015, 11, e1004647.	3.2	34
15	HIV-1 immune activation induces Siglec-1 expression and enhances viral trans-infection in blood and tissue myeloid cells. <i>Retrovirology</i> , 2015, 12, 37.	2.0	85
16	Identification of potential HIV restriction factors by combining evolutionary genomic signatures with functional analyses. <i>Retrovirology</i> , 2015, 12, 41.	2.0	78
17	<i>scell</i> : an R/Bioconductor package for statistical assessment of cell-state hierarchies from single-cell RNA-seq. <i>Bioinformatics</i> , 2015, 31, 3380-3382.	4.1	61
18	Evolutionary genomics and HIV restriction factors. <i>Current Opinion in HIV and AIDS</i> , 2015, 10, 79-83.	3.8	13

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19	Analysis of Stop-Gain and Frameshift Variants in Human Innate Immunity Genes. PLoS Computational Biology, 2014, 10, e1003757.	3.2	32
20	Hippocampal Extracellular Matrix Levels and Stochasticity in Synaptic Protein Expression Increase with Age and Are Associated with Age-dependent Cognitive Decline. Molecular and Cellular Proteomics, 2014, 13, 2975-2985.	3.8	52
21	Transcriptional dissection of pancreatic tumors engrafted in mice. Genome Medicine, 2014, 6, 27.	8.2	41
22	Genomics of host-pathogen interactions. Current Opinion in Immunology, 2014, 30, 32-38.	5.5	30
23	Immune-responsive gene 1 protein links metabolism to immunity by catalyzing itaconic acid production. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 7820-7825.	7.1	765
24	HIV and innate immunity - a genomics perspective. F1000prime Reports, 2013, 5, 29.	5.9	10
25	On Different Aspects of Network Analysis in Systems Biology. , 2013, , 181-207.		3
26	JDet: interactive calculation and visualization of function-related conservation patterns in multiple sequence alignments and structures. Bioinformatics, 2012, 28, 584-586.	4.1	20
27	The Ras protein superfamily: Evolutionary tree and role of conserved amino acids. Journal of Cell Biology, 2012, 196, 189-201.	5.2	321
28	Protein interactions and ligand binding: From protein subfamilies to functional specificity. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 1995-2000.	7.1	132
29	Modern genome annotation: the BioSapiens network. , 2008, , 213-238.		2
30	Phylogeny-independent detection of functional residues. Bioinformatics, 2006, 22, 1440-1448.	4.1	60
31	The translation initiation factor eIF1A is an important determinant in the tolerance to NaCl stress in yeast and plants. Plant Journal, 2003, 34, 257-267.	5.7	111
32	FUNCTIONAL GENOMICS OF SALT TOLERANCE: THE YEAST OVEREXPRESSION APPROACH. Acta Horticulturae, 2003, , 31-38.	0.2	6