## Antonio Rausell

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4709240/publications.pdf

Version: 2024-02-01

32 papers

2,405 citations

394421 19 h-index 414414 32 g-index

40 all docs

40 docs citations

times ranked

40

5375 citing authors

#	Article	IF	CITATIONS
1	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
2	The Ras protein superfamily: Evolutionary tree and role of conserved amino acids. Journal of Cell Biology, 2012, 196, 189-201.	5.2	321
3	Distinctive roles of age, sex, and genetics in shaping transcriptional variation of human immune responses to microbial challenges. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E488-E497.	7.1	181
4	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
5	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
6	HIV-1 immune activation induces Siglec-1 expression and enhances viral trans-infection in blood and tissue myeloid cells. Retrovirology, 2015, 12, 37.	2.0	85
7	Identification of potential HIV restriction factors by combining evolutionary genomic signatures with functional analyses. Retrovirology, 2015, 12, 41.	2.0	78
8	Gene signature extraction and cell identity recognition at the single-cell level with Cell-ID. Nature Biotechnology, 2021, 39, 1095-1102.	17.5	75
9	The SIB Swiss Institute of Bioinformatics' resources: focus on curated databases. Nucleic Acids Research, 2016, 44, D27-D37.	14.5	64
10	$\langle i \rangle$ Sincell $\langle i \rangle$ : an R/Bioconductor package for statistical assessment of cell-state hierarchies from single-cell RNA-seq. Bioinformatics, 2015, 31, 3380-3382.	4.1	61
11	Phylogeny-independent detection of functional residues. Bioinformatics, 2006, 22, 1440-1448.	4.1	60
12	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
13	NCBoost classifies pathogenic non-coding variants in Mendelian diseases through supervised learning on purifying selection signals in humans. Genome Biology, 2019, 20, 32.	8.8	47
14	Single-cell analysis identifies cellular markers of the HIV permissive cell. PLoS Pathogens, 2017, 13, e1006678.	4.7	44
15	Transcriptional dissection of pancreatic tumors engrafted in mice. Genome Medicine, 2014, 6, 27.	8.2	41
16	The Characteristics of Heterozygous Protein Truncating Variants in the Human Genome. PLoS Computational Biology, 2015, 11, e1004647.	3.2	34
17	Primary immunodeficiencies suggest redundancy within the human immune system. Science Immunology, 2016, 1, .	11.9	33
18	Analysis of Stop-Gain and Frameshift Variants in Human Innate Immunity Genes. PLoS Computational Biology, 2014, 10, e1003757.	3.2	32

#	Article	IF	CITATIONS
19	Genomics of host–pathogen interactions. Current Opinion in Immunology, 2014, 30, 32-38.	5.5	30
20	JDet: interactive calculation and visualization of function-related conservation patterns in multiple sequence alignments and structures. Bioinformatics, 2012, 28, 584-586.	4.1	20
21	Common homozygosity for predicted loss-of-function variants reveals both redundant and advantageous effects of dispensable human genes. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 13626-13636.	7.1	18
22	Innate immune defects in HIV permissive cell lines. Retrovirology, 2016, 13, 43.	2.0	17
23	Generation of adult human T-cell progenitors for immunotherapeutic applications. Journal of Allergy and Clinical Immunology, 2018, 141, 1491-1494.e4.	2.9	15
24	What do primary immunodeficiencies tell us about the essentiality/redundancy of immune responses?. Seminars in Immunology, 2018, 36, 13-16.	5.6	14
25	CNVxplorer: a web tool to assist clinical interpretation of CNVs in rare disease patients. Nucleic Acids Research, 2021, 49, W93-W103.	14.5	14
26	Evolutionary genomics and HIV restriction factors. Current Opinion in HIV and AIDS, 2015, 10, 79-83.	3.8	13
27	HIV and innate immunity – a genomics perspective. F1000prime Reports, 2013, 5, 29.	5.9	10
28	Integrative genetic and immune cell analysis of plasma proteins in healthy donors identifies novel associations involving primary immune deficiency genes. Genome Medicine, 2022, 14, 28.	8.2	8
29	FUNCTIONAL GENOMICS OF SALT TOLERANCE: THE YEAST OVEREXPRESSION APPROACH. Acta Horticulturae, 2003, , 31-38.	0.2	6
30	A DL-4- and TNFα-based culture system to generate high numbers of nonmodified or genetically modified immunotherapeutic human T-lymphoid progenitors. Cellular and Molecular Immunology, 2021, 18, 1662-1676.	10.5	6
31	On Different Aspects of Network Analysis in Systems Biology. , 2013, , 181-207.		3
32	Modern genome annotation: the BioSapiens network. , 2008, , 213-238.		2