

Luigi Grassi

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5414990/publications.pdf>

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12
papers

2,330
citations

933410

10
h-index

1199563

12
g-index

17
all docs

17
docs citations

17
times ranked

7936
citing authors

#	ARTICLE	IF	CITATIONS
1	DetectIS: a pipeline to rapidly detect exogenous DNA integration sites using DNA or RNA paired-end sequencing data. <i>Bioinformatics</i> , 2021, 37, 4230-4232.	4.1	1
2	Assessment of a complete and classified platelet proteome from genome-wide transcripts of human platelets and megakaryocytes covering platelet functions. <i>Scientific Reports</i> , 2021, 11, 12358.	3.3	40
3	Germline mutations in the transcription factor IKZF5 cause thrombocytopenia. <i>Blood</i> , 2019, 134, 2070-2081.	1.4	29
4	Identification and characterization of an IgG sequence variant with an 11 kDa heavy chain C-terminal extension using a combination of mass spectrometry and high-throughput sequencing analysis. <i>MAbs</i> , 2019, 11, 1452-1463.	5.2	9
5	Dynamic Transcriptome-Proteome Correlation Networks Reveal Human Myeloid Differentiation and Neutrophil-Specific Programming. <i>Cell Reports</i> , 2019, 29, 2505-2519.e4.	6.4	70
6	Nbeal2 interacts with Dock7, Sec16a, and Vac14. <i>Blood</i> , 2018, 131, 1000-1011.	1.4	29
7	A synthesis approach of mouse studies to identify genes and proteins in arterial thrombosis and bleeding. <i>Blood</i> , 2018, 132, e35-e46.	1.4	29
8	Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. <i>Cell Reports</i> , 2018, 24, 2784-2794.	6.4	104
9	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. <i>Nature Communications</i> , 2017, 8, 16058.	12.8	50
10	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. <i>Cell</i> , 2016, 167, 1369-1384.e19.	28.9	863
11	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. <i>Cell</i> , 2016, 167, 1415-1429.e19.	28.9	1,052
12	FIDEA: a server for the functional interpretation of differential expression analysis. <i>Nucleic Acids Research</i> , 2013, 41, W84-W88.	14.5	39