Lionel Spinelli

List of Publications by Citations

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29 856 14 29 g-index

39 1,189 11.1 3.94 ext. papers ext. citations avg, IF L-index

#	Paper	IF	Citations
29	High-Dimensional Single-Cell Analysis Identifies Organ-Specific Signatures and Conserved NK Cell Subsets in Humans and Mice. <i>Immunity</i> , 2018 , 49, 971-986.e5	32.3	190
28	Extreme multifunctional proteins identified from a human protein interaction network. <i>Nature Communications</i> , 2015 , 6, 7412	17.4	76
27	Human germinal center transcriptional programs are de-synchronized in B cell lymphoma. <i>Nature Immunology</i> , 2018 , 19, 1013-1024	19.1	64
26	Tyrosine phosphorylation of RNA polymerase II CTD is associated with antisense promoter transcription and active enhancers in mammalian cells. <i>ELife</i> , 2014 , 3, e02105	8.9	58
25	BubbleGUM: automatic extraction of phenotype molecular signatures and comprehensive visualization of multiple Gene Set Enrichment Analyses. <i>BMC Genomics</i> , 2015 , 16, 814	4.5	52
24	Protein complex scaffolding predicted as a prevalent function of long non-coding RNAs. <i>Nucleic Acids Research</i> , 2018 , 46, 917-928	20.1	51
23	Topology and phase transitions: paradigmatic evidence. <i>Physical Review Letters</i> , 2000 , 84, 2774-7	7.4	44
22	Protein synthesis inhibition and GADD34 control IFN-Iheterogeneous expression in response toldsRNA. <i>EMBO Journal</i> , 2017 , 36, 761-782	13	40
21	Clust&See: a Cytoscape plugin for the identification, visualization and manipulation of network clusters. <i>BioSystems</i> , 2013 , 113, 91-5	1.9	33
20	Topological aspects of geometrical signatures of phase transitions. <i>Physical Review E</i> , 1999 , 60, R5009-	12.4	33
19	Topology and phase transitions I. Preliminary results. <i>Nuclear Physics B</i> , 2007 , 782, 189-218	2.8	29
18	Reticular Fibroblasts Expressing the Transcription Factor WT1 Define a Stromal Niche that Maintains and Replenishes Splenic Red Pulp Macrophages. <i>Immunity</i> , 2020 , 53, 127-142.e7	32.3	27
17	Perturbed human sub-networks by Fusobacterium nucleatum candidate virulence proteins. <i>Microbiome</i> , 2017 , 5, 89	16.6	19
16	Generation of a versatile BiFC ORFeome library for analyzing protein-protein interactions in live. <i>ELife</i> , 2018 , 7,	8.9	15
15	Post-transcriptional regulatory patterns revealed by protein-RNA interactions. <i>Scientific Reports</i> , 2019 , 9, 4302	4.9	14
14	Pasha: a versatile R package for piling chromatin HTS data. <i>Bioinformatics</i> , 2016 , 32, 2528-30	7.2	14
13	Guanabenz inhibits TLR9 signaling through a pathway that is independent of eIF2 dephosphorylation by the GADD34/PP1c complex. <i>Science Signaling</i> , 2018 , 11,	8.8	13

LIST OF PUBLICATIONS

12	Experimental detection of long-distance interactions between biomolecules through their diffusion behavior: numerical study. <i>Physical Review E</i> , 2014 , 90, 022703	2.4	13
11	MoonDB 2.0: an updated database of extreme multifunctional and moonlighting proteins. <i>Nucleic Acids Research</i> , 2019 , 47, D398-D402	20.1	13
10	FB5P-seq: FACS-Based 5-Prime End Single-Cell RNA-seq for Integrative Analysis of Transcriptome and Antigen Receptor Repertoire in B and T Cells. <i>Frontiers in Immunology</i> , 2020 , 11, 216	8.4	11
9	Guanabenz Prevents d-Galactosamine/Lipopolysaccharide-Induced Liver Damage and Mortality. <i>Frontiers in Immunology</i> , 2017 , 8, 679	8.4	11
8	Distinct Waves from the Hemogenic Endothelium Give Rise to Layered Lymphoid Tissue Inducer Cell Ontogeny. <i>Cell Reports</i> , 2020 , 32, 108004	10.6	10
7	Differentiation Paths of Peyeræ Patch LysoDCs Are Linked to Sampling Site Positioning, Migration, and T Cell Priming. <i>Cell Reports</i> , 2020 , 31, 107479	10.6	8
6	FB5P-seq: FACS-based 5-prime end single-cell RNAseq for integrative analysis of transcriptome and antigen receptor repertoire in B and T cells		4
5	Flux through a Markov chain. <i>Chaos, Solitons and Fractals</i> , 2016 , 93, 136-146	9.3	3
4	Framework for cosmography at high redshift. <i>Monthly Notices of the Royal Astronomical Society</i> , 1996 , 279, 564-570	4.3	2
3	Single-Cell RNA Sequencing Identifies a Pseudo-Immune Differentiation Axis As the Main Source of Functional Heterogeneity in Follicular Lymphoma B-Cells. <i>Blood</i> , 2019 , 134, 548-548	2.2	2
2	MetamORF: a repository of unique short open reading frames identified by both experimental and computational approaches for gene and metagene analyses. <i>Database: the Journal of Biological Databases and Curation</i> , 2021 , 2021,	5	2
1	Type 1 Innate Lymphoid Cells Limit the Antitumoral Immune Response. <i>Frontiers in Immunology</i> , 2021 , 12, 768989	8.4	1