

# Lionel Spinelli

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

29  
papers

856  
citations

14  
h-index

29  
g-index

39  
ext. papers

1,189  
ext. citations

11.1  
avg, IF

3.94  
L-index

#	Paper	IF	Citations
29	Type 1 Innate Lymphoid Cells Limit the Antitumoral Immune Response. <i>Frontiers in Immunology</i> , <b>2021</b> , 12, 768989	8.4	1
28	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> , <b>2021</b> , 2021,	5	2
27	Reticular Fibroblasts Expressing the Transcription Factor WT1 Define a Stromal Niche that Maintains and Replenishes Splenic Red Pulp Macrophages. <i>Immunity</i> , <b>2020</b> , 53, 127-142.e7	32.3	27
26	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> , <b>2020</b> , 11, 216	8.4	11
25	Distinct Waves from the Hemogenic Endothelium Give Rise to Layered Lymphoid Tissue Inducer Cell Ontogeny. <i>Cell Reports</i> , <b>2020</b> , 32, 108004	10.6	10
24	Differentiation Paths of Peyer's Patch LysoDCs Are Linked to Sampling Site Positioning, Migration, and T Cell Priming. <i>Cell Reports</i> , <b>2020</b> , 31, 107479	10.6	8
23	Post-transcriptional regulatory patterns revealed by protein-RNA interactions. <i>Scientific Reports</i> , <b>2019</b> , 9, 4302	4.9	14
22	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> , <b>2019</b> , 134, 548-548	2.2	2
21	MoonDB 2.0: an updated database of extreme multifunctional and moonlighting proteins. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D398-D402	20.1	13
20	Guanabenz inhibits TLR9 signaling through a pathway that is independent of eIF2 $\alpha$ dephosphorylation by the GADD34/PP1c complex. <i>Science Signaling</i> , <b>2018</b> , 11,	8.8	13
19	Protein complex scaffolding predicted as a prevalent function of long non-coding RNAs. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, 917-928	20.1	51
18	Human germinal center transcriptional programs are de-synchronized in B cell lymphoma. <i>Nature Immunology</i> , <b>2018</b> , 19, 1013-1024	19.1	64
17	Generation of a versatile BiFC ORFeome library for analyzing protein-protein interactions in live. <i>ELife</i> , <b>2018</b> , 7,	8.9	15
16	High-Dimensional Single-Cell Analysis Identifies Organ-Specific Signatures and Conserved NK Cell Subsets in Humans and Mice. <i>Immunity</i> , <b>2018</b> , 49, 971-986.e5	32.3	190
15	Protein synthesis inhibition and GADD34 control IFN- $\gamma$ heterogeneous expression in response to dsRNA. <i>EMBO Journal</i> , <b>2017</b> , 36, 761-782	13	40
14	Perturbed human sub-networks by <i>Fusobacterium nucleatum</i> candidate virulence proteins. <i>Microbiome</i> , <b>2017</b> , 5, 89	16.6	19
13	Guanabenz Prevents d-Galactosamine/Lipopolysaccharide-Induced Liver Damage and Mortality. <i>Frontiers in Immunology</i> , <b>2017</b> , 8, 679	8.4	11

12	Flux through a Markov chain. <i>Chaos, Solitons and Fractals</i> , <b>2016</b> , 93, 136-146	9.3	3
11	Pasha: a versatile R package for piling chromatin HTS data. <i>Bioinformatics</i> , <b>2016</b> , 32, 2528-30	7.2	14
10	BubbleGUM: automatic extraction of phenotype molecular signatures and comprehensive visualization of multiple Gene Set Enrichment Analyses. <i>BMC Genomics</i> , <b>2015</b> , 16, 814	4.5	52
9	Extreme multifunctional proteins identified from a human protein interaction network. <i>Nature Communications</i> , <b>2015</b> , 6, 7412	17.4	76
8	Experimental detection of long-distance interactions between biomolecules through their diffusion behavior: numerical study. <i>Physical Review E</i> , <b>2014</b> , 90, 022703	2.4	13
7	Tyrosine phosphorylation of RNA polymerase II CTD is associated with antisense promoter transcription and active enhancers in mammalian cells. <i>ELife</i> , <b>2014</b> , 3, e02105	8.9	58
6	Clust&See: a Cytoscape plugin for the identification, visualization and manipulation of network clusters. <i>BioSystems</i> , <b>2013</b> , 113, 91-5	1.9	33
5	Topology and phase transitions I. Preliminary results. <i>Nuclear Physics B</i> , <b>2007</b> , 782, 189-218	2.8	29
4	Topology and phase transitions: paradigmatic evidence. <i>Physical Review Letters</i> , <b>2000</b> , 84, 2774-7	7.4	44
3	Topological aspects of geometrical signatures of phase transitions. <i>Physical Review E</i> , <b>1999</b> , 60, R5009-12	2.4	33
2	Framework for cosmography at high redshift. <i>Monthly Notices of the Royal Astronomical Society</i> , <b>1996</b> , 279, 564-570	4.3	2
1	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