

# Søren Møller

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/230120/publications.pdf>

Version: 2024-02-01

17  
papers

2,139  
citations

567281

15  
h-index

940533

16  
g-index

18  
all docs

18  
docs citations

18  
times ranked

3692  
citing authors

#	ARTICLE	IF	CITATIONS
1	Gremlin 1+ fibroblastic niche maintains dendritic cell homeostasis in lymphoid tissues. <i>Nature Immunology</i> , 2021, 22, 571-585.	14.5	44
2	Interpretation of T cell states from single-cell transcriptomics data using reference atlases. <i>Nature Communications</i> , 2021, 12, 2965.	12.8	210
3	Cross-tissue organization of the fibroblast lineage. <i>Nature</i> , 2021, 593, 575-579.	27.8	463
4	A bird's eye view of fibroblast heterogeneity: A pan-disease, pan-cancer perspective. <i>Immunological Reviews</i> , 2021, 302, 299-320.	6.0	23
5	Single-Cell RNA Sequencing Reveals Stromal Evolution into LRR15+ Myofibroblasts as a Determinant of Patient Response to Cancer Immunotherapy. <i>Cancer Discovery</i> , 2020, 10, 232-253.	9.4	466
6	Outer Radial Glia-like Cancer Stem Cells Contribute to Heterogeneity of Glioblastoma. <i>Cell Stem Cell</i> , 2020, 26, 48-63.e6.	11.1	222
7	The Phenotypes of Proliferating Glioblastoma Cells Reside on a Single Axis of Variation. <i>Cancer Discovery</i> , 2019, 9, 1708-1719.	9.4	205
8	Coexpression of Inhibitory Receptors Enriches for Activated and Functional CD8+ T Cells in Murine Syngeneic Tumor Models. <i>Cancer Immunology Research</i> , 2019, 7, 963-976.	3.4	36
9	CONICS integrates scRNA-seq with DNA sequencing to map gene expression to tumor sub-clones. <i>Bioinformatics</i> , 2018, 34, 3217-3219.	4.1	87
10	Single-cell Co-expression Subnetwork Analysis. <i>Scientific Reports</i> , 2017, 7, 15066.	3.3	19
11	Transcriptomic Analyses of Adipocyte Differentiation From Human Mesenchymal Stromal Cells (MSC). <i>Journal of Cellular Physiology</i> , 2017, 232, 771-784.	4.1	29
12	GENT-22. SINGLE-CELL PROFILING OF GLIOBLASTOMA BIOPSIES IDENTIFIES A FAMILY OF ACTIVATING PDGF-RECEPTOR DELETIONS. <i>Neuro-Oncology</i> , 2016, 18, vi78-vi78.	1.2	0
13	Exploring the miRNA-mRNA Regulatory Network in Clear Cell Renal Cell Carcinomas by Next-Generation Sequencing Expression Profiles. <i>BioMed Research International</i> , 2014, 2014, 1-11.	1.9	36
14	Massive analysis of cDNA Ends (MACE) and miRNA expression profiling identifies proatherogenic pathways in chronic kidney disease. <i>Epigenetics</i> , 2014, 9, 161-172.	2.7	107
15	In silico analysis of regulatory networks underlines the role of miR-10b-5p and its target BDNF in huntington's disease. <i>Translational Neurodegeneration</i> , 2014, 3, 17.	8.0	34
16	APADB: a database for alternative polyadenylation and microRNA regulation events. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau076-bau076.	3.0	90
17	omiRas: a Web server for differential expression analysis of miRNAs derived from small RNA-Seq data. <i>Bioinformatics</i> , 2013, 29, 2651-2652.	4.1	67