

# Daniel Ramskjöld

## List of Publications by Year in descending order

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Version: 2024-02-01

34  
papers

5,423  
citations

304743

22  
h-index

414414

32  
g-index

38  
all docs

38  
docs citations

38  
times ranked

10680  
citing authors

#	ARTICLE	IF	CITATIONS
1	Full-length mRNA-Seq from single-cell levels of RNA and individual circulating tumor cells. <i>Nature Biotechnology</i> , 2012, 30, 777-782.	17.5	1,347
2	Single-Cell RNA-Seq Reveals Dynamic, Random Monoallelic Gene Expression in Mammalian Cells. <i>Science</i> , 2014, 343, 193-196.	12.6	1,164
3	An Abundance of Ubiquitously Expressed Genes Revealed by Tissue Transcriptome Sequence Data. <i>PLoS Computational Biology</i> , 2009, 5, e1000598.	3.2	777
4	Single-cell RNA counting at allele and isoform resolution using Smart-seq3. <i>Nature Biotechnology</i> , 2020, 38, 708-714.	17.5	399
5	Sequentially acting Sox transcription factors in neural lineage development. <i>Genes and Development</i> , 2011, 25, 2453-2464.	5.9	263
6	BMP Signaling and Its pSMAD1/5 Target Genes Differentially Regulate Hair Follicle Stem Cell Lineages. <i>Cell Stem Cell</i> , 2014, 15, 619-633.	11.1	145
7	Transcription factor Nurr1 maintains fiber integrity and nuclear-encoded mitochondrial gene expression in dopamine neurons. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2360-2365.	7.1	143
8	Analysis of allelic expression patterns in clonal somatic cells by single-cell RNA-seq. <i>Nature Genetics</i> , 2016, 48, 1430-1435.	21.4	142
9	Non-canonical Notch signaling activates IL-6/JAK/STAT signaling in breast tumor cells and is controlled by p53 and IKK1/IKK2. <i>Oncogene</i> , 2013, 32, 4892-4902.	5.9	121
10	Genome-wide mapping of promoter-anchored interactions with close to single-enhancer resolution. <i>Genome Biology</i> , 2015, 16, 156.	8.8	108
11	Recognition of Amino Acid Motifs, Rather Than Specific Proteins, by Human Plasma Cell-Derived Monoclonal Antibodies to Posttranslationally Modified Proteins in Rheumatoid Arthritis. <i>Arthritis and Rheumatology</i> , 2019, 71, 196-209.	5.6	99
12	Mouse Model of Alagille Syndrome and Mechanisms of Jagged1 Missense Mutations. <i>Gastroenterology</i> , 2018, 154, 1080-1095.	1.3	92
13	B cell alterations during BAFF inhibition with belimumab in SLE. <i>EBioMedicine</i> , 2019, 40, 517-527.	6.1	88
14	Smoking and pre-existing organ damage reduce the efficacy of belimumab in systemic lupus erythematosus. <i>Autoimmunity Reviews</i> , 2017, 16, 343-351.	5.8	80
15	The RNA WikiProject: Community annotation of RNA families. <i>Rna</i> , 2008, 14, 2462-2464.	3.5	66
16	B cells expressing the IgA receptor FcRL4 participate in the autoimmune response in patients with rheumatoid arthritis. <i>Journal of Autoimmunity</i> , 2017, 81, 34-43.	6.5	59
17	RNA Helicase A Is a Downstream Mediator of KIF1B <sup>Δ2</sup> Tumor-Suppressor Function in Neuroblastoma. <i>Cancer Discovery</i> , 2014, 4, 434-451.	9.4	48
18	Integration of Known DNA, RNA and Protein Biomarkers Provides Prediction of Anti-TNF Response in Rheumatoid Arthritis: Results from the COMBINE Study. <i>Molecular Medicine</i> , 2016, 22, 322-328.	4.4	39

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19	EOMESâ€positive CD4<sup>+</sup> Tâ€cells are increased in <i>PTPN22</i> (1858T) risk allele carriers. European Journal of Immunology, 2018, 48, 655-669.	2.9	33
20	Loss of CSL Unlocks a Hypoxic Response and Enhanced Tumor Growth Potential in Breast Cancer Cells. Stem Cell Reports, 2016, 6, 643-651.	4.8	31
21	Efficient and Comprehensive Representation of Uniqueness for Next-Generation Sequencing by Minimum Unique Length Analyses. PLoS ONE, 2013, 8, e53822.	2.5	29
22	T cells are influenced by a long non-coding RNA in the autoimmune associated PTPN2 locus. Journal of Autoimmunity, 2018, 90, 28-38.	6.5	29
23	How to Analyze Gene Expression Using RNA-Sequencing Data. Methods in Molecular Biology, 2012, 802, 259-274.	0.9	23
24	Intussusceptive Vascular Remodeling Precedes Pathological Neovascularization. Arteriosclerosis, Thrombosis, and Vascular Biology, 2019, 39, 1402-1418.	2.4	20
25	Systematic approach demonstrates enrichment of multiple interactions between non-<i>HLA</i> risk variants and <i>HLA-DRB1</i> risk alleles in rheumatoid arthritis. Annals of the Rheumatic Diseases, 2018, 77, 1454-1462.	0.9	19
26	Disruption of the Extracellular Matrix Progressively Impairs Central Nervous System Vascular Maturation Downstream of Î²-Catenin Signaling. Arteriosclerosis, Thrombosis, and Vascular Biology, 2019, 39, 1432-1447.	2.4	14
27	Decoding breast cancer tissueâ€stroma interactions using species-specific sequencing. Breast Cancer Research, 2015, 17, 109.	5.0	11
28	Effect of CTLA4â€Ig (abatacept) treatment on T cells and B cells in peripheral blood of patients with polymyositis and dermatomyositis. Scandinavian Journal of Immunology, 2019, 89, e12732.	2.7	8
29	Understanding interactions between risk factors, and assessing the utility of the additive and multiplicative models through simulations. PLoS ONE, 2021, 16, e0250282.	2.5	5
30	Immunoglobulin characteristics and RNAseq data of FcRL4+ B cells sorted from synovial fluid and tissue of patients with rheumatoid arthritis. Data in Brief, 2017, 13, 356-370.	1.0	3
31	Auxilin is a novel susceptibility gene for congenital heart block which directly impacts fetal heart function. Annals of the Rheumatic Diseases, 2022, 81, 1151-1161.	0.9	3
32	Circulating melanoma cells isolated from clinical blood samples and characterized by full-length mRNA sequencing at single-cell level.. Journal of Clinical Oncology, 2012, 30, 10539-10539.	1.6	1
33	08.41 cloning of gingival tissue b cells from an acpa+ ra patient with periodontitis. , 2017, , .		0
34	SAT0016â€...RHEUMATOID ARTHRITIS PATIENTS DISPLAY B-CELL DYSREGULATION ALREADY IN THE NAËVE REPERTOIRE. , 2019, , .		0