

Åsa K Bjorklund

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

9,610
citations

236925

25
h-index

361022

35
g-index

41
all docs

41
docs citations

41
times ranked

19056
citing authors

#	ARTICLE	IF	CITATIONS
1	Full-length RNA-seq from single cells using Smart-seq2. <i>Nature Protocols</i> , 2014, 9, 171-181.	12.0	3,308
2	Smart-seq2 for sensitive full-length transcriptome profiling in single cells. <i>Nature Methods</i> , 2013, 10, 1096-1098.	19.0	2,022
3	Tn5 transposase and tagmentation procedures for massively scaled sequencing projects. <i>Genome Research</i> , 2014, 24, 2033-2040.	5.5	692
4	Spatially and functionally distinct subclasses of breast cancer-associated fibroblasts revealed by single cell RNA sequencing. <i>Nature Communications</i> , 2018, 9, 5150.	12.8	496
5	The heterogeneity of human CD127+ innate lymphoid cells revealed by single-cell RNA sequencing. <i>Nature Immunology</i> , 2016, 17, 451-460.	14.5	416
6	What properties characterize the hub proteins of the protein-protein interaction network of <i>Saccharomyces cerevisiae</i> ?. <i>Genome Biology</i> , 2006, 7, R45.	9.6	337
7	Multi-domain Proteins in the Three Kingdoms of Life: Orphan Domains and Other Unassigned Regions. <i>Journal of Molecular Biology</i> , 2005, 348, 231-243.	4.2	230
8	Expansion of Protein Domain Repeats. <i>PLoS Computational Biology</i> , 2006, 2, e114.	3.2	225
9	Transcriptional Convergence of Oligodendrocyte Lineage Progenitors during Development. <i>Developmental Cell</i> , 2018, 46, 504-517.e7.	7.0	199
10	Arrangements in the modular evolution of proteins. <i>Trends in Biochemical Sciences</i> , 2008, 33, 444-451.	7.5	193
11	Domain Rearrangements in Protein Evolution. <i>Journal of Molecular Biology</i> , 2005, 353, 911-923.	4.2	190
12	Single-cell RNA sequencing reveals midbrain dopamine neuron diversity emerging during mouse brain development. <i>Nature Communications</i> , 2019, 10, 581.	12.8	189
13	Single-Cell Analysis Reveals a Close Relationship between Differentiating Dopamine and Subthalamic Nucleus Neuronal Lineages. <i>Cell Stem Cell</i> , 2017, 20, 29-40.	11.1	127
14	Prostaglandin E 2 suppresses human group 2 innate lymphoid cell function. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 1761-1773.e6.	2.9	119
15	Neuropilin-1 Is Expressed on Lymphoid Tissue Residing LTI-like Group 3 Innate Lymphoid Cells and Associated with Ectopic Lymphoid Aggregates. <i>Cell Reports</i> , 2017, 18, 1761-1773.	6.4	98
16	Tissue-specific transcriptional imprinting and heterogeneity in human innate lymphoid cells revealed by full-length single-cell RNA-sequencing. <i>Cell Research</i> , 2021, 31, 554-568.	12.0	97
17	Quantification of the Elevated Rate of Domain Rearrangements in Metazoa. <i>Journal of Molecular Biology</i> , 2007, 372, 1337-1348.	4.2	96
18	Supervised identification of allergen-representative peptides for <i>in silico</i> detection of potentially allergenic proteins. <i>Bioinformatics</i> , 2005, 21, 39-50.	4.1	88

#	ARTICLE	IF	CITATIONS
19	Single cell transcriptomics identifies stem cell-derived graft composition in a model of Parkinsonâ€™s disease. <i>Nature Communications</i> , 2020, 11, 2434.	12.8	54
20	A reference transcriptome and inferred proteome for the salamander <i>Notophthalmus viridescens</i> . <i>Experimental Cell Research</i> , 2013, 319, 1187-1197.	2.6	49
21	Nebulin: A Study of Protein Repeat Evolution. <i>Journal of Molecular Biology</i> , 2010, 402, 38-51.	4.2	47
22	Prototypical pacemaker neurons interact with the resident microbiota. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 17854-17863.	7.1	47
23	Limited access to antigen drives generation of early B cell memory while restraining the plasmablast response. <i>Immunity</i> , 2021, 54, 2005-2023.e10.	14.3	46
24	Sequentially acting SOX proteins orchestrate astrocyteâ€•and oligodendrocyteâ€•specific gene expression. <i>EMBO Reports</i> , 2018, 19, .	4.5	38
25	Spatio-molecular domains identified in the mouse subthalamic nucleus and neighboring glutamatergic and GABAergic brain structures. <i>Communications Biology</i> , 2020, 3, 338.	4.4	38
26	A comprehensive map coupling histone modifications with gene regulation in adult dopaminergic and serotonergic neurons. <i>Nature Communications</i> , 2018, 9, 1226.	12.8	35
27	Exploring parasite heterogeneity using single-cell RNA-seq reveals a gene signature among sexual stage <i>Plasmodium falciparum</i> parasites. <i>Experimental Cell Research</i> , 2018, 371, 130-138.	2.6	31
28	Characterization of the nuclear and cytosolic transcriptomes in human brain tissue reveals new insights into the subcellular distribution of RNA transcripts. <i>Scientific Reports</i> , 2021, 11, 4076.	3.3	27
29	Quantitative assessment of the structural bias in proteinâ€•protein interaction assays. <i>Proteomics</i> , 2008, 8, 4657-4667.	2.2	22
30	Conbase: a software for unsupervised discovery of clonal somatic mutations in single cells through read phasing. <i>Genome Biology</i> , 2019, 20, 68.	8.8	21
31	External cross-validation for unbiased evaluation of protein family detectors: Application to allergens. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 918-925.	2.6	7
32	The Use of Phylogenetic Profiles for Gene Predictions Revisited. <i>Current Genomics</i> , 2006, 7, 79-86.	1.6	1
33	Expansion of protein domain repeats. <i>PLoS Computational Biology</i> , 2005, preprint, e114.	3.2	0