

# Sarah A Teichmann

## List of Publications by Citations

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268  
papers

32,660  
citations

90  
h-index

178  
g-index

299  
ext. papers

44,354  
ext. citations

19.1  
avg, IF

7.54  
L-index

#	Paper	IF	Citations
268	Evolution of genes and genomes on the Drosophila phylogeny. <i>Nature</i> , <b>2007</b> , 450, 203-18	50.4	1586
267	SARS-CoV-2 Receptor ACE2 Is an Interferon-Stimulated Gene in Human Airway Epithelial Cells and Is Detected in Specific Cell Subsets across Tissues. <i>Cell</i> , <b>2020</b> , 181, 1016-1035.e19	56.2	1326
266	A census of human transcription factors: function, expression and evolution. <i>Nature Reviews Genetics</i> , <b>2009</b> , 10, 252-63	30.1	1090
265	Common variants near MC4R are associated with fat mass, weight and risk of obesity. <i>Nature Genetics</i> , <b>2008</b> , 40, 768-75	36.3	1048
264	Targeting CXCL12 from FAP-expressing carcinoma-associated fibroblasts synergizes with anti-PD-L1 immunotherapy in pancreatic cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 20212-7	11.5	1041
263	The Human Cell Atlas. <i>ELife</i> , <b>2017</b> , 6,	8.9	937
262	Single-cell reconstruction of the early maternal-fetal interface in humans. <i>Nature</i> , <b>2018</b> , 563, 347-353	50.4	792
261	Computational analysis of cell-to-cell heterogeneity in single-cell RNA-sequencing data reveals hidden subpopulations of cells. <i>Nature Biotechnology</i> , <b>2015</b> , 33, 155-60	44.5	778
260	Genomic analysis of regulatory network dynamics reveals large topological changes. <i>Nature</i> , <b>2004</b> , 431, 308-12	50.4	767
259	Computational and analytical challenges in single-cell transcriptomics. <i>Nature Reviews Genetics</i> , <b>2015</b> , 16, 133-45	30.1	736
258	Accounting for technical noise in single-cell RNA-seq experiments. <i>Nature Methods</i> , <b>2013</b> , 10, 1093-5	21.6	659
257	The technology and biology of single-cell RNA sequencing. <i>Molecular Cell</i> , <b>2015</b> , 58, 610-20	17.6	650
256	Structure and evolution of transcriptional regulatory networks. <i>Current Opinion in Structural Biology</i> , <b>2004</b> , 14, 283-91	8.1	556
255	An atlas of combinatorial transcriptional regulation in mouse and man. <i>Cell</i> , <b>2010</b> , 140, 744-52	56.2	555
254	CellPhoneDB: inferring cell-cell communication from combined expression of multi-subunit ligand-receptor complexes. <i>Nature Protocols</i> , <b>2020</b> , 15, 1484-1506	18.8	534
253	Evolution of the protein repertoire. <i>Science</i> , <b>2003</b> , 300, 1701-3	33.3	419
252	Gene regulatory network growth by duplication. <i>Nature Genetics</i> , <b>2004</b> , 36, 492-6	36.3	406

251	Exponential scaling of single-cell RNA-seq in the past decade. <i>Nature Protocols</i> , <b>2018</b> , 13, 599-604	18.8	400
250	Domain combinations in archaeal, eubacterial and eukaryotic proteomes. <i>Journal of Molecular Biology</i> , <b>2001</b> , 310, 311-25	6.5	389
249	Tight regulation of unstructured proteins: from transcript synthesis to protein degradation. <i>Science</i> , <b>2008</b> , 322, 1365-8	33.3	364
248	Power analysis of single-cell RNA-sequencing experiments. <i>Nature Methods</i> , <b>2017</b> , 14, 381-387	21.6	357
247	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , <b>2009</b> , 41, 553-62	36.3	356
246	Single Cell RNA-Sequencing of Pluripotent States Unlocks Modular Transcriptional Variation. <i>Cell Stem Cell</i> , <b>2015</b> , 17, 471-85	18	343
245	A cellular census of human lungs identifies novel cell states in health and in asthma. <i>Nature Medicine</i> , <b>2019</b> , 25, 1153-1163	50.5	334
244	A practical guide to single-cell RNA-sequencing for biomedical research and clinical applications. <i>Genome Medicine</i> , <b>2017</b> , 9, 75	14.4	332
243	Classification of low quality cells from single-cell RNA-seq data. <i>Genome Biology</i> , <b>2016</b> , 17, 29	18.3	329
242	Assembly reflects evolution of protein complexes. <i>Nature</i> , <b>2008</b> , 453, 1262-5	50.4	316
241	The Human Cell Atlas: from vision to reality. <i>Nature</i> , <b>2017</b> , 550, 451-453	50.4	310
240	T cell fate and clonality inference from single-cell transcriptomes. <i>Nature Methods</i> , <b>2016</b> , 13, 329-332	21.6	302
239	Structure, function and evolution of multidomain proteins. <i>Current Opinion in Structural Biology</i> , <b>2004</b> , 14, 208-16	8.1	299
238	Single-cell transcriptomes from human kidneys reveal the cellular identity of renal tumors. <i>Science</i> , <b>2018</b> , 361, 594-599	33.3	282
237	Single-cell transcriptomics to explore the immune system in health and disease. <i>Science</i> , <b>2017</b> , 358, 58-63	33.3	275
236	Cells of the adult human heart. <i>Nature</i> , <b>2020</b> , 588, 466-472	50.4	274
235	The importance of sequence diversity in the aggregation and evolution of proteins. <i>Nature</i> , <b>2005</b> , 438, 878-81	50.4	263
234	Computational assignment of cell-cycle stage from single-cell transcriptome data. <i>Methods</i> , <b>2015</b> , 85, 54-61	4.6	259

233	The folding and evolution of multidomain proteins. <i>Nature Reviews Molecular Cell Biology</i> , <b>2007</b> , 8, 319-348.7	257
232	3D complex: a structural classification of protein complexes. <i>PLoS Computational Biology</i> , <b>2006</b> , 2, e155	256
231	Evolution of transcription factors and the gene regulatory network in Escherichia coli. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 1234-44	20.1 234
230	Structure, dynamics, assembly, and evolution of protein complexes. <i>Annual Review of Biochemistry</i> , <b>2015</b> , 84, 551-75	29.1 227
229	DBD--taxonomically broad transcription factor predictions: new content and functionality. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D88-92	20.1 226
228	Polycomb associates genome-wide with a specific RNA polymerase II variant, and regulates metabolic genes in ESCs. <i>Cell Stem Cell</i> , <b>2012</b> , 10, 157-70	18 221
227	Depletion of stromal cells expressing fibroblast activation protein-1 from skeletal muscle and bone marrow results in cachexia and anemia. <i>Journal of Experimental Medicine</i> , <b>2013</b> , 210, 1137-51	16.6 219
226	RNA sequencing reveals two major classes of gene expression levels in metazoan cells. <i>Molecular Systems Biology</i> , <b>2011</b> , 7, 497	12.2 219
225	Evolutionary dynamics of prokaryotic transcriptional regulatory networks. <i>Journal of Molecular Biology</i> , <b>2006</b> , 358, 614-33	6.5 217
224	Decoding human fetal liver haematopoiesis. <i>Nature</i> , <b>2019</b> , 574, 365-371	50.4 200
223	A HaemAtlas: characterizing gene expression in differentiated human blood cells. <i>Blood</i> , <b>2009</b> , 113, e1-92.2	193
222	Single-cell RNA-seq identifies a PD-1 ILC progenitor and defines its development pathway. <i>Nature</i> , <b>2016</b> , 539, 102-106	50.4 186
221	Single-Cell Transcriptomics of Regulatory T Cells Reveals Trajectories of Tissue Adaptation. <i>Immunity</i> , <b>2019</b> , 50, 493-504.e7	32.3 175
220	SARS-CoV-2 infection of the oral cavity and saliva. <i>Nature Medicine</i> , <b>2021</b> , 27, 892-903	50.5 175
219	Single-cell RNA-seq and computational analysis using temporal mixture modelling resolves Th1/Tfh fate bifurcation in malaria. <i>Science Immunology</i> , <b>2017</b> , 2,	28 171
218	A cell atlas of human thymic development defines T cell repertoire formation. <i>Science</i> , <b>2020</b> , 367,	33.3 171
217	DBD: a transcription factor prediction database. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D74-81	20.1 163
216	Expression Atlas update: from tissues to single cells. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, D77-D83	20.1 159

215	Aging increases cell-to-cell transcriptional variability upon immune stimulation. <i>Science</i> , <b>2017</b> , 355, 1433-1436	14.3	158
214	Characterizing noise structure in single-cell RNA-seq distinguishes genuine from technical stochastic allelic expression. <i>Nature Communications</i> , <b>2015</b> , 6, 8687	17.4	154
213	BBKNN: fast batch alignment of single cell transcriptomes. <i>Bioinformatics</i> , <b>2020</b> , 36, 964-965	7.2	154
212	SpatialDE: identification of spatially variable genes. <i>Nature Methods</i> , <b>2018</b> , 15, 343-346	21.6	153
211	Protein complexes are under evolutionary selection to assemble via ordered pathways. <i>Cell</i> , <b>2013</b> , 153, 461-70	56.2	153
210	Circulating and Tissue-Resident CD4 T Cells With Reactivity to Intestinal Microbiota Are Abundant in Healthy Individuals and Function Is Altered During Inflammation. <i>Gastroenterology</i> , <b>2017</b> , 153, 1320-1337.e16	13.2	150
209	Mapping protein family interactions: intramolecular and intermolecular protein family interaction repertoires in the PDB and yeast. <i>Journal of Molecular Biology</i> , <b>2001</b> , 307, 929-38	6.5	148
208	Spatiotemporal immune zonation of the human kidney. <i>Science</i> , <b>2019</b> , 365, 1461-1466	33.3	145
207	Relative rates of gene fusion and fission in multi-domain proteins. <i>Trends in Genetics</i> , <b>2005</b> , 21, 25-30	8.5	144
206	Single-cell RNA sequencing reveals T helper cells synthesizing steroids de novo to contribute to immune homeostasis. <i>Cell Reports</i> , <b>2014</b> , 7, 1130-42	10.6	143
205	Principles of assembly reveal a periodic table of protein complexes. <i>Science</i> , <b>2015</b> , 350, aaa2245	33.3	142
204	A test metric for assessing single-cell RNA-seq batch correction. <i>Nature Methods</i> , <b>2019</b> , 16, 43-49	21.6	140
203	Evolution of protein complexes by duplication of homomeric interactions. <i>Genome Biology</i> , <b>2007</b> , 8, R51	18.3	139
202	Supra-domains: evolutionary units larger than single protein domains. <i>Journal of Molecular Biology</i> , <b>2004</b> , 336, 809-23	6.5	139
201	The interface of protein structure, protein biophysics, and molecular evolution. <i>Protein Science</i> , <b>2012</b> , 21, 769-85	6.3	136
200	The relationship between domain duplication and recombination. <i>Journal of Molecular Biology</i> , <b>2005</b> , 346, 355-65	6.5	131
199	Establishment of mouse expanded potential stem cells. <i>Nature</i> , <b>2017</b> , 550, 393-397	50.4	128
198	Establishment of porcine and human expanded potential stem cells. <i>Nature Cell Biology</i> , <b>2019</b> , 21, 687-699	39.4	127

197	Advances in structural genomics. <i>Current Opinion in Structural Biology</i> , <b>1999</b> , 9, 390-9	8.1	121
196	Cellular crowding imposes global constraints on the chemistry and evolution of proteomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 20461-6	11.5	120
195	Relative solvent accessible surface area predicts protein conformational changes upon binding. <i>Structure</i> , <b>2011</b> , 19, 859-67	5.2	120
194	Single-Cell RNA-Sequencing Reveals a Continuous Spectrum of Differentiation in Hematopoietic Cells. <i>Cell Reports</i> , <b>2016</b> , 14, 966-977	10.6	119
193	Single-Cell Transcriptomics Uncovers Zonation of Function in the Mesenchyme during Liver Fibrosis. <i>Cell Reports</i> , <b>2019</b> , 29, 1832-1847.e8	10.6	115
192	The origins and evolution of functional modules: lessons from protein complexes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2006</b> , 361, 507-17	5.8	113
191	MERVL/Zscan4 Network Activation Results in Transient Genome-wide DNA Demethylation of mESCs. <i>Cell Reports</i> , <b>2016</b> , 17, 179-192	10.6	111
190	Longitudinal Multi-omics Analyses Identify Responses of Megakaryocytes, Erythroid Cells, and Plasmablasts as Hallmarks of Severe COVID-19. <i>Immunity</i> , <b>2020</b> , 53, 1296-1314.e9	32.3	109
189	Genomic repertoires of DNA-binding transcription factors across the tree of life. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, 7364-77	20.1	102
188	Single-cell multi-omics analysis of the immune response in COVID-19. <i>Nature Medicine</i> , <b>2021</b> , 27, 904-916	50.5	101
187	The transcriptional program controlled by the stem cell leukemia gene Scl/Tal1 during early embryonic hematopoietic development. <i>Blood</i> , <b>2009</b> , 113, 5456-65	2.2	100
186	The Human Lung Cell Atlas: A High-Resolution Reference Map of the Human Lung in Health and Disease. <i>American Journal of Respiratory Cell and Molecular Biology</i> , <b>2019</b> , 61, 31-41	5.7	98
185	Altered TMPRSS2 usage by SARS-CoV-2 Omicron impacts tropism and fusogenicity.. <i>Nature</i> , <b>2022</b> ,	50.4	95
184	Gene expression variability across cells and species shapes innate immunity. <i>Nature</i> , <b>2018</b> , 563, 197-202	50.4	94
183	Single cell RNA-seq and ATAC-seq analysis of cardiac progenitor cell transition states and lineage settlement. <i>Nature Communications</i> , <b>2018</b> , 9, 4877	17.4	93
182	Distinct microbial and immune niches of the human colon. <i>Nature Immunology</i> , <b>2020</b> , 21, 343-353	19.1	92
181	The constraints protein-protein interactions place on sequence divergence. <i>Journal of Molecular Biology</i> , <b>2002</b> , 324, 399-407	6.5	92
180	The evolution and structural anatomy of the small molecule metabolic pathways in Escherichia coli. <i>Journal of Molecular Biology</i> , <b>2001</b> , 311, 693-708	6.5	91

179	A rapid and robust method for single cell chromatin accessibility profiling. <i>Nature Communications</i> , <b>2018</b> , 9, 5345	17.4	91
178	The immunoglobulin superfamily in <i>Drosophila melanogaster</i> and <i>Caenorhabditis elegans</i> and the evolution of complexity. <i>Development (Cambridge)</i> , <b>2003</b> , 130, 6317-28	6.6	89
177	Wounding induces dedifferentiation of epidermal Gata6 cells and acquisition of stem cell properties. <i>Nature Cell Biology</i> , <b>2017</b> , 19, 603-613	23.4	87
176	Probing the diverse landscape of protein flexibility and binding. <i>Current Opinion in Structural Biology</i> , <b>2012</b> , 22, 643-50	8.1	87
175	Immunoglobulin superfamily proteins in <i>Caenorhabditis elegans</i> . <i>Journal of Molecular Biology</i> , <b>2000</b> , 296, 1367-83	6.5	87
174	FlyTF: a systematic review of site-specific transcription factors in the fruit fly <i>Drosophila melanogaster</i> . <i>Bioinformatics</i> , <b>2006</b> , 22, 1532-3	7.2	79
173	Conservation of gene co-regulation in prokaryotes and eukaryotes. <i>Trends in Biotechnology</i> , <b>2002</b> , 20, 407-10; discussion 410	15.1	79
172	Structural, evolutionary, and assembly principles of protein oligomerization. <i>Progress in Molecular Biology and Translational Science</i> , <b>2013</b> , 117, 25-51	4	77
171	Computational approaches for interpreting scRNA-seq data. <i>FEBS Letters</i> , <b>2017</b> , 591, 2213-2225	3.8	75
170	Single-cell transcriptomic reconstruction reveals cell cycle and multi-lineage differentiation defects in Bcl11a-deficient hematopoietic stem cells. <i>Genome Biology</i> , <b>2015</b> , 16, 178	18.3	74
169	Multi-domain protein families and domain pairs: comparison with known structures and a random model of domain recombination. <i>Journal of Structural and Functional Genomics</i> , <b>2003</b> , 4, 67-78		74
168	Statistical analysis of domains in interacting protein pairs. <i>Bioinformatics</i> , <b>2005</b> , 21, 993-1001	7.2	73
167	Genome-wide CRISPR Screens in T Helper Cells Reveal Pervasive Crosstalk between Activation and Differentiation. <i>Cell</i> , <b>2019</b> , 176, 882-896.e18	56.2	72
166	The role of salt bridges, charge density, and subunit flexibility in determining disassembly routes of protein complexes. <i>Structure</i> , <b>2013</b> , 21, 1325-37	5.2	71
165	Novel specificities emerge by stepwise duplication of functional modules. <i>Genome Research</i> , <b>2005</b> , 15, 552-9	9.7	70
164	Computational methods for single-cell omics across modalities. <i>Nature Methods</i> , <b>2020</b> , 17, 14-17	21.6	70
163	Functional determinants of transcription factors in <i>Escherichia coli</i> : protein families and binding sites. <i>Trends in Genetics</i> , <b>2003</b> , 19, 75-9	8.5	69
162	Is there a phylogenetic signal in prokaryote proteins?. <i>Journal of Molecular Evolution</i> , <b>1999</b> , 49, 98-107	3.1	64

161	Single-Cell RNA Sequencing Reveals a Dynamic Stromal Niche That Supports Tumor Growth. <i>Cell Reports</i> , <b>2020</b> , 31, 107628	10.6	63
160	Developmental cell programs are co-opted in inflammatory skin disease. <i>Science</i> , <b>2021</b> , 371,	33.3	63
159	The emergence of protein complexes: quaternary structure, dynamics and allostery. Colworth Medal Lecture. <i>Biochemical Society Transactions</i> , <b>2012</b> , 40, 475-91	5.1	61
158	FlyTF: improved annotation and enhanced functionality of the Drosophila transcription factor database. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D443-7	20.1	61
157	Single-cell transcriptome analysis of fish immune cells provides insight into the evolution of vertebrate immune cell types. <i>Genome Research</i> , <b>2017</b> , 27, 451-461	9.7	59
156	Single cell transcriptomics comes of age. <i>Nature Communications</i> , <b>2020</b> , 11, 4307	17.4	59
155	From Tissues to Cell Types and Back: Single-Cell Gene Expression Analysis of Tissue Architecture. <i>Annual Review of Biomedical Data Science</i> , <b>2018</b> , 1, 29-51	5.6	59
154	Divergence of interdomain geometry in two-domain proteins. <i>Structure</i> , <b>2006</b> , 14, 935-45	5.2	58
153	Assessing computational methods of cis-regulatory module prediction. <i>PLoS Computational Biology</i> , <b>2010</b> , 6, e1001020	5	57
152	The (in)dependence of alternative splicing and gene duplication. <i>PLoS Computational Biology</i> , <b>2007</b> , 3, e33	5	57
151	Protein flexibility facilitates quaternary structure assembly and evolution. <i>PLoS Biology</i> , <b>2014</b> , 12, e1001870	18.7	56
150	How do proteins gain new domains?. <i>Genome Biology</i> , <b>2010</b> , 11, 126	18.3	56
149	LifeTime and improving European healthcare through cell-based interceptive medicine. <i>Nature</i> , <b>2020</b> , 587, 377-386	50.4	56
148	Polychromic Reporter Mice Reveal Unappreciated Innate Lymphoid Cell Progenitor Heterogeneity and Elusive ILC3 Progenitors in Bone Marrow. <i>Immunity</i> , <b>2019</b> , 51, 104-118.e7	32.3	53
147	Single cell analysis of human foetal liver captures the transcriptional profile of hepatobiliary hybrid progenitors. <i>Nature Communications</i> , <b>2019</b> , 10, 3350	17.4	52
146	An atlas of mouse CD4(+) T cell transcriptomes. <i>Biology Direct</i> , <b>2015</b> , 10, 14	7.2	50
145	Evolution of oligomeric state through allosteric pathways that mimic ligand binding. <i>Science</i> , <b>2014</b> , 346, 1254346	33.3	49
144	BraCeR: B-cell-receptor reconstruction and clonality inference from single-cell RNA-seq. <i>Nature Methods</i> , <b>2018</b> , 15, 563-565	21.6	48



143	Parallel dynamics and evolution: Protein conformational fluctuations and assembly reflect evolutionary changes in sequence and structure. <i>BioEssays</i> , <b>2014</b> , 36, 209-18	4.1	48
142	Comparative analysis of sequencing technologies for single-cell transcriptomics. <i>Genome Biology</i> , <b>2019</b> , 20, 70	18.3	47
141	Single-Cell Sequencing of Developing Human Gut Reveals Transcriptional Links to Childhood Crohn's Disease. <i>Developmental Cell</i> , <b>2020</b> , 55, 771-783.e5	10.2	47
140	Single-cell analysis of CD4+ T-cell differentiation reveals three major cell states and progressive acceleration of proliferation. <i>Genome Biology</i> , <b>2016</b> , 17, 103	18.3	46
139	Regulation of protein-protein binding by coupling between phosphorylation and intrinsic disorder: analysis of human protein complexes. <i>Molecular BioSystems</i> , <b>2013</b> , 9, 1620-6		45
138	Cholangiocyte organoids can repair bile ducts after transplantation in the human liver. <i>Science</i> , <b>2021</b> , 371, 839-846	33.3	45
137	Regulation, evolution and consequences of cotranslational protein complex assembly. <i>Current Opinion in Structural Biology</i> , <b>2017</b> , 42, 90-97	8.1	44
136	Homology, pathway distance and chromosomal localization of the small molecule metabolism enzymes in Escherichia coli. <i>Journal of Molecular Biology</i> , <b>2002</b> , 318, 911-32	6.5	44
135	Fast assignment of protein structures to sequences using the intermediate sequence library PDB-ISL. <i>Bioinformatics</i> , <b>2000</b> , 16, 117-24	7.2	44
134	Immunology Driven by Large-Scale Single-Cell Sequencing. <i>Trends in Immunology</i> , <b>2019</b> , 40, 1011-1021	14.4	43
133	Flipping between Polycomb repressed and active transcriptional states introduces noise in gene expression. <i>Nature Communications</i> , <b>2017</b> , 8, 36	17.4	43
132	The Human Cell Atlas <b>2017</b> ,		41
131	High-Resolution mRNA and Secretome Atlas of Human Enteroendocrine Cells. <i>Cell</i> , <b>2020</b> , 181, 1291-1306.e19	9.1	41
130	Protein domain organisation: adding order. <i>BMC Bioinformatics</i> , <b>2009</b> , 10, 39	3.6	41
129	Functional protein divergence in the evolution of Homo sapiens. <i>Genome Biology</i> , <b>2008</b> , 9, R33	18.3	41
128	The impact of genomic neighborhood on the evolution of human and chimpanzee transcriptome. <i>Genome Research</i> , <b>2009</b> , 19, 785-94	9.7	40
127	Cells of the human intestinal tract mapped across space and time. <i>Nature</i> , <b>2021</b> , 597, 250-255	50.4	40
126	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. <i>Developmental Cell</i> , <b>2019</b> , 49, 10-29	10.2	39

125	Prenatal development of human immunity. <i>Science</i> , <b>2020</b> , 368, 600-603	33.3	39
124	Single-cell analysis of human B cell maturation predicts how antibody class switching shapes selection dynamics. <i>Science Immunology</i> , <b>2021</b> , 6,	28	39
123	Evolution of oligomeric state through geometric coupling of protein interfaces. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 8127-32	11.5	38
122	Intrinsic transcriptional heterogeneity in B cells controls early class switching to IgE. <i>Journal of Experimental Medicine</i> , <b>2017</b> , 214, 183-196	16.6	35
121	Construction of a large extracellular protein interaction network and its resolution by spatiotemporal expression profiling. <i>Molecular and Cellular Proteomics</i> , <b>2010</b> , 9, 2654-65	7.6	35
120	Lineage-specific expansion of DNA-binding transcription factor families. <i>Trends in Genetics</i> , <b>2010</b> , 26, 388-93	8.5	35
119	Nasal DNA methylation profiling of asthma and rhinitis. <i>Journal of Allergy and Clinical Immunology</i> , <b>2020</b> , 145, 1655-1663	11.5	34
118	EpiChIP: gene-by-gene quantification of epigenetic modification levels. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, e27	20.1	34
117	Single-cell transcriptomics identifies CD44 as a marker and regulator of endothelial to haematopoietic transition. <i>Nature Communications</i> , <b>2020</b> , 11, 586	17.4	33
116	Single-cell sequencing reveals clonal expansions of pro-inflammatory synovial CD8 T cells expressing tissue-homing receptors in psoriatic arthritis. <i>Nature Communications</i> , <b>2020</b> , 11, 4767	17.4	33
115	Mapping the temporal and spatial dynamics of the human endometrium in vivo and in vitro. <i>Nature Genetics</i> , <b>2021</b> , 53, 1698-1711	36.3	32
114	Integrated scRNA-Seq Identifies Human Postnatal Thymus Seeding Progenitors and Regulatory Dynamics of Differentiating Immature Thymocytes. <i>Immunity</i> , <b>2020</b> , 52, 1088-1104.e6	32.3	31
113	Putative cell type discovery from single-cell gene expression data. <i>Nature Methods</i> , <b>2020</b> , 17, 621-628	21.6	30
112	BloodExpress: a database of gene expression in mouse haematopoiesis. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D873-9	20.1	30
111	The Organoid Cell Atlas. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 13-17	44.5	30
110	Structural and evolutionary versatility in protein complexes with uneven stoichiometry. <i>Nature Communications</i> , <b>2015</b> , 6, 6394	17.4	29
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108	Unbiased classification of mosquito blood cells by single-cell genomics and high-content imaging. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, E7568-E7577	11.5	28

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