

Sarah A Teichmann

List of Publications by Year in descending order

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239
papers

53,032
citations

1893

102
h-index

1980

206
g-index

299
all docs

299
docs citations

299
times ranked

64078
citing authors

#	ARTICLE	IF	CITATIONS
1	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> , 2020, 181, 1016-1035.e19.	28.9	1,956
2	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	27.8	1,886
3	CellPhoneDB: inferring cell-cell communication from combined expression of multi-subunit ligand-receptor complexes. <i>Nature Protocols</i> , 2020, 15, 1484-1506.	12.0	1,768
4	The Human Cell Atlas. <i>ELife</i> , 2017, 6, .	6.0	1,547
5	Single-cell reconstruction of the early maternal-fetal interface in humans. <i>Nature</i> , 2018, 563, 347-353.	27.8	1,547
6	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> , 2013, 110, 20212-20217.	7.1	1,482
7	A census of human transcription factors: function, expression and evolution. <i>Nature Reviews Genetics</i> , 2009, 10, 252-263.	16.3	1,357
8	Common variants near MC4R are associated with fat mass, weight and risk of obesity. <i>Nature Genetics</i> , 2008, 40, 768-775.	21.4	1,179
9	Computational analysis of cell-to-cell heterogeneity in single-cell RNA-sequencing data reveals hidden subpopulations of cells. <i>Nature Biotechnology</i> , 2015, 33, 155-160.	17.5	1,068
10	Computational and analytical challenges in single-cell transcriptomics. <i>Nature Reviews Genetics</i> , 2015, 16, 133-145.	16.3	1,043
11	The Technology and Biology of Single-Cell RNA Sequencing. <i>Molecular Cell</i> , 2015, 58, 610-620.	9.7	1,014
12	Accounting for technical noise in single-cell RNA-seq experiments. <i>Nature Methods</i> , 2013, 10, 1093-1095.	19.0	929
13	Genomic analysis of regulatory network dynamics reveals large topological changes. <i>Nature</i> , 2004, 431, 308-312.	27.8	921
14	Cells of the adult human heart. <i>Nature</i> , 2020, 588, 466-472.	27.8	852
15	Altered TMPRSS2 usage by SARS-CoV-2 Omicron impacts infectivity and fusogenicity. <i>Nature</i> , 2022, 603, 706-714.	27.8	756
16	A practical guide to single-cell RNA-sequencing for biomedical research and clinical applications. <i>Genome Medicine</i> , 2017, 9, 75.	8.2	712
17	Exponential scaling of single-cell RNA-seq in the past decade. <i>Nature Protocols</i> , 2018, 13, 599-604.	12.0	704
18	Structure and evolution of transcriptional regulatory networks. <i>Current Opinion in Structural Biology</i> , 2004, 14, 283-291.	5.7	683

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19	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. Cell, 2010, 140, 744-752.	28.9	667
20	A cellular census of human lungs identifies novel cell states in health and in asthma. Nature Medicine, 2019, 25, 1153-1163.	30.7	631
21	Classification of low quality cells from single-cell RNA-seq data. Genome Biology, 2016, 17, 29.	8.8	572
22	SARS-CoV-2 infection of the oral cavity and saliva. Nature Medicine, 2021, 27, 892-903.	30.7	527
23	BBKNN: fast batch alignment of single cell transcriptomes. Bioinformatics, 2020, 36, 964-965.	4.1	517
24	Single-cell transcriptomes from human kidneys reveal the cellular identity of renal tumors. Science, 2018, 361, 594-599.	12.6	511
25	The Human Cell Atlas: from vision to reality. Nature, 2017, 550, 451-453.	27.8	511
26	Single Cell RNA-Sequencing of Pluripotent States Unlocks Modular Transcriptional Variation. Cell Stem Cell, 2015, 17, 471-485.	11.1	505
27	Power analysis of single-cell RNA-sequencing experiments. Nature Methods, 2017, 14, 381-387.	19.0	496
28	Evolution of the Protein Repertoire. Science, 2003, 300, 1701-1703.	12.6	494
29	Gene regulatory network growth by duplication. Nature Genetics, 2004, 36, 492-496.	21.4	475
30	Domain combinations in archaeal, eubacterial and eukaryotic proteomes. Journal of Molecular Biology, 2001, 310, 311-325.	4.2	452
31	Single-cell multi-omics analysis of the immune response in COVID-19. Nature Medicine, 2021, 27, 904-916.	30.7	452
32	Single-cell transcriptomics to explore the immune system in health and disease. Science, 2017, 358, 58-63.	12.6	440
33	Tight Regulation of Unstructured Proteins: From Transcript Synthesis to Protein Degradation. Science, 2008, 322, 1365-1368.	12.6	419
34	T cell fate and clonality inference from single-cell transcriptomes. Nature Methods, 2016, 13, 329-332.	19.0	411
35	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. Nature Genetics, 2009, 41, 553-562.	21.4	408
36	Decoding human fetal liver haematopoiesis. Nature, 2019, 574, 365-371.	27.8	392

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37	Assembly reflects evolution of protein complexes. <i>Nature</i> , 2008, 453, 1262-1265.	27.8	383
38	SpatialDE: identification of spatially variable genes. <i>Nature Methods</i> , 2018, 15, 343-346.	19.0	382
39	Computational assignment of cell-cycle stage from single-cell transcriptome data. <i>Methods</i> , 2015, 85, 54-61.	3.8	381
40	Structure, function and evolution of multidomain proteins. <i>Current Opinion in Structural Biology</i> , 2004, 14, 208-216.	5.7	379
41	A cell atlas of human thymic development defines T cell repertoire formation. <i>Science</i> , 2020, 367, .	12.6	368
42	Expression Atlas update: from tissues to single cells. <i>Nucleic Acids Research</i> , 2020, 48, D77-D83.	14.5	363
43	Single-Cell Transcriptomics of Regulatory T Cells Reveals Trajectories of Tissue Adaptation. <i>Immunity</i> , 2019, 50, 493-504.e7.	14.3	352
44	Structure, Dynamics, Assembly, and Evolution of Protein Complexes. <i>Annual Review of Biochemistry</i> , 2015, 84, 551-575.	11.1	351
45	The folding and evolution of multidomain proteins. <i>Nature Reviews Molecular Cell Biology</i> , 2007, 8, 319-330.	37.0	341
46	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> , 2013, 210, 1137-1151.	8.5	304
47	3D Complex: A Structural Classification of Protein Complexes. <i>PLoS Computational Biology</i> , 2006, 2, e155.	3.2	299
48	The importance of sequence diversity in the aggregation and evolution of proteins. <i>Nature</i> , 2005, 438, 878-881.	27.8	291
49	Evolution of transcription factors and the gene regulatory network in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2003, 31, 1234-1244.	14.5	283
50	Spatiotemporal immune zonation of the human kidney. <i>Science</i> , 2019, 365, 1461-1466.	12.6	281
51	A test metric for assessing single-cell RNA-seq batch correction. <i>Nature Methods</i> , 2019, 16, 43-49.	19.0	278
52	Longitudinal Multi-omics Analyses Identify Responses of Megakaryocytes, Erythroid Cells, and Plasmablasts as Hallmarks of Severe COVID-19. <i>Immunity</i> , 2020, 53, 1296-1314.e9.	14.3	278
53	Cells of the human intestinal tract mapped across space and time. <i>Nature</i> , 2021, 597, 250-255.	27.8	266
54	RNA sequencing reveals two major classes of gene expression levels in metazoan cells. <i>Molecular Systems Biology</i> , 2011, 7, 497.	7.2	265

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55	Aging increases cell-to-cell transcriptional variability upon immune stimulation. <i>Science</i> , 2017, 355, 1433-1436.	12.6	265
56	Cross-tissue immune cell analysis reveals tissue-specific features in humans. <i>Science</i> , 2022, 376, eabl5197.	12.6	265
57	Developmental cell programs are co-opted in inflammatory skin disease. <i>Science</i> , 2021, 371, .	12.6	264
58	Polycomb Associates Genome-wide with a Specific RNA Polymerase II Variant, and Regulates Metabolic Genes in ESCs. <i>Cell Stem Cell</i> , 2012, 10, 157-170.	11.1	261
59	Single-Cell Transcriptomics Uncovers Zonation of Function in the Mesenchyme during Liver Fibrosis. <i>Cell Reports</i> , 2019, 29, 1832-1847.e8.	6.4	261
60	Establishment of porcine and human expanded potential stem cells. <i>Nature Cell Biology</i> , 2019, 21, 687-699.	10.3	261
61	Single-cell RNA-seq and computational analysis using temporal mixture modeling resolves T _H 1/T _{FH} fate bifurcation in malaria. <i>Science Immunology</i> , 2017, 2, .	11.9	258
62	Single-cell RNA-seq identifies a PD-1hi ILC progenitor and defines its development pathway. <i>Nature</i> , 2016, 539, 102-106.	27.8	257
63	Evolutionary Dynamics of Prokaryotic Transcriptional Regulatory Networks. <i>Journal of Molecular Biology</i> , 2006, 358, 614-633.	4.2	254
64	DBDâ€™s taxonomically broad transcription factor predictions: new content and functionality. <i>Nucleic Acids Research</i> , 2008, 36, D88-D92.	14.5	254
65	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> , 2017, 153, 1320-1337.e16.	1.3	246
66	Mapping the temporal and spatial dynamics of the human endometrium in vivo and in vitro. <i>Nature Genetics</i> , 2021, 53, 1698-1711.	21.4	238
67	Differential abundance testing on single-cell data using k-nearest neighbor graphs. <i>Nature Biotechnology</i> , 2022, 40, 245-253.	17.5	229
68	Establishment of mouse expanded potential stem cells. <i>Nature</i> , 2017, 550, 393-397.	27.8	223
69	A HaemAtlas: characterizing gene expression in differentiated human blood cells. <i>Blood</i> , 2009, 113, e1-e9.	1.4	215
70	Protein Complexes Are under Evolutionary Selection to Assemble via Ordered Pathways. <i>Cell</i> , 2013, 153, 461-470.	28.9	215
71	Characterizing noise structure in single-cell RNA-seq distinguishes genuine from technical stochastic allelic expression. <i>Nature Communications</i> , 2015, 6, 8687.	12.8	213
72	Single-Cell RNA Sequencing Reveals T Helper Cells Synthesizing Steroids De Novo to Contribute to Immune Homeostasis. <i>Cell Reports</i> , 2014, 7, 1130-1142.	6.4	198

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73	Principles of assembly reveal a periodic table of protein complexes. <i>Science</i> , 2015, 350, aaa2245.	12.6	198
74	Single cell transcriptomics comes of age. <i>Nature Communications</i> , 2020, 11, 4307.	12.8	194
75	The interface of protein structure, protein biophysics, and molecular evolution. <i>Protein Science</i> , 2012, 21, 769-785.	7.6	188
76	A rapid and robust method for single cell chromatin accessibility profiling. <i>Nature Communications</i> , 2018, 9, 5345.	12.8	188
77	DBD: a transcription factor prediction database. <i>Nucleic Acids Research</i> , 2006, 34, D74-D81.	14.5	186
78	Single-Cell RNA Sequencing Reveals a Dynamic Stromal Niche That Supports Tumor Growth. <i>Cell Reports</i> , 2020, 31, 107628.	6.4	186
79	Integrated Single-Cell Atlas of Endothelial Cells of the Human Lung. <i>Circulation</i> , 2021, 144, 286-302.	1.6	181
80	Local and systemic responses to SARS-CoV-2 infection in children and adults. <i>Nature</i> , 2022, 602, 321-327.	27.8	179
81	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> , 2019, 61, 31-41.	2.9	178
82	Distinct microbial and immune niches of the human colon. <i>Nature Immunology</i> , 2020, 21, 343-353.	14.5	175
83	Relative Solvent Accessible Surface Area Predicts Protein Conformational Changes upon Binding. <i>Structure</i> , 2011, 19, 859-867.	3.3	174
84	MERVL/Zscan4 Network Activation Results in Transient Genome-wide DNA Demethylation of mESCs. <i>Cell Reports</i> , 2016, 17, 179-192.	6.4	174
85	Single cell RNA-seq and ATAC-seq analysis of cardiac progenitor cell transition states and lineage settlement. <i>Nature Communications</i> , 2018, 9, 4877.	12.8	174
86	Relative rates of gene fusion and fission in multi-domain proteins. <i>Trends in Genetics</i> , 2005, 21, 25-30.	6.7	173
87	Cholangiocyte organoids can repair bile ducts after transplantation in the human liver. <i>Science</i> , 2021, 371, 839-846.	12.6	170
88	Mapping protein family interactions: intramolecular and intermolecular protein family interaction repertoires in the PDB and yeast ¹¹ Edited by J. Karn. <i>Journal of Molecular Biology</i> , 2001, 307, 929-938.	4.2	167
89	Gene expression variability across cells and species shapes innate immunity. <i>Nature</i> , 2018, 563, 197-202.	27.8	165
90	Single-Cell RNA-Sequencing Reveals a Continuous Spectrum of Differentiation in Hematopoietic Cells. <i>Cell Reports</i> , 2016, 14, 966-977.	6.4	164

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91	Single-Cell Sequencing of Developing Human Gut Reveals Transcriptional Links to Childhood Crohn's Disease. <i>Developmental Cell</i> , 2020, 55, 771-783.e5.	7.0	164
92	Evolution of protein complexes by duplication of homomeric interactions. <i>Genome Biology</i> , 2007, 8, R51.	9.6	163
93	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> , 2012, 109, 20461-20466.	7.1	161
94	Supra-domains: Evolutionary Units Larger than Single Protein Domains. <i>Journal of Molecular Biology</i> , 2004, 336, 809-823.	4.2	157
95	Computational methods for single-cell omics across modalities. <i>Nature Methods</i> , 2020, 17, 14-17.	19.0	156
96	The Relationship Between Domain Duplication and Recombination. <i>Journal of Molecular Biology</i> , 2005, 346, 355-365.	4.2	154
97	Single-cell analysis of human B cell maturation predicts how antibody class switching shapes selection dynamics. <i>Science Immunology</i> , 2021, 6, .	11.9	149
98	Genomic repertoires of DNA-binding transcription factors across the tree of life. <i>Nucleic Acids Research</i> , 2010, 38, 7364-7377.	14.5	140
99	Wounding induces dedifferentiation of epidermal Gata6+ cells and acquisition of stem cell properties. <i>Nature Cell Biology</i> , 2017, 19, 603-613.	10.3	138
100	Advances in structural genomics. <i>Current Opinion in Structural Biology</i> , 1999, 9, 390-399.	5.7	137
101	Genome-wide CRISPR Screens in T Helper Cells Reveal Pervasive Crosstalk between Activation and Differentiation. <i>Cell</i> , 2019, 176, 882-896.e18.	28.9	135
102	The origins and evolution of functional modules: lessons from protein complexes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 507-517.	4.0	134
103	Single-cell transcriptome analysis of fish immune cells provides insight into the evolution of vertebrate immune cell types. <i>Genome Research</i> , 2017, 27, 451-461.	5.5	126
104	Mapping the developing human immune system across organs. <i>Science</i> , 2022, 376, eabo0510.	12.6	126
105	A roadmap for the Human Developmental Cell Atlas. <i>Nature</i> , 2021, 597, 196-205.	27.8	114
106	Computational approaches for interpreting single-cell RNA-seq data. <i>FEBS Letters</i> , 2017, 591, 2213-2225.	2.8	112
107	Cell-type specialization is encoded by specific chromatin topologies. <i>Nature</i> , 2021, 599, 684-691.	27.8	112
108	Conservation of gene co-regulation in prokaryotes and eukaryotes. <i>Trends in Biotechnology</i> , 2002, 20, 407-410.	9.3	111

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109	High-Resolution mRNA and Secretome Atlas of Human Enteroendocrine Cells. <i>Cell</i> , 2020, 181, 1291-1306.e19.	28.9	110
110	LifeTime and improving European healthcare through cell-based interceptive medicine. <i>Nature</i> , 2020, 587, 377-386.	27.8	108
111	Single-cell sequencing reveals clonal expansions of pro-inflammatory synovial CD8 T cells expressing tissue-homing receptors in psoriatic arthritis. <i>Nature Communications</i> , 2020, 11, 4767.	12.8	108
112	The transcriptional program controlled by the stem cell leukemia gene <i>Scl/Tal1</i> during early embryonic hematopoietic development. <i>Blood</i> , 2009, 113, 5456-5465.	1.4	107
113	Structural, Evolutionary, and Assembly Principles of Protein Oligomerization. <i>Progress in Molecular Biology and Translational Science</i> , 2013, 117, 25-51.	1.7	107
114	The immunoglobulin superfamily in <i>Drosophila melanogaster</i> and <i>Caenorhabditis elegans</i> and the evolution of complexity. <i>Development (Cambridge)</i> , 2003, 130, 6317-6328.	2.5	106
115	Immunoglobulin superfamily proteins in <i>Caenorhabditis elegans</i> 1 Edited by G. von Heijne. <i>Journal of Molecular Biology</i> , 2000, 296, 1367-1383.	4.2	101
116	The evolution and structural anatomy of the small molecule metabolic pathways in <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2001, 311, 693-708.	4.2	101
117	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> , 2003, 4, 67-78.	1.2	100
118	The Constraints Proteinâ€“Protein Interactions Place on Sequence Divergence. <i>Journal of Molecular Biology</i> , 2002, 324, 399-407.	4.2	99
119	Molecular phenotyping reveals the identity of Barrettâ€™s esophagus and its malignant transition. <i>Science</i> , 2021, 373, 760-767.	12.6	99
120	The Organoid Cell Atlas. <i>Nature Biotechnology</i> , 2021, 39, 13-17.	17.5	96
121	Probing the diverse landscape of protein flexibility and binding. <i>Current Opinion in Structural Biology</i> , 2012, 22, 643-650.	5.7	94
122	Polychromatic Reporter Mice Reveal Unappreciated Innate Lymphoid Cell Progenitor Heterogeneity and Elusive ILC3 Progenitors in Bone Marrow. <i>Immunity</i> , 2019, 51, 104-118.e7.	14.3	94
123	From Tissues to Cell Types and Back: Single-Cell Gene Expression Analysis of Tissue Architecture. <i>Annual Review of Biomedical Data Science</i> , 2018, 1, 29-51.	6.5	91
124	Putative cell type discovery from single-cell gene expression data. <i>Nature Methods</i> , 2020, 17, 621-628.	19.0	91
125	FlyTF: a systematic review of site-specific transcription factors in the fruit fly <i>Drosophila melanogaster</i> . <i>Bioinformatics</i> , 2006, 22, 1532-1533.	4.1	90
126	Prenatal development of human immunity. <i>Science</i> , 2020, 368, 600-603.	12.6	90

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127	Protein Flexibility Facilitates Quaternary Structure Assembly and Evolution. PLoS Biology, 2014, 12, e1001870.	5.6	89
128	Single-cell transcriptomic reconstruction reveals cell cycle and multi-lineage differentiation defects in Bcl11a-deficient hematopoietic stem cells. Genome Biology, 2015, 16, 178.	8.8	86
129	BraCeR: B-cell-receptor reconstruction and clonality inference from single-cell RNA-seq. Nature Methods, 2018, 15, 563-565.	19.0	84
130	The Role of Salt Bridges, Charge Density, and Subunit Flexibility in Determining Disassembly Routes of Protein Complexes. Structure, 2013, 21, 1325-1337.	3.3	82
131	An atlas of mouse CD4+ T cell transcriptomes. Biology Direct, 2015, 10, 14.	4.6	82
132	Single cell analysis of human foetal liver captures the transcriptional profile of hepatobiliary hybrid progenitors. Nature Communications, 2019, 10, 3350.	12.8	82
133	Comparative analysis of sequencing technologies for single-cell transcriptomics. Genome Biology, 2019, 20, 70.	8.8	82
134	Statistical analysis of domains in interacting protein pairs. Bioinformatics, 2005, 21, 993-1001.	4.1	81
135	Integrated scRNA-Seq Identifies Human Postnatal Thymus Seeding Progenitors and Regulatory Dynamics of Differentiating Immature Thymocytes. Immunity, 2020, 52, 1088-1104.e6.	14.3	79
136	Novel specificities emerge by stepwise duplication of functional modules. Genome Research, 2005, 15, 552-559.	5.5	78
137	Tumor to normal single-cell mRNA comparisons reveal a pan-neuroblastoma cancer cell. Science Advances, 2021, 7, .	10.3	78
138	Expression Atlas update: gene and protein expression in multiple species. Nucleic Acids Research, 2022, 50, D129-D140.	14.5	78
139	Is There a Phylogenetic Signal in Prokaryote Proteins?. Journal of Molecular Evolution, 1999, 49, 98-107.	1.8	76
140	Functional determinants of transcription factors in Escherichia coli: protein families and binding sites. Trends in Genetics, 2003, 19, 75-79.	6.7	75
141	The emergence of protein complexes: quaternary structure, dynamics and allostery. Biochemical Society Transactions, 2012, 40, 475-491.	3.4	75
142	Blood and immune development in human fetal bone marrow and Down syndrome. Nature, 2021, 598, 327-331.	27.8	73
143	Cell type ontologies of the Human Cell Atlas. Nature Cell Biology, 2021, 23, 1129-1135.	10.3	71
144	Single-cell atlases: shared and tissue-specific cell types across human organs. Nature Reviews Genetics, 2022, 23, 395-410.	16.3	71

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145	Assessing Computational Methods of Cis-Regulatory Module Prediction. PLoS Computational Biology, 2010, 6, e1001020.	3.2	70
146	FlyTF: improved annotation and enhanced functionality of the Drosophila transcription factor database. Nucleic Acids Research, 2010, 38, D443-D447.	14.5	70
147	How do proteins gain new domains?. Genome Biology, 2010, 11, 126.	9.6	70
148	Single-cell transcriptomics identifies CD44 as a marker and regulator of endothelial to haematopoietic transition. Nature Communications, 2020, 11, 586.	12.8	69
149	Parallel dynamics and evolution: Protein conformational fluctuations and assembly reflect evolutionary changes in sequence and structure. BioEssays, 2014, 36, 209-218.	2.5	68
150	Mosquito cellular immunity at single-cell resolution. Science, 2020, 369, 1128-1132.	12.6	68
151	Anatomical structures, cell types and biomarkers of the Human Reference Atlas. Nature Cell Biology, 2021, 23, 1117-1128.	10.3	68
152	Genome-wide analyses reveal the IRE1a-XBP1 pathway promotes T helper cell differentiation by resolving secretory stress and accelerating proliferation. Genome Medicine, 2018, 10, 76.	8.2	67
153	The (In)dependence of Alternative Splicing and Gene Duplication. PLoS Computational Biology, 2007, 3, e33.	3.2	66
154	Single-cell analysis of CD4+ T-cell differentiation reveals three major cell states and progressive acceleration of proliferation. Genome Biology, 2016, 17, 103.	8.8	65
155	Evolution of oligomeric state through allosteric pathways that mimic ligand binding. Science, 2014, 346, 1254346.	12.6	62
156	Regulation, evolution and consequences of cotranslational protein complex assembly. Current Opinion in Structural Biology, 2017, 42, 90-97.	5.7	62
157	Flipping between Polycomb repressed and active transcriptional states introduces noise in gene expression. Nature Communications, 2017, 8, 36.	12.8	62
158	Immunology Driven by Large-Scale Single-Cell Sequencing. Trends in Immunology, 2019, 40, 1011-1021.	6.8	62
159	Divergence of Interdomain Geometry in Two-Domain Proteins. Structure, 2006, 14, 935-945.	3.3	60
160	Regulation of protein-protein binding by coupling between phosphorylation and intrinsic disorder: analysis of human protein complexes. Molecular BioSystems, 2013, 9, 1620.	2.9	60
161	Towards a Human Cell Atlas: Taking Notes from the Past. Trends in Genetics, 2021, 37, 625-630.	6.7	59
162	Unbiased classification of mosquito blood cells by single-cell genomics and high-content imaging. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E7568-E7577.	7.1	57

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163	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. <i>Developmental Cell</i> , 2019, 49, 10-29.	7.0	57
164	Immunology in the Era of Single-Cell Technologies. <i>Annual Review of Immunology</i> , 2020, 38, 727-757.	21.8	57
165	Nasal DNA methylation profiling of asthma and rhinitis. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 145, 1655-1663.	2.9	56
166	Tumors induce de novo steroid biosynthesis in T cells to evade immunity. <i>Nature Communications</i> , 2020, 11, 3588.	12.8	54
167	INSIGHT: A population-scale COVID-19 testing strategy combining point-of-care diagnosis with centralized high-throughput sequencing. <i>Science Advances</i> , 2021, 7, .	10.3	54
168	Protein domain organisation: adding order. <i>BMC Bioinformatics</i> , 2009, 10, 39.	2.6	52
169	<i>Malat1</i> Suppresses Immunity to Infection through Promoting Expression of Maf and IL-10 in Th Cells. <i>Journal of Immunology</i> , 2020, 204, 2949-2960.	0.8	52
170	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> , 2012, 109, 8127-8132.	7.1	49
171	Intrinsic transcriptional heterogeneity in B cells controls early class switching to IgE. <i>Journal of Experimental Medicine</i> , 2017, 214, 183-196.	8.5	49
172	Homology, Pathway Distance and Chromosomal Localization of the Small Molecule Metabolism Enzymes in <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2002, 318, 911-932.	4.2	48
173	Functional protein divergence in the evolution of <i>Homo sapiens</i> . <i>Genome Biology</i> , 2008, 9, R33.	9.6	48
174	Structural and evolutionary versatility in protein complexes with uneven stoichiometry. <i>Nature Communications</i> , 2015, 6, 6394.	12.8	48
175	Cardelino: computational integration of somatic clonal substructure and single-cell transcriptomes. <i>Nature Methods</i> , 2020, 17, 414-421.	19.0	48
176	Fast assignment of protein structures to sequences using the Intermediate Sequence Library PDB-ISL. <i>Bioinformatics</i> , 2000, 16, 117-124.	4.1	45
177	The impact of genomic neighborhood on the evolution of human and chimpanzee transcriptome. <i>Genome Research</i> , 2009, 19, 785-794.	5.5	44
178	Cotranslational protein assembly imposes evolutionary constraints on homomeric proteins. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 279-288.	8.2	43
179	Transcriptome dynamics of CD4+ T cells during malaria maps gradual transit from effector to memory. <i>Nature Immunology</i> , 2020, 21, 1597-1610.	14.5	43
180	Reconstitution of a functional human thymus by postnatal stromal progenitor cells and natural whole-organ scaffolds. <i>Nature Communications</i> , 2020, 11, 6372.	12.8	42

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