

Sarah A Teichmann

List of Publications by Year in descending order

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239
papers

53,032
citations

1888

102
h-index

1980

206
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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.	13.5	1,956
2	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	13.7	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.	5.5	1,768
4	The Human Cell Atlas. <i>ELife</i> , 2017, 6, .	2.8	1,547
5	Single-cell reconstruction of the early maternal-fetal interface in humans. <i>Nature</i> , 2018, 563, 347-353.	13.7	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.	3.3	1,482
7	A census of human transcription factors: function, expression and evolution. <i>Nature Reviews Genetics</i> , 2009, 10, 252-263.	7.7	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.	9.4	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.	9.4	1,068
10	Computational and analytical challenges in single-cell transcriptomics. <i>Nature Reviews Genetics</i> , 2015, 16, 133-145.	7.7	1,043
11	The Technology and Biology of Single-Cell RNA Sequencing. <i>Molecular Cell</i> , 2015, 58, 610-620.	4.5	1,014
12	Accounting for technical noise in single-cell RNA-seq experiments. <i>Nature Methods</i> , 2013, 10, 1093-1095.	9.0	929
13	Genomic analysis of regulatory network dynamics reveals large topological changes. <i>Nature</i> , 2004, 431, 308-312.	13.7	921
14	Cells of the adult human heart. <i>Nature</i> , 2020, 588, 466-472.	13.7	852
15	Altered TMPRSS2 usage by SARS-CoV-2 Omicron impacts infectivity and fusogenicity. <i>Nature</i> , 2022, 603, 706-714.	13.7	756
16	A practical guide to single-cell RNA-sequencing for biomedical research and clinical applications. <i>Genome Medicine</i> , 2017, 9, 75.	3.6	712
17	Exponential scaling of single-cell RNA-seq in the past decade. <i>Nature Protocols</i> , 2018, 13, 599-604.	5.5	704
18	Structure and evolution of transcriptional regulatory networks. <i>Current Opinion in Structural Biology</i> , 2004, 14, 283-291.	2.6	683

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19	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , 2010, 140, 744-752.	13.5	667
20	A cellular census of human lungs identifies novel cell states in health and in asthma. <i>Nature Medicine</i> , 2019, 25, 1153-1163.	15.2	631
21	Classification of low quality cells from single-cell RNA-seq data. <i>Genome Biology</i> , 2016, 17, 29.	3.8	572
22	SARS-CoV-2 infection of the oral cavity and saliva. <i>Nature Medicine</i> , 2021, 27, 892-903.	15.2	527
23	BBKNN: fast batch alignment of single cell transcriptomes. <i>Bioinformatics</i> , 2020, 36, 964-965.	1.8	517
24	Single-cell transcriptomes from human kidneys reveal the cellular identity of renal tumors. <i>Science</i> , 2018, 361, 594-599.	6.0	511
25	The Human Cell Atlas: from vision to reality. <i>Nature</i> , 2017, 550, 451-453.	13.7	511
26	Single Cell RNA-Sequencing of Pluripotent States Unlocks Modular Transcriptional Variation. <i>Cell Stem Cell</i> , 2015, 17, 471-485.	5.2	505
27	Power analysis of single-cell RNA-sequencing experiments. <i>Nature Methods</i> , 2017, 14, 381-387.	9.0	496
28	Evolution of the Protein Repertoire. <i>Science</i> , 2003, 300, 1701-1703.	6.0	494
29	Gene regulatory network growth by duplication. <i>Nature Genetics</i> , 2004, 36, 492-496.	9.4	475
30	Domain combinations in archaeal, eubacterial and eukaryotic proteomes. <i>Journal of Molecular Biology</i> , 2001, 310, 311-325.	2.0	452
31	Single-cell multi-omics analysis of the immune response in COVID-19. <i>Nature Medicine</i> , 2021, 27, 904-916.	15.2	452
32	Single-cell transcriptomics to explore the immune system in health and disease. <i>Science</i> , 2017, 358, 58-63.	6.0	440
33	Tight Regulation of Unstructured Proteins: From Transcript Synthesis to Protein Degradation. <i>Science</i> , 2008, 322, 1365-1368.	6.0	419
34	T cell fate and clonality inference from single-cell transcriptomes. <i>Nature Methods</i> , 2016, 13, 329-332.	9.0	411
35	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	9.4	408
36	Decoding human fetal liver haematopoiesis. <i>Nature</i> , 2019, 574, 365-371.	13.7	392

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37	Assembly reflects evolution of protein complexes. <i>Nature</i> , 2008, 453, 1262-1265.	13.7	383
38	SpatialDE: identification of spatially variable genes. <i>Nature Methods</i> , 2018, 15, 343-346.	9.0	382
39	Computational assignment of cell-cycle stage from single-cell transcriptome data. <i>Methods</i> , 2015, 85, 54-61.	1.9	381
40	Structure, function and evolution of multidomain proteins. <i>Current Opinion in Structural Biology</i> , 2004, 14, 208-216.	2.6	379
41	A cell atlas of human thymic development defines T cell repertoire formation. <i>Science</i> , 2020, 367, .	6.0	368
42	Expression Atlas update: from tissues to single cells. <i>Nucleic Acids Research</i> , 2020, 48, D77-D83.	6.5	363
43	Single-Cell Transcriptomics of Regulatory T Cells Reveals Trajectories of Tissue Adaptation. <i>Immunity</i> , 2019, 50, 493-504.e7.	6.6	352
44	Structure, Dynamics, Assembly, and Evolution of Protein Complexes. <i>Annual Review of Biochemistry</i> , 2015, 84, 551-575.	5.0	351
45	The folding and evolution of multidomain proteins. <i>Nature Reviews Molecular Cell Biology</i> , 2007, 8, 319-330.	16.1	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.	4.2	304
47	3D Complex: A Structural Classification of Protein Complexes. <i>PLoS Computational Biology</i> , 2006, 2, e155.	1.5	299
48	The importance of sequence diversity in the aggregation and evolution of proteins. <i>Nature</i> , 2005, 438, 878-881.	13.7	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.	6.5	283
50	Spatiotemporal immune zonation of the human kidney. <i>Science</i> , 2019, 365, 1461-1466.	6.0	281
51	A test metric for assessing single-cell RNA-seq batch correction. <i>Nature Methods</i> , 2019, 16, 43-49.	9.0	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.	6.6	278
53	Cells of the human intestinal tract mapped across space and time. <i>Nature</i> , 2021, 597, 250-255.	13.7	266
54	RNA sequencing reveals two major classes of gene expression levels in metazoan cells. <i>Molecular Systems Biology</i> , 2011, 7, 497.	3.2	265

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55	Aging increases cell-to-cell transcriptional variability upon immune stimulation. <i>Science</i> , 2017, 355, 1433-1436.	6.0	265
56	Cross-tissue immune cell analysis reveals tissue-specific features in humans. <i>Science</i> , 2022, 376, eabl5197.	6.0	265
57	Developmental cell programs are co-opted in inflammatory skin disease. <i>Science</i> , 2021, 371, .	6.0	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.	5.2	261
59	Single-Cell Transcriptomics Uncovers Zonation of Function in the Mesenchyme during Liver Fibrosis. <i>Cell Reports</i> , 2019, 29, 1832-1847.e8.	2.9	261
60	Establishment of porcine and human expanded potential stem cells. <i>Nature Cell Biology</i> , 2019, 21, 687-699.	4.6	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, .	5.6	258
62	Single-cell RNA-seq identifies a PD-1hi ILC progenitor and defines its development pathway. <i>Nature</i> , 2016, 539, 102-106.	13.7	257
63	Evolutionary Dynamics of Prokaryotic Transcriptional Regulatory Networks. <i>Journal of Molecular Biology</i> , 2006, 358, 614-633.	2.0	254
64	DBDâ€™s taxonomically broad transcription factor predictions: new content and functionality. <i>Nucleic Acids Research</i> , 2008, 36, D88-D92.	6.5	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.	0.6	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.	9.4	238
67	Differential abundance testing on single-cell data using k-nearest neighbor graphs. <i>Nature Biotechnology</i> , 2022, 40, 245-253.	9.4	229
68	Establishment of mouse expanded potential stem cells. <i>Nature</i> , 2017, 550, 393-397.	13.7	223
69	A HaemAtlas: characterizing gene expression in differentiated human blood cells. <i>Blood</i> , 2009, 113, e1-e9.	0.6	215
70	Protein Complexes Are under Evolutionary Selection to Assemble via Ordered Pathways. <i>Cell</i> , 2013, 153, 461-470.	13.5	215
71	Characterizing noise structure in single-cell RNA-seq distinguishes genuine from technical stochastic allelic expression. <i>Nature Communications</i> , 2015, 6, 8687.	5.8	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.	2.9	198

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73	Principles of assembly reveal a periodic table of protein complexes. <i>Science</i> , 2015, 350, aaa2245.	6.0	198
74	Single cell transcriptomics comes of age. <i>Nature Communications</i> , 2020, 11, 4307.	5.8	194
75	The interface of protein structure, protein biophysics, and molecular evolution. <i>Protein Science</i> , 2012, 21, 769-785.	3.1	188
76	A rapid and robust method for single cell chromatin accessibility profiling. <i>Nature Communications</i> , 2018, 9, 5345.	5.8	188
77	DBD: a transcription factor prediction database. <i>Nucleic Acids Research</i> , 2006, 34, D74-D81.	6.5	186
78	Single-Cell RNA Sequencing Reveals a Dynamic Stromal Niche That Supports Tumor Growth. <i>Cell Reports</i> , 2020, 31, 107628.	2.9	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.	13.7	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.	1.4	178
82	Distinct microbial and immune niches of the human colon. <i>Nature Immunology</i> , 2020, 21, 343-353.	7.0	175
83	Relative Solvent Accessible Surface Area Predicts Protein Conformational Changes upon Binding. <i>Structure</i> , 2011, 19, 859-867.	1.6	174
84	MERVL/Zscan4 Network Activation Results in Transient Genome-wide DNA Demethylation of mESCs. <i>Cell Reports</i> , 2016, 17, 179-192.	2.9	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.	5.8	174
86	Relative rates of gene fusion and fission in multi-domain proteins. <i>Trends in Genetics</i> , 2005, 21, 25-30.	2.9	173
87	Cholangiocyte organoids can repair bile ducts after transplantation in the human liver. <i>Science</i> , 2021, 371, 839-846.	6.0	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.	2.0	167
89	Gene expression variability across cells and species shapes innate immunity. <i>Nature</i> , 2018, 563, 197-202.	13.7	165
90	Single-Cell RNA-Sequencing Reveals a Continuous Spectrum of Differentiation in Hematopoietic Cells. <i>Cell Reports</i> , 2016, 14, 966-977.	2.9	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.	3.1	164
92	Evolution of protein complexes by duplication of homomeric interactions. <i>Genome Biology</i> , 2007, 8, R51.	13.9	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.	3.3	161
94	Supra-domains: Evolutionary Units Larger than Single Protein Domains. <i>Journal of Molecular Biology</i> , 2004, 336, 809-823.	2.0	157
95	Computational methods for single-cell omics across modalities. <i>Nature Methods</i> , 2020, 17, 14-17.	9.0	156
96	The Relationship Between Domain Duplication and Recombination. <i>Journal of Molecular Biology</i> , 2005, 346, 355-365.	2.0	154
97	Single-cell analysis of human B cell maturation predicts how antibody class switching shapes selection dynamics. <i>Science Immunology</i> , 2021, 6, .	5.6	149
98	Genomic repertoires of DNA-binding transcription factors across the tree of life. <i>Nucleic Acids Research</i> , 2010, 38, 7364-7377.	6.5	140
99	Wounding induces dedifferentiation of epidermal Gata6+ cells and acquisition of stem cell properties. <i>Nature Cell Biology</i> , 2017, 19, 603-613.	4.6	138
100	Advances in structural genomics. <i>Current Opinion in Structural Biology</i> , 1999, 9, 390-399.	2.6	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.	13.5	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.	1.8	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.	2.4	126
104	Mapping the developing human immune system across organs. <i>Science</i> , 2022, 376, eabo0510.	6.0	126
105	A roadmap for the Human Developmental Cell Atlas. <i>Nature</i> , 2021, 597, 196-205.	13.7	114
106	Computational approaches for interpreting scRNA-seq data. <i>FEBS Letters</i> , 2017, 591, 2213-2225.	1.3	112
107	Cell-type specialization is encoded by specific chromatin topologies. <i>Nature</i> , 2021, 599, 684-691.	13.7	112
108	Conservation of gene co-regulation in prokaryotes and eukaryotes. <i>Trends in Biotechnology</i> , 2002, 20, 407-410.	4.9	111

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109	High-Resolution mRNA and Secretome Atlas of Human Enteroendocrine Cells. <i>Cell</i> , 2020, 181, 1291-1306.e19.	13.5	110
110	LifeTime and improving European healthcare through cell-based interceptive medicine. <i>Nature</i> , 2020, 587, 377-386.	13.7	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.	5.8	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.	0.6	107
113	Structural, Evolutionary, and Assembly Principles of Protein Oligomerization. <i>Progress in Molecular Biology and Translational Science</i> , 2013, 117, 25-51.	0.9	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.	1.2	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.	2.0	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.	2.0	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 Protein-Protein Interactions Place on Sequence Divergence. <i>Journal of Molecular Biology</i> , 2002, 324, 399-407.	2.0	99
119	Molecular phenotyping reveals the identity of Barrett's esophagus and its malignant transition. <i>Science</i> , 2021, 373, 760-767.	6.0	99
120	The Organoid Cell Atlas. <i>Nature Biotechnology</i> , 2021, 39, 13-17.	9.4	96
121	Probing the diverse landscape of protein flexibility and binding. <i>Current Opinion in Structural Biology</i> , 2012, 22, 643-650.	2.6	94
122	Polychromic Reporter Mice Reveal Unappreciated Innate Lymphoid Cell Progenitor Heterogeneity and Elusive ILC3 Progenitors in Bone Marrow. <i>Immunity</i> , 2019, 51, 104-118.e7.	6.6	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.	2.8	91
124	Putative cell type discovery from single-cell gene expression data. <i>Nature Methods</i> , 2020, 17, 621-628.	9.0	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.	1.8	90
126	Prenatal development of human immunity. <i>Science</i> , 2020, 368, 600-603.	6.0	90

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127	Protein Flexibility Facilitates Quaternary Structure Assembly and Evolution. <i>PLoS Biology</i> , 2014, 12, e1001870.	2.6	89
128	Single-cell transcriptomic reconstruction reveals cell cycle and multi-lineage differentiation defects in <i>Bcl11a</i> -deficient hematopoietic stem cells. <i>Genome Biology</i> , 2015, 16, 178.	3.8	86
129	BraCeR: B-cell-receptor reconstruction and clonality inference from single-cell RNA-seq. <i>Nature Methods</i> , 2018, 15, 563-565.	9.0	84
130	The Role of Salt Bridges, Charge Density, and Subunit Flexibility in Determining Disassembly Routes of Protein Complexes. <i>Structure</i> , 2013, 21, 1325-1337.	1.6	82
131	An atlas of mouse CD4+ T cell transcriptomes. <i>Biology Direct</i> , 2015, 10, 14.	1.9	82
132	Single cell analysis of human foetal liver captures the transcriptional profile of hepatobiliary hybrid progenitors. <i>Nature Communications</i> , 2019, 10, 3350.	5.8	82
133	Comparative analysis of sequencing technologies for single-cell transcriptomics. <i>Genome Biology</i> , 2019, 20, 70.	3.8	82
134	Statistical analysis of domains in interacting protein pairs. <i>Bioinformatics</i> , 2005, 21, 993-1001.	1.8	81
135	Integrated scRNA-Seq Identifies Human Postnatal Thymus Seeding Progenitors and Regulatory Dynamics of Differentiating Immature Thymocytes. <i>Immunity</i> , 2020, 52, 1088-1104.e6.	6.6	79
136	Novel specificities emerge by stepwise duplication of functional modules. <i>Genome Research</i> , 2005, 15, 552-559.	2.4	78
137	Tumor to normal single-cell mRNA comparisons reveal a pan-neuroblastoma cancer cell. <i>Science Advances</i> , 2021, 7, .	4.7	78
138	Expression Atlas update: gene and protein expression in multiple species. <i>Nucleic Acids Research</i> , 2022, 50, D129-D140.	6.5	78
139	Is There a Phylogenetic Signal in Prokaryote Proteins?. <i>Journal of Molecular Evolution</i> , 1999, 49, 98-107.	0.8	76
140	Functional determinants of transcription factors in <i>Escherichia coli</i> : protein families and binding sites. <i>Trends in Genetics</i> , 2003, 19, 75-79.	2.9	75
141	The emergence of protein complexes: quaternary structure, dynamics and allostery. <i>Biochemical Society Transactions</i> , 2012, 40, 475-491.	1.6	75
142	Blood and immune development in human fetal bone marrow and Down syndrome. <i>Nature</i> , 2021, 598, 327-331.	13.7	73
143	Cell type ontologies of the Human Cell Atlas. <i>Nature Cell Biology</i> , 2021, 23, 1129-1135.	4.6	71
144	Single-cell atlases: shared and tissue-specific cell types across human organs. <i>Nature Reviews Genetics</i> , 2022, 23, 395-410.	7.7	71

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145	Assessing Computational Methods of Cis-Regulatory Module Prediction. <i>PLoS Computational Biology</i> , 2010, 6, e1001020.	1.5	70
146	FlyTF: improved annotation and enhanced functionality of the <i>Drosophila</i> transcription factor database. <i>Nucleic Acids Research</i> , 2010, 38, D443-D447.	6.5	70
147	How do proteins gain new domains?. <i>Genome Biology</i> , 2010, 11, 126.	13.9	70
148	Single-cell transcriptomics identifies CD44 as a marker and regulator of endothelial to haematopoietic transition. <i>Nature Communications</i> , 2020, 11, 586.	5.8	69
149	Parallel dynamics and evolution: Protein conformational fluctuations and assembly reflect evolutionary changes in sequence and structure. <i>BioEssays</i> , 2014, 36, 209-218.	1.2	68
150	Mosquito cellular immunity at single-cell resolution. <i>Science</i> , 2020, 369, 1128-1132.	6.0	68
151	Anatomical structures, cell types and biomarkers of the Human Reference Atlas. <i>Nature Cell Biology</i> , 2021, 23, 1117-1128.	4.6	68
152	Genome-wide analyses reveal the IRE1a-XBP1 pathway promotes T helper cell differentiation by resolving secretory stress and accelerating proliferation. <i>Genome Medicine</i> , 2018, 10, 76.	3.6	67
153	The (In)dependence of Alternative Splicing and Gene Duplication. <i>PLoS Computational Biology</i> , 2007, 3, e33.	1.5	66
154	Single-cell analysis of CD4+ T-cell differentiation reveals three major cell states and progressive acceleration of proliferation. <i>Genome Biology</i> , 2016, 17, 103.	3.8	65
155	Evolution of oligomeric state through allosteric pathways that mimic ligand binding. <i>Science</i> , 2014, 346, 1254-346.	6.0	62
156	Regulation, evolution and consequences of cotranslational protein complex assembly. <i>Current Opinion in Structural Biology</i> , 2017, 42, 90-97.	2.6	62
157	Flipping between Polycomb repressed and active transcriptional states introduces noise in gene expression. <i>Nature Communications</i> , 2017, 8, 36.	5.8	62
158	Immunology Driven by Large-Scale Single-Cell Sequencing. <i>Trends in Immunology</i> , 2019, 40, 1011-1021.	2.9	62
159	Divergence of Interdomain Geometry in Two-Domain Proteins. <i>Structure</i> , 2006, 14, 935-945.	1.6	60
160	Regulation of protein-protein binding by coupling between phosphorylation and intrinsic disorder: analysis of human protein complexes. <i>Molecular BioSystems</i> , 2013, 9, 1620.	2.9	60
161	Towards a Human Cell Atlas: Taking Notes from the Past. <i>Trends in Genetics</i> , 2021, 37, 625-630.	2.9	59
162	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> , 2018, 115, E7568-E7577.	3.3	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.	3.1	57
164	Immunology in the Era of Single-Cell Technologies. <i>Annual Review of Immunology</i> , 2020, 38, 727-757.	9.5	57
165	Nasal DNA methylation profiling of asthma and rhinitis. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 145, 1655-1663.	1.5	56
166	Tumors induce de novo steroid biosynthesis in T cells to evade immunity. <i>Nature Communications</i> , 2020, 11, 3588.	5.8	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, .	4.7	54
168	Protein domain organisation: adding order. <i>BMC Bioinformatics</i> , 2009, 10, 39.	1.2	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.	0.4	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.	3.3	49
171	Intrinsic transcriptional heterogeneity in B cells controls early class switching to IgE. <i>Journal of Experimental Medicine</i> , 2017, 214, 183-196.	4.2	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.	2.0	48
173	Functional protein divergence in the evolution of <i>Homo sapiens</i> . <i>Genome Biology</i> , 2008, 9, R33.	13.9	48
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