

Sarah A Teichmann

List of Publications by Year in descending order

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239
papers

53,032
citations

1883

102
h-index

1974

206
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299
all docs

299
docs citations

299
times ranked

64078
citing authors

#	ARTICLE	IF	CITATIONS
1	Differential abundance testing on single-cell data using k-nearest neighbor graphs. <i>Nature Biotechnology</i> , 2022, 40, 245-253.	9.4	229
2	An Integrated Taxonomy for Monogenic Inflammatory Bowel Disease. <i>Gastroenterology</i> , 2022, 162, 859-876.	0.6	37
3	Expression Atlas update: gene and protein expression in multiple species. <i>Nucleic Acids Research</i> , 2022, 50, D129-D140.	6.5	78
4	Altered TMPRSS2 usage by SARS-CoV-2 Omicron impacts infectivity and fusogenicity. <i>Nature</i> , 2022, 603, 706-714.	13.7	756
5	Single-cell atlases: shared and tissue-specific cell types across human organs. <i>Nature Reviews Genetics</i> , 2022, 23, 395-410.	7.7	71
6	Single-cell transcriptomics links malignant T cells to the tumor immune landscape in cutaneous T cell lymphoma. <i>Nature Communications</i> , 2022, 13, 1158.	5.8	29
7	Single-cell transcriptomics reveals a distinct developmental state of KMT2A-rearranged infant B-cell acute lymphoblastic leukemia. <i>Nature Medicine</i> , 2022, 28, 743-751.	15.2	35
8	Local and systemic responses to SARS-CoV-2 infection in children and adults. <i>Nature</i> , 2022, 602, 321-327.	13.7	179
9	Mapping the developing human immune system across organs. <i>Science</i> , 2022, 376, eabo0510.	6.0	126
10	Cross-tissue immune cell analysis reveals tissue-specific features in humans. <i>Science</i> , 2022, 376, eabl5197.	6.0	265
11	Community voices: policy proposals to promote inclusion in academia through the lens of women in science. <i>Nature Communications</i> , 2022, 13, .	5.8	3
12	Integrated single cell and spatial transcriptomics reveal autoreactive differentiated B cells in joints of early rheumatoid arthritis. <i>Scientific Reports</i> , 2022, 12, .	1.6	18
13	Developmental cell programs are co-opted in inflammatory skin disease. <i>Science</i> , 2021, 371, .	6.0	264
14	Cholangiocyte organoids can repair bile ducts after transplantation in the human liver. <i>Science</i> , 2021, 371, 839-846.	6.0	170
15	Tumor to normal single-cell mRNA comparisons reveal a pan-neuroblastoma cancer cell. <i>Science Advances</i> , 2021, 7, .	4.7	78
16	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
17	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
18	User-friendly, scalable tools and workflows for single-cell RNA-seq analysis. <i>Nature Methods</i> , 2021, 18, 327-328.	9.0	26

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19	Transcriptional characterization of human megakaryocyte polyploidization and lineage commitment. <i>Journal of Thrombosis and Haemostasis</i> , 2021, 19, 1236-1249.	1.9	15
20	SARS-CoV-2 infection of the oral cavity and saliva. <i>Nature Medicine</i> , 2021, 27, 892-903.	15.2	527
21	The Human Lung Cell Atlas: a transformational resource for cells of the respiratory system. , 2021, , 158-174.		3
22	Single-cell multi-omics analysis of the immune response in COVID-19. <i>Nature Medicine</i> , 2021, 27, 904-916.	15.2	452
23	CLICK-enabled analogues reveal pregnenolone interactomes in cancer and immune cells. <i>IScience</i> , 2021, 24, 102485.	1.9	6
24	Developmental bifurcation of human T follicular regulatory cells. <i>Science Immunology</i> , 2021, 6, .	5.6	22
25	High-throughput full-length single-cell RNA-seq automation. <i>Nature Protocols</i> , 2021, 16, 2886-2915.	5.5	13
26	Mapping Rora expression in resting and activated CD4+ T cells. <i>PLoS ONE</i> , 2021, 16, e0251233.	1.1	29
27	Single cell derived mRNA signals across human kidney tumors. <i>Nature Communications</i> , 2021, 12, 3896.	5.8	27
28	Towards a Human Cell Atlas: Taking Notes from the Past. <i>Trends in Genetics</i> , 2021, 37, 625-630.	2.9	59
29	Integrated Single-Cell Atlas of Endothelial Cells of the Human Lung. <i>Circulation</i> , 2021, 144, 286-302.	1.6	181
30	Molecular phenotyping reveals the identity of Barrett's esophagus and its malignant transition. <i>Science</i> , 2021, 373, 760-767.	6.0	99
31	Evidence generation and reproducibility in cell and gene therapy research: A call to action. <i>Molecular Therapy - Methods and Clinical Development</i> , 2021, 22, 11-14.	1.8	13
32	Cells of the human intestinal tract mapped across space and time. <i>Nature</i> , 2021, 597, 250-255.	13.7	266
33	Blood and immune development in human fetal bone marrow and Down syndrome. <i>Nature</i> , 2021, 598, 327-331.	13.7	73
34	A roadmap for the Human Developmental Cell Atlas. <i>Nature</i> , 2021, 597, 196-205.	13.7	114
35	The Organoid Cell Atlas. <i>Nature Biotechnology</i> , 2021, 39, 13-17.	9.4	96
36	Anatomical structures, cell types and biomarkers of the Human Reference Atlas. <i>Nature Cell Biology</i> , 2021, 23, 1117-1128.	4.6	68

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37	Cell type ontologies of the Human Cell Atlas. <i>Nature Cell Biology</i> , 2021, 23, 1129-1135.	4.6	71
38	Cell-type specialization is encoded by specific chromatin topologies. <i>Nature</i> , 2021, 599, 684-691.	13.7	112
39	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
40	MultiMAP: dimensionality reduction and integration of multimodal data. <i>Genome Biology</i> , 2021, 22, 346.	3.8	27
41	Completing the cancer jigsaw puzzle with single-cell multiomics. <i>Nature Cancer</i> , 2021, 2, 1260-1262.	5.7	3
42	BBKNN: fast batch alignment of single cell transcriptomes. <i>Bioinformatics</i> , 2020, 36, 964-965.	1.8	517
43	Expression Atlas update: from tissues to single cells. <i>Nucleic Acids Research</i> , 2020, 48, D77-D83.	6.5	363
44	Computational methods for single-cell omics across modalities. <i>Nature Methods</i> , 2020, 17, 14-17.	9.0	156
45	Transcriptome dynamics of CD4+ T cells during malaria maps gradual transit from effector to memory. <i>Nature Immunology</i> , 2020, 21, 1597-1610.	7.0	43
46	Tumors induce de novo steroid biosynthesis in T cells to evade immunity. <i>Nature Communications</i> , 2020, 11, 3588.	5.8	54
47	Cells of the adult human heart. <i>Nature</i> , 2020, 588, 466-472.	13.7	852
48	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
49	Guidelines for reporting single-cell RNA-seq experiments. <i>Nature Biotechnology</i> , 2020, 38, 1384-1386.	9.4	27
50	LifeTime and improving European healthcare through cell-based interceptive medicine. <i>Nature</i> , 2020, 587, 377-386.	13.7	108
51	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
52	Mosquito cellular immunity at single-cell resolution. <i>Science</i> , 2020, 369, 1128-1132.	6.0	68
53	Single cell transcriptomics comes of age. <i>Nature Communications</i> , 2020, 11, 4307.	5.8	194
54	Gene signatures from scRNA-seq accurately quantify mast cells in biopsies in asthma. <i>Clinical and Experimental Allergy</i> , 2020, 50, 1428-1431.	1.4	16

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55	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
56	Reconstitution of a functional human thymus by postnatal stromal progenitor cells and natural whole-organ scaffolds. <i>Nature Communications</i> , 2020, 11, 6372.	5.8	42
57	Putative cell type discovery from single-cell gene expression data. <i>Nature Methods</i> , 2020, 17, 621-628.	9.0	91
58	Malat1 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
59	Prenatal development of human immunity. <i>Science</i> , 2020, 368, 600-603.	6.0	90
60	High-Resolution mRNA and Secretome Atlas of Human Enteroendocrine Cells. <i>Cell</i> , 2020, 181, 1291-1306.e19.	13.5	110
61	Cardelino: computational integration of somatic clonal substructure and single-cell transcriptomes. <i>Nature Methods</i> , 2020, 17, 414-421.	9.0	48
62	The network effect: studying COVID-19 pathology with the Human Cell Atlas. <i>Nature Reviews Molecular Cell Biology</i> , 2020, 21, 415-416.	16.1	12
63	Distinct microbial and immune niches of the human colon. <i>Nature Immunology</i> , 2020, 21, 343-353.	7.0	175
64	Immunology in the Era of Single-Cell Technologies. <i>Annual Review of Immunology</i> , 2020, 38, 727-757.	9.5	57
65	A cell atlas of human thymic development defines T cell repertoire formation. <i>Science</i> , 2020, 367, .	6.0	368
66	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
67	Nasal DNA methylation profiling of asthma and rhinitis. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 145, 1655-1663.	1.5	56
68	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
69	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
70	Single-Cell RNA Sequencing Reveals a Dynamic Stromal Niche That Supports Tumor Growth. <i>Cell Reports</i> , 2020, 31, 107628.	2.9	186
71	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
72	Cell Atlas technologies and insights into tissue architecture. <i>Biochemical Journal</i> , 2020, 477, 1427-1442.	1.7	32

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73	Single-cell transcriptomics of alloreactive CD4+ T cells over time reveals divergent fates during gut graft-versus-host disease. <i>JCI Insight</i> , 2020, 5, .	2.3	12
74	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
75	Immunology Driven by Large-Scale Single-Cell Sequencing. <i>Trends in Immunology</i> , 2019, 40, 1011-1021.	2.9	62
76	Decoding human fetal liver haematopoiesis. <i>Nature</i> , 2019, 574, 365-371.	13.7	392
77	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
78	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
79	Spatiotemporal immune zonation of the human kidney. <i>Science</i> , 2019, 365, 1461-1466.	6.0	281
80	Single-Cell Transcriptomics of Regulatory T Cells Reveals Trajectories of Tissue Adaptation. <i>Immunity</i> , 2019, 50, 493-504.e7.	6.6	352
81	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
82	Establishment of porcine and human expanded potential stem cells. <i>Nature Cell Biology</i> , 2019, 21, 687-699.	4.6	261
83	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
84	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
85	Comparative analysis of sequencing technologies for single-cell transcriptomics. <i>Genome Biology</i> , 2019, 20, 70.	3.8	82
86	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
87	A test metric for assessing single-cell RNA-seq batch correction. <i>Nature Methods</i> , 2019, 16, 43-49.	9.0	278
88	Exponential scaling of single-cell RNA-seq in the past decade. <i>Nature Protocols</i> , 2018, 13, 599-604.	5.5	704
89	Mapping human development at single-cell resolution. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	30
90	Cotranslational protein assembly imposes evolutionary constraints on homomeric proteins. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 279-288.	3.6	43

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91	SpatialDE: identification of spatially variable genes. <i>Nature Methods</i> , 2018, 15, 343-346.	9.0	382
92	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
93	Single-cell reconstruction of the early maternal-fetal interface in humans. <i>Nature</i> , 2018, 563, 347-353.	13.7	1,547
94	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
95	A rapid and robust method for single cell chromatin accessibility profiling. <i>Nature Communications</i> , 2018, 9, 5345.	5.8	188
96	Gene expression variability across cells and species shapes innate immunity. <i>Nature</i> , 2018, 563, 197-202.	13.7	165
97	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
98	BraCeR: B-cell-receptor reconstruction and clonality inference from single-cell RNA-seq. <i>Nature Methods</i> , 2018, 15, 563-565.	9.0	84
99	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
100	Single-cell transcriptomes from human kidneys reveal the cellular identity of renal tumors. <i>Science</i> , 2018, 361, 594-599.	6.0	511
101	Distinctive features of lincRNA gene expression suggest widespread RNA-independent functions. <i>Life Science Alliance</i> , 2018, 1, e201800124.	1.3	32
102	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
103	Power analysis of single-cell RNA-sequencing experiments. <i>Nature Methods</i> , 2017, 14, 381-387.	9.0	496
104	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
105	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
106	Computational approaches for interpreting scRNA-seq data. <i>FEBS Letters</i> , 2017, 591, 2213-2225.	1.3	112
107	Ageing increases cell-to-cell transcriptional variability upon immune stimulation. <i>Science</i> , 2017, 355, 1433-1436.	6.0	265
108	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

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109	Regulation, evolution and consequences of cotranslational protein complex assembly. <i>Current Opinion in Structural Biology</i> , 2017, 42, 90-97.	2.6	62
110	Single-cell transcriptomics to explore the immune system in health and disease. <i>Science</i> , 2017, 358, 58-63.	6.0	440
111	Establishment of mouse expanded potential stem cells. <i>Nature</i> , 2017, 550, 393-397.	13.7	223
112	Single-cell insights into transcriptomic diversity in immunity. <i>Current Opinion in Systems Biology</i> , 2017, 5, 63-71.	1.3	5
113	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
114	Flipping between Polycomb repressed and active transcriptional states introduces noise in gene expression. <i>Nature Communications</i> , 2017, 8, 36.	5.8	62
115	Single cell transcriptomics of pluripotent stem cells: reprogramming and differentiation. <i>Current Opinion in Genetics and Development</i> , 2017, 46, 66-76.	1.5	17
116	The Human Cell Atlas. <i>ELife</i> , 2017, 6, .	2.8	1,547
117	A practical guide to single-cell RNA-sequencing for biomedical research and clinical applications. <i>Genome Medicine</i> , 2017, 9, 75.	3.6	712
118	The Human Cell Atlas: from vision to reality. <i>Nature</i> , 2017, 550, 451-453.	13.7	511
119	Data on publications, structural analyses, and queries used to build and utilize the AlloRep database. <i>Data in Brief</i> , 2016, 8, 948-957.	0.5	2
120	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
121	MERVL/Zscan4 Network Activation Results in Transient Genome-wide DNA Demethylation of mESCs. <i>Cell Reports</i> , 2016, 17, 179-192.	2.9	174
122	Genetics and immunity in the era of single-cell genomics. <i>Human Molecular Genetics</i> , 2016, 25, R141-R148.	1.4	19
123	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
124	Classification of low quality cells from single-cell RNA-seq data. <i>Genome Biology</i> , 2016, 17, 29.	3.8	572
125	AlloRep: A Repository of Sequence, Structural and Mutagenesis Data for the LacI/GalR Transcription Regulators. <i>Journal of Molecular Biology</i> , 2016, 428, 671-678.	2.0	18
126	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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127	T cell fate and clonality inference from single-cell transcriptomes. <i>Nature Methods</i> , 2016, 13, 329-332.	9.0	411
128	The Regulatory T Cell Lineage Factor Foxp3 Regulates Gene Expression through Several Distinct Mechanisms Mostly Independent of Direct DNA Binding. <i>PLoS Genetics</i> , 2015, 11, e1005251.	1.5	35
129	The Technology and Biology of Single-Cell RNA Sequencing. <i>Molecular Cell</i> , 2015, 58, 610-620.	4.5	1,014
130	Single-cell transcriptomic reconstruction reveals cell cycle and multi-lineage differentiation defects in Bcl11a-deficient hematopoietic stem cells. <i>Genome Biology</i> , 2015, 16, 178.	3.8	86
131	Principles of assembly reveal a periodic table of protein complexes. <i>Science</i> , 2015, 350, aaa2245.	6.0	198
132	Computational and analytical challenges in single-cell transcriptomics. <i>Nature Reviews Genetics</i> , 2015, 16, 133-145.	7.7	1,043
133	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
134	Computational assignment of cell-cycle stage from single-cell transcriptome data. <i>Methods</i> , 2015, 85, 54-61.	1.9	381
135	An atlas of mouse CD4+ T cell transcriptomes. <i>Biology Direct</i> , 2015, 10, 14.	1.9	82
136	Structural and evolutionary versatility in protein complexes with uneven stoichiometry. <i>Nature Communications</i> , 2015, 6, 6394.	5.8	48
137	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
138	Single Cell RNA-Sequencing of Pluripotent States Unlocks Modular Transcriptional Variation. <i>Cell Stem Cell</i> , 2015, 17, 471-485.	5.2	505
139	Structure, Dynamics, Assembly, and Evolution of Protein Complexes. <i>Annual Review of Biochemistry</i> , 2015, 84, 551-575.	5.0	351
140	Protein Flexibility Facilitates Quaternary Structure Assembly and Evolution. <i>PLoS Biology</i> , 2014, 12, e1001870.	2.6	89
141	Evolution of oligomeric state through allosteric pathways that mimic ligand binding. <i>Science</i> , 2014, 346, 1254346.	6.0	62
142	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
143	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
144	Evolution of protein structures and interactions from the perspective of residue contact networks. <i>Current Opinion in Structural Biology</i> , 2013, 23, 954-963.	2.6	33

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145	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
146	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
147	Accounting for technical noise in single-cell RNA-seq experiments. <i>Nature Methods</i> , 2013, 10, 1093-1095.	9.0	929
148	Protein Complexes Are under Evolutionary Selection to Assemble via Ordered Pathways. <i>Cell</i> , 2013, 153, 461-470.	13.5	215
149	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
150	Structural, Evolutionary, and Assembly Principles of Protein Oligomerization. <i>Progress in Molecular Biology and Translational Science</i> , 2013, 117, 25-51.	0.9	107
151	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
152	Immunology meets genomics. <i>Briefings in Functional Genomics</i> , 2013, 12, 469-470.	1.3	0
153	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
154	Uncovering the interplay between DNA sequence preferences of transcription factors and nucleosomes. <i>Cell Cycle</i> , 2012, 11, 4487-4488.	1.3	6
155	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
156	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
157	DNA Sequence Preferences of Transcriptional Activators Correlate More Strongly than Repressors with Nucleosomes. <i>Molecular Cell</i> , 2012, 47, 183-192.	4.5	26
158	The emergence of protein complexes: quaternary structure, dynamics and allostery. <i>Biochemical Society Transactions</i> , 2012, 40, 475-491.	1.6	75
159	Probing the diverse landscape of protein flexibility and binding. <i>Current Opinion in Structural Biology</i> , 2012, 22, 643-650.	2.6	94
160	How Do You Find Transcription Factors? Computational Approaches to Compile and Annotate Repertoires of Regulators for Any Genome. <i>Methods in Molecular Biology</i> , 2012, 786, 3-19.	0.4	11
161	The interface of protein structure, protein biophysics, and molecular evolution. <i>Protein Science</i> , 2012, 21, 769-785.	3.1	188
162	Duel of the fates: the role of transcriptional circuits and noise in CD4+ cells. <i>Current Opinion in Cell Biology</i> , 2012, 24, 350-358.	2.6	14

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163	Analysis and simulation of gene expression profiles in pure and mixed cell populations. <i>Physical Biology</i> , 2011, 8, 035013.	0.8	17
164	Relative Solvent Accessible Surface Area Predicts Protein Conformational Changes upon Binding. <i>Structure</i> , 2011, 19, 859-867.	1.6	174
165	RNA sequencing reveals two major classes of gene expression levels in metazoan cells. <i>Molecular Systems Biology</i> , 2011, 7, 497.	3.2	265
166	EpiChIP: gene-by-gene quantification of epigenetic modification levels. <i>Nucleic Acids Research</i> , 2011, 39, e27-e27.	6.5	36
167	Sequences and topology: evolution of proteins and evolution of computational approaches. <i>Current Opinion in Structural Biology</i> , 2010, 20, 333-334.	2.6	1
168	Lineage-specific expansion of DNA-binding transcription factor families. <i>Trends in Genetics</i> , 2010, 26, 388-393.	2.9	40
169	Genomic repertoires of DNA-binding transcription factors across the tree of life. <i>Nucleic Acids Research</i> , 2010, 38, 7364-7377.	6.5	140
170	Assessing Computational Methods of Cis-Regulatory Module Prediction. <i>PLoS Computational Biology</i> , 2010, 6, e1001020.	1.5	70
171	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
172	The Impact of Gene Expression Regulation on Evolution of Extracellular Signaling Pathways. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2666-2677.	2.5	8
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