

Sarah A Teichmann

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Altered TMPRSS2 usage by SARS-CoV-2 Omicron impacts tropism and fusogenicity.. <i>Nature</i> , 2022 ,	50.4	95
267	Single-cell atlases: shared and tissue-specific cell types across human organs.. <i>Nature Reviews Genetics</i> , 2022 ,	30.1	4
266	Single-cell transcriptomics links malignant T cells to the tumor immune landscape in cutaneous T cell lymphoma.. <i>Nature Communications</i> , 2022 , 13, 1158	17.4	1
265	Mapping the developing human immune system across organs.. <i>Science</i> , 2022 , eabo0510	33.3	10
264	Cross-tissue immune cell analysis reveals tissue-specific features in humans.. <i>Science</i> , 2022 , 376, eabl51973	33.3	13
263	Anatomical structures, cell types and biomarkers of the Human Reference Atlas. <i>Nature Cell Biology</i> , 2021 , 23, 1117-1128	23.4	6
262	Cell type ontologies of the Human Cell Atlas. <i>Nature Cell Biology</i> , 2021 , 23, 1129-1135	23.4	6
261	An integrated taxonomy for monogenic inflammatory bowel disease. <i>Gastroenterology</i> , 2021 ,	13.3	4
260	Expression Atlas update: gene and protein expression in multiple species. <i>Nucleic Acids Research</i> , 2021 ,	20.1	8
259	Cell-type specialization is encoded by specific chromatin topologies. <i>Nature</i> , 2021 , 599, 684-691	50.4	10
258	Mapping the temporal and spatial dynamics of the human endometrium in vivo and in vitro. <i>Nature Genetics</i> , 2021 , 53, 1698-1711	36.3	32
257	The Organoid Cell Atlas. <i>Nature Biotechnology</i> , 2021 , 39, 13-17	44.5	30
256	Transcriptional characterization of human megakaryocyte polyploidization and lineage commitment. <i>Journal of Thrombosis and Haemostasis</i> , 2021 , 19, 1236-1249	15.4	3
255	SARS-CoV-2 infection of the oral cavity and saliva. <i>Nature Medicine</i> , 2021 , 27, 892-903	50.5	175
254	The Human Lung Cell Atlas: a transformational resource for cells of the respiratory system 2021 , 158-174		0
253	Single-cell multi-omics analysis of the immune response in COVID-19. <i>Nature Medicine</i> , 2021 , 27, 904-916	50.5	101
252	CLICK-enabled analogues reveal pregnenolone interactomes in cancer and immune cells. <i>IScience</i> , 2021 , 24, 102485	6.1	1

251	Developmental bifurcation of human T follicular regulatory cells. <i>Science Immunology</i> , 2021 , 6,	28	5
250	High-throughput full-length single-cell RNA-seq automation. <i>Nature Protocols</i> , 2021 , 16, 2886-2915	18.8	2
249	Mapping Rora expression in resting and activated CD4+ T cells. <i>PLoS ONE</i> , 2021 , 16, e0251233	3.7	8
248	Single cell derived mRNA signals across human kidney tumors. <i>Nature Communications</i> , 2021 , 12, 3896	17.4	4
247	Towards a Human Cell Atlas: Taking Notes from the Past. <i>Trends in Genetics</i> , 2021 , 37, 625-630	8.5	17
246	Developmental cell programs are co-opted in inflammatory skin disease. <i>Science</i> , 2021 , 371,	33.3	63
245	Cholangiocyte organoids can repair bile ducts after transplantation in the human liver. <i>Science</i> , 2021 , 371, 839-846	33.3	45
244	Tumor to normal single-cell mRNA comparisons reveal a pan-neuroblastoma cancer cell. <i>Science Advances</i> , 2021 , 7,	14.3	23
243	Single-cell analysis of human B cell maturation predicts how antibody class switching shapes selection dynamics. <i>Science Immunology</i> , 2021 , 6,	28	39
242	INSIGHT: A population-scale COVID-19 testing strategy combining point-of-care diagnosis with centralized high-throughput sequencing. <i>Science Advances</i> , 2021 , 7,	14.3	22
241	User-friendly, scalable tools and workflows for single-cell RNA-seq analysis. <i>Nature Methods</i> , 2021 , 18, 327-328	21.6	9
240	Integrated Single-Cell Atlas of Endothelial Cells of the Human Lung. <i>Circulation</i> , 2021 , 144, 286-302	16.7	22
239	Molecular phenotyping reveals the identity of Barrett's esophagus and its malignant transition. <i>Science</i> , 2021 , 373, 760-767	33.3	18
238	Cells of the human intestinal tract mapped across space and time. <i>Nature</i> , 2021 , 597, 250-255	50.4	40
237	Differential abundance testing on single-cell data using k-nearest neighbor graphs. <i>Nature Biotechnology</i> , 2021 ,	44.5	8
236	Blood and immune development in human fetal bone marrow and Down syndrome. <i>Nature</i> , 2021 , 598, 327-331	50.4	10
235	A roadmap for the Human Developmental Cell Atlas. <i>Nature</i> , 2021 , 597, 196-205	50.4	18
234	MultiMAP: dimensionality reduction and integration of multimodal data.. <i>Genome Biology</i> , 2021 , 22, 346	18.3	2

233	Local and systemic responses to SARS-CoV-2 infection in children and adults.. <i>Nature</i> , 2021 ,	50.4	17
232	Completing the cancer jigsaw puzzle with single-cell multiomics.. <i>Nature Cancer</i> , 2021 , 2, 1260-1262	15.4	0
231	Single-Cell Sequencing of Developing Human Gut Reveals Transcriptional Links to Childhood Crohn's Disease. <i>Developmental Cell</i> , 2020 , 55, 771-783.e5	10.2	47
230	Reconstitution of a functional human thymus by postnatal stromal progenitor cells and natural whole-organ scaffolds. <i>Nature Communications</i> , 2020 , 11, 6372	17.4	15
229	Putative cell type discovery from single-cell gene expression data. <i>Nature Methods</i> , 2020 , 17, 621-628	21.6	30
228	Suppresses Immunity to Infection through Promoting Expression of Maf and IL-10 in Th Cells. <i>Journal of Immunology</i> , 2020 , 204, 2949-2960	5.3	19
227	Prenatal development of human immunity. <i>Science</i> , 2020 , 368, 600-603	33.3	39
226	High-Resolution mRNA and Secretome Atlas of Human Enteroendocrine Cells. <i>Cell</i> , 2020 , 181, 1291-1306.e19	56.1	41
225	Cardelino: computational integration of somatic clonal substructure and single-cell transcriptomes. <i>Nature Methods</i> , 2020 , 17, 414-421	21.6	17
224	The network effect: studying COVID-19 pathology with the Human Cell Atlas. <i>Nature Reviews Molecular Cell Biology</i> , 2020 , 21, 415-416	48.7	7
223	Distinct microbial and immune niches of the human colon. <i>Nature Immunology</i> , 2020 , 21, 343-353	19.1	92
222	Immunology in the Era of Single-Cell Technologies. <i>Annual Review of Immunology</i> , 2020 , 38, 727-757	34.7	27
221	A cell atlas of human thymic development defines T cell repertoire formation. <i>Science</i> , 2020 , 367,	33.3	171
220	CellPhoneDB: inferring cell-cell communication from combined expression of multi-subunit ligand-receptor complexes. <i>Nature Protocols</i> , 2020 , 15, 1484-1506	18.8	534
219	Nasal DNA methylation profiling of asthma and rhinitis. <i>Journal of Allergy and Clinical Immunology</i> , 2020 , 145, 1655-1663	11.5	34
218	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	56.2	1326
217	BBKNN: fast batch alignment of single cell transcriptomes. <i>Bioinformatics</i> , 2020 , 36, 964-965	7.2	154
216	Expression Atlas update: from tissues to single cells. <i>Nucleic Acids Research</i> , 2020 , 48, D77-D83	20.1	159

215	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,	9.9	3
214	Single-Cell RNA Sequencing Reveals a Dynamic Stromal Niche That Supports Tumor Growth. <i>Cell Reports</i> , 2020 , 31, 107628	10.6	63
213	Single-cell transcriptomics identifies CD44 as a marker and regulator of endothelial to haematopoietic transition. <i>Nature Communications</i> , 2020 , 11, 586	17.4	33
212	Cell Atlas technologies and insights into tissue architecture. <i>Biochemical Journal</i> , 2020 , 477, 1427-1442	3.8	20
211	Computational methods for single-cell omics across modalities. <i>Nature Methods</i> , 2020 , 17, 14-17	21.6	70
210	Transcriptome dynamics of CD4 T cells during malaria maps gradual transit from effector to memory. <i>Nature Immunology</i> , 2020 , 21, 1597-1610	19.1	10
209	Tumors induce de novo steroid biosynthesis in T cells to evade immunity. <i>Nature Communications</i> , 2020 , 11, 3588	17.4	19
208	Cells of the adult human heart. <i>Nature</i> , 2020 , 588, 466-472	50.4	274
207	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	32.3	109
206	Guidelines for reporting single-cell RNA-seq experiments. <i>Nature Biotechnology</i> , 2020 , 38, 1384-1386	44.5	9
205	LifeTime and improving European healthcare through cell-based interceptive medicine. <i>Nature</i> , 2020 , 587, 377-386	50.4	56
204	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	17.4	33
203	Mosquito cellular immunity at single-cell resolution. <i>Science</i> , 2020 , 369, 1128-1132	33.3	26
202	Single cell transcriptomics comes of age. <i>Nature Communications</i> , 2020 , 11, 4307	17.4	59
201	Gene signatures from scRNA-seq accurately quantify mast cells in biopsies in asthma. <i>Clinical and Experimental Allergy</i> , 2020 , 50, 1428-1431	4.1	6
200	Integrated scRNA-Seq Identifies Human Postnatal Thymus Seeding Progenitors and Regulatory Dynamics of Differentiating Immature Thymocytes. <i>Immunity</i> , 2020 , 52, 1088-1104.e6	32.3	31
199	Spatiotemporal immune zonation of the human kidney. <i>Science</i> , 2019 , 365, 1461-1466	33.3	145
198	Single-Cell Transcriptomics of Regulatory T Cells Reveals Trajectories of Tissue Adaptation. <i>Immunity</i> , 2019 , 50, 493-504.e7	32.3	175

197	A cellular census of human lungs identifies novel cell states in health and in asthma. <i>Nature Medicine</i> , 2019 , 25, 1153-1163	50.5	334
196	Establishment of porcine and human expanded potential stem cells. <i>Nature Cell Biology</i> , 2019 , 21, 687-699.	39.4	127
195	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	32.3	53
194	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	5.7	98
193	Comparative analysis of sequencing technologies for single-cell transcriptomics. <i>Genome Biology</i> , 2019 , 20, 70	18.3	47
192	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. <i>Developmental Cell</i> , 2019 , 49, 10-29	10.2	39
191	Single cell analysis of human foetal liver captures the transcriptional profile of hepatobiliary hybrid progenitors. <i>Nature Communications</i> , 2019 , 10, 3350	17.4	52
190	Immunology Driven by Large-Scale Single-Cell Sequencing. <i>Trends in Immunology</i> , 2019 , 40, 1011-1021	14.4	43
189	Decoding human fetal liver haematopoiesis. <i>Nature</i> , 2019 , 574, 365-371	50.4	200
188	Single-Cell Transcriptomics Uncovers Zonation of Function in the Mesenchyme during Liver Fibrosis. <i>Cell Reports</i> , 2019 , 29, 1832-1847.e8	10.6	115
187	Genome-wide CRISPR Screens in T Helper Cells Reveal Pervasive Crosstalk between Activation and Differentiation. <i>Cell</i> , 2019 , 176, 882-896.e18	56.2	72
186	A test metric for assessing single-cell RNA-seq batch correction. <i>Nature Methods</i> , 2019 , 16, 43-49	21.6	140
185	Exponential scaling of single-cell RNA-seq in the past decade. <i>Nature Protocols</i> , 2018 , 13, 599-604	18.8	400
184	Mapping human development at single-cell resolution. <i>Development (Cambridge)</i> , 2018 , 145,	6.6	24
183	Cotranslational protein assembly imposes evolutionary constraints on homomeric proteins. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 279-288	17.6	19
182	SpatialDE: identification of spatially variable genes. <i>Nature Methods</i> , 2018 , 15, 343-346	21.6	153
181	BraCeR: B-cell-receptor reconstruction and clonality inference from single-cell RNA-seq. <i>Nature Methods</i> , 2018 , 15, 563-565	21.6	48
180	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	11.5	28

179	Single-cell transcriptomes from human kidneys reveal the cellular identity of renal tumors. <i>Science</i> , 2018 , 361, 594-599	33.3	282
178	Distinctive features of lincRNA gene expression suggest widespread RNA-independent functions. <i>Life Science Alliance</i> , 2018 , 1, e201800124	5.8	21
177	Single cell RNA-seq and ATAC-seq analysis of cardiac progenitor cell transition states and lineage settlement. <i>Nature Communications</i> , 2018 , 9, 4877	17.4	93
176	Single-cell reconstruction of the early maternal-fetal interface in humans. <i>Nature</i> , 2018 , 563, 347-353	50.4	792
175	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	14.4	21
174	A rapid and robust method for single cell chromatin accessibility profiling. <i>Nature Communications</i> , 2018 , 9, 5345	17.4	91
173	Gene expression variability across cells and species shapes innate immunity. <i>Nature</i> , 2018 , 563, 197-202	50.4	94
172	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	5.6	59
171	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	9.7	59
170	Power analysis of single-cell RNA-sequencing experiments. <i>Nature Methods</i> , 2017 , 14, 381-387	21.6	357
169	Single-cell RNA-seq and computational analysis using temporal mixture modelling resolves Th1/Tfh fate bifurcation in malaria. <i>Science Immunology</i> , 2017 , 2,	28	171
168	Wounding induces dedifferentiation of epidermal Gata6 cells and acquisition of stem cell properties. <i>Nature Cell Biology</i> , 2017 , 19, 603-613	23.4	87
167	Computational approaches for interpreting scRNA-seq data. <i>FEBS Letters</i> , 2017 , 591, 2213-2225	3.8	75
166	Aging increases cell-to-cell transcriptional variability upon immune stimulation. <i>Science</i> , 2017 , 355, 1433-1436	35.3	158
165	Intrinsic transcriptional heterogeneity in B cells controls early class switching to IgE. <i>Journal of Experimental Medicine</i> , 2017 , 214, 183-196	16.6	35
164	Regulation, evolution and consequences of cotranslational protein complex assembly. <i>Current Opinion in Structural Biology</i> , 2017 , 42, 90-97	8.1	44
163	The Human Cell Atlas 2017 ,		41
162	Single-cell transcriptomics to explore the immune system in health and disease. <i>Science</i> , 2017 , 358, 58-63	33.3	275

161	Establishment of mouse expanded potential stem cells. <i>Nature</i> , 2017 , 550, 393-397	50.4	128
160	A practical guide to single-cell RNA-sequencing for biomedical research and clinical applications. <i>Genome Medicine</i> , 2017 , 9, 75	14.4	332
159	Single-cell insights into transcriptomic diversity in immunity. <i>Current Opinion in Systems Biology</i> , 2017 , 5, 63-71	3.2	4
158	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	13.3	150
157	Flipping between Polycomb repressed and active transcriptional states introduces noise in gene expression. <i>Nature Communications</i> , 2017 , 8, 36	17.4	43
156	Single cell transcriptomics of pluripotent stem cells: reprogramming and differentiation. <i>Current Opinion in Genetics and Development</i> , 2017 , 46, 66-76	4.9	14
155	The Human Cell Atlas. <i>ELife</i> , 2017 , 6,	8.9	937
154	The Human Cell Atlas: from vision to reality. <i>Nature</i> , 2017 , 550, 451-453	50.4	310
153	Genetics and immunity in the era of single-cell genomics. <i>Human Molecular Genetics</i> , 2016 , 25, R141-R148.	8.6	18
152	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	18.3	46
151	Classification of low quality cells from single-cell RNA-seq data. <i>Genome Biology</i> , 2016 , 17, 29	18.3	329
150	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	6.5	13
149	Single-Cell RNA-Sequencing Reveals a Continuous Spectrum of Differentiation in Hematopoietic Cells. <i>Cell Reports</i> , 2016 , 14, 966-977	10.6	119
148	T cell fate and clonality inference from single-cell transcriptomes. <i>Nature Methods</i> , 2016 , 13, 329-332	21.6	302
147	Data on publications, structural analyses, and queries used to build and utilize the AlloRep database. <i>Data in Brief</i> , 2016 , 8, 948-57	1.2	1
146	Single-cell RNA-seq identifies a PD-1 ILC progenitor and defines its development pathway. <i>Nature</i> , 2016 , 539, 102-106	50.4	186
145	MERVL/Zscan4 Network Activation Results in Transient Genome-wide DNA Demethylation of mESCs. <i>Cell Reports</i> , 2016 , 17, 179-192	10.6	111
144	Computational analysis of cell-to-cell heterogeneity in single-cell RNA-sequencing data reveals hidden subpopulations of cells. <i>Nature Biotechnology</i> , 2015 , 33, 155-60	44.5	778

143	Computational assignment of cell-cycle stage from single-cell transcriptome data. <i>Methods</i> , 2015 , 85, 54-61	4.6	259
142	An atlas of mouse CD4(+) T cell transcriptomes. <i>Biology Direct</i> , 2015 , 10, 14	7.2	50
141	Structural and evolutionary versatility in protein complexes with uneven stoichiometry. <i>Nature Communications</i> , 2015 , 6, 6394	17.4	29
140	Characterizing noise structure in single-cell RNA-seq distinguishes genuine from technical stochastic allelic expression. <i>Nature Communications</i> , 2015 , 6, 8687	17.4	154
139	Single Cell RNA-Sequencing of Pluripotent States Unlocks Modular Transcriptional Variation. <i>Cell Stem Cell</i> , 2015 , 17, 471-85	18	343
138	Structure, dynamics, assembly, and evolution of protein complexes. <i>Annual Review of Biochemistry</i> , 2015 , 84, 551-75	29.1	227
137	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	6	27
136	The technology and biology of single-cell RNA sequencing. <i>Molecular Cell</i> , 2015 , 58, 610-20	17.6	650
135	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	18.3	74
134	Principles of assembly reveal a periodic table of protein complexes. <i>Science</i> , 2015 , 350, aaa2245	33.3	142
133	Computational and analytical challenges in single-cell transcriptomics. <i>Nature Reviews Genetics</i> , 2015 , 16, 133-45	30.1	736
132	Single-cell RNA sequencing reveals T helper cells synthesizing steroids de novo to contribute to immune homeostasis. <i>Cell Reports</i> , 2014 , 7, 1130-42	10.6	143
131	Protein flexibility facilitates quaternary structure assembly and evolution. <i>PLoS Biology</i> , 2014 , 12, e1001870	18.70	56
130	Evolution of oligomeric state through allosteric pathways that mimic ligand binding. <i>Science</i> , 2014 , 346, 1254346	33.3	49
129	Parallel dynamics and evolution: Protein conformational fluctuations and assembly reflect evolutionary changes in sequence and structure. <i>BioEssays</i> , 2014 , 36, 209-18	4.1	48
128	Evolution of protein structures and interactions from the perspective of residue contact networks. <i>Current Opinion in Structural Biology</i> , 2013 , 23, 954-63	8.1	29
127	The role of salt bridges, charge density, and subunit flexibility in determining disassembly routes of protein complexes. <i>Structure</i> , 2013 , 21, 1325-37	5.2	71
126	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, 20212-7	11.5	1041

125	Accounting for technical noise in single-cell RNA-seq experiments. <i>Nature Methods</i> , 2013 , 10, 1093-5	21.6	659
124	Protein complexes are under evolutionary selection to assemble via ordered pathways. <i>Cell</i> , 2013 , 153, 461-70	56.2	153
123	Regulation of protein-protein binding by coupling between phosphorylation and intrinsic disorder: analysis of human protein complexes. <i>Molecular BioSystems</i> , 2013 , 9, 1620-6		45
122	Structural, evolutionary, and assembly principles of protein oligomerization. <i>Progress in Molecular Biology and Translational Science</i> , 2013 , 117, 25-51	4	77
121	Families of Sequence-Specific DNA-Binding Domains in Transcription Factors across the Tree of Life 2013 , 383-420		
120	Depletion of stromal cells expressing fibroblast activation protein- Γ from skeletal muscle and bone marrow results in cachexia and anemia. <i>Journal of Experimental Medicine</i> , 2013 , 210, 1137-51	16.6	219
119	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, 20461-6	11.5	120
118	Polycomb associates genome-wide with a specific RNA polymerase II variant, and regulates metabolic genes in ESCs. <i>Cell Stem Cell</i> , 2012 , 10, 157-70	18	221
117	DNA sequence preferences of transcriptional activators correlate more strongly than repressors with nucleosomes. <i>Molecular Cell</i> , 2012 , 47, 183-92	17.6	21
116	The emergence of protein complexes: quaternary structure, dynamics and allostery. Colworth Medal Lecture. <i>Biochemical Society Transactions</i> , 2012 , 40, 475-91	5.1	61
115	Probing the diverse landscape of protein flexibility and binding. <i>Current Opinion in Structural Biology</i> , 2012 , 22, 643-50	8.1	87
114	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	1.4	6
113	The interface of protein structure, protein biophysics, and molecular evolution. <i>Protein Science</i> , 2012 , 21, 769-85	6.3	136
112	Duel of the fates: the role of transcriptional circuits and noise in CD4+ cells. <i>Current Opinion in Cell Biology</i> , 2012 , 24, 350-8	9	11
111	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, 8127-32	11.5	38
110	Analysis and simulation of gene expression profiles in pure and mixed cell populations. <i>Physical Biology</i> , 2011 , 8, 035013	3	15
109	Relative solvent accessible surface area predicts protein conformational changes upon binding. <i>Structure</i> , 2011 , 19, 859-67	5.2	120
108	RNA sequencing reveals two major classes of gene expression levels in metazoan cells. <i>Molecular Systems Biology</i> , 2011 , 7, 497	12.2	219

107	EpiChIP: gene-by-gene quantification of epigenetic modification levels. <i>Nucleic Acids Research</i> , 2011 , 39, e27	20.1	34
106	Genomic repertoires of DNA-binding transcription factors across the tree of life. <i>Nucleic Acids Research</i> , 2010 , 38, 7364-77	20.1	102
105	Assessing computational methods of cis-regulatory module prediction. <i>PLoS Computational Biology</i> , 2010 , 6, e1001020	5	57
104	FlyTF: improved annotation and enhanced functionality of the Drosophila transcription factor database. <i>Nucleic Acids Research</i> , 2010 , 38, D443-7	20.1	61
103	The impact of gene expression regulation on evolution of extracellular signaling pathways. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 2666-77	7.6	8
102	Construction of a large extracellular protein interaction network and its resolution by spatiotemporal expression profiling. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 2654-65	7.6	35
101	An atlas of combinatorial transcriptional regulation in mouse and man. <i>Cell</i> , 2010 , 140, 744-52	56.2	555
100	Homomeric protein complexes: evolution and assembly. <i>Biochemical Society Transactions</i> , 2010 , 38, 879-82	8.2	24
99	How do proteins gain new domains?. <i>Genome Biology</i> , 2010 , 11, 126	18.3	56
98	The developmental expression dynamics of Drosophila melanogaster transcription factors. <i>Genome Biology</i> , 2010 , 11, R40	18.3	16
97	Lineage-specific expansion of DNA-binding transcription factor families. <i>Trends in Genetics</i> , 2010 , 26, 388-93	8.5	35
96	The impact of genomic neighborhood on the evolution of human and chimpanzee transcriptome. <i>Genome Research</i> , 2009 , 19, 785-94	9.7	40
95	BloodExpress: a database of gene expression in mouse haematopoiesis. <i>Nucleic Acids Research</i> , 2009 , 37, D873-9	20.1	30
94	Protein domain organisation: adding order. <i>BMC Bioinformatics</i> , 2009 , 10, 39	3.6	41
93	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009 , 41, 553-62	36.3	356
92	A census of human transcription factors: function, expression and evolution. <i>Nature Reviews Genetics</i> , 2009 , 10, 252-63	30.1	1090
91	A HaemAtlas: characterizing gene expression in differentiated human blood cells. <i>Blood</i> , 2009 , 113, e1-92.2		193
90	The transcriptional program controlled by the stem cell leukemia gene Scl/Tal1 during early embryonic hematopoietic development. <i>Blood</i> , 2009 , 113, 5456-65	2.2	100

89	Assembly reflects evolution of protein complexes. <i>Nature</i> , 2008 , 453, 1262-5	50.4	316
88	Common variants near MC4R are associated with fat mass, weight and risk of obesity. <i>Nature Genetics</i> , 2008 , 40, 768-75	36.3	1048
87	Patterns of evolutionary constraints on genes in humans. <i>BMC Evolutionary Biology</i> , 2008 , 8, 275	3	13
86	Chance and necessity in chromosomal gene distributions. <i>Trends in Genetics</i> , 2008 , 24, 216-9	8.5	19
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34	A spatial multi-omics atlas of the human lung reveals a novel immune cell survival niche	8
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30	BraCeR: Reconstruction of B-cell receptor sequences and clonality inference from single-cell RNA-sequencing	4
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