

Lars M Steinmetz

List of Publications by Citations

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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.

181
papers

19,426
citations

64
h-index

138
g-index

214
ext. papers

23,905
ext. citations

16
avg, IF

6.57
L-index

#	Paper	IF	Citations
181	A genome-wide transcriptional analysis of the mitotic cell cycle. <i>Molecular Cell</i> , 1998 , 2, 65-73	17.6	1659
180	Insights into RNA biology from an atlas of mammalian mRNA-binding proteins. <i>Cell</i> , 2012 , 149, 1393-406	56.2	1328
179	Bidirectional promoters generate pervasive transcription in yeast. <i>Nature</i> , 2009 , 457, 1033-7	50.4	725
178	Evolutionary rate in the protein interaction network. <i>Science</i> , 2002 , 296, 750-2	33.3	704
177	Role of duplicate genes in genetic robustness against null mutations. <i>Nature</i> , 2003 , 421, 63-6	50.4	670
176	A global genetic interaction network maps a wiring diagram of cellular function. <i>Science</i> , 2016 , 353,	33.3	626
175	Assembly of functionally integrated human forebrain spheroids. <i>Nature</i> , 2017 , 545, 54-59	50.4	604
174	A high-resolution map of transcription in the yeast genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 5320-5	11.5	546
173	Ultrasensitive proteome analysis using paramagnetic bead technology. <i>Molecular Systems Biology</i> , 2014 , 10, 757	12.2	497
172	Widespread bidirectional promoters are the major source of cryptic transcripts in yeast. <i>Nature</i> , 2009 , 457, 1038-42	50.4	462
171	Human haematopoietic stem cell lineage commitment is a continuous process. <i>Nature Cell Biology</i> , 2017 , 19, 271-281	23.4	441
170	High-resolution mapping of meiotic crossovers and non-crossovers in yeast. <i>Nature</i> , 2008 , 454, 479-85	50.4	441
169	Systematic screen for human disease genes in yeast. <i>Nature Genetics</i> , 2002 , 31, 400-4	36.3	431
168	Gene regulation by antisense transcription. <i>Nature Reviews Genetics</i> , 2013 , 14, 880-93	30.1	429
167	Dissecting the architecture of a quantitative trait locus in yeast. <i>Nature</i> , 2002 , 416, 326-30	50.4	429
166	Cytosine base editor generates substantial off-target single-nucleotide variants in mouse embryos. <i>Science</i> , 2019 , 364, 289-292	33.3	381
165	Transcriptional regulation and function during the human cell cycle. <i>Nature Genetics</i> , 2001 , 27, 48-54	36.3	330

164	A new fate mapping system reveals context-dependent random or clonal expansion of microglia. <i>Nature Neuroscience</i> , 2017 , 20, 793-803	25.5	316
163	Extensive transcriptional heterogeneity revealed by isoform profiling. <i>Nature</i> , 2013 , 497, 127-31	50.4	280
162	Extensive variation in chromatin states across humans. <i>Science</i> , 2013 , 342, 750-2	33.3	276
161	Yeast Sen1 helicase protects the genome from transcription-associated instability. <i>Molecular Cell</i> , 2011 , 41, 21-32	17.6	251
160	Inflammation-Induced Emergency Megakaryopoiesis Driven by Hematopoietic Stem Cell-like Megakaryocyte Progenitors. <i>Cell Stem Cell</i> , 2015 , 17, 422-34	18	245
159	Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions. <i>Cell</i> , 2015 , 162, 1051-65	56.2	240
158	Combined single-cell and spatial transcriptomics reveal the molecular, cellular and spatial bone marrow niche organization. <i>Nature Cell Biology</i> , 2020 , 22, 38-48	23.4	221
157	Genome sequencing and comparative analysis of <i>Saccharomyces cerevisiae</i> strain YJM789. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 12825-30	11.5	214
156	Polyadenylation site-induced decay of upstream transcripts enforces promoter directionality. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 923-8	17.6	207
155	Extensive degradation of RNA precursors by the exosome in wild-type cells. <i>Molecular Cell</i> , 2012 , 48, 409-21	17.6	176
154	Gene loops enhance transcriptional directionality. <i>Science</i> , 2012 , 338, 671-5	33.3	175
153	Widespread Co-translational RNA Decay Reveals Ribosome Dynamics. <i>Cell</i> , 2015 , 161, 1400-12	56.2	171
152	Integrative analysis of the mitochondrial proteome in yeast. <i>PLoS Biology</i> , 2004 , 2, e160	9.7	165
151	Antisense artifacts in transcriptome microarray experiments are resolved by actinomycin D. <i>Nucleic Acids Research</i> , 2007 , 35, e128	20.1	162
150	Functional consequences of bidirectional promoters. <i>Trends in Genetics</i> , 2011 , 27, 267-76	8.5	155
149	Set3 HDAC mediates effects of overlapping noncoding transcription on gene induction kinetics. <i>Cell</i> , 2012 , 150, 1158-69	56.2	143
148	System-wide identification of RNA-binding proteins by interactome capture. <i>Nature Protocols</i> , 2013 , 8, 491-500	18.8	135
147	Magnetic levitation of single cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E3661-8	11.5	132

146	Antisense expression increases gene expression variability and locus interdependency. <i>Molecular Systems Biology</i> , 2011 , 7, 468	12.2	131
145	Genetic analysis of variation in transcription factor binding in yeast. <i>Nature</i> , 2010 , 464, 1187-91	50.4	130
144	RNA polymerase II collision interrupts convergent transcription. <i>Molecular Cell</i> , 2012 , 48, 365-74	17.6	120
143	Transcript mapping with high-density oligonucleotide tiling arrays. <i>Bioinformatics</i> , 2006 , 22, 1963-70	7.2	120
142	Trans-acting antisense RNAs mediate transcriptional gene cosuppression in <i>S. cerevisiae</i> . <i>Genes and Development</i> , 2009 , 23, 1534-45	12.6	119
141	Myt1l safeguards neuronal identity by actively repressing many non-neuronal fates. <i>Nature</i> , 2017 , 544, 245-249	50.4	112
140	Thymic tuft cells promote an IL-4-enriched medulla and shape thymocyte development. <i>Nature</i> , 2018 , 559, 627-631	50.4	111
139	Quantitative CRISPR interference screens in yeast identify chemical-genetic interactions and new rules for guide RNA design. <i>Genome Biology</i> , 2016 , 17, 45	18.3	110
138	HEX: A heterologous expression platform for the discovery of fungal natural products. <i>Science Advances</i> , 2018 , 4, eaar5459	14.3	106
137	Sequential elimination of major-effect contributors identifies additional quantitative trait loci conditioning high-temperature growth in yeast. <i>Genetics</i> , 2008 , 180, 1661-70	4	106
136	Conventional and Neo-antigenic Peptides Presented by β Cells Are Targeted by Circulating Naive CD8+ T Cells in Type 1 Diabetic and Healthy Donors. <i>Cell Metabolism</i> , 2018 , 28, 946-960.e6	24.6	104
135	Execution of the meiotic noncoding RNA expression program and the onset of gametogenesis in yeast require the conserved exosome subunit Rrp6. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 1058-63	11.5	103
134	Biological plasticity rescues target activity in CRISPR knock outs. <i>Nature Methods</i> , 2019 , 16, 1087-1093	21.6	94
133	Complex genetic interactions in a quantitative trait locus. <i>PLoS Genetics</i> , 2006 , 2, e13	6	94
132	Multiplexed precision genome editing with trackable genomic barcodes in yeast. <i>Nature Biotechnology</i> , 2018 , 36, 512-520	44.5	91
131	Single-cell transcriptome analysis reveals coordinated ectopic gene-expression patterns in medullary thymic epithelial cells. <i>Nature Immunology</i> , 2015 , 16, 933-41	19.1	88
130	Elevated evolutionary rates in the laboratory strain of <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 1092-7	11.5	85
129	Inhibition of NGLY1 Inactivates the Transcription Factor Nrf1 and Potentiates Proteasome Inhibitor Cytotoxicity. <i>ACS Central Science</i> , 2017 , 3, 1143-1155	16.8	84

128	Yeast as a system for modeling mitochondrial disease mechanisms and discovering therapies. <i>DMM Disease Models and Mechanisms</i> , 2015 , 8, 509-26	4.1	83
127	Dissecting the genetic basis of resistance to malaria parasites in <i>Anopheles gambiae</i> . <i>Science</i> , 2009 , 326, 147-50	33.3	82
126	An efficient method for genome-wide polyadenylation site mapping and RNA quantification. <i>Nucleic Acids Research</i> , 2013 , 41, e65	20.1	81
125	High-resolution transcription atlas of the mitotic cell cycle in budding yeast. <i>Genome Biology</i> , 2010 , 11, R24	18.3	81
124	The baker's yeast diploid genome is remarkably stable in vegetative growth and meiosis. <i>PLoS Genetics</i> , 2010 , 6, e1001109	6	79
123	Maximizing the potential of functional genomics. <i>Nature Reviews Genetics</i> , 2004 , 5, 190-201	30.1	79
122	Drift and conservation of differential exon usage across tissues in primate species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 15377-82	11.5	73
121	Opposing T cell responses in experimental autoimmune encephalomyelitis. <i>Nature</i> , 2019 , 572, 481-487	50.4	70
120	Control of Cdc28 CDK1 by a stress-induced lncRNA. <i>Molecular Cell</i> , 2014 , 53, 549-61	17.6	70
119	Alternative polyadenylation diversifies post-transcriptional regulation by selective RNA-protein interactions. <i>Molecular Systems Biology</i> , 2014 , 10, 719	12.2	64
118	Rrp6p controls mRNA poly(A) tail length and its decoration with poly(A) binding proteins. <i>Molecular Cell</i> , 2012 , 47, 267-80	17.6	64
117	Modulation of mRNA and lncRNA expression dynamics by the Set2-Rpd3S pathway. <i>Nature Communications</i> , 2016 , 7, 13534	17.4	64
116	Genotype-environment interactions reveal causal pathways that mediate genetic effects on phenotype. <i>PLoS Genetics</i> , 2013 , 9, e1003803	6	63
115	Assessing systems properties of yeast mitochondria through an interaction map of the organelle. <i>PLoS Genetics</i> , 2006 , 2, e170	6	63
114	A yeast-based assay identifies drugs active against human mitochondrial disorders. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 11989-94	11.5	60
113	An evaluation of high-throughput approaches to QTL mapping in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2014 , 196, 853-65	4	56
112	Large-Scale Low-Cost NGS Library Preparation Using a Robust Tn5 Purification and Tagmentation Protocol. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 79-89	3.2	54
111	Principles for RNA metabolism and alternative transcription initiation within closely spaced promoters. <i>Nature Genetics</i> , 2016 , 48, 984-94	36.3	53

110	Regional Variation in RBM20 Causes a Highly Penetrant Arrhythmogenic Cardiomyopathy. <i>Circulation: Heart Failure</i> , 2019 , 12, e005371	7.6	51
109	Multitarget, quantitative nanoplasmonic electrical field-enhanced resonating device (NE2RD) for diagnostics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E4354-63	11.5	49
108	A genome-wide map of mitochondrial DNA recombination in yeast. <i>Genetics</i> , 2014 , 198, 755-71	4	49
107	Genome-wide identification of transcript start and end sites by transcript isoform sequencing. <i>Nature Protocols</i> , 2014 , 9, 1740-59	18.8	46
106	Targeted Perturb-seq enables genome-scale genetic screens in single cells. <i>Nature Methods</i> , 2020 , 17, 629-635	21.6	41
105	Roadblock termination by reb1p restricts cryptic and readthrough transcription. <i>Molecular Cell</i> , 2014 , 56, 667-80	17.6	41
104	Single-cell polyadenylation site mapping reveals 3Sisoform choice variability. <i>Molecular Systems Biology</i> , 2015 , 11, 812	12.2	40
103	Genome-wide H4 K16 acetylation by SAS-I is deposited independently of transcription and histone exchange. <i>Nucleic Acids Research</i> , 2012 , 40, 65-74	20.1	39
102	Landscape and Dynamics of Transcription Initiation in the Malaria Parasite Plasmodium falciparum. <i>Cell Reports</i> , 2016 , 14, 2463-75	10.6	38
101	Protein Abundance Control by Non-coding Antisense Transcription. <i>Cell Reports</i> , 2016 , 15, 2625-36	10.6	37
100	Role of histone modifications and early termination in pervasive transcription and antisense-mediated gene silencing in yeast. <i>Nucleic Acids Research</i> , 2014 , 42, 4348-62	20.1	37
99	Genotyping 1000 yeast strains by next-generation sequencing. <i>BMC Genomics</i> , 2013 , 14, 90	4.5	37
98	Expression of nuclear and mitochondrial genes encoding ATP synthase is synchronized by disassembly of a multisynthetase complex. <i>Molecular Cell</i> , 2014 , 56, 763-76	17.6	37
97	Gain of CTCF-Anchored Chromatin Loops Marks the Exit from Naive Pluripotency. <i>Cell Systems</i> , 2018 , 7, 482-495.e10	10.6	37
96	Mosaic genome architecture of the Anopheles gambiae species complex. <i>PLoS ONE</i> , 2007 , 2, e1249	3.7	36
95	Comprehensive Identification of RNA-Binding Proteins by RNA Interactome Capture. <i>Methods in Molecular Biology</i> , 2016 , 1358, 131-9	1.4	36
94	Systematic screens for human disease genes, from yeast to human and back. <i>Molecular BioSystems</i> , 2008 , 4, 18-29		35
93	The Not5 subunit of the ccr4-not complex connects transcription and translation. <i>PLoS Genetics</i> , 2014 , 10, e1004569	6	34

92	Heritability and genetic basis of protein level variation in an outbred population. <i>Genome Research</i> , 2014 , 24, 1363-70	9.7	34
91	Select sequencing of clonally expanded CD8 T cells reveals limits to clonal expansion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 8995-9001	11.5	33
90	The Nuclear PolyA-Binding Protein Nab2p Is Essential for mRNA Production. <i>Cell Reports</i> , 2015 , 12, 128-139	11.6	33
89	Experimental relocation of the mitochondrial ATP9 gene to the nucleus reveals forces underlying mitochondrial genome evolution. <i>PLoS Genetics</i> , 2012 , 8, e1002876	6	32
88	Sensitive high-throughput single-cell RNA-seq reveals within-clonal transcript correlations in yeast populations. <i>Nature Microbiology</i> , 2019 , 4, 683-692	26.6	32
87	Integrating Cell Phone Imaging with Magnetic Levitation (i-LEV) for Label-Free Blood Analysis at the Point-of-Living. <i>Small</i> , 2016 , 12, 1222-1229	11	31
86	The cellular growth rate controls overall mRNA turnover, and modulates either transcription or degradation rates of particular gene regulons. <i>Nucleic Acids Research</i> , 2016 , 44, 3643-58	20.1	31
85	Genome-wide quantification of 5Sphosphorylated mRNA degradation intermediates for analysis of ribosome dynamics. <i>Nature Protocols</i> , 2016 , 11, 359-76	18.8	30
84	Natural sequence variants of yeast environmental sensors confer cell-to-cell expression variability. <i>Molecular Systems Biology</i> , 2013 , 9, 695	12.2	29
83	Translational Capacity of a Cell Is Determined during Transcription Elongation via the Ccr4-Not Complex. <i>Cell Reports</i> , 2016 , 15, 1782-94	10.6	28
82	Genome-wide allele- and strand-specific expression profiling. <i>Molecular Systems Biology</i> , 2009 , 5, 274	12.2	28
81	Transcription mediated insulation and interference direct gene cluster expression switches. <i>ELife</i> , 2014 , 3, e03635	8.9	28
80	Negative feedback buffers effects of regulatory variants. <i>Molecular Systems Biology</i> , 2015 , 11, 785	12.2	27
79	Accumulation of noncoding RNA due to an RNase P defect in <i>Saccharomyces cerevisiae</i> . <i>Rna</i> , 2011 , 17, 1441-50	5.8	27
78	A method for high-throughput production of sequence-verified DNA libraries and strain collections. <i>Molecular Systems Biology</i> , 2017 , 13, 913	12.2	26
77	Identification of leukemic and pre-leukemic stem cells by clonal tracking from single-cell transcriptomics. <i>Nature Communications</i> , 2021 , 12, 1366	17.4	26
76	Yeast growth plasticity is regulated by environment-specific multi-QTL interactions. <i>G3: Genes, Genomes, Genetics</i> , 2014 , 4, 769-77	3.2	23
75	Single-cell analyses reveal SARS-CoV-2 interference with intrinsic immune response in the human gut. <i>Molecular Systems Biology</i> , 2021 , 17, e10232	12.2	23

74	Chromatin Dynamics and the RNA Exosome Function in Concert to Regulate Transcriptional Homeostasis. <i>Cell Reports</i> , 2015 , 13, 1610-22	10.6	22
73	A high-throughput CHIP-Seq for large-scale chromatin studies. <i>Molecular Systems Biology</i> , 2015 , 11, 777	12.2	22
72	Chromatin-dependent regulation of RNA polymerases II and III activity throughout the transcription cycle. <i>Nucleic Acids Research</i> , 2015 , 43, 787-802	20.1	21
71	Genome Dynamics of Hybrid During Vegetative and Meiotic Divisions. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 3669-3679	3.2	20
70	Multiple genomic changes associated with reorganization of gene regulation and adaptation in yeast. <i>Molecular Biology and Evolution</i> , 2013 , 30, 1514-26	8.3	20
69	NAD(P)HX repair deficiency causes central metabolic perturbations in yeast and human cells. <i>FEBS Journal</i> , 2018 , 285, 3376-3401	5.7	19
68	The chaperone-binding activity of the mitochondrial surface receptor Tom70 protects the cytosol against mitoprotein-induced stress. <i>Cell Reports</i> , 2021 , 35, 108936	10.6	19
67	Variation in crossover frequencies perturb crossover assurance without affecting meiotic chromosome segregation in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2015 , 199, 399-412	4	18
66	A privacy-preserving solution for compressed storage and selective retrieval of genomic data. <i>Genome Research</i> , 2016 , 26, 1687-1696	9.7	18
65	Mitochondrial protein sorting as a therapeutic target for ATP synthase disorders. <i>Nature Communications</i> , 2014 , 5, 5585	17.4	18
64	Genome-wide polyadenylation site mapping. <i>Methods in Enzymology</i> , 2012 , 513, 271-96	1.7	18
63	Modulating Crossover Frequency and Interference for Obligate Crossovers in Meiosis. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 1511-1524	3.2	17
62	Rpd3L HDAC links H3K4me3 to transcriptional repression memory. <i>Nucleic Acids Research</i> , 2018 , 46, 8261-8274	18.2	17
61	Genome-wide survey of post-meiotic segregation during yeast recombination. <i>Genome Biology</i> , 2011 , 12, R36	18.3	17
60	The conserved histone deacetylase Rpd3 and its DNA binding subunit Ume6 control dynamic transcript architecture during mitotic growth and meiotic development. <i>Nucleic Acids Research</i> , 2015 , 43, 115-28	20.1	16
59	High-speed fluorescence image-enabled cell sorting.. <i>Science</i> , 2022 , 375, 315-320	33.3	16
58	Condensin controls cellular RNA levels through the accurate segregation of chromosomes instead of directly regulating transcription. <i>ELife</i> , 2018 , 7,	8.9	16
57	Dysregulated ribonucleoprotein granules promote cardiomyopathy in RBM20 gene-edited pigs. <i>Nature Medicine</i> , 2020 , 26, 1788-1800	50.5	16

56	High-frequency actionable pathogenic exome variants in an average-risk cohort. <i>Journal of Physical Education and Sports Management</i> , 2018 , 4,	2.8	15
55	KIRCD8 T cells suppress pathogenic T cells and are active in autoimmune diseases and COVID-19.. <i>Science</i> , 2022 , 376, eabi9591	33.3	15
54	The role of Ctk1 kinase in termination of small non-coding RNAs. <i>PLoS ONE</i> , 2013 , 8, e80495	3.7	14
53	Antagonistic changes in sensitivity to antifungal drugs by mutations of an important ABC transporter gene in a fungal pathogen. <i>PLoS ONE</i> , 2010 , 5, e11309	3.7	13
52	Natural single-nucleosome epi-polymorphisms in yeast. <i>PLoS Genetics</i> , 2010 , 6, e1000913	6	13
51	Combined transient ablation and single-cell RNA-sequencing reveals the development of medullary thymic epithelial cells. <i>ELife</i> , 2020 , 9,	8.9	13
50	iPSC Modeling of RBM20-Deficient DCM Identifies Upregulation of RBM20 as a Therapeutic Strategy. <i>Cell Reports</i> , 2020 , 32, 108117	10.6	13
49	Functional interplay between MSL1 and CDK7 controls RNA polymerase II Ser5 phosphorylation. <i>Nature Structural and Molecular Biology</i> , 2016 , 23, 580-9	17.6	12
48	Temporal expression profiling identifies pathways mediating effect of causal variant on phenotype. <i>PLoS Genetics</i> , 2015 , 11, e1005195	6	11
47	Loss of the Yeast SR Protein Npl3 Alters Gene Expression Due to Transcription Readthrough. <i>PLoS Genetics</i> , 2015 , 11, e1005735	6	11
46	GOT1, a method to identify genome-wide off-target effects of genome editing in mouse embryos. <i>Nature Protocols</i> , 2020 , 15, 3009-3029	18.8	11
45	Combining genome sequences and new technologies for dissecting the genetics of complex phenotypes. <i>Trends in Plant Science</i> , 2000 , 5, 397-401	13.1	10
44	Liver-specific deletion of Ngly1 causes abnormal nuclear morphology and lipid metabolism under food stress. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2020 , 1866, 165588	6.9	10
43	Identification of mitochondrial disease genes through integrative analysis of multiple datasets. <i>Methods</i> , 2008 , 46, 248-55	4.6	9
42	Capturing cellular machines by systematic screens of protein complexes. <i>Trends in Microbiology</i> , 2006 , 14, 336-9	12.4	9
41	Evolthon: A community endeavor to evolve lab evolution. <i>PLoS Biology</i> , 2019 , 17, e3000182	9.7	8
40	High-density arrays and insights into genome function. <i>Biotechnology and Genetic Engineering Reviews</i> , 2000 , 17, 109-46	4.1	8
39	Induced mutations in yeast cell populations adapting to an unforeseen challenge. <i>PLoS ONE</i> , 2014 , 9, e111133	3.7	8

38	Silencing of genes and alleles by RNAi in <i>Anopheles gambiae</i> . <i>Methods in Molecular Biology</i> , 2013 , 923, 161-76	1.4	7
37	Re-analysis of data and its integration. <i>FEBS Letters</i> , 2005 , 579, 1802-7	3.8	7
36	Genome-wide transcriptome analysis in yeast using high-density tiling arrays. <i>Methods in Molecular Biology</i> , 2011 , 759, 107-23	1.4	7
35	Single-cell analyses reveal SARS-CoV-2 interference with intrinsic immune response in the human gut		6
34	INO80 represses osmostress induced gene expression by resetting promoter proximal nucleosomes. <i>Nucleic Acids Research</i> , 2017 , 45, 3752-3766	20.1	6
33	Chromatin-sensitive cryptic promoters putatively drive expression of alternative protein isoforms in yeast. <i>Genome Research</i> , 2019 , 29, 1974-1984	9.7	6
32	Array-based genotyping in <i>S.cerevisiae</i> using semi-supervised clustering. <i>Bioinformatics</i> , 2009 , 25, 1056-622		5
31	Genetic modifiers of chromatin acetylation antagonize the reprogramming of epi-polymorphisms. <i>PLoS Genetics</i> , 2012 , 8, e1002958	6	5
30	DChIPRep, an R/Bioconductor package for differential enrichment analysis in chromatin studies. <i>PeerJ</i> , 2016 , 4, e1981	3.1	5
29	Loss of N-Glycanase 1 Alters Transcriptional and Translational Regulation in K562 Cell Lines. <i>G3: Genes, Genomes, Genetics</i> , 2020 , 10, 1585-1597	3.2	5
28	CRISPRi screens reveal genes modulating yeast growth in lignocellulose hydrolysate. <i>Biotechnology for Biofuels</i> , 2021 , 14, 41	7.8	5
27	Gene function on a genomic scale. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2002 , 782, 151-63	3.2	4
26	Biological Plasticity Rescues Target Activity in CRISPR Knockouts		4
25	TIF-Seq2 disentangles overlapping isoforms in complex human transcriptomes. <i>Nucleic Acids Research</i> , 2020 , 48, e104	20.1	4
24	Case-control study evaluating risk factors for SARS-CoV-2 outbreak amongst healthcare personnel at a tertiary care center. <i>American Journal of Infection Control</i> , 2021 , 49, 1457-1463	3.8	4
23	Multiplexed ChIP-Seq Using Direct Nucleosome Barcoding: A Tool for High-Throughput Chromatin Analysis. <i>Methods in Molecular Biology</i> , 2018 , 1689, 177-194	1.4	3
22	High-throughput functional characterization of protein phosphorylation sites in yeast. <i>Nature Biotechnology</i> , 2021 ,	44.5	3
21	The mitochondrial surface receptor Tom70 protects the cytosol against mitoprotein-induced stress		3

20	Combined single-cell and spatial transcriptomics reveals the molecular, cellular and spatial bone marrow niche organization		3
19	Meiotic Interactors of a Mitotic Gene TAO3 Revealed by Functional Analysis of its Rare Variant. <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 2255-63	3.2	3
18	Gene dosage screens in yeast reveal core signalling pathways controlling heat adaptation		2
17	RNA degradation analysis reveals ribosome dynamics in complex microbiome samples		2
16	High-Throughput Nucleotide Resolution Predictions of Assay Limitations Increase the Reliability and Concordance of Clinical Tests. <i>JCO Clinical Cancer Informatics</i> , 2021 , 5, 1085-1095	5.2	1
15	Integrated single-cell transcriptomics and epigenomics reveals strong germinal center-associated etiology of autoimmune risk loci. <i>Science Immunology</i> , 2021 , 6, eabh3768	28	1
14	Yeast Single-cell RNA-seq, Cell by Cell and Step by Step. <i>Bio-protocol</i> , 2019 , 9, e3359	0.9	1
13	Genome-Wide Identification of Alternative Polyadenylation Events Using 3T-Fill. <i>Methods in Molecular Biology</i> , 2016 , 1358, 295-302	1.4	1
12	Fast and inexpensive whole-genome sequencing library preparation from intact yeast cells. <i>G3: Genes, Genomes, Genetics</i> , 2021 , 11,	3.2	1
11	Principles for RNA metabolism and alternative transcription initiation within closely spaced promoters		1
10	Combined transient ablation and single cell RNA sequencing reveals the development of medullary thymic epithelial cells		1
9	Single-molecule, full-length transcript isoform sequencing reveals disease-associated RNA isoforms in cardiomyocytes. <i>Nature Communications</i> , 2021 , 12, 4203	17.4	1
8	Patient-derived gene and protein expression signatures of NGLY1 deficiency		1
7	Regulation of Msh4-Msh5 association with meiotic chromosomes in budding yeast. <i>Genetics</i> , 2021 , 219,	4	1
6	Transcriptional neighborhoods regulate transcript isoform lengths and expression levels.. <i>Science</i> , 2022 , 375, 1000-1005	33.3	1
5	Patient-derived gene and protein expression signatures of NGLY1 deficiency. <i>Journal of Biochemistry</i> , 2021 ,	3.1	1
4	Stem Cell-like Megakaryocyte Progenitors As Driving Forces of IFN-Induced Emergency Megakaryopoiesis. <i>Blood</i> , 2015 , 126, 2391-2391	2.2	0
3	A functional connection between translation elongation and protein folding at the ribosome exit tunnel in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2021 , 49, 206-220	20.1	0

- 2 High-density tiling microarray analysis of the full transcriptional activity of yeast. *Methods in Molecular Biology*, **2014**, 1205, 257-73 1.4
- 1 SYGNALing a Red Light for Glioblastoma. *Cell Systems*, **2016**, 3, 118-120 10.6