

Lars M Steinmetz

List of Publications by Year in descending order

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179
papers

26,670
citations

11639
70
h-index

7511
151
g-index

214
all docs

214
docs citations

214
times ranked

34811
citing authors

#	ARTICLE	IF	CITATIONS
1	A Genome-Wide Transcriptional Analysis of the Mitotic Cell Cycle. <i>Molecular Cell</i> , 1998, 2, 65-73.	4.5	1,927
2	Insights into RNA Biology from an Atlas of Mammalian mRNA-Binding Proteins. <i>Cell</i> , 2012, 149, 1393-1406.	13.5	1,765
3	A global genetic interaction network maps a wiring diagram of cellular function. <i>Science</i> , 2016, 353, .	6.0	979
4	Assembly of functionally integrated human forebrain spheroids. <i>Nature</i> , 2017, 545, 54-59.	13.7	931
5	Bidirectional promoters generate pervasive transcription in yeast. <i>Nature</i> , 2009, 457, 1033-1037.	13.7	872
6	Ultrasensitive proteome analysis using paramagnetic bead technology. <i>Molecular Systems Biology</i> , 2014, 10, 757.	3.2	835
7	Evolutionary Rate in the Protein Interaction Network. <i>Science</i> , 2002, 296, 750-752.	6.0	798
8	Role of duplicate genes in genetic robustness against null mutations. <i>Nature</i> , 2003, 421, 63-66.	13.7	790
9	Human haematopoietic stem cell lineage commitment is a continuous process. <i>Nature Cell Biology</i> , 2017, 19, 271-281.	4.6	709
10	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, 5320-5325.	3.3	613
11	Cytosine base editor generates substantial off-target single-nucleotide variants in mouse embryos. <i>Science</i> , 2019, 364, 289-292.	6.0	573
12	Widespread bidirectional promoters are the major source of cryptic transcripts in yeast. <i>Nature</i> , 2009, 457, 1038-1042.	13.7	557
13	Gene regulation by antisense transcription. <i>Nature Reviews Genetics</i> , 2013, 14, 880-893.	7.7	556
14	High-resolution mapping of meiotic crossovers and non-crossovers in yeast. <i>Nature</i> , 2008, 454, 479-485.	13.7	554
15	Dissecting the architecture of a quantitative trait locus in yeast. <i>Nature</i> , 2002, 416, 326-330.	13.7	524
16	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.	4.6	521
17	Systematic screen for human disease genes in yeast. <i>Nature Genetics</i> , 2002, 31, 400-404.	9.4	503
18	A new fate mapping system reveals context-dependent random or clonal expansion of microglia. <i>Nature Neuroscience</i> , 2017, 20, 793-803.	7.1	446

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19	Extensive transcriptional heterogeneity revealed by isoform profiling. <i>Nature</i> , 2013, 497, 127-131.	13.7	408
20	Transcriptional regulation and function during the human cell cycle. <i>Nature Genetics</i> , 2001, 27, 48-54.	9.4	399
21	Inflammation-Induced Emergency Megakaryopoiesis Driven by Hematopoietic Stem Cell-like Megakaryocyte Progenitors. <i>Cell Stem Cell</i> , 2015, 17, 422-434.	5.2	353
22	Extensive Variation in Chromatin States Across Humans. <i>Science</i> , 2013, 342, 750-752.	6.0	338
23	Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions. <i>Cell</i> , 2015, 162, 1051-1065.	13.5	304
24	Yeast Sen1 Helicase Protects the Genome from Transcription-Associated Instability. <i>Molecular Cell</i> , 2011, 41, 21-32.	4.5	301
25	Polyadenylation site-induced decay of upstream transcripts enforces promoter directionality. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 923-928.	3.6	258
26	Widespread Co-translational RNA Decay Reveals Ribosome Dynamics. <i>Cell</i> , 2015, 161, 1400-1412.	13.5	246
27	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, 12825-12830.	3.3	240
28	Thymic tuft cells promote an IL-4-enriched medulla and shape thymocyte development. <i>Nature</i> , 2018, 559, 627-631.	13.7	221
29	Gene Loops Enhance Transcriptional Directionality. <i>Science</i> , 2012, 338, 671-675.	6.0	219
30	Extensive Degradation of RNA Precursors by the Exosome in Wild-Type Cells. <i>Molecular Cell</i> , 2012, 48, 409-421.	4.5	218
31	Functional consequences of bidirectional promoters. <i>Trends in Genetics</i> , 2011, 27, 267-276.	2.9	194
32	Magnetic levitation of single cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E3661-8.	3.3	192
33	Integrative Analysis of the Mitochondrial Proteome in Yeast. <i>PLoS Biology</i> , 2004, 2, e160.	2.6	181
34	Antisense artifacts in transcriptome microarray experiments are resolved by actinomycin D. <i>Nucleic Acids Research</i> , 2007, 35, e128.	6.5	180
35	Myt1l safeguards neuronal identity by actively repressing many non-neuronal fates. <i>Nature</i> , 2017, 544, 245-249.	13.7	180
36	Conventional and Neo-antigenic Peptides Presented by β^2 Cells Are Targeted by Circulating Na ⁺ ve CD8 ⁺ T Cells in Type 1 Diabetic and Healthy Donors. <i>Cell Metabolism</i> , 2018, 28, 946-960.e6.	7.2	177

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37	Set3 HDAC Mediates Effects of Overlapping Noncoding Transcription on Gene Induction Kinetics. <i>Cell</i> , 2012, 150, 1158-1169.	13.5	176
38	System-wide identification of RNA-binding proteins by interactome capture. <i>Nature Protocols</i> , 2013, 8, 491-500.	5.5	176
39	Antisense expression increases gene expression variability and locus interdependency. <i>Molecular Systems Biology</i> , 2011, 7, 468.	3.2	173
40	HEx: A heterologous expression platform for the discovery of fungal natural products. <i>Science Advances</i> , 2018, 4, eaar5459.	4.7	167
41	Quantitative CRISPR interference screens in yeast identify chemical-genetic interactions and new rules for guide RNA design. <i>Genome Biology</i> , 2016, 17, 45.	3.8	165
42	Genetic analysis of variation in transcription factor binding in yeast. <i>Nature</i> , 2010, 464, 1187-1191.	13.7	162
43	Biological plasticity rescues target activity in CRISPR knock outs. <i>Nature Methods</i> , 2019, 16, 1087-1093.	9.0	159
44	RNA Polymerase II Collision Interrupts Convergent Transcription. <i>Molecular Cell</i> , 2012, 48, 365-374.	4.5	149
45	Single-cell transcriptome analysis reveals coordinated ectopic gene-expression patterns in medullary thymic epithelial cells. <i>Nature Immunology</i> , 2015, 16, 933-941.	7.0	148
46	Inhibition of NGLY1 Inactivates the Transcription Factor Nrf1 and Potentiates Proteasome Inhibitor Cytotoxicity. <i>ACS Central Science</i> , 2017, 3, 1143-1155.	5.3	146
47	Sequential Elimination of Major-Effect Contributors Identifies Additional Quantitative Trait Loci Conditioning High-Temperature Growth in Yeast. <i>Genetics</i> , 2008, 180, 1661-1670.	1.2	145
48	Opposing T cell responses in experimental autoimmune encephalomyelitis. <i>Nature</i> , 2019, 572, 481-487.	13.7	141
49	Targeted Perturb-seq enables genome-scale genetic screens in single cells. <i>Nature Methods</i> , 2020, 17, 629-635.	9.0	139
50	<i>Trans</i> -acting antisense RNAs mediate transcriptional gene cosuppression in <i>S. cerevisiae</i> . <i>Genes and Development</i> , 2009, 23, 1534-1545.	2.7	138
51	Multiplexed precision genome editing with trackable genomic barcodes in yeast. <i>Nature Biotechnology</i> , 2018, 36, 512-520.	9.4	138
52	Transcript mapping with high-density oligonucleotide tiling arrays. <i>Bioinformatics</i> , 2006, 22, 1963-1970.	1.8	134
53	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, 1058-1063.	3.3	124
54	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.	0.8	124

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55	High-speed fluorescence image-enabled cell sorting. <i>Science</i> , 2022, 375, 315-320.	6.0	121
56	Complex Genetic Interactions in a Quantitative Trait Locus. <i>PLoS Genetics</i> , 2006, 2, e13.	1.5	117
57	Yeast as a system for modeling mitochondrial disease mechanisms and discovering therapies. <i>DMM Disease Models and Mechanisms</i> , 2015, 8, 509-526.	1.2	115
58	KIR ⁺ CD8 ⁺ T cells suppress pathogenic T cells and are active in autoimmune diseases and COVID-19. <i>Science</i> , 2022, 376, eabi9591.	6.0	113
59	Dissecting the Genetic Basis of Resistance to Malaria Parasites in <i>Anopheles gambiae</i> . <i>Science</i> , 2009, 326, 147-150.	6.0	106
60	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, 15377-15382.	3.3	103
61	High-resolution transcription atlas of the mitotic cell cycle in budding yeast. <i>Genome Biology</i> , 2010, 11, R24.	13.9	99
62	An efficient method for genome-wide polyadenylation site mapping and RNA quantification. <i>Nucleic Acids Research</i> , 2013, 41, e65-e65.	6.5	98
63	Regional Variation in <i>RBM20</i> Causes a Highly Penetrant Arrhythmogenic Cardiomyopathy. <i>Circulation: Heart Failure</i> , 2019, 12, e005371.	1.6	96
64	Modulation of mRNA and lncRNA expression dynamics by the Set2-Rpd3S pathway. <i>Nature Communications</i> , 2016, 7, 13534.	5.8	93
65	Alternative polyadenylation diversifies post-transcriptional regulation by selective RNA-protein interactions. <i>Molecular Systems Biology</i> , 2014, 10, 719.	3.2	91
66	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, 1092-1097.	3.3	90
67	The Baker's Yeast Diploid Genome Is Remarkably Stable in Vegetative Growth and Meiosis. <i>PLoS Genetics</i> , 2010, 6, e1001109.	1.5	89
68	An Evaluation of High-Throughput Approaches to QTL Mapping in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2014, 196, 853-865.	1.2	86
69	Control of Cdc28 CDK1 by a Stress-Induced lncRNA. <i>Molecular Cell</i> , 2014, 53, 549-561.	4.5	85
70	Maximizing the potential of functional genomics. <i>Nature Reviews Genetics</i> , 2004, 5, 190-201.	7.7	83
71	Single-cell analyses reveal SARS-CoV-2 interference with intrinsic immune response in the human gut. <i>Molecular Systems Biology</i> , 2021, 17, e10232.	3.2	78
72	A Genome-Wide Map of Mitochondrial DNA Recombination in Yeast. <i>Genetics</i> , 2014, 198, 755-771.	1.2	76

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73	Principles for RNA metabolism and alternative transcription initiation within closely spaced promoters. <i>Nature Genetics</i> , 2016, 48, 984-994.	9.4	75
74	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, 11989-11994.	3.3	73
75	Genotype-Environment Interactions Reveal Causal Pathways That Mediate Genetic Effects on Phenotype. <i>PLoS Genetics</i> , 2013, 9, e1003803.	1.5	72
76	Rrp6p Controls mRNA Poly(A) Tail Length and Its Decoration with Poly(A) Binding Proteins. <i>Molecular Cell</i> , 2012, 47, 267-280.	4.5	69
77	Identification of leukemic and pre-leukemic stem cells by clonal tracking from single-cell transcriptomics. <i>Nature Communications</i> , 2021, 12, 1366.	5.8	69
78	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.	3.3	68
79	Assessing Systems Properties of Yeast Mitochondria through an Interaction Map of the Organelle. <i>PLoS Genetics</i> , 2006, 2, e170.	1.5	67
80	Gain of CTCF-Anchored Chromatin Loops Marks the Exit from Naive Pluripotency. <i>Cell Systems</i> , 2018, 7, 482-495.e10.	2.9	62
81	Sensitive high-throughput single-cell RNA-seq reveals within-clonal transcript correlations in yeast populations. <i>Nature Microbiology</i> , 2019, 4, 683-692.	5.9	61
82	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.	6.5	60
83	Dysregulated ribonucleoprotein granules promote cardiomyopathy in RBM20 gene-edited pigs. <i>Nature Medicine</i> , 2020, 26, 1788-1800.	15.2	58
84	Genome-wide identification of transcript start and end sites by transcript isoform sequencing. <i>Nature Protocols</i> , 2014, 9, 1740-1759.	5.5	57
85	Genome Dynamics of Hybrid <i>Saccharomyces cerevisiae</i> During Vegetative and Meiotic Divisions. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3669-3679.	0.8	57
86	The Not5 Subunit of the Ccr4-Not Complex Connects Transcription and Translation. <i>PLoS Genetics</i> , 2014, 10, e1004569.	1.5	56
87	Multitarget, quantitative nanoplasmonic electrical field-enhanced resonating device (NE Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50) States of America, 2015, 112, E4354-63.	3.3	56
88	Roadblock Termination by Reb1p Restricts Cryptic and Readthrough Transcription. <i>Molecular Cell</i> , 2014, 56, 667-680.	4.5	53
89	Comprehensive Identification of RNA-Binding Proteins by RNA Interactome Capture. <i>Methods in Molecular Biology</i> , 2016, 1358, 131-139.	0.4	53
90	Combined transient ablation and single-cell RNA-sequencing reveals the development of medullary thymic epithelial cells. <i>ELife</i> , 2020, 9, .	2.8	53

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91	Single-cell polyadenylation site mapping reveals 3' isoform choice variability. <i>Molecular Systems Biology</i> , 2015, 11, 812.	3.2	52
92	Heritability and genetic basis of protein level variation in an outbred population. <i>Genome Research</i> , 2014, 24, 1363-1370.	2.4	51
93	Landscape and Dynamics of Transcription Initiation in the Malaria Parasite <i>Plasmodium falciparum</i> . <i>Cell Reports</i> , 2016, 14, 2463-2475.	2.9	51
94	Protein Abundance Control by Non-coding Antisense Transcription. <i>Cell Reports</i> , 2016, 15, 2625-2636.	2.9	51
95	Role of histone modifications and early termination in pervasive transcription and antisense-mediated gene silencing in yeast. <i>Nucleic Acids Research</i> , 2014, 42, 4348-4362.	6.5	50
96	Experimental Relocation of the Mitochondrial ATP9 Gene to the Nucleus Reveals Forces Underlying Mitochondrial Genome Evolution. <i>PLoS Genetics</i> , 2012, 8, e1002876.	1.5	48
97	Genotyping 1000 yeast strains by next-generation sequencing. <i>BMC Genomics</i> , 2013, 14, 90.	1.2	47
98	The Nuclear PolyA-Binding Protein Nab2p Is Essential for mRNA Production. <i>Cell Reports</i> , 2015, 12, 128-139.	2.9	47
99	The chaperone-binding activity of the mitochondrial surface receptor Tom70 protects the cytosol against mitoprotein-induced stress. <i>Cell Reports</i> , 2021, 35, 108936.	2.9	47
100	Translational Capacity of a Cell Is Determined during Transcription Elongation via the Ccr4-Not Complex. <i>Cell Reports</i> , 2016, 15, 1782-1794.	2.9	46
101	Systematic screens for human disease genes, from yeast to human and back. <i>Molecular BioSystems</i> , 2008, 4, 18-29.	2.9	45
102	Genome-wide quantification of 5'-phosphorylated mRNA degradation intermediates for analysis of ribosome dynamics. <i>Nature Protocols</i> , 2016, 11, 359-376.	5.5	45
103	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, 3643-3658.	6.5	45
104	Expression of Nuclear and Mitochondrial Genes Encoding ATP Synthase Is Synchronized by Disassembly of a Multisynthetase Complex. <i>Molecular Cell</i> , 2014, 56, 763-776.	4.5	43
105	Natural sequence variants of yeast environmental sensors confer cell-to-cell expression variability. <i>Molecular Systems Biology</i> , 2013, 9, 695.	3.2	42
106	A method for high-throughput production of sequence-verified <sc>DNA</sc> libraries and strain collections. <i>Molecular Systems Biology</i> , 2017, 13, 913.	3.2	41
107	Rpd3L HDAC links H3K4me3 to transcriptional repression memory. <i>Nucleic Acids Research</i> , 2018, 46, 8261-8274.	6.5	41
108	Mosaic Genome Architecture of the <i>Anopheles gambiae</i> Species Complex. <i>PLoS ONE</i> , 2007, 2, e1249.	1.1	41

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109	iPSC Modeling of RBM20-Deficient DCM Identifies Upregulation of RBM20 as a Therapeutic Strategy. <i>Cell Reports</i> , 2020, 32, 108117.	2.9	40
110	Integrating Cell Phone Imaging with Magnetic Levitation (iCLEV) for Label-Free Blood Analysis at the Point-of-Care Living. <i>Small</i> , 2016, 12, 1222-1229.	5.2	39
111	Transcription mediated insulation and interference direct gene cluster expression switches. <i>ELife</i> , 2014, 3, e03635.	2.8	35
112	Accumulation of noncoding RNA due to an RNase P defect in <i>Saccharomyces cerevisiae</i> . <i>Rna</i> , 2011, 17, 1441-1450.	1.6	34
113	Yeast Growth Plasticity Is Regulated by Environment-Specific Multi-QTL Interactions. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 769-777.	0.8	34
114	Chromatin Dynamics and the RNA Exosome Function in Concert to Regulate Transcriptional Homeostasis. <i>Cell Reports</i> , 2015, 13, 1610-1622.	2.9	34
115	Negative feedback buffers effects of regulatory variants. <i>Molecular Systems Biology</i> , 2015, 11, 785.	3.2	33
116	Genome-wide allele- and strand-specific expression profiling. <i>Molecular Systems Biology</i> , 2009, 5, 274.	3.2	31
117	Variation in Crossover Frequencies Perturb Crossover Assurance Without Affecting Meiotic Chromosome Segregation in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2015, 199, 399-412.	1.2	30
118	Mitochondrial protein sorting as a therapeutic target for ATP synthase disorders. <i>Nature Communications</i> , 2014, 5, 5585.	5.8	29
119	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, 115-128.	6.5	29
120	The State of Systems Genetics in 2017. <i>Cell Systems</i> , 2017, 4, 7-15.	2.9	29
121	A high-throughput ChIP-seq for large-scale chromatin studies. <i>Molecular Systems Biology</i> , 2015, 11, 777.	3.2	28
122	NAD(P)HX repair deficiency causes central metabolic perturbations in yeast and human cells. <i>FEBS Journal</i> , 2018, 285, 3376-3401.	2.2	28
123	Modulating Crossover Frequency and Interference for Obligate Crossovers in <i>Saccharomyces cerevisiae</i> Meiosis. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1511-1524.	0.8	27
124	A privacy-preserving solution for compressed storage and selective retrieval of genomic data. <i>Genome Research</i> , 2016, 26, 1687-1696.	2.4	26
125	GOTI, a method to identify genome-wide off-target effects of genome editing in mouse embryos. <i>Nature Protocols</i> , 2020, 15, 3009-3029.	5.5	24
126	Single-molecule, full-length transcript isoform sequencing reveals disease-associated RNA isoforms in cardiomyocytes. <i>Nature Communications</i> , 2021, 12, 4203.	5.8	24

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127	Condensin controls cellular RNA levels through the accurate segregation of chromosomes instead of directly regulating transcription. <i>ELife</i> , 2018, 7, .	2.8	24
128	High-throughput functional characterization of protein phosphorylation sites in yeast. <i>Nature Biotechnology</i> , 2022, 40, 382-390.	9.4	24
129	Multiple Genomic Changes Associated with Reorganization of Gene Regulation and Adaptation in Yeast. <i>Molecular Biology and Evolution</i> , 2013, 30, 1514-1526.	3.5	23
130	Loss of the Yeast SR Protein Npl3 Alters Gene Expression Due to Transcription Readthrough. <i>PLoS Genetics</i> , 2015, 11, e1005735.	1.5	23
131	Chromatin-dependent regulation of RNA polymerases II and III activity throughout the transcription cycle. <i>Nucleic Acids Research</i> , 2015, 43, 787-802.	6.5	23
132	High-frequency actionable pathogenic exome variants in an average-risk cohort. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a003178.	0.5	23
133	Transcriptional neighborhoods regulate transcript isoform lengths and expression levels. <i>Science</i> , 2022, 375, 1000-1005.	6.0	23
134	Genome-wide survey of post-meiotic segregation during yeast recombination. <i>Genome Biology</i> , 2011, 12, R36.	3.8	22
135	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.	1.8	22
136	Genome-Wide Polyadenylation Site Mapping. <i>Methods in Enzymology</i> , 2012, 513, 271-296.	0.4	21
137	Chromatin-sensitive cryptic promoters putatively drive expression of alternative protein isoforms in yeast. <i>Genome Research</i> , 2019, 29, 1974-1984.	2.4	20
138	RBM20-Related Cardiomyopathy: Current Understanding and Future Options. <i>Journal of Clinical Medicine</i> , 2021, 10, 4101.	1.0	20
139	Functional interplay between MSL1 and CDK7 controls RNA polymerase II Ser5 phosphorylation. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 580-589.	3.6	19
140	Integrated single-cell transcriptomics and epigenomics reveals strong germinal center-associated etiology of autoimmune risk loci. <i>Science Immunology</i> , 2021, 6, eabh3768.	5.6	19
141	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.	1.1	17
142	Temporal Expression Profiling Identifies Pathways Mediating Effect of Causal Variant on Phenotype. <i>PLoS Genetics</i> , 2015, 11, e1005195.	1.5	17
143	The Role of Ctk1 Kinase in Termination of Small Non-Coding RNAs. <i>PLoS ONE</i> , 2013, 8, e80495.	1.1	15
144	INO80 represses osmostress induced gene expression by resetting promoter proximal nucleosomes. <i>Nucleic Acids Research</i> , 2017, 45, gkw1292.	6.5	15

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145	CRISPRi screens reveal genes modulating yeast growth in lignocellulose hydrolysate. <i>Biotechnology for Biofuels</i> , 2021, 14, 41.	6.2	15
146	Natural Single-Nucleosome Epi-Polymorphisms in Yeast. <i>PLoS Genetics</i> , 2010, 6, e1000913.	1.5	14
147	Loss of N-Glycanase 1 Alters Transcriptional and Translational Regulation in K562 Cell Lines. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1585-1597.	0.8	14
148	Combining genome sequences and new technologies for dissecting the genetics of complex phenotypes. <i>Trends in Plant Science</i> , 2000, 5, 397-401.	4.3	12
149	High-Density Arrays and Insights into Genome function. <i>Biotechnology and Genetic Engineering Reviews</i> , 2000, 17, 109-146.	2.4	11
150	Capturing cellular machines by systematic screens of protein complexes. <i>Trends in Microbiology</i> , 2006, 14, 336-339.	3.5	10
151	Identification of mitochondrial disease genes through integrative analysis of multiple datasets. <i>Methods</i> , 2008, 46, 248-255.	1.9	10
152	Evolthon: A community endeavor to evolve lab evolution. <i>PLoS Biology</i> , 2019, 17, e3000182.	2.6	10
153	TIF-Seq2 disentangles overlapping isoforms in complex human transcriptomes. <i>Nucleic Acids Research</i> , 2020, 48, e104-e104.	6.5	10
154	Induced Mutations in Yeast Cell Populations Adapting to an Unforeseen Challenge. <i>PLoS ONE</i> , 2014, 9, e111133.	1.1	10
155	Patient-derived gene and protein expression signatures of NGLY1 deficiency. <i>Journal of Biochemistry</i> , 2022, 171, 187-199.	0.9	9
156	Re-analysis of data and its integration. <i>FEBS Letters</i> , 2005, 579, 1802-1807.	1.3	8
157	Silencing of Genes and Alleles by RNAi in <i>Anopheles gambiae</i> . <i>Methods in Molecular Biology</i> , 2012, 923, 161-176.	0.4	8
158	Sensing a revolution. <i>Molecular Systems Biology</i> , 2016, 12, 867.	3.2	8
159	Regulation of Msh4-Msh5 association with meiotic chromosomes in budding yeast. <i>Genetics</i> , 2021, 219, .	1.2	8
160	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.	1.1	8
161	Genome-Wide Transcriptome Analysis in Yeast Using High-Density Tiling Arrays. <i>Methods in Molecular Biology</i> , 2011, 759, 107-123.	0.4	8
162	<i>DChIPRep</i> , an R/Bioconductor package for differential enrichment analysis in chromatin studies. <i>PeerJ</i> , 2016, 4, e1981.	0.9	8

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163	Array-based genotyping in <i>S.cerevisiae</i> using semi-supervised clustering. <i>Bioinformatics</i> , 2009, 25, 1056-1062.	1.8	7
164	Genetic Modifiers of Chromatin Acetylation Antagonize the Reprogramming of Epi-Polymorphisms. <i>PLoS Genetics</i> , 2012, 8, e1002958.	1.5	7
165	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.	6.5	6
166	Gene function on a genomic scale. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2002, 782, 151-163.	1.2	5
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