

Lars M Steinmetz

List of Publications by Year in descending order

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Version: 2024-02-01

179
papers

26,670
citations

11608

70
h-index

7496

151
g-index

214
all docs

214
docs citations

214
times ranked

34811
citing authors

#	ARTICLE	IF	CITATIONS
1	High-throughput functional characterization of protein phosphorylation sites in yeast. <i>Nature Biotechnology</i> , 2022, 40, 382-390.	9.4	24
2	High-speed fluorescence image-enabled cell sorting. <i>Science</i> , 2022, 375, 315-320.	6.0	121
3	Assembly-dependent translation of subunits <i>Atp6</i> and <i>Atp9</i> of ATP synthase in yeast mitochondria. <i>Genetics</i> , 2022, 220, .	1.2	5
4	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
5	Transcriptional neighborhoods regulate transcript isoform lengths and expression levels. <i>Science</i> , 2022, 375, 1000-1005.	6.0	23
6	Patient-derived gene and protein expression signatures of NGLY1 deficiency. <i>Journal of Biochemistry</i> , 2022, 171, 187-199.	0.9	9
7	CRISPRi screens reveal genes modulating yeast growth in lignocellulose hydrolysate. <i>Biotechnology for Biofuels</i> , 2021, 14, 41.	6.2	15
8	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
9	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
10	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
11	Single-molecule, full-length transcript isoform sequencing reveals disease-associated RNA isoforms in cardiomyocytes. <i>Nature Communications</i> , 2021, 12, 4203.	5.8	24
12	Regulation of Msh4-Msh5 association with meiotic chromosomes in budding yeast. <i>Genetics</i> , 2021, 219, .	1.2	8
13	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
14	RBM20-Related Cardiomyopathy: Current Understanding and Future Options. <i>Journal of Clinical Medicine</i> , 2021, 10, 4101.	1.0	20
15	Fast and inexpensive whole-genome sequencing library preparation from intact yeast cells. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	5
16	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
17	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
18	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.	1.0	4

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19	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
20	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
21	iPSC Modeling of RBM20-Deficient DCM Identifies Upregulation of RBM20 as a Therapeutic Strategy. <i>Cell Reports</i> , 2020, 32, 108117.	2.9	40
22	Dysregulated ribonucleoprotein granules promote cardiomyopathy in RBM20 gene-edited pigs. <i>Nature Medicine</i> , 2020, 26, 1788-1800.	15.2	58
23	GOT1, 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
24	TIF-Seq2 disentangles overlapping isoforms in complex human transcriptomes. <i>Nucleic Acids Research</i> , 2020, 48, e104-e104.	6.5	10
25	Targeted Perturb-seq enables genome-scale genetic screens in single cells. <i>Nature Methods</i> , 2020, 17, 629-635.	9.0	139
26	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
27	Combined transient ablation and single-cell RNA-sequencing reveals the development of medullary thymic epithelial cells. <i>ELife</i> , 2020, 9, .	2.8	53
28	Opposing T cell responses in experimental autoimmune encephalomyelitis. <i>Nature</i> , 2019, 572, 481-487.	13.7	141
29	Biological plasticity rescues target activity in CRISPR knock outs. <i>Nature Methods</i> , 2019, 16, 1087-1093.	9.0	159
30	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
31	Cytosine base editor generates substantial off-target single-nucleotide variants in mouse embryos. <i>Science</i> , 2019, 364, 289-292.	6.0	573
32	Regional Variation in <i>RBM20</i> Causes a Highly Penetrant Arrhythmogenic Cardiomyopathy. <i>Circulation: Heart Failure</i> , 2019, 12, e005371.	1.6	96
33	Evolthon: A community endeavor to evolve lab evolution. <i>PLoS Biology</i> , 2019, 17, e3000182.	2.6	10
34	Chromatin-sensitive cryptic promoters putatively drive expression of alternative protein isoforms in yeast. <i>Genome Research</i> , 2019, 29, 1974-1984.	2.4	20
35	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
36	Yeast Single-cell RNA-seq, Cell by Cell and Step by Step. <i>Bio-protocol</i> , 2019, 9, e3359.	0.2	4

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37	HEx: A heterologous expression platform for the discovery of fungal natural products. <i>Science Advances</i> , 2018, 4, eaar5459.	4.7	167
38	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
39	Multiplexed ChIP-Seq Using Direct Nucleosome Barcoding: A Tool for High-Throughput Chromatin Analysis. <i>Methods in Molecular Biology</i> , 2018, 1689, 177-194.	0.4	5
40	Gain of CTCF-Anchored Chromatin Loops Marks the Exit from Naive Pluripotency. <i>Cell Systems</i> , 2018, 7, 482-495.e10.	2.9	62
41	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
42	Conventional and Neo-antigenic Peptides Presented by \hat{I}^2 Cells Are Targeted by Circulating Na \hat{A} -ve CD8+ T Cells in Type 1 Diabetic and Healthy Donors. <i>Cell Metabolism</i> , 2018, 28, 946-960.e6.	7.2	177
43	Thymic tuft cells promote an IL-4-enriched medulla and shape thymocyte development. <i>Nature</i> , 2018, 559, 627-631.	13.7	221
44	Rpd3L HDAC links H3K4me3 to transcriptional repression memory. <i>Nucleic Acids Research</i> , 2018, 46, 8261-8274.	6.5	41
45	Multiplexed precision genome editing with trackable genomic barcodes in yeast. <i>Nature Biotechnology</i> , 2018, 36, 512-520.	9.4	138
46	Multi-Layered Single-Cell Transcriptional Profiling of All Bone and Bone Marrow Populations Provides a Systems View of the Mesenchymal and Hematopoietic Stem Cell Niche. <i>Experimental Hematology</i> , 2018, 64, S47-S48.	0.2	0
47	<sc>NAD</sc>(P)<sc>HX</sc> repair deficiency causes central metabolic perturbations in yeast and human cells. <i>FEBS Journal</i> , 2018, 285, 3376-3401.	2.2	28
48	Condensin controls cellular RNA levels through the accurate segregation of chromosomes instead of directly regulating transcription. <i>ELife</i> , 2018, 7, .	2.8	24
49	INO80 represses osmostress induced gene expression by resetting promoter proximal nucleosomes. <i>Nucleic Acids Research</i> , 2017, 45, gkw1292.	6.5	15
50	The State of Systems Genetics in 2017. <i>Cell Systems</i> , 2017, 4, 7-15.	2.9	29
51	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
52	Assembly of functionally integrated human forebrain spheroids. <i>Nature</i> , 2017, 545, 54-59.	13.7	931
53	Myt1l safeguards neuronal identity by actively repressing many non-neuronal fates. <i>Nature</i> , 2017, 544, 245-249.	13.7	180
54	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

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55	Human haematopoietic stem cell lineage commitment is a continuous process. <i>Nature Cell Biology</i> , 2017, 19, 271-281.	4.6	709
56	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
57	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
58	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
59	Human haematopoietic stem cell differentiation follows a continuous waddington-like landscape. <i>Experimental Hematology</i> , 2017, 53, S101.	0.2	0
60	Meiotic Interactors of a Mitotic Gene <i>TAO3</i> Revealed by Functional Analysis of its Rare Variant. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2255-2263.	0.8	5
61	Sensing a revolution. <i>Molecular Systems Biology</i> , 2016, 12, 867.	3.2	8
62	Modulation of mRNA and lncRNA expression dynamics by the Set2-Rpd3S pathway. <i>Nature Communications</i> , 2016, 7, 13534.	5.8	93
63	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
64	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
65	SYGNALing a Red Light for Glioblastoma. <i>Cell Systems</i> , 2016, 3, 118-120.	2.9	0
66	A global genetic interaction network maps a wiring diagram of cellular function. <i>Science</i> , 2016, 353, .	6.0	979
67	Principles for RNA metabolism and alternative transcription initiation within closely spaced promoters. <i>Nature Genetics</i> , 2016, 48, 984-994.	9.4	75
68	Human haematopoietic stem cell differentiation follows a continuous waddington-like landscape. <i>Experimental Hematology</i> , 2016, 44, S77.	0.2	0
69	A privacy-preserving solution for compressed storage and selective retrieval of genomic data. <i>Genome Research</i> , 2016, 26, 1687-1696.	2.4	26
70	Integrating Cell Phone Imaging with Magnetic Levitation (iCLEV) for Label-Free Blood Analysis at the Point-of-Living. <i>Small</i> , 2016, 12, 1222-1229.	5.2	39
71	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
72	Protein Abundance Control by Non-coding Antisense Transcription. <i>Cell Reports</i> , 2016, 15, 2625-2636.	2.9	51

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73	Genome-wide quantification of 5â€²-phosphorylated mRNA degradation intermediates for analysis of ribosome dynamics. <i>Nature Protocols</i> , 2016, 11, 359-376.	5.5	45
74	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
75	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
76	Genome-Wide Identification of Alternative Polyadenylation Events Using 3â€²T-Fill. <i>Methods in Molecular Biology</i> , 2016, 1358, 295-302.	0.4	2
77	Comprehensive Identification of RNA-Binding Proteins by RNA Interactome Capture. <i>Methods in Molecular Biology</i> , 2016, 1358, 131-139.	0.4	53
78	<i>DChIPRep</i> , an R/Bioconductor package for differential enrichment analysis in chromatin studies. <i>PeerJ</i> , 2016, 4, e1981.	0.9	8
79	A high-throughput ChIP-seq protocol for large-scale chromatin studies. <i>Molecular Systems Biology</i> , 2015, 11, 777.	3.2	28
80	Single-cell polyadenylation site mapping reveals 3â€² isoform choice variability. <i>Molecular Systems Biology</i> , 2015, 11, 812.	3.2	52
81	Temporal Expression Profiling Identifies Pathways Mediating Effect of Causal Variant on Phenotype. <i>PLoS Genetics</i> , 2015, 11, e1005195.	1.5	17
82	Loss of the Yeast SR Protein Npl3 Alters Gene Expression Due to Transcription Readthrough. <i>PLoS Genetics</i> , 2015, 11, e1005735.	1.5	23
83	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
84	Widespread Co-translational RNA Decay Reveals Ribosome Dynamics. <i>Cell</i> , 2015, 161, 1400-1412.	13.5	246
85	Negative feedback buffers effects of regulatory variants. <i>Molecular Systems Biology</i> , 2015, 11, 785.	3.2	33
86	Multitarget, quantitative nanoplasmonic electrical field-enhanced resonating device (NE Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 227 Td (States of America, 2015, 112, E4354-63.	3.3	56
87	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
88	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
89	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
90	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

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91	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
92	Inflammation-Induced Emergency Megakaryopoiesis Driven by Hematopoietic Stem Cell-like Megakaryocyte Progenitors. <i>Cell Stem Cell</i> , 2015, 17, 422-434.	5.2	353
93	Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions. <i>Cell</i> , 2015, 162, 1051-1065.	13.5	304
94	The Nuclear PolyA-Binding Protein Nab2p Is Essential for mRNA Production. <i>Cell Reports</i> , 2015, 12, 128-139.	2.9	47
95	Chromatin Dynamics and the RNA Exosome Function in Concert to Regulate Transcriptional Homeostasis. <i>Cell Reports</i> , 2015, 13, 1610-1622.	2.9	34
96	Stem Cell-like Megakaryocyte Progenitors As Driving Forces of IFN-Induced Emergency Megakaryopoiesis. <i>Blood</i> , 2015, 126, 2391-2391.	0.6	1
97	A Genome-Wide Map of Mitochondrial DNA Recombination in Yeast. <i>Genetics</i> , 2014, 198, 755-771.	1.2	76
98	The Not5 Subunit of the Ccr4-Not Complex Connects Transcription and Translation. <i>PLoS Genetics</i> , 2014, 10, e1004569.	1.5	56
99	Heritability and genetic basis of protein level variation in an outbred population. <i>Genome Research</i> , 2014, 24, 1363-1370.	2.4	51
100	An Evaluation of High-Throughput Approaches to QTL Mapping in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2014, 196, 853-865.	1.2	86
101	Mitochondrial protein sorting as a therapeutic target for ATP synthase disorders. <i>Nature Communications</i> , 2014, 5, 5585.	5.8	29
102	Roadblock Termination by Reb1p Restricts Cryptic and Readthrough Transcription. <i>Molecular Cell</i> , 2014, 56, 667-680.	4.5	53
103	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
104	Alternative polyadenylation diversifies post-transcriptional regulation by selective RNA-protein interactions. <i>Molecular Systems Biology</i> , 2014, 10, 719.	3.2	91
105	Yeast Growth Plasticity Is Regulated by Environment-Specific Multi-QTL Interactions. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 769-777.	0.8	34
106	Control of Cdc28 CDK1 by a Stress-Induced lncRNA. <i>Molecular Cell</i> , 2014, 53, 549-561.	4.5	85
107	Ultrasensitive proteome analysis using paramagnetic bead technology. <i>Molecular Systems Biology</i> , 2014, 10, 757.	3.2	835
108	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

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109	Genome-wide identification of transcript start and end sites by transcript isoform sequencing. <i>Nature Protocols</i> , 2014, 9, 1740-1759.	5.5	57
110	Induced Mutations in Yeast Cell Populations Adapting to an Unforeseen Challenge. <i>PLoS ONE</i> , 2014, 9, e111133.	1.1	10
111	Transcription mediated insulation and interference direct gene cluster expression switches. <i>ELife</i> , 2014, 3, e03635.	2.8	35
112	High-Density Tiling Microarray Analysis of the Full Transcriptional Activity of Yeast. <i>Methods in Molecular Biology</i> , 2014, 1205, 257-273.	0.4	0
113	Polyadenylation site-induced decay of upstream transcripts enforces promoter directionality. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 923-928.	3.6	258
114	Genotyping 1000 yeast strains by next-generation sequencing. <i>BMC Genomics</i> , 2013, 14, 90.	1.2	47
115	Extensive Variation in Chromatin States Across Humans. <i>Science</i> , 2013, 342, 750-752.	6.0	338
116	Gene regulation by antisense transcription. <i>Nature Reviews Genetics</i> , 2013, 14, 880-893.	7.7	556
117	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
118	System-wide identification of RNA-binding proteins by interactome capture. <i>Nature Protocols</i> , 2013, 8, 491-500.	5.5	176
119	Extensive transcriptional heterogeneity revealed by isoform profiling. <i>Nature</i> , 2013, 497, 127-131.	13.7	408
120	An efficient method for genome-wide polyadenylation site mapping and RNA quantification. <i>Nucleic Acids Research</i> , 2013, 41, e65-e65.	6.5	98
121	Genotype-Environment Interactions Reveal Causal Pathways That Mediate Genetic Effects on Phenotype. <i>PLoS Genetics</i> , 2013, 9, e1003803.	1.5	72
122	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
123	Natural sequence variants of yeast environmental sensors confer cell-to-cell expression variability. <i>Molecular Systems Biology</i> , 2013, 9, 695.	3.2	42
124	The Role of Ctk1 Kinase in Termination of Small Non-Coding RNAs. <i>PLoS ONE</i> , 2013, 8, e80495.	1.1	15
125	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
126	Genetic Modifiers of Chromatin Acetylation Antagonize the Reprogramming of Epi-Polymorphisms. <i>PLoS Genetics</i> , 2012, 8, e1002958.	1.5	7

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127	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
128	Genome-Wide Polyadenylation Site Mapping. <i>Methods in Enzymology</i> , 2012, 513, 271-296.	0.4	21
129	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
130	Set3 HDAC Mediates Effects of Overlapping Noncoding Transcription on Gene Induction Kinetics. <i>Cell</i> , 2012, 150, 1158-1169.	13.5	176
131	Gene Loops Enhance Transcriptional Directionality. <i>Science</i> , 2012, 338, 671-675.	6.0	219
132	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
133	Insights into RNA Biology from an Atlas of Mammalian mRNA-Binding Proteins. <i>Cell</i> , 2012, 149, 1393-1406.	13.5	1,765
134	Extensive Degradation of RNA Precursors by the Exosome in Wild-Type Cells. <i>Molecular Cell</i> , 2012, 48, 409-421.	4.5	218
135	RNA Polymerase II Collision Interrupts Convergent Transcription. <i>Molecular Cell</i> , 2012, 48, 365-374.	4.5	149
136	Genome-wide survey of post-meiotic segregation during yeast recombination. <i>Genome Biology</i> , 2011, 12, R36.	3.8	22
137	Yeast Sen1 Helicase Protects the Genome from Transcription-Associated Instability. <i>Molecular Cell</i> , 2011, 41, 21-32.	4.5	301
138	Functional consequences of bidirectional promoters. <i>Trends in Genetics</i> , 2011, 27, 267-276.	2.9	194
139	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
140	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
141	Antisense expression increases gene expression variability and locus interdependency. <i>Molecular Systems Biology</i> , 2011, 7, 468.	3.2	173
142	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
143	Genome-Wide Transcriptome Analysis in Yeast Using High-Density Tiling Arrays. <i>Methods in Molecular Biology</i> , 2011, 759, 107-123.	0.4	8
144	Genetic analysis of variation in transcription factor binding in yeast. <i>Nature</i> , 2010, 464, 1187-1191.	13.7	162

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145	The Baker's Yeast Diploid Genome Is Remarkably Stable in Vegetative Growth and Meiosis. <i>PLoS Genetics</i> , 2010, 6, e1001109.	1.5	89
146	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
147	Natural Single-Nucleosome Epi-Polymorphisms in Yeast. <i>PLoS Genetics</i> , 2010, 6, e1000913.	1.5	14
148	High-resolution transcription atlas of the mitotic cell cycle in budding yeast. <i>Genome Biology</i> , 2010, 11, R24.	13.9	99
149	Genome-wide allele- and strand-specific expression profiling. <i>Molecular Systems Biology</i> , 2009, 5, 274.	3.2	31
150	Array-based genotyping in <i>S.cerevisiae</i> using semi-supervised clustering. <i>Bioinformatics</i> , 2009, 25, 1056-1062.	1.8	7
151	<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
152	Bidirectional promoters generate pervasive transcription in yeast. <i>Nature</i> , 2009, 457, 1033-1037.	13.7	872
153	Widespread bidirectional promoters are the major source of cryptic transcripts in yeast. <i>Nature</i> , 2009, 457, 1038-1042.	13.7	557
154	Dissecting the Genetic Basis of Resistance to Malaria Parasites in <i>Anopheles gambiae</i> . <i>Science</i> , 2009, 326, 147-150.	6.0	106
155	High-resolution mapping of meiotic crossovers and non-crossovers in yeast. <i>Nature</i> , 2008, 454, 479-485.	13.7	554
156	Identification of mitochondrial disease genes through integrative analysis of multiple datasets. <i>Methods</i> , 2008, 46, 248-255.	1.9	10
157	Systematic screens for human disease genes, from yeast to human and back. <i>Molecular BioSystems</i> , 2008, 4, 18-29.	2.9	45
158	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
159	Antisense artifacts in transcriptome microarray experiments are resolved by actinomycin D. <i>Nucleic Acids Research</i> , 2007, 35, e128.	6.5	180
160	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
161	Mosaic Genome Architecture of the <i>Anopheles gambiae</i> Species Complex. <i>PLoS ONE</i> , 2007, 2, e1249.	1.1	41
162	Capturing cellular machines by systematic screens of protein complexes. <i>Trends in Microbiology</i> , 2006, 14, 336-339.	3.5	10

#	ARTICLE	IF	CITATIONS
163	Assessing Systems Properties of Yeast Mitochondria through an Interaction Map of the Organelle. PLoS Genetics, 2006, 2, e170.	1.5	67
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