

Jonathan S Weissman

List of Publications by Year in descending order

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234
papers

96,637
citations

470

129
h-index

721

250
g-index

319
all docs

319
docs citations

319
times ranked

92775
citing authors

#	ARTICLE	IF	CITATIONS
1	CRISPR technologies for genome, epigenome and transcriptome editing. Nature Reviews Molecular Cell Biology, 2024, 25, 464-487.	37.3	17
2	Deciphering cell states and genealogies of human haematopoiesis. Nature, 2024, 627, 389-398.	36.2	16
3	CRISPR technologies for genome, epigenome and transcriptome editing. Nature Reviews Molecular Cell Biology, 2024, 25, 464-487.	37.3	0
4	Triaging of Î±-helical proteins to the mitochondrial outer membrane by distinct chaperone machinery based on substrate topology. Molecular Cell, 2024, 84, 1101-1119.e9.	9.6	2
5	Neuronal activity rapidly reprograms dendritic translation via eIF4G2:uORF binding. Nature Neuroscience, 2024, 27, 822-835.	14.5	2
6	Microfluidics-free single-cell genomics with templated emulsification. Nature Biotechnology, 2023, 41, 1557-1566.	20.8	64
7	Systematic functional interrogation of SARS-CoV-2 host factors using Perturb-seq. Nature Communications, 2023, 14, .	13.2	8
8	Functional single-cell genomics of human cytomegalovirus infection. Nature Biotechnology, 2022, 40, 391-401.	20.8	70
9	The dark proteome: translation from noncanonical open reading frames. Trends in Cell Biology, 2022, 32, 243-258.	8.1	85
10	BRD2 inhibition blocks SARS-CoV-2 infection by reducing transcription of the host cell receptor ACE2. Nature Cell Biology, 2022, 24, 24-34.	10.0	59
11	Peroxisome function relies on organelle-associated mRNA translation. Science Advances, 2022, 8, eabk2141.	10.9	19
12	Mapping transcriptomic vector fields of single cells. Cell, 2022, 185, 690-711.e45.	27.8	218
13	High-content CRISPR screening. Nature Reviews Methods Primers, 2022, 2, .	18.8	237
14	OpenCell: Endogenous tagging for the cartography of human cellular organization. Science, 2022, 375, eabi6983.	20.9	239
15	Lineage tracing reveals the phylodynamics, plasticity, and paths of tumor evolution. Cell, 2022, 185, 1905-1923.e25.	27.8	141
16	Mapping information-rich genotype-phenotype landscapes with genome-scale Perturb-seq. Cell, 2022, 185, 2559-2575.e28.	27.8	232
17	Variant to function mapping at single-cell resolution through network propagation. Nature Biotechnology, 2022, 40, 1644-1653.	20.8	34
18	Standardized annotation of translated open reading frames. Nature Biotechnology, 2022, 40, 994-999.	20.8	112

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19	Ras-mutant cancers are sensitive to small molecule inhibition of V-type ATPases in mice. <i>Nature Biotechnology</i> , 2022, 40, 1834-1844.	20.8	15
20	Cellular barcoding to decipher clonal dynamics in disease. <i>Science</i> , 2022, 378, .	20.9	32
21	Single-cell lineages reveal the rates, routes, and drivers of metastasis in cancer xenografts. <i>Science</i> , 2021, 371, .	20.9	182
22	Regulation of translation by methylation multiplicity of 18S rRNA. <i>Cell Reports</i> , 2021, 34, 108825.	6.3	22
23	CRISPR-based functional genomics in human dendritic cells. <i>ELife</i> , 2021, 10, .	5.9	15
24	Genome-wide programmable transcriptional memory by CRISPR-based epigenome editing. <i>Cell</i> , 2021, 184, 2503-2519.e17.	27.8	382
25	Genome-wide CRISPRi screening identifies OCIAD1 as a prohibitin client and regulatory determinant of mitochondrial Complex III assembly in human cells. <i>ELife</i> , 2021, 10, .	5.9	24
26	Efficient C-to-G base editors developed using CRISPRi screens, target-library analysis, and machine learning. <i>Nature Biotechnology</i> , 2021, 39, 1414-1425.	20.8	140
27	An engineered transcriptional reporter of protein localization identifies regulators of mitochondrial and ER membrane protein trafficking in high-throughput CRISPRi screens. <i>ELife</i> , 2021, 10, .	5.9	20
28	Structured elements drive extensive circular RNA translation. <i>Molecular Cell</i> , 2021, 81, 4300-4318.e13.	9.6	140
29	High-content imaging-based pooled CRISPR screens in mammalian cells. <i>Journal of Cell Biology</i> , 2021, 220, .	5.2	58
30	A CRISPR/Cas9-Engineered <i>ARID1A</i> -Deficient Human Gastric Cancer Organoid Model Reveals Essential and Nonessential Modes of Oncogenic Transformation. <i>Cancer Discovery</i> , 2021, 11, 1562-1581.	14.2	93
31	Genome-Scale Perturbation of Long Noncoding RNA Expression Using CRISPR Interference. <i>Methods in Molecular Biology</i> , 2021, 2254, 323-338.	0.0	5
32	Enhanced prime editing systems by manipulating cellular determinants of editing outcomes. <i>Cell</i> , 2021, 184, 5635-5652.e29.	27.8	417
33	Mapping the genetic landscape of DNA double-strand break repair. <i>Cell</i> , 2021, 184, 5653-5669.e25.	27.8	114
34	The microtubule regulator <i>ringer</i> functions downstream from the RNA repair/splicing pathway to promote axon regeneration. <i>Genes and Development</i> , 2020, 34, 194-208.	5.9	16
35	Mismatch-CRISPRi Reveals the Co-varying Expression-Fitness Relationships of Essential Genes in <i>Escherichia coli</i> and <i>Bacillus subtilis</i> . <i>Cell Systems</i> , 2020, 11, 523-535.e9.	6.2	88
36	Conserved Functions of Ether Lipids and Sphingolipids in the Early Secretory Pathway. <i>Current Biology</i> , 2020, 30, 3775-3787.e7.	4.0	61

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37	Pharmaceutical-Grade Rigosertib Is a Microtubule-Destabilizing Agent. <i>Molecular Cell</i> , 2020, 79, 191-198.e3.	9.6	27
38	GIGYF2 and 4EHP Inhibit Translation Initiation of Defective Messenger RNAs to Assist Ribosome-Associated Quality Control. <i>Molecular Cell</i> , 2020, 79, 950-962.e6.	9.6	127
39	Life span extension by glucose restriction is abrogated by methionine supplementation: Cross-talk between glucose and methionine and implication of methionine as a key regulator of life span. <i>Science Advances</i> , 2020, 6, eaba1306.	10.9	55
40	Therapy-Induced Evolution of Human Lung Cancer Revealed by Single-Cell RNA Sequencing. <i>Cell</i> , 2020, 182, 1232-1251.e22.	27.8	421
41	Combinatorial single-cell CRISPR screens by direct guide RNA capture and targeted sequencing. <i>Nature Biotechnology</i> , 2020, 38, 954-961.	20.8	269
42	Polysomes Bypass a 50-Nucleotide Coding Gap Less Efficiently Than Monosomes Due to Attenuation of a 5' mRNA Stem-Loop and Enhanced Drop-off. <i>Journal of Molecular Biology</i> , 2020, 432, 4369-4387.	4.3	6
43	Fitness effects of CRISPR/Cas9-targeting of long noncoding RNA genes. <i>Nature Biotechnology</i> , 2020, 38, 573-576.	20.8	28
44	Titration of gene expression using libraries of systematically attenuated CRISPR guide RNAs. <i>Nature Biotechnology</i> , 2020, 38, 355-364.	20.8	125
45	Inference of single-cell phylogenies from lineage tracing data using Cassiopeia. <i>Genome Biology</i> , 2020, 21, 92.	9.2	71
46	CRISPRi-based radiation modifier screen identifies long non-coding RNA therapeutic targets in glioma. <i>Genome Biology</i> , 2020, 21, 83.	9.2	88
47	Structural and mechanistic basis of the EMC-dependent biogenesis of distinct transmembrane clients. <i>ELife</i> , 2020, 9, .	5.9	71
48	Ribosome Profiling: Global Views of Translation. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019, 11, a032698.	5.4	223
49	Exploring genetic interaction manifolds constructed from rich single-cell phenotypes. <i>Science</i> , 2019, 365, 786-793.	20.9	172
50	MULTI-seq: sample multiplexing for single-cell RNA sequencing using lipid-tagged indices. <i>Nature Methods</i> , 2019, 16, 619-626.	19.6	478
51	Molecular recording of mammalian embryogenesis. <i>Nature</i> , 2019, 570, 77-82.	36.2	280
52	Chaperone-mediated reflux of secretory proteins to the cytosol during endoplasmic reticulum stress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11291-11298.	7.6	41
53	Probing the Global Cellular Responses to Lipotoxicity Caused by Saturated Fatty Acids. <i>Molecular Cell</i> , 2019, 74, 32-44.e8.	9.6	188
54	Cellular response to small molecules that selectively stall protein synthesis by the ribosome. <i>PLoS Genetics</i> , 2019, 15, e1008057.	3.4	32

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55	Cycloheximide can distort measurements of mRNA levels and translation efficiency. <i>Nucleic Acids Research</i> , 2019, 47, 4974-4985.	14.0	65
56	New factors for protein transport identified by a genome-wide CRISPRi screen in mammalian cells. <i>Journal of Cell Biology</i> , 2019, 218, 3861-3879.	5.2	26
57	Chaperones block the unfolded protein response sensor ATF6 β by inducing a neomorphic inter-organelle tether. <i>ELife</i> , 2019, 8, .	5.9	48
58	The ER membrane protein complex is required to ensure correct topology and stable expression of flavivirus polyproteins. <i>ELife</i> , 2019, 8, .	5.9	50
59	A Stress Response that Monitors and Regulates mRNA Structure Is Central to Cold Shock Adaptation. <i>Molecular Cell</i> , 2018, 70, 274-286.e7.	9.6	163
60	Lipid Homeostasis Is Maintained by Dual Targeting of the Mitochondrial PE Biosynthesis Enzyme to the ER. <i>Developmental Cell</i> , 2018, 44, 261-270.e6.	7.0	84
61	CRISPR Approaches to Small Molecule Target Identification. <i>ACS Chemical Biology</i> , 2018, 13, 366-375.	3.6	72
62	Promoter of lncRNA Gene PVT1 Is a Tumor-Suppressor DNA Boundary Element. <i>Cell</i> , 2018, 173, 1398-1412.e22.	27.8	387
63	Combinatorial genetics in liver repopulation and carcinogenesis with a <i>in vivo</i> CRISPR activation platform. <i>Hepatology</i> , 2018, 68, 663-676.	8.1	67
64	The ER membrane protein complex interacts cotranslationally to enable biogenesis of multipass membrane proteins. <i>ELife</i> , 2018, 7, .	5.9	174
65	The helicase Ded1p controls use of near-cognate translation initiation codons in 5' UTRs. <i>Nature</i> , 2018, 559, 130-134.	36.2	155
66	Exploration of Benzothiazole Rhodacyanines as Allosteric Inhibitors of Protein-Protein Interactions with Heat Shock Protein 70 (Hsp70). <i>Journal of Medicinal Chemistry</i> , 2018, 61, 6163-6177.	6.6	89
67	Identification of a transporter complex responsible for the cytosolic entry of nitrogen-containing bisphosphonates. <i>ELife</i> , 2018, 7, .	5.9	44
68	Targeting RAS-driven human cancer cells with antibodies to upregulated and essential cell-surface proteins. <i>ELife</i> , 2018, 7, .	5.9	78
69	Reprogramming human T cell function and specificity with non-viral genome targeting. <i>Nature</i> , 2018, 559, 405-409.	36.2	664
70	Engineering ER-stress dependent non-conventional mRNA splicing. <i>ELife</i> , 2018, 7, .	5.9	18
71	Mapping the Genetic Landscape of Human Cells. <i>Cell</i> , 2018, 174, 953-967.e22.	27.8	243
72	Translation from unconventional 5' start sites drives tumour initiation. <i>Nature</i> , 2017, 541, 494-499.	36.2	292

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73	Suppression of B-cell development genes is key to glucocorticoid efficacy in treatment of acute lymphoblastic leukemia. <i>Blood</i> , 2017, 129, 3000-3008.	1.4	50
74	Model-guided optogenetic study of PKA signaling in budding yeast. <i>Molecular Biology of the Cell</i> , 2017, 28, 221-227.	2.5	20
75	CRISPRi-based genome-scale identification of functional long noncoding RNA loci in human cells. <i>Science</i> , 2017, 355, .	20.9	605
76	Inducible and multiplex gene regulation using CRISPRa-Cpf1-based transcription factors. <i>Nature Methods</i> , 2017, 14, 1163-1166.	19.6	176
77	Combined CRISPRi/a-Based Chemical Genetic Screens Reveal that Rigosertib Is a Microtubule-Destabilizing Agent. <i>Molecular Cell</i> , 2017, 68, 210-223.e6.	9.6	209
78	DMS-MaPseq for genome-wide or targeted RNA structure probing in vivo. <i>Nature Methods</i> , 2017, 14, 75-82.	19.6	339
79	The Human Cell Atlas. <i>ELife</i> , 2017, 6, .	5.9	1,677
80	Operon mRNAs are organized into ORF-centric structures that predict translation efficiency. <i>ELife</i> , 2017, 6, .	5.9	142
81	Compact and highly active next-generation libraries for CRISPR-mediated gene repression and activation. <i>ELife</i> , 2016, 5, .	5.9	672
82	Htm1p-Pdi1p is a folding-sensitive mannosidase that marks N-glycoproteins for ER-associated protein degradation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4015-24.	7.6	27
83	The SND proteins constitute an alternative targeting route to the endoplasmic reticulum. <i>Nature</i> , 2016, 540, 134-138.	36.2	174
84	Plastid: nucleotide-resolution analysis of next-generation sequencing and genomics data. <i>BMC Genomics</i> , 2016, 17, 958.	2.9	140
85	Perturb-Seq: Dissecting Molecular Circuits with Scalable Single-Cell RNA Profiling of Pooled Genetic Screens. <i>Cell</i> , 2016, 167, 1853-1866.e17.	27.8	1,234
86	A Multiplexed Single-Cell CRISPR Screening Platform Enables Systematic Dissection of the Unfolded Protein Response. <i>Cell</i> , 2016, 167, 1867-1882.e21.	27.8	876
87	The mTOR Complex Controls HIV Latency. <i>Cell Host and Microbe</i> , 2016, 20, 785-797.	11.0	184
88	A Comprehensive, CRISPR-based Functional Analysis of Essential Genes in Bacteria. <i>Cell</i> , 2016, 165, 1493-1506.	27.8	624
89	Single-cell analysis of long non-coding RNAs in the developing human neocortex. <i>Genome Biology</i> , 2016, 17, 67.	9.2	307
90	Combined chemical-genetic approach identifies cytosolic HSP70 dependence in rhabdomyosarcoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9015-9020.	7.6	33

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91	Versatile protein tagging in cells with split fluorescent protein. <i>Nature Communications</i> , 2016, 7, 11046.	13.2	361
92	Dynamic translation regulation in <i>Caulobacter</i> cell cycle control. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E6859-E6867.	7.6	59
93	Ligand-binding domains of nuclear receptors facilitate tight control of split CRISPR activity. <i>Nature Communications</i> , 2016, 7, 12009.	13.2	96
94	A scalable strategy for high-throughput GFP tagging of endogenous human proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3501-8.	7.6	220
95	Versatile in vivo regulation of tumor phenotypes by dCas9-mediated transcriptional perturbation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3892-900.	7.6	90
96	CRISPR Interference Efficiently Induces Specific and Reversible Gene Silencing in Human iPSCs. <i>Cell Stem Cell</i> , 2016, 18, 541-553.	11.0	440
97	Nucleosomes impede Cas9 access to DNA in vivo and in vitro. <i>ELife</i> , 2016, 5, .	5.9	364
98	Response to Comment on "Principles of ER cotranslational translocation revealed by proximity-specific ribosome profiling". <i>Science</i> , 2015, 348, 1217-1217.	20.9	12
99	[KIL-d] Protein Element Confers Antiviral Activity via Catastrophic Viral Mutagenesis. <i>Molecular Cell</i> , 2015, 60, 651-660.	9.6	8
100	A Regression-Based Analysis of Ribosome-Profiling Data Reveals a Conserved Complexity to Mammalian Translation. <i>Molecular Cell</i> , 2015, 60, 816-827.	9.6	206
101	Dynamic profiling of the protein life cycle in response to pathogens. <i>Science</i> , 2015, 347, 1259038.	20.9	420
102	Validation of the Hsp70-Bag3 Protein-Protein Interaction as a Potential Therapeutic Target in Cancer. <i>Molecular Cancer Therapeutics</i> , 2015, 14, 642-648.	3.7	110
103	Next-generation libraries for robust RNA interference-based genome-wide screens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E3384-91.	7.6	84
104	A prudent path forward for genomic engineering and germline gene modification. <i>Science</i> , 2015, 348, 36-38.	20.9	552
105	Ribosome profiling reveals the what, when, where and how of protein synthesis. <i>Nature Reviews Molecular Cell Biology</i> , 2015, 16, 651-664.	37.3	417
106	Targeting the AAA ATPase p97 as an Approach to Treat Cancer through Disruption of Protein Homeostasis. <i>Cancer Cell</i> , 2015, 28, 653-665.	16.8	341
107	Engineering Complex Synthetic Transcriptional Programs with CRISPR RNA Scaffolds. <i>Cell</i> , 2015, 160, 339-350.	27.8	828
108	Pharmacological dimerization and activation of the exchange factor eIF2B antagonizes the integrated stress response. <i>ELife</i> , 2015, 4, e07314.	5.9	216

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109	Regulation of mRNA translation during mitosis. <i>ELife</i> , 2015, 4, .	5.9	151
110	Paradoxical resistance of multiple myeloma to proteasome inhibitors by decreased levels of 19S proteasomal subunits. <i>ELife</i> , 2015, 4, e08153.	5.9	88
111	Ribosome Profiling Reveals Pervasive Translation Outside of Annotated Protein-Coding Genes. <i>Cell Reports</i> , 2014, 8, 1365-1379.	6.3	609
112	A high-coverage shRNA screen identifies TMEM129 as an E3 ligase involved in ER-associated protein degradation. <i>Nature Communications</i> , 2014, 5, 3832.	13.2	115
113	Causal signals between codon bias, mRNA structure, and the efficiency of translation and elongation. <i>Molecular Systems Biology</i> , 2014, 10, 770.	7.5	233
114	The Coding and Noncoding Architecture of the <i>Caulobacter crescentus</i> Genome. <i>PLoS Genetics</i> , 2014, 10, e1004463.	3.4	137
115	Genetic Influences on Translation in Yeast. <i>PLoS Genetics</i> , 2014, 10, e1004692.	3.4	78
116	KSHV 2.0: A Comprehensive Annotation of the Kaposi's Sarcoma-Associated Herpesvirus Genome Using Next-Generation Sequencing Reveals Novel Genomic and Functional Features. <i>PLoS Pathogens</i> , 2014, 10, e1003847.	4.1	273
117	Differential Scales of Protein Quality Control. <i>Cell</i> , 2014, 157, 52-64.	27.8	215
118	Quantifying Absolute Protein Synthesis Rates Reveals Principles Underlying Allocation of Cellular Resources. <i>Cell</i> , 2014, 157, 624-635.	27.8	1,169
119	Extensive and coordinated control of allele-specific expression by both transcription and translation in <i>Candida albicans</i> . <i>Genome Research</i> , 2014, 24, 963-973.	5.6	53
120	Genome-wide probing of RNA structure reveals active unfolding of mRNA structures in vivo. <i>Nature</i> , 2014, 505, 701-705.	36.2	772
121	Principles of ER cotranslational translocation revealed by proximity-specific ribosome profiling. <i>Science</i> , 2014, 346, 1257521.	20.9	369
122	The general mode of translation inhibition by macrolide antibiotics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15958-15963.	7.6	147
123	Genome-Scale CRISPR-Mediated Control of Gene Repression and Activation. <i>Cell</i> , 2014, 159, 647-661.	27.8	2,285
124	A Protein-Tagging System for Signal Amplification in Gene Expression and Fluorescence Imaging. <i>Cell</i> , 2014, 159, 635-646.	27.8	1,310
125	Misfolded Proteins Induce Aggregation of the Lectin Yos9. <i>Journal of Biological Chemistry</i> , 2014, 289, 25670-25677.	3.5	5
126	Unraveling the mechanism of cell death induced by chemical fibrils. <i>Nature Chemical Biology</i> , 2014, 10, 969-976.	8.0	43

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127	Uniform nomenclature for the mitochondrial contact site and cristae organizing system. <i>Journal of Cell Biology</i> , 2014, 204, 1083-1086.	5.2	226
128	CRISPR-Mediated Modular RNA-Guided Regulation of Transcription in Eukaryotes. <i>Cell</i> , 2013, 154, 442-451.	27.8	3,123
129	The Contribution of Systematic Approaches to Characterizing the Proteins and Functions of the Endoplasmic Reticulum. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013, 5, a013284-a013284.	5.4	12
130	Msn2 Coordinates a Stoichiometric Gene Expression Program. <i>Current Biology</i> , 2013, 23, 2336-2345.	4.0	52
131	Dynamic Imaging of Genomic Loci in Living Human Cells by an Optimized CRISPR/Cas System. <i>Cell</i> , 2013, 155, 1479-1491.	27.8	1,750
132	A Systematic Mammalian Genetic Interaction Map Reveals Pathways Underlying Ricin Susceptibility. <i>Cell</i> , 2013, 152, 909-922.	27.8	340
133	Next-Generation NAMPT Inhibitors Identified by Sequential High-Throughput Phenotypic Chemical and Functional Genomic Screens. <i>Chemistry and Biology</i> , 2013, 20, 1352-1363.	6.2	74
134	Repurposing CRISPR as an RNA-Guided Platform for Sequence-Specific Control of Gene Expression. <i>Cell</i> , 2013, 152, 1173-1183.	27.8	4,252
135	Integrated platform for genome-wide screening and construction of high-density genetic interaction maps in mammalian cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2317-26.	7.6	123
136	Genome-Wide Annotation and Quantitation of Translation by Ribosome Profiling. <i>Current Protocols in Molecular Biology</i> , 2013, 103, Unit 4.18.	3.7	57
137	Ribosome Profiling Provides Evidence that Large Noncoding RNAs Do Not Encode Proteins. <i>Cell</i> , 2013, 154, 240-251.	27.8	704
138	rRNA:mRNA pairing alters the length and the symmetry of mRNA-protected fragments in ribosome profiling experiments. <i>Bioinformatics</i> , 2013, 29, 1488-1491.	4.2	50
139	A developmentally regulated translational control pathway establishes the meiotic chromosome segregation pattern. <i>Genes and Development</i> , 2013, 27, 2147-2163.	5.9	93
140	Aneuploid yeast strains exhibit defects in cell growth and passage through START. <i>Molecular Biology of the Cell</i> , 2013, 24, 1274-1289.	2.5	81
141	Ribosome profiling reveals pervasive and regulated stop codon readthrough in <i>Drosophila melanogaster</i> . <i>ELife</i> , 2013, 2, e01179.	5.9	342
142	A Ribosome-Bound Quality Control Complex Triggers Degradation of Nascent Peptides and Signals Translation Stress. <i>Cell</i> , 2012, 151, 1042-1054.	27.8	556
143	Proto-genes and de novo gene birth. <i>Nature</i> , 2012, 487, 370-374.	36.2	576
144	High-Resolution View of the Yeast Meiotic Program Revealed by Ribosome Profiling. <i>Science</i> , 2012, 335, 552-557.	20.9	510

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145	Cellular Noise Regulons Underlie Fluctuations in <i>Saccharomyces cerevisiae</i> . <i>Molecular Cell</i> , 2012, 45, 483-493.	9.6	149
146	Functional Repurposing Revealed by Comparing <i>S. pombe</i> and <i>S. cerevisiae</i> Genetic Interactions. <i>Cell</i> , 2012, 149, 1339-1352.	27.8	156
147	Native Elongating Transcript Sequencing (NET-seq). <i>Current Protocols in Molecular Biology</i> , 2012, 98, Unit 4.14.1-17.	3.7	70
148	The translational landscape of mTOR signalling steers cancer initiation and metastasis. <i>Nature</i> , 2012, 485, 55-61.	36.2	1,141
149	The anti-Shine-Dalgarno sequence drives translational pausing and codon choice in bacteria. <i>Nature</i> , 2012, 484, 538-541.	36.2	577
150	Road to Ruin: Targeting Proteins for Degradation in the Endoplasmic Reticulum. <i>Science</i> , 2011, 334, 1086-1090.	20.9	567
151	Ganglion-specific splicing of TRPV1 underlies infrared sensation in vampire bats. <i>Nature</i> , 2011, 476, 88-91.	36.2	213
152	Selective Ribosome Profiling Reveals the Cotranslational Chaperone Action of Trigger Factor In Vivo. <i>Cell</i> , 2011, 147, 1295-1308.	27.8	428
153	Ribosome Profiling of Mouse Embryonic Stem Cells Reveals the Complexity and Dynamics of Mammalian Proteomes. <i>Cell</i> , 2011, 147, 789-802.	27.8	1,969
154	Radically Different Amyloid Conformations Dictate the Seeding Specificity of a Chimeric Sup35 Prion. <i>Journal of Molecular Biology</i> , 2011, 408, 1-8.	4.3	12
155	Strain conformation, primary structure and the propagation of the yeast prion [PSI ⁺]. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 493-499.	8.1	41
156	Nascent transcript sequencing visualizes transcription at nucleotide resolution. <i>Nature</i> , 2011, 469, 368-373.	36.2	727
157	Amyloid Structure: Conformational Diversity and Consequences. <i>Annual Review of Biochemistry</i> , 2011, 80, 557-585.	11.2	263
158	Systematic Screen of <i>Schizosaccharomyces pombe</i> Deletion Collection Uncovers Parallel Evolution of the Phosphate Signal Transduction Pathway in Yeasts. <i>Eukaryotic Cell</i> , 2011, 10, 198-206.	3.3	51
159	A mitochondrial-focused genetic interaction map reveals a scaffold-like complex required for inner membrane organization in mitochondria. <i>Journal of Cell Biology</i> , 2011, 195, 323-340.	5.2	413
160	Protein kinase Ypk1 phosphorylates regulatory proteins Orm1 and Orm2 to control sphingolipid homeostasis in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 19222-19227.	7.6	266
161	Automated identification of pathways from quantitative genetic interaction data. <i>Molecular Systems Biology</i> , 2010, 6, 379.	7.5	70
162	A general lack of compensation for gene dosage in yeast. <i>Molecular Systems Biology</i> , 2010, 6, 368.	7.5	119

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163	Orm family proteins mediate sphingolipid homeostasis. <i>Nature</i> , 2010, 463, 1048-1053.	36.2	551
164	Molecular basis of infrared detection by snakes. <i>Nature</i> , 2010, 464, 1006-1011.	36.2	389
165	Mammalian microRNAs predominantly act to decrease target mRNA levels. <i>Nature</i> , 2010, 466, 835-840.	36.2	3,550
166	Differences in prion strain conformations result from non-native interactions in a nucleus. <i>Nature Chemical Biology</i> , 2010, 6, 225-230.	8.0	70
167	J Domain Co-chaperone Specificity Defines the Role of BiP during Protein Translocation. <i>Journal of Biological Chemistry</i> , 2010, 285, 22484-22494.	3.5	43
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