

Jonathan S Weissman

List of Publications by Year in descending order

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244
papers

92,728
citations

528

127
h-index

946

239
g-index

298
all docs

298
docs citations

298
times ranked

77719
citing authors

#	ARTICLE	IF	CITATIONS
1	Repurposing CRISPR as an RNA-Guided Platform for Sequence-Specific Control of Gene Expression. <i>Cell</i> , 2013, 152, 1173-1183.	13.5	4,090
2	Global analysis of protein localization in budding yeast. <i>Nature</i> , 2003, 425, 686-691.	13.7	3,884
3	Mammalian microRNAs predominantly act to decrease target mRNA levels. <i>Nature</i> , 2010, 466, 835-840.	13.7	3,513
4	Global analysis of protein expression in yeast. <i>Nature</i> , 2003, 425, 737-741.	13.7	3,407
5	Genome-Wide Analysis in Vivo of Translation with Nucleotide Resolution Using Ribosome Profiling. <i>Science</i> , 2009, 324, 218-223.	6.0	3,283
6	CRISPR-Mediated Modular RNA-Guided Regulation of Transcription in Eukaryotes. <i>Cell</i> , 2013, 154, 442-451.	13.5	3,012
7	Global landscape of protein complexes in the yeast <i>Saccharomyces cerevisiae</i> . <i>Nature</i> , 2006, 440, 637-643.	13.7	2,681
8	Genome-Scale CRISPR-Mediated Control of Gene Repression and Activation. <i>Cell</i> , 2014, 159, 647-661.	13.5	2,176
9	Ribosome Profiling of Mouse Embryonic Stem Cells Reveals the Complexity and Dynamics of Mammalian Proteomes. <i>Cell</i> , 2011, 147, 789-802.	13.5	1,904
10	Functional and Genomic Analyses Reveal an Essential Coordination between the Unfolded Protein Response and ER-Associated Degradation. <i>Cell</i> , 2000, 101, 249-258.	13.5	1,777
11	Dynamic Imaging of Genomic Loci in Living Human Cells by an Optimized CRISPR/Cas System. <i>Cell</i> , 2013, 155, 1479-1491.	13.5	1,695
12	The Human Cell Atlas. <i>ELife</i> , 2017, 6, .	2.8	1,547
13	Single-cell proteomic analysis of <i>S. cerevisiae</i> reveals the architecture of biological noise. <i>Nature</i> , 2006, 441, 840-846.	13.7	1,434
14	Molecular Chaperones and Protein Quality Control. <i>Cell</i> , 2006, 125, 443-451.	13.5	1,352
15	A Protein-Tagging System for Signal Amplification in Gene Expression and Fluorescence Imaging. <i>Cell</i> , 2014, 159, 635-646.	13.5	1,245
16	Perturb-Seq: Dissecting Molecular Circuits with Scalable Single-Cell RNA Profiling of Pooled Genetic Screens. <i>Cell</i> , 2016, 167, 1853-1866.e17.	13.5	1,144
17	Quantifying Absolute Protein Synthesis Rates Reveals Principles Underlying Allocation of Cellular Resources. <i>Cell</i> , 2014, 157, 624-635.	13.5	1,137
18	An ER-Mitochondria Tethering Complex Revealed by a Synthetic Biology Screen. <i>Science</i> , 2009, 325, 477-481.	6.0	1,129

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19	The translational landscape of mTOR signalling steers cancer initiation and metastasis. <i>Nature</i> , 2012, 485, 55-61.	13.7	1,114
20	Decay of Endoplasmic Reticulum-Localized mRNAs During the Unfolded Protein Response. <i>Science</i> , 2006, 313, 104-107.	6.0	1,094
21	The ribosome profiling strategy for monitoring translation in vivo by deep sequencing of ribosome-protected mRNA fragments. <i>Nature Protocols</i> , 2012, 7, 1534-1550.	5.5	1,045
22	Oxidative protein folding in eukaryotes. <i>Journal of Cell Biology</i> , 2004, 164, 341-346.	2.3	934
23	CRISPR interference (CRISPRi) for sequence-specific control of gene expression. <i>Nature Protocols</i> , 2013, 8, 2180-2196.	5.5	930
24	Regulated Ire1-dependent decay of messenger RNAs in mammalian cells. <i>Journal of Cell Biology</i> , 2009, 186, 323-331.	2.3	841
25	A Multiplexed Single-Cell CRISPR Screening Platform Enables Systematic Dissection of the Unfolded Protein Response. <i>Cell</i> , 2016, 167, 1867-1882.e21.	13.5	819
26	Engineering Complex Synthetic Transcriptional Programs with CRISPR RNA Scaffolds. <i>Cell</i> , 2015, 160, 339-350.	13.5	809
27	Functional dissection of protein complexes involved in yeast chromosome biology using a genetic interaction map. <i>Nature</i> , 2007, 446, 806-810.	13.7	806
28	Exploration of the Function and Organization of the Yeast Early Secretory Pathway through an Epistatic Miniarray Profile. <i>Cell</i> , 2005, 123, 507-519.	13.5	804
29	Genome-wide probing of RNA structure reveals active unfolding of mRNA structures in vivo. <i>Nature</i> , 2014, 505, 701-705.	13.7	753
30	Conformational variations in an infectious protein determine prion strain differences. <i>Nature</i> , 2004, 428, 323-328.	13.7	747
31	Cotranscriptional Set2 Methylation of Histone H3 Lysine 36 Recruits a Repressive Rpd3 Complex. <i>Cell</i> , 2005, 123, 593-605.	13.5	712
32	Nascent transcript sequencing visualizes transcription at nucleotide resolution. <i>Nature</i> , 2011, 469, 368-373.	13.7	706
33	Toward a Comprehensive Atlas of the Physical Interactome of <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Proteomics</i> , 2007, 6, 439-450.	2.5	692
34	Ribosome Profiling Provides Evidence that Large Noncoding RNAs Do Not Encode Proteins. <i>Cell</i> , 2013, 154, 240-251.	13.5	678
35	Comprehensive Characterization of Genes Required for Protein Folding in the Endoplasmic Reticulum. <i>Science</i> , 2009, 323, 1693-1697.	6.0	646
36	Reprogramming human T cell function and specificity with non-viral genome targeting. <i>Nature</i> , 2018, 559, 405-409.	13.7	630

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37	Compact and highly active next-generation libraries for CRISPR-mediated gene repression and activation. <i>ELife</i> , 2016, 5, .	2.8	609
38	A Comprehensive, CRISPR-based Functional Analysis of Essential Genes in Bacteria. <i>Cell</i> , 2016, 165, 1493-1506.	13.5	593
39	Ribosome Profiling Reveals Pervasive Translation Outside of Annotated Protein-Coding Genes. <i>Cell Reports</i> , 2014, 8, 1365-1379.	2.9	591
40	The anti-Shine-Dalgarno sequence drives translational pausing and codon choice in bacteria. <i>Nature</i> , 2012, 484, 538-541.	13.7	566
41	CRISPRi-based genome-scale identification of functional long noncoding RNA loci in human cells. <i>Science</i> , 2017, 355, .	6.0	566
42	Road to Ruin: Targeting Proteins for Degradation in the Endoplasmic Reticulum. <i>Science</i> , 2011, 334, 1086-1090.	6.0	559
43	Proto-genes and de novo gene birth. <i>Nature</i> , 2012, 487, 370-374.	13.7	555
44	The physical basis of how prion conformations determine strain phenotypes. <i>Nature</i> , 2006, 442, 585-589.	13.7	552
45	Decoding Human Cytomegalovirus. <i>Science</i> , 2012, 338, 1088-1093.	6.0	546
46	Orm family proteins mediate sphingolipid homeostasis. <i>Nature</i> , 2010, 463, 1048-1053.	13.7	544
47	A prudent path forward for genomic engineering and germline gene modification. <i>Science</i> , 2015, 348, 36-38.	6.0	541
48	A Ribosome-Bound Quality Control Complex Triggers Degradation of Nascent Peptides and Signals Translation Stress. <i>Cell</i> , 2012, 151, 1042-1054.	13.5	536
49	High-Resolution View of the Yeast Meiotic Program Revealed by Ribosome Profiling. <i>Science</i> , 2012, 335, 552-557.	6.0	496
50	A comprehensive strategy enabling high-resolution functional analysis of the yeast genome. <i>Nature Methods</i> , 2008, 5, 711-718.	9.0	473
51	Mechanism of Prion Propagation: Amyloid Growth Occurs by Monomer Addition. <i>PLoS Biology</i> , 2004, 2, e321.	2.6	466
52	The GET Complex Mediates Insertion of Tail-Anchored Proteins into the ER Membrane. <i>Cell</i> , 2008, 134, 634-645.	13.5	460
53	Ero1p: A Novel and Ubiquitous Protein with an Essential Role in Oxidative Protein Folding in the Endoplasmic Reticulum. <i>Molecular Cell</i> , 1998, 1, 171-182.	4.5	424
54	MULTI-seq: sample multiplexing for single-cell RNA sequencing using lipid-tagged indices. <i>Nature Methods</i> , 2019, 16, 619-626.	9.0	421

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55	Selective Ribosome Profiling Reveals the Cotranslational Chaperone Action of Trigger Factor In Vivo. <i>Cell</i> , 2011, 147, 1295-1308.	13.5	419
56	CRISPR Interference Efficiently Induces Specific and Reversible Gene Silencing in Human iPSCs. <i>Cell Stem Cell</i> , 2016, 18, 541-553.	5.2	418
57	Dynamic profiling of the protein life cycle in response to pathogens. <i>Science</i> , 2015, 347, 1259038.	6.0	408
58	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.	2.3	402
59	Pervasive functional translation of noncanonical human open reading frames. <i>Science</i> , 2020, 367, 1140-1146.	6.0	400
60	Characterization of the Active Intermediate of a GroEL-GroES-Mediated Protein Folding Reaction. <i>Cell</i> , 1996, 84, 481-490.	13.5	395
61	Ribosome profiling reveals the what, when, where and how of protein synthesis. <i>Nature Reviews Molecular Cell Biology</i> , 2015, 16, 651-664.	16.1	389
62	Biochemical Basis of Oxidative Protein Folding in the Endoplasmic Reticulum. , 2000, 290, 1571-1574.		382
63	A Luminal Surveillance Complex that Selects Misfolded Glycoproteins for ER-Associated Degradation. <i>Cell</i> , 2006, 126, 349-359.	13.5	381
64	Molecular basis of infrared detection by snakes. <i>Nature</i> , 2010, 464, 1006-1011.	13.7	378
65	The FAD- and O ₂ -Dependent Reaction Cycle of Ero1-Mediated Oxidative Protein Folding in the Endoplasmic Reticulum. <i>Molecular Cell</i> , 2002, 10, 983-994.	4.5	374
66	Therapy-Induced Evolution of Human Lung Cancer Revealed by Single-Cell RNA Sequencing. <i>Cell</i> , 2020, 182, 1232-1251.e22.	13.5	371
67	A Critical Role for Amino-Terminal Glutamine/Asparagine Repeats in the Formation and Propagation of a Yeast Prion. <i>Cell</i> , 1998, 93, 1241-1252.	13.5	365
68	Promoter of lncRNA Gene PVT1 Is a Tumor-Suppressor DNA Boundary Element. <i>Cell</i> , 2018, 173, 1398-1412.e22.	13.5	362
69	Principles of ER cotranslational translocation revealed by proximity-specific ribosome profiling. <i>Science</i> , 2014, 346, 1257521.	6.0	350
70	Nucleosomes impede Cas9 access to DNA in vivo and in vitro. <i>ELife</i> , 2016, 5, .	2.8	349
71	Targeting and plasticity of mitochondrial proteins revealed by proximity-specific ribosome profiling. <i>Science</i> , 2014, 346, 748-751.	6.0	345
72	Ribosome profiling reveals pervasive and regulated stop codon readthrough in <i>Drosophila melanogaster</i> . <i>ELife</i> , 2013, 2, e01179.	2.8	335

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73	A Systematic Mammalian Genetic Interaction Map Reveals Pathways Underlying Ricin Susceptibility. <i>Cell</i> , 2013, 152, 909-922.	13.5	332
74	Enhanced prime editing systems by manipulating cellular determinants of editing outcomes. <i>Cell</i> , 2021, 184, 5635-5652.e29.	13.5	332
75	Versatile protein tagging in cells with split fluorescent protein. <i>Nature Communications</i> , 2016, 7, 11046.	5.8	331
76	Conservation and Rewiring of Functional Modules Revealed by an Epistasis Map in Fission Yeast. <i>Science</i> , 2008, 322, 405-410.	6.0	328
77	The structural basis of yeast prion strain variants. <i>Nature</i> , 2007, 449, 233-237.	13.7	324
78	Targeting the AAA ATPase p97 as an Approach to Treat Cancer through Disruption of Protein Homeostasis. <i>Cancer Cell</i> , 2015, 28, 653-665.	7.7	319
79	Emerging Principles of Conformation-Based Prion Inheritance. <i>Annual Review of Biochemistry</i> , 2004, 73, 617-656.	5.0	317
80	Genome-wide programmable transcriptional memory by CRISPR-based epigenome editing. <i>Cell</i> , 2021, 184, 2503-2519.e17.	13.5	312
81	DMS-MaPseq for genome-wide or targeted RNA structure probing in vivo. <i>Nature Methods</i> , 2017, 14, 75-82.	9.0	309
82	Multiple Gln/Asn-Rich Prion Domains Confer Susceptibility to Induction of the Yeast [PSI ⁺] Prion. <i>Cell</i> , 2001, 106, 183-194.	13.5	303
83	Single-cell analysis of long non-coding RNAs in the developing human neocortex. <i>Genome Biology</i> , 2016, 17, 67.	3.8	295
84	A strategy for extracting and analyzing large-scale quantitative epistatic interaction data. <i>Genome Biology</i> , 2006, 7, R63.	13.9	287
85	Translation from unconventional 5' start sites drives tumour initiation. <i>Nature</i> , 2017, 541, 494-499.	13.7	282
86	A pause sequence enriched at translation start sites drives transcription dynamics in vivo. <i>Science</i> , 2014, 344, 1042-1047.	6.0	280
87	The Action of Molecular Chaperones in the Early Secretory Pathway. <i>Annual Review of Genetics</i> , 2001, 35, 149-191.	3.2	279
88	Molecular Basis of a Yeast Prion Species Barrier. <i>Cell</i> , 2000, 100, 277-288.	13.5	269
89	Deadly Conformations—Protein Misfolding in Prion Disease. <i>Cell</i> , 1997, 89, 499-510.	13.5	265
90	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.	2.1	264

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91	Protein kinase Ypk1 phosphorylates regulatory proteins Orm1 and Orm2 to control sphingolipid homeostasis in <i>Saccharomyces cerevisiae</i> . Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 19222-19227.	3.3	260
92	Molecular recording of mammalian embryogenesis. Nature, 2019, 570, 77-82.	13.7	257
93	Amyloid Structure: Conformational Diversity and Consequences. Annual Review of Biochemistry, 2011, 80, 557-585.	5.0	256
94	A Molecular Caliper Mechanism for Determining Very Long-Chain Fatty Acid Length. Cell, 2007, 130, 663-677.	13.5	245
95	Rqc2p and 60S ribosomal subunits mediate mRNA-independent elongation of nascent chains. Science, 2015, 347, 75-78.	6.0	245
96	Small-molecule aggregates inhibit amyloid polymerization. Nature Chemical Biology, 2008, 4, 197-199.	3.9	244
97	Functional Organization of the <i>S. cerevisiae</i> Phosphorylation Network. Cell, 2009, 136, 952-963.	13.5	235
98	Combinatorial single-cell CRISPR screens by direct guide RNA capture and targeted sequencing. Nature Biotechnology, 2020, 38, 954-961.	9.4	232
99	Causal signals between codon bias, mRNA structure, and the efficiency of translation and elongation. Molecular Systems Biology, 2014, 10, 770.	3.2	231
100	Mapping the Genetic Landscape of Human Cells. Cell, 2018, 174, 953-967.e22.	13.5	226
101	A Genetic Interaction Map of RNA-Processing Factors Reveals Links between Sem1/Dss1-Containing Complexes and mRNA Export and Splicing. Molecular Cell, 2008, 32, 735-746.	4.5	221
102	Efficient catalysis of disulphide bond rearrangements by protein disulphide isomerase. Nature, 1993, 365, 185-188.	13.7	219
103	Uniform nomenclature for the mitochondrial contact site and cristae organizing system. Journal of Cell Biology, 2014, 204, 1083-1086.	2.3	219
104	High-throughput, quantitative analyses of genetic interactions in <i>E. coli</i> . Nature Methods, 2008, 5, 781-787.	9.0	214
105	Pharmacological dimerization and activation of the exchange factor eIF2B antagonizes the integrated stress response. ELife, 2015, 4, e07314.	2.8	212
106	Defining the Glycan Destruction Signal for Endoplasmic Reticulum-Associated Degradation. Molecular Cell, 2008, 32, 870-877.	4.5	211
107	Ganglion-specific splicing of TRPV1 underlies infrared sensation in vampire bats. Nature, 2011, 476, 88-91.	13.7	208
108	A scalable strategy for high-throughput GFP tagging of endogenous human proteins. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3501-8.	3.3	208

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109	Differential Scales of Protein Quality Control. <i>Cell</i> , 2014, 157, 52-64.	13.5	207
110	Membranes in Balance: Mechanisms of Sphingolipid Homeostasis. <i>Molecular Cell</i> , 2010, 40, 267-279.	4.5	206
111	Ribosome Profiling: Global Views of Translation. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019, 11, a032698.	2.3	205
112	Exploration of the Topological Requirements of ERAD Identifies Yos9p as a Lectin Sensor of Misfolded Glycoproteins in the ER Lumen. <i>Molecular Cell</i> , 2005, 19, 741-751.	4.5	204
113	A Regression-Based Analysis of Ribosome-Profiling Data Reveals a Conserved Complexity to Mammalian Translation. <i>Molecular Cell</i> , 2015, 60, 816-827.	4.5	200
114	Combined CRISPRi/a-Based Chemical Genetic Screens Reveal that Rigosertib Is a Microtubule-Destabilizing Agent. <i>Molecular Cell</i> , 2017, 68, 210-223.e6.	4.5	197
115	The mTOR Complex Controls HIV Latency. <i>Cell Host and Microbe</i> , 2016, 20, 785-797.	5.1	179
116	Dissection and Design of Yeast Prions. <i>PLoS Biology</i> , 2004, 2, e86.	2.6	175
117	OpenCell: Endogenous tagging for the cartography of human cellular organization. <i>Science</i> , 2022, 375, eabi6983.	6.0	174
118	Mechanism of Cross-Species Prion Transmission. <i>Cell</i> , 2005, 121, 49-62.	13.5	172
119	Inducible and multiplex gene regulation using CRISPR-Cpf1-based transcription factors. <i>Nature Methods</i> , 2017, 14, 1163-1166.	9.0	170
120	Probing the Global Cellular Responses to Lipotoxicity Caused by Saturated Fatty Acids. <i>Molecular Cell</i> , 2019, 74, 32-44.e8.	4.5	170
121	Mapping information-rich genotype-phenotype landscapes with genome-scale Perturb-seq. <i>Cell</i> , 2022, 185, 2559-2575.e28.	13.5	169
122	The SND proteins constitute an alternative targeting route to the endoplasmic reticulum. <i>Nature</i> , 2016, 540, 134-138.	13.7	168
123	Mapping transcriptomic vector fields of single cells. <i>Cell</i> , 2022, 185, 690-711.e45.	13.5	167
124	Single-cell lineages reveal the rates, routes, and drivers of metastasis in cancer xenografts. <i>Science</i> , 2021, 371, .	6.0	166
125	Defining the physiological role of SRP in protein-targeting efficiency and specificity. <i>Science</i> , 2018, 359, 689-692.	6.0	164
126	In Vivo Monitoring of the Prion Replication Cycle Reveals a Critical Role for Sis1 in Delivering Substrates to Hsp104. <i>Molecular Cell</i> , 2008, 32, 584-591.	4.5	160

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127	The ER membrane protein complex interacts cotranslationally to enable biogenesis of multipass membrane proteins. <i>ELife</i> , 2018, 7, .	2.8	160
128	A Stress Response that Monitors and Regulates mRNA Structure Is Central to Cold Shock Adaptation. <i>Molecular Cell</i> , 2018, 70, 274-286.e7.	4.5	157
129	Exploring genetic interaction manifolds constructed from rich single-cell phenotypes. <i>Science</i> , 2019, 365, 786-793.	6.0	155
130	High-content CRISPR screening. <i>Nature Reviews Methods Primers</i> , 2022, 2, .	11.8	155
131	Evidence for the Prion Hypothesis: Induction of the Yeast [PSI ⁺] Factor by in Vitro- Converted Sup35 Protein. <i>Science</i> , 2000, 289, 595-599.	6.0	154
132	Functional Repurposing Revealed by Comparing <i>S.Âpombe</i> and <i>S.Âcerevisiae</i> Genetic Interactions. <i>Cell</i> , 2012, 149, 1339-1352.	13.5	154
133	Conformational diversity in a yeast prion dictates its seeding specificity. <i>Nature</i> , 2001, 410, 223-227.	13.7	150
134	High-throughput genetic interaction mapping in the fission yeast <i>Schizosaccharomyces pombe</i> . <i>Nature Methods</i> , 2007, 4, 861-866.	9.0	146
135	Backup without redundancy: genetic interactions reveal the cost of duplicate gene loss. <i>Molecular Systems Biology</i> , 2007, 3, 86.	3.2	143
136	Cellular Noise Regulons Underlie Fluctuations in <i>Saccharomyces cerevisiae</i> . <i>Molecular Cell</i> , 2012, 45, 483-493.	4.5	143
137	The helicase Ded1p controls use of near-cognate translation initiation codons in 5â€² UTRs. <i>Nature</i> , 2018, 559, 130-134.	13.7	143
138	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.	3.3	142
139	Regulation of mRNA translation during mitosis. <i>ELife</i> , 2015, 4, .	2.8	138
140	Directed Evolution of Substrate-Optimized GroEL/S Chaperonins. <i>Cell</i> , 2002, 111, 1027-1039.	13.5	137
141	The Coding and Noncoding Architecture of the <i>Caulobacter crescentus</i> Genome. <i>PLoS Genetics</i> , 2014, 10, e1004463.	1.5	136
142	Plastid: nucleotide-resolution analysis of next-generation sequencing and genomics data. <i>BMC Genomics</i> , 2016, 17, 958.	1.2	136
143	Operon mRNAs are organized into ORF-centric structures that predict translation efficiency. <i>ELife</i> , 2017, 6, .	2.8	128
144	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.	3.3	121

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145	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.	4.5	119
146	A general lack of compensation for gene dosage in yeast. <i>Molecular Systems Biology</i> , 2010, 6, 368.	3.2	118
147	Efficient C-to-G base editors developed using CRISPRi screens, target-library analysis, and machine learning. <i>Nature Biotechnology</i> , 2021, 39, 1414-1425.	9.4	118
148	Mec1/Tel1 Phosphorylation of the INO80 Chromatin Remodeling Complex Influences DNA Damage Checkpoint Responses. <i>Cell</i> , 2007, 130, 499-511.	13.5	116
149	A high-coverage shRNA screen identifies TMEM129 as an E3 ligase involved in ER-associated protein degradation. <i>Nature Communications</i> , 2014, 5, 3832.	5.8	113
150	CAT-tailing as a fail-safe mechanism for efficient degradation of stalled nascent polypeptides. <i>Science</i> , 2017, 357, 414-417.	6.0	113
151	Selective ribosome profiling as a tool for studying the interaction of chaperones and targeting factors with nascent polypeptide chains and ribosomes. <i>Nature Protocols</i> , 2013, 8, 2212-2239.	5.5	112
152	Titrating gene expression using libraries of systematically attenuated CRISPR guide RNAs. <i>Nature Biotechnology</i> , 2020, 38, 355-364.	9.4	108
153	Structured elements drive extensive circular RNA translation. <i>Molecular Cell</i> , 2021, 81, 4300-4318.e13.	4.5	108
154	Lineage tracing reveals the phylodynamics, plasticity, and paths of tumor evolution. <i>Cell</i> , 2022, 185, 1905-1923.e25.	13.5	108
155	Validation of the Hsp70- Bag3 Protein-Protein Interaction as a Potential Therapeutic Target in Cancer. <i>Molecular Cancer Therapeutics</i> , 2015, 14, 642-648.	1.9	105
156	Mapping the genetic landscape of DNA double-strand break repair. <i>Cell</i> , 2021, 184, 5653-5669.e25.	13.5	98
157	Generation of prion transmission barriers by mutational control of amyloid conformations. <i>Nature</i> , 2003, 424, 948-951.	13.7	97
158	Rapid creation and quantitative monitoring of high coverage shRNA libraries. <i>Nature Methods</i> , 2009, 6, 443-445.	9.0	92
159	Release of both native and non-native proteins from a cis-only GroEL ternary complex. <i>Nature</i> , 1996, 383, 96-99.	13.7	90
160	A developmentally regulated translational control pathway establishes the meiotic chromosome segregation pattern. <i>Genes and Development</i> , 2013, 27, 2147-2163.	2.7	90
161	Ligand-binding domains of nuclear receptors facilitate tight control of split CRISPR activity. <i>Nature Communications</i> , 2016, 7, 12009.	5.8	90
162	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.	3.3	87

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163	Standardized annotation of translated open reading frames. <i>Nature Biotechnology</i> , 2022, 40, 994-999.	9.4	86
164	A kinetic explanation for the rearrangement pathway of BPTI folding. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 1123-1130.	3.6	84
165	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.	2.9	84
166	Paradoxical resistance of multiple myeloma to proteasome inhibitors by decreased levels of 19S proteasomal subunits. <i>ELife</i> , 2015, 4, e08153.	2.8	84
167	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.	3.3	83
168	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.	3.1	83
169	Construction, Verification and Experimental Use of Two Epitope-Tagged Collections of Budding Yeast Strains. <i>Comparative and Functional Genomics</i> , 2005, 6, 2-16.	2.0	80
170	Aneuploid yeast strains exhibit defects in cell growth and passage through START. <i>Molecular Biology of the Cell</i> , 2013, 24, 1274-1289.	0.9	79
171	Functional genomics platform for pooled screening and generation of mammalian genetic interaction maps. <i>Nature Protocols</i> , 2014, 9, 1825-1847.	5.5	79
172	Genetic Influences on Translation in Yeast. <i>PLoS Genetics</i> , 2014, 10, e1004692.	1.5	77
173	CRISPRi-based radiation modifier screen identifies long non-coding RNA therapeutic targets in glioma. <i>Genome Biology</i> , 2020, 21, 83.	3.8	76
174	CCR4/NOT complex associates with the proteasome and regulates histone methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 5836-5841.	3.3	75
175	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.	7.7	75
176	Domain Architecture of Protein-disulfide Isomerase Facilitates Its Dual Role as an Oxidase and an Isomerase in Ero1p-mediated Disulfide Formation. <i>Journal of Biological Chemistry</i> , 2006, 281, 876-884.	1.6	73
177	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	72
178	Targeting RAS-driven human cancer cells with antibodies to upregulated and essential cell-surface proteins. <i>ELife</i> , 2018, 7, .	2.8	72
179	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.	2.9	72
180	Automated identification of pathways from quantitative genetic interaction data. <i>Molecular Systems Biology</i> , 2010, 6, 379.	3.2	70

#	ARTICLE	IF	CITATIONS
181	Differences in prion strain conformations result from non-native interactions in a nucleus. <i>Nature Chemical Biology</i> , 2010, 6, 225-230.	3.9	70
182	CRISPR Approaches to Small Molecule Target Identification. <i>ACS Chemical Biology</i> , 2018, 13, 366-375.	1.6	68
183	Native Elongating Transcript Sequencing (NET-seq). <i>Current Protocols in Molecular Biology</i> , 2012, 98, Unit 4.14.1-17.	2.9	67
184	Structural and mechanistic basis of the EMC-dependent biogenesis of distinct transmembrane clients. <i>ELife</i> , 2020, 9, .	2.8	66
185	Origins and kinetic consequences of diversity in Sup35 yeast prion fibers. , 2002, 9, 389-96.		64
186	Combinatorial genetics in liver repopulation and carcinogenesis with a in vivo CRISPR activation platform. <i>Hepatology</i> , 2018, 68, 663-676.	3.6	63
187	The dark proteome: translation from noncanonical open reading frames. <i>Trends in Cell Biology</i> , 2022, 32, 243-258.	3.6	63
188	Cycloheximide can distort measurements of mRNA levels and translation efficiency. <i>Nucleic Acids Research</i> , 2019, 47, 4974-4985.	6.5	62
189	Inference of single-cell phylogenies from lineage tracing data using Cassiopeia. <i>Genome Biology</i> , 2020, 21, 92.	3.8	61
190	Functional single-cell genomics of human cytomegalovirus infection. <i>Nature Biotechnology</i> , 2022, 40, 391-401.	9.4	60
191	Conserved Functions of Ether Lipids and Sphingolipids in the Early Secretory Pathway. <i>Current Biology</i> , 2020, 30, 3775-3787.e7.	1.8	59
192	Global cellular response to chemotherapy-induced apoptosis. <i>ELife</i> , 2013, 2, e01236.	2.8	59
193	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.	3.3	57
194	Genome-wide Annotation and Quantitation of Translation by Ribosome Profiling. <i>Current Protocols in Molecular Biology</i> , 2013, 103, Unit 4.18.	2.9	55
195	The Utility of Prions. <i>Developmental Cell</i> , 2002, 2, 143-151.	3.1	54
196	Identification of yeast proteins necessary for cell-surface function of a potassium channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 18079-18084.	3.3	53
197	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.	2.4	53
198	High-content imaging-based pooled CRISPR screens in mammalian cells. <i>Journal of Cell Biology</i> , 2021, 220, .	2.3	53

#	ARTICLE	IF	CITATIONS
199	Msn2 Coordinates a Stoichiometric Gene Expression Program. <i>Current Biology</i> , 2013, 23, 2336-2345.	1.8	51
200	rRNA:mRNA pairing alters the length and the symmetry of mRNA-protected fragments in ribosome profiling experiments. <i>Bioinformatics</i> , 2013, 29, 1488-1491.	1.8	50
201	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.	4.7	49
202	Suppression of B-cell development genes is key to glucocorticoid efficacy in treatment of acute lymphoblastic leukemia. <i>Blood</i> , 2017, 129, 3000-3008.	0.6	48
203	BRD2 inhibition blocks SARS-CoV-2 infection by reducing transcription of the host cell receptor ACE2. <i>Nature Cell Biology</i> , 2022, 24, 24-34.	4.6	47
204	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.	3.4	46
205	Ceapins block the unfolded protein response sensor ATF6 β by inducing a neomorphic inter-organelle tether. <i>ELife</i> , 2019, 8, .	2.8	46
206	An Efficient Protein Transformation Protocol for Introducing Prions into Yeast. <i>Methods in Enzymology</i> , 2006, 412, 185-200.	0.4	45
207	J Domain Co-chaperone Specificity Defines the Role of BiP during Protein Translocation. <i>Journal of Biological Chemistry</i> , 2010, 285, 22484-22494.	1.6	43
208	Unraveling the mechanism of cell death induced by chemical fibrils. <i>Nature Chemical Biology</i> , 2014, 10, 969-976.	3.9	43
209	Identification of a transporter complex responsible for the cytosolic entry of nitrogen-containing bisphosphonates. <i>ELife</i> , 2018, 7, .	2.8	42
210	The ER membrane protein complex is required to ensure correct topology and stable expression of flavivirus polyproteins. <i>ELife</i> , 2019, 8, .	2.8	42
211	Strain conformation, primary structure and the propagation of the yeast prion [PSI ⁺]. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 493-499.	3.6	39
212	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.	3.3	36
213	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.	3.3	33
214	Cellular response to small molecules that selectively stall protein synthesis by the ribosome. <i>PLoS Genetics</i> , 2019, 15, e1008057.	1.5	31
215	Fitness effects of CRISPR/Cas9-targeting of long noncoding RNA genes. <i>Nature Biotechnology</i> , 2020, 38, 573-576.	9.4	27
216	Htm1p 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.	3.3	26

#	ARTICLE	IF	CITATIONS
217	[11] Construction of single-ring and two-ring hybrid versions of bacterial chaperonin GroEL. <i>Methods in Enzymology</i> , 1998, 290, 141-146.	0.4	25
218	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.	2.3	25
219	Variant to function mapping at single-cell resolution through network propagation. <i>Nature Biotechnology</i> , 2022, 40, 1644-1653.	9.4	25
220	Putting a lid on protein folding: structure and function of the co-chaperonin, GroES. <i>Chemistry and Biology</i> , 1996, 3, 157-161.	6.2	23
221	Pharmaceutical-Grade Rigosertib Is a Microtubule-Destabilizing Agent. <i>Molecular Cell</i> , 2020, 79, 191-198.e3.	4.5	22
222	Model-guided optogenetic study of PKA signaling in budding yeast. <i>Molecular Biology of the Cell</i> , 2017, 28, 221-227.	0.9	20
223	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, .	2.8	20
224	Peroxisome function relies on organelle-associated mRNA translation. <i>Science Advances</i> , 2022, 8, eabk2141.	4.7	18
225	Thinking outside the box: new insights into the mechanism of GroEL-mediated protein folding. , 1999, 6, 597-600.		17
226	Engineering ER-stress dependent non-conventional mRNA splicing. <i>ELife</i> , 2018, 7, .	2.8	17
227	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, .	2.8	17
228	Regulation of translation by methylation multiplicity of 18S rRNA. <i>Cell Reports</i> , 2021, 34, 108825.	2.9	16
229	From information to knowledge: new technologies for defining gene function. <i>Nature Methods</i> , 2009, 6, 721-723.	9.0	15
230	Many things from one. <i>Nature</i> , 2006, 444, 561-562.	13.7	14
231	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.	2.7	13
232	Radically Different Amyloid Conformations Dictate the Seeding Specificity of a Chimeric Sup35 Prion. <i>Journal of Molecular Biology</i> , 2011, 408, 1-8.	2.0	12
233	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.	2.3	12
234	Response to Comment on "Principles of ER cotranslational translocation revealed by proximity-specific ribosome profiling". <i>Science</i> , 2015, 348, 1217-1217.	6.0	12

#	ARTICLE	IF	CITATIONS
235	CRISPR-based functional genomics in human dendritic cells. <i>ELife</i> , 2021, 10, .	2.8	10
236	The Ins and Outs of GroEL-Mediated Protein Folding. <i>Molecular Cell</i> , 2001, 8, 730-732.	4.5	9
237	Functional genomic approaches to understanding molecular chaperones and stress responses. <i>Advances in Protein Chemistry</i> , 2001, 59, 345-390.	4.4	8
238	[KIL-d] Protein Element Confers Antiviral Activity via Catastrophic Viral Mutagenesis. <i>Molecular Cell</i> , 2015, 60, 651-660.	4.5	8
239	Misfolded Proteins Induce Aggregation of the Lectin Yos9. <i>Journal of Biological Chemistry</i> , 2014, 289, 25670-25677.	1.6	5
240	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.	2.0	5
241	Genome-Scale Perturbation of Long Noncoding RNA Expression Using CRISPR Interference. <i>Methods in Molecular Biology</i> , 2021, 2254, 323-338.	0.4	5
242	The Epistemology of Cell Biology. <i>Molecular Biology of the Cell</i> , 2010, 21, 3825-3825.	0.9	1
243	2004 Irving Sigal Young Investigator Award. <i>Protein Science</i> , 2009, 13, 3333-3335.	3.1	0
244	Integrated genomic analysis of EGFR-mutant non-small cell lung cancer immediately following erlotinib initiation in patients.. <i>Journal of Clinical Oncology</i> , 2013, 31, 11067-11067.	0.8	0