

Jonathan S Weissman

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

264
papers

70,235
citations

119
h-index

265
g-index

298
ext. papers

83,675
ext. citations

26.7
avg, IF

7.99
L-index

#	Paper	IF	Citations
264	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	23.4	5
263	Peroxisome function relies on organelle-associated mRNA translation.. <i>Science Advances</i> , 2022 , 8, eabk21415	14.5	2
262	Mapping transcriptomic vector fields of single cells.. <i>Cell</i> , 2022 ,	56.2	9
261	High-content CRISPR screening. <i>Nature Reviews Methods Primers</i> , 2022 , 2,		10
260	OpenCell: Endogenous tagging for the cartography of human cellular organization.. <i>Science</i> , 2022 , 375, eabi6983	33.3	9
259	Lineage tracing reveals the phylodynamics, plasticity, and paths of tumor evolution.. <i>Cell</i> , 2022 ,	56.2	4
258	The dark proteome: translation from noncanonical open reading frames. <i>Trends in Cell Biology</i> , 2021 ,	18.3	4
257	Functional single-cell genomics of human cytomegalovirus infection. <i>Nature Biotechnology</i> , 2021 ,	44.5	11
256	Enhanced prime editing systems by manipulating cellular determinants of editing outcomes. <i>Cell</i> , 2021 , 184, 5635-5652.e29	56.2	48
255	Mapping the genetic landscape of DNA double-strand break repair. <i>Cell</i> , 2021 , 184, 5653-5669.e25	56.2	12
254	Regulation of translation by methylation multiplicity of 18S rRNA. <i>Cell Reports</i> , 2021 , 34, 108825	10.6	5
253	CRISPR-based functional genomics in human dendritic cells. <i>ELife</i> , 2021 , 10,	8.9	2
252	Genome-wide programmable transcriptional memory by CRISPR-based epigenome editing. <i>Cell</i> , 2021 , 184, 2503-2519.e17	56.2	80
251	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,	8.9	8
250	Efficient C-to-G base editors developed using CRISPRi screens, target-library analysis, and machine learning. <i>Nature Biotechnology</i> , 2021 , 39, 1414-1425	44.5	32
249	BRD2 inhibition blocks SARS-CoV-2 infection in vitro by reducing transcription of the host cell receptor ACE2 2021 ,		5
248	Single-cell lineages reveal the rates, routes, and drivers of metastasis in cancer xenografts. <i>Science</i> , 2021 , 371,	33.3	51

247	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,	8.9	3
246	Structured elements drive extensive circular RNA translation. <i>Molecular Cell</i> , 2021 , 81, 4300-4318.e13	17.6	13
245	High-content imaging-based pooled CRISPR screens in mammalian cells. <i>Journal of Cell Biology</i> , 2021 , 220,	7.3	15
244	A CRISPR/Cas9-Engineered -Deficient Human Gastric Cancer Organoid Model Reveals Essential and Nonessential Modes of Oncogenic Transformation. <i>Cancer Discovery</i> , 2021 , 11, 1562-1581	24.4	19
243	Genome-Scale Perturbation of Long Noncoding RNA Expression Using CRISPR Interference. <i>Methods in Molecular Biology</i> , 2021 , 2254, 323-338	1.4	2
242	Pervasive functional translation of noncanonical human open reading frames. <i>Science</i> , 2020 , 367, 1140-1146	33.6	168
241	Combinatorial single-cell CRISPR screens by direct guide RNA capture and targeted sequencing. <i>Nature Biotechnology</i> , 2020 , 38, 954-961	44.5	85
240	Polysomes Bypass a 50-Nucleotide Coding Gap Less Efficiently Than Monosomes Due to Attenuation of a 5RmRNA Stem-Loop and Enhanced Drop-off. <i>Journal of Molecular Biology</i> , 2020 , 432, 4369-4387	6.5	3
239	Fitness effects of CRISPR/Cas9-targeting of long noncoding RNA genes. <i>Nature Biotechnology</i> , 2020 , 38, 573-576	44.5	15
238	Titrating gene expression using libraries of systematically attenuated CRISPR guide RNAs. <i>Nature Biotechnology</i> , 2020 , 38, 355-364	44.5	50
237	Structural and mechanistic basis of the EMC-dependent biogenesis of distinct transmembrane clients. <i>ELife</i> , 2020 , 9,	8.9	21
236	The microtubule regulator functions downstream from the RNA repair/splicing pathway to promote axon regeneration. <i>Genes and Development</i> , 2020 , 34, 194-208	12.6	7
235	Mismatch-CRISPRi Reveals the Co-varying Expression-Fitness Relationships of Essential Genes in Escherichia coli and Bacillus subtilis. <i>Cell Systems</i> , 2020 , 11, 523-535.e9	10.6	17
234	Conserved Functions of Ether Lipids and Sphingolipids in the Early Secretory Pathway. <i>Current Biology</i> , 2020 , 30, 3775-3787.e7	6.3	19
233	Pharmaceutical-Grade Rigosertib Is a Microtubule-Destabilizing Agent. <i>Molecular Cell</i> , 2020 , 79, 191-198.e36	17.6	7
232	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	17.6	36
231	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	14.3	17
230	Therapy-Induced Evolution of Human Lung Cancer Revealed by Single-Cell RNA Sequencing. <i>Cell</i> , 2020 , 182, 1232-1251.e22	56.2	116

229	Inference of single-cell phylogenies from lineage tracing data using <i>Cassiopeia</i> . <i>Genome Biology</i> , 2020 , 21, 92	18.3	16
228	CRISPRi-based radiation modifier screen identifies long non-coding RNA therapeutic targets in glioma. <i>Genome Biology</i> , 2020 , 21, 83	18.3	39
227	MULTI-seq: sample multiplexing for single-cell RNA sequencing using lipid-tagged indices. <i>Nature Methods</i> , 2019 , 16, 619-626	21.6	169
226	Molecular recording of mammalian embryogenesis. <i>Nature</i> , 2019 , 570, 77-82	50.4	140
225	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 ¹⁷	11.5	17
224	Probing the Global Cellular Responses to Lipotoxicity Caused by Saturated Fatty Acids. <i>Molecular Cell</i> , 2019 , 74, 32-44.e8	17.6	84
223	Cellular response to small molecules that selectively stall protein synthesis by the ribosome. <i>PLoS Genetics</i> , 2019 , 15, e1008057	6	19
222	Cycloheximide can distort measurements of mRNA levels and translation efficiency. <i>Nucleic Acids Research</i> , 2019 , 47, 4974-4985	20.1	31
221	Ribosome Profiling: Global Views of Translation. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019 , 11,	10.2	94
220	Exploring genetic interaction manifolds constructed from rich single-cell phenotypes. <i>Science</i> , 2019 , 365, 786-793	33.3	64
219	Ceapins block the unfolded protein response sensor ATF6 β by inducing a neomorphic inter-organelle tether. <i>ELife</i> , 2019 , 8,	8.9	29
218	The ER membrane protein complex is required to ensure correct topology and stable expression of flavivirus polyproteins. <i>ELife</i> , 2019 , 8,	8.9	25
217	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	7.3	12
216	A Stress Response that Monitors and Regulates mRNA Structure Is Central to Cold Shock Adaptation. <i>Molecular Cell</i> , 2018 , 70, 274-286.e7	17.6	82
215	Defining the physiological role of SRP in protein-targeting efficiency and specificity. <i>Science</i> , 2018 , 359, 689-692	33.3	108
214	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	10.2	60
213	CRISPR Approaches to Small Molecule Target Identification. <i>ACS Chemical Biology</i> , 2018 , 13, 366-375	4.9	41
212	Promoter of lncRNA Gene PVT1 Is a Tumor-Suppressor DNA Boundary Element. <i>Cell</i> , 2018 , 173, 1398-1410.e22226	10.2	226

211	Combinatorial genetics in liver repopulation and carcinogenesis with a in vivo CRISPR activation platform. <i>Hepatology</i> , 2018 , 68, 663-676	11.2	36
210	Reprogramming human T cell function and specificity with non-viral genome targeting. <i>Nature</i> , 2018 , 559, 405-409	50.4	367
209	Engineering ER-stress dependent non-conventional mRNA splicing. <i>ELife</i> , 2018 , 7,	8.9	12
208	Mapping the Genetic Landscape of Human Cells. <i>Cell</i> , 2018 , 174, 953-967.e22	56.2	136
207	The ER membrane protein complex interacts cotranslationally to enable biogenesis of multipass membrane proteins. <i>ELife</i> , 2018 , 7,	8.9	92
206	The helicase Ded1p controls use of near-cognate translation initiation codons in 5RUTRs. <i>Nature</i> , 2018 , 559, 130-134	50.4	87
205	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	8.3	54
204	Identification of a transporter complex responsible for the cytosolic entry of nitrogen-containing bisphosphonates. <i>ELife</i> , 2018 , 7,	8.9	20
203	Targeting RAS-driven human cancer cells with antibodies to upregulated and essential cell-surface proteins. <i>ELife</i> , 2018 , 7,	8.9	44
202	Translation from unconventional 5Rstart sites drives tumour initiation. <i>Nature</i> , 2017 , 541, 494-499	50.4	185
201	Suppression of B-cell development genes is key to glucocorticoid efficacy in treatment of acute lymphoblastic leukemia. <i>Blood</i> , 2017 , 129, 3000-3008	2.2	33
200	Model-guided optogenetic study of PKA signaling in budding yeast. <i>Molecular Biology of the Cell</i> , 2017 , 28, 221-227	3.5	13
199	CRISPRi-based genome-scale identification of functional long noncoding RNA loci in human cells. <i>Science</i> , 2017 , 355,	33.3	404
198	Inducible and multiplex gene regulation using CRISPR-Cpf1-based transcription factors. <i>Nature Methods</i> , 2017 , 14, 1163-1166	21.6	132
197	Combined CRISPRi/a-Based Chemical Genetic Screens Reveal that Rigosertib Is a Microtubule-Destabilizing Agent. <i>Molecular Cell</i> , 2017 , 68, 210-223.e6	17.6	127
196	CAT-tailing as a fail-safe mechanism for efficient degradation of stalled nascent polypeptides. <i>Science</i> , 2017 , 357, 414-417	33.3	69
195	DMS-MaPseq for genome-wide or targeted RNA structure probing in vivo. <i>Nature Methods</i> , 2017 , 14, 75-82	21.6	192
194	The Human Cell Atlas. <i>ELife</i> , 2017 , 6,	8.9	937

193	Operon mRNAs are organized into ORF-centric structures that predict translation efficiency. <i>ELife</i> , 2017 , 6,	8.9	82
192	Author response: The Human Cell Atlas 2017 ,		10
191	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, 9015-20	11.5	21
190	Versatile protein tagging in cells with split fluorescent protein. <i>Nature Communications</i> , 2016 , 7, 11046	17.4	206
189	Dynamic translation regulation in Caulobacter cell cycle control. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E6859-E6867	11.5	33
188	Ligand-binding domains of nuclear receptors facilitate tight control of split CRISPR activity. <i>Nature Communications</i> , 2016 , 7, 12009	17.4	73
187	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	11.5	141
186	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	11.5	76
185	CRISPR Interference Efficiently Induces Specific and Reversible Gene Silencing in Human iPSCs. <i>Cell Stem Cell</i> , 2016 , 18, 541-53	18	271
184	Nucleosomes impede Cas9 access to DNA in vivo and in vitro. <i>ELife</i> , 2016 , 5,	8.9	243
183	Author response: Compact and highly active next-generation libraries for CRISPR-mediated gene repression and activation 2016 ,		3
182	Compact and highly active next-generation libraries for CRISPR-mediated gene repression and activation. <i>ELife</i> , 2016 , 5,	8.9	343
181	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	11.5	19
180	The SND proteins constitute an alternative targeting route to the endoplasmic reticulum. <i>Nature</i> , 2016 , 540, 134-138	50.4	120
179	Plastid: nucleotide-resolution analysis of next-generation sequencing and genomics data. <i>BMC Genomics</i> , 2016 , 17, 958	4.5	90
178	Perturb-Seq: Dissecting Molecular Circuits with Scalable Single-Cell RNA Profiling of Pooled Genetic Screens. <i>Cell</i> , 2016 , 167, 1853-1866.e17	56.2	675
177	A Multiplexed Single-Cell CRISPR Screening Platform Enables Systematic Dissection of the Unfolded Protein Response. <i>Cell</i> , 2016 , 167, 1867-1882.e21	56.2	518
176	The mTOR Complex Controls HIV Latency. <i>Cell Host and Microbe</i> , 2016 , 20, 785-797	23.4	115

175	A Comprehensive, CRISPR-based Functional Analysis of Essential Genes in Bacteria. <i>Cell</i> , 2016 , 165, 1493-1506	367
174	Single-cell analysis of long non-coding RNAs in the developing human neocortex. <i>Genome Biology</i> , 2016 , 17, 67	18.3 224
173	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	11.5 64
172	Biotechnology. A prudent path forward for genomic engineering and germline gene modification. <i>Science</i> , 2015 , 348, 36-8	33.3 413
171	Ribosome profiling reveals the what, when, where and how of protein synthesis. <i>Nature Reviews Molecular Cell Biology</i> , 2015 , 16, 651-64	48.7 244
170	Targeting the AAA ATPase p97 as an Approach to Treat Cancer through Disruption of Protein Homeostasis. <i>Cancer Cell</i> , 2015 , 28, 653-665	24.3 225
169	Engineering complex synthetic transcriptional programs with CRISPR RNA scaffolds. <i>Cell</i> , 2015 , 160, 339-50	56.2 648
168	LOCAL TRANSLATION. Response to Comment on "Principles of ER cotranslational translocation revealed by proximity-specific ribosome profiling". <i>Science</i> , 2015 , 348, 1217	33.3 12
167	[KIL-d] Protein Element Confers Antiviral Activity via Catastrophic Viral Mutagenesis. <i>Molecular Cell</i> , 2015 , 60, 651-60	17.6 6
166	A Regression-Based Analysis of Ribosome-Profiling Data Reveals a Conserved Complexity to Mammalian Translation. <i>Molecular Cell</i> , 2015 , 60, 816-827	17.6 133
165	Protein synthesis. Rqc2p and 60S ribosomal subunits mediate mRNA-independent elongation of nascent chains. <i>Science</i> , 2015 , 347, 75-8	33.3 180
164	Immunogenetics. Dynamic profiling of the protein life cycle in response to pathogens. <i>Science</i> , 2015 , 347, 1259038	33.3 284
163	Validation of the Hsp70-Bag3 protein-protein interaction as a potential therapeutic target in cancer. <i>Molecular Cancer Therapeutics</i> , 2015 , 14, 642-8	6.1 79
162	Pharmacological dimerization and activation of the exchange factor eIF2B antagonizes the integrated stress response. <i>ELife</i> , 2015 , 4, e07314	8.9 160
161	Regulation of mRNA translation during mitosis. <i>ELife</i> , 2015 , 4,	8.9 92
160	Paradoxical resistance of multiple myeloma to proteasome inhibitors by decreased levels of 19S proteasomal subunits. <i>ELife</i> , 2015 , 4, e08153	8.9 54
159	Differential scales of protein quality control. <i>Cell</i> , 2014 , 157, 52-64	56.2 172
158	Quantifying absolute protein synthesis rates reveals principles underlying allocation of cellular resources. <i>Cell</i> , 2014 , 157, 624-35	56.2 802

157	A pause sequence enriched at translation start sites drives transcription dynamics in vivo. <i>Science</i> , 2014 , 344, 1042-7	33.3	209
156	Extensive and coordinated control of allele-specific expression by both transcription and translation in <i>Candida albicans</i> . <i>Genome Research</i> , 2014 , 24, 963-73	9.7	43
155	Genome-wide probing of RNA structure reveals active unfolding of mRNA structures in vivo. <i>Nature</i> , 2014 , 505, 701-5	50.4	560
154	Principles of ER cotranslational translocation revealed by proximity-specific ribosome profiling. <i>Science</i> , 2014 , 346, 1257-521	33.3	238
153	Targeting and plasticity of mitochondrial proteins revealed by proximity-specific ribosome profiling. <i>Science</i> , 2014 , 346, 748-51	33.3	231
152	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, 15958-63	11.5	107
151	Genome-Scale CRISPR-Mediated Control of Gene Repression and Activation. <i>Cell</i> , 2014 , 159, 647-61	56.2	1556
150	A protein-tagging system for signal amplification in gene expression and fluorescence imaging. <i>Cell</i> , 2014 , 159, 635-46	56.2	874
149	Functional genomics platform for pooled screening and generation of mammalian genetic interaction maps. <i>Nature Protocols</i> , 2014 , 9, 1825-47	18.8	58
148	Misfolded proteins induce aggregation of the lectin Yos9. <i>Journal of Biological Chemistry</i> , 2014 , 289, 25670-7	5.4	4
147	Unraveling the mechanism of cell death induced by chemical fibrils. <i>Nature Chemical Biology</i> , 2014 , 10, 969-76	11.7	40
146	Uniform nomenclature for the mitochondrial contact site and cristae organizing system. <i>Journal of Cell Biology</i> , 2014 , 204, 1083-6	7.3	177
145	Ribosome profiling reveals pervasive translation outside of annotated protein-coding genes. <i>Cell Reports</i> , 2014 , 8, 1365-79	10.6	416
144	A high-coverage shRNA screen identifies TMEM129 as an E3 ligase involved in ER-associated protein degradation. <i>Nature Communications</i> , 2014 , 5, 3832	17.4	91
143	Causal signals between codon bias, mRNA structure, and the efficiency of translation and elongation. <i>Molecular Systems Biology</i> , 2014 , 10, 770	12.2	180
142	The coding and noncoding architecture of the <i>Caulobacter crescentus</i> genome. <i>PLoS Genetics</i> , 2014 , 10, e1004463	6	101
141	Genetic influences on translation in yeast. <i>PLoS Genetics</i> , 2014 , 10, e1004692	6	58
140	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	7.6	195

139	CRISPR-mediated modular RNA-guided regulation of transcription in eukaryotes. <i>Cell</i> , 2013 , 154, 442-51	56.2	2255
138	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	10.2	11
137	CRISPR interference (CRISPRi) for sequence-specific control of gene expression. <i>Nature Protocols</i> , 2013 , 8, 2180-96	18.8	677
136	Msn2 coordinates a stoichiometric gene expression program. <i>Current Biology</i> , 2013 , 23, 2336-45	6.3	32
135	Dynamic imaging of genomic loci in living human cells by an optimized CRISPR/Cas system. <i>Cell</i> , 2013 , 155, 1479-91	56.2	1306
134	A systematic mammalian genetic interaction map reveals pathways underlying ricin susceptibility. <i>Cell</i> , 2013 , 152, 909-22	56.2	264
133	Next-generation NAMPT inhibitors identified by sequential high-throughput phenotypic chemical and functional genomic screens. <i>Chemistry and Biology</i> , 2013 , 20, 1352-63		60
132	Repurposing CRISPR as an RNA-guided platform for sequence-specific control of gene expression. <i>Cell</i> , 2013 , 152, 1173-83	56.2	2988
131	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	11.5	90
130	Genome-wide annotation and quantitation of translation by ribosome profiling. <i>Current Protocols in Molecular Biology</i> , 2013 , Chapter 4, Unit 4.18	2.9	45
129	Ribosome profiling provides evidence that large noncoding RNAs do not encode proteins. <i>Cell</i> , 2013 , 154, 240-51	56.2	537
128	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, 2212-39	18.8	80
127	rRNA:mRNA pairing alters the length and the symmetry of mRNA-protected fragments in ribosome profiling experiments. <i>Bioinformatics</i> , 2013 , 29, 1488-91	7.2	44
126	A developmentally regulated translational control pathway establishes the meiotic chromosome segregation pattern. <i>Genes and Development</i> , 2013 , 27, 2147-63	12.6	53
125	Aneuploid yeast strains exhibit defects in cell growth and passage through START. <i>Molecular Biology of the Cell</i> , 2013 , 24, 1274-89	3.5	69
124	Ribosome profiling reveals pervasive and regulated stop codon readthrough in <i>Drosophila melanogaster</i> . <i>ELife</i> , 2013 , 2, e01179	8.9	244
123	Global cellular response to chemotherapy-induced apoptosis. <i>ELife</i> , 2013 , 2, e01236	8.9	48
122	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	2.2	

121	Decoding human cytomegalovirus. <i>Science</i> , 2012 , 338, 1088-93	33.3	430
120	A ribosome-bound quality control complex triggers degradation of nascent peptides and signals translation stress. <i>Cell</i> , 2012 , 151, 1042-54	56.2	392
119	Proto-genes and de novo gene birth. <i>Nature</i> , 2012 , 487, 370-4	50.4	379
118	The ribosome profiling strategy for monitoring translation in vivo by deep sequencing of ribosome-protected mRNA fragments. <i>Nature Protocols</i> , 2012 , 7, 1534-50	18.8	742
117	High-resolution view of the yeast meiotic program revealed by ribosome profiling. <i>Science</i> , 2012 , 335, 552-7	33.3	378
116	Cellular noise regulons underlie fluctuations in <i>Saccharomyces cerevisiae</i> . <i>Molecular Cell</i> , 2012 , 45, 483-93	37.6	117
115	Functional repurposing revealed by comparing <i>S. pombe</i> and <i>S. cerevisiae</i> genetic interactions. <i>Cell</i> , 2012 , 149, 1339-52	56.2	122
114	Native elongating transcript sequencing (NET-seq). <i>Current Protocols in Molecular Biology</i> , 2012 , Chapter 4, Unit 4.14.1-17	2.9	47
113	The translational landscape of mTOR signalling steers cancer initiation and metastasis. <i>Nature</i> , 2012 , 485, 55-61	50.4	903
112	The anti-Shine-Dalgarno sequence drives translational pausing and codon choice in bacteria. <i>Nature</i> , 2012 , 484, 538-41	50.4	464
111	Road to ruin: targeting proteins for degradation in the endoplasmic reticulum. <i>Science</i> , 2011 , 334, 1086-90	39.3	476
110	Ganglion-specific splicing of TRPV1 underlies infrared sensation in vampire bats. <i>Nature</i> , 2011 , 476, 88-91	30.4	156
109	Selective ribosome profiling reveals the cotranslational chaperone action of trigger factor in vivo. <i>Cell</i> , 2011 , 147, 1295-308	56.2	326
108	Ribosome profiling of mouse embryonic stem cells reveals the complexity and dynamics of mammalian proteomes. <i>Cell</i> , 2011 , 147, 789-802	56.2	1469
107	Radically different amyloid conformations dictate the seeding specificity of a chimeric Sup35 prion. <i>Journal of Molecular Biology</i> , 2011 , 408, 1-8	6.5	10
106	Strain conformation, primary structure and the propagation of the yeast prion [PSI ⁺]. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 493-9	17.6	33
105	Nascent transcript sequencing visualizes transcription at nucleotide resolution. <i>Nature</i> , 2011 , 469, 368-73	30.4	571
104	Amyloid structure: conformational diversity and consequences. <i>Annual Review of Biochemistry</i> , 2011 , 80, 557-85	29.1	205

103	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		33
102	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, 323-40	7.3	335
101	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, 19222-7	11.5	215
100	Orm family proteins mediate sphingolipid homeostasis. <i>Nature</i> , 2010 , 463, 1048-53	50.4	450
99	Molecular basis of infrared detection by snakes. <i>Nature</i> , 2010 , 464, 1006-11	50.4	287
98	Mammalian microRNAs predominantly act to decrease target mRNA levels. <i>Nature</i> , 2010 , 466, 835-40	50.4	3074
97	Differences in prion strain conformations result from non-native interactions in a nucleus. <i>Nature Chemical Biology</i> , 2010 , 6, 225-230	11.7	63
96	The epistemology of cell biology. <i>Molecular Biology of the Cell</i> , 2010 , 21, 3825	3.5	1
95	J domain co-chaperone specificity defines the role of BiP during protein translocation. <i>Journal of Biological Chemistry</i> , 2010 , 285, 22484-94	5.4	36
94	Membranes in balance: mechanisms of sphingolipid homeostasis. <i>Molecular Cell</i> , 2010 , 40, 267-79	17.6	170
93	Automated identification of pathways from quantitative genetic interaction data. <i>Molecular Systems Biology</i> , 2010 , 6, 379	12.2	57
92	A general lack of compensation for gene dosage in yeast. <i>Molecular Systems Biology</i> , 2010 , 6, 368	12.2	99
91	Regulated Ire1-dependent decay of messenger RNAs in mammalian cells. <i>Journal of Cell Biology</i> , 2009 , 186, 323-31	7.3	691
90	Rapid creation and quantitative monitoring of high coverage shRNA libraries. <i>Nature Methods</i> , 2009 , 6, 443-5	21.6	82
89	From information to knowledge: new technologies for defining gene function. <i>Nature Methods</i> , 2009 , 6, 721-23	21.6	13
88	Genome-wide analysis in vivo of translation with nucleotide resolution using ribosome profiling. <i>Science</i> , 2009 , 324, 218-23	33.3	2472
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19	Exploring genetic interaction manifolds constructed from rich phenotypes		2
18	Design and specificity of long ssDNA donors for CRISPR-based knock-in		29
17	Single-cell lineages reveal the rates, routes, and drivers of metastasis in cancer xenografts		4
16	Approaches to maximize sgRNA-barcode coupling in Perturb-seq screens		14
15	MULTI-seq: Scalable sample multiplexing for single-cell RNA sequencing using lipid-tagged indices		12
14	Direct capture of CRISPR guides enables scalable, multiplexed, and multi-omic Perturb-seq		9

13	New factors for protein transport identified by a genome-wide CRISPRi screen in mammalian cells	1
12	Mapping Transcriptomic Vector Fields of Single Cells	17
11	Titration of gene expression with series of systematically compromised CRISPR guide RNAs	2
10	Functional single-cell genomics of human cytomegalovirus infection	5
9	GIGYF2 and 4EHP Inhibit Translation Initiation of Defective Messenger RNAs to Assist Ribosome-Associated Quality Control	4
8	Inference of Single-Cell Phylogenies from Lineage Tracing Data	1
7	Modulated efficacy CRISPRi reveals evolutionary conservation of essential gene expression-fitness relationships in bacteria	5
6	Deep profiling reveals substantial heterogeneity of integration outcomes in CRISPR knock-in experiments	19
5	Inducible, tunable and multiplex human gene regulation using CRISPR-Cpf1-based transcription factors	1
4	OpenCell: proteome-scale endogenous tagging enables the cartography of human cellular organization	4
3	A community-driven roadmap to advance research on translated open reading frames detected by Ribo-seq	4
2	Mapping the Genetic Landscape of DNA Double-strand Break Repair	2
1	Coupled protein quality control during nonsense mediated mRNA decay	3