

Jonathan S Weissman

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264
papers

70,235
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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	Global analysis of protein localization in budding yeast. <i>Nature</i> , 2003 , 425, 686-91	50.4	3330
263	Mammalian microRNAs predominantly act to decrease target mRNA levels. <i>Nature</i> , 2010 , 466, 835-40	50.4	3074
262	Global analysis of protein expression in yeast. <i>Nature</i> , 2003 , 425, 737-41	50.4	3045
261	Repurposing CRISPR as an RNA-guided platform for sequence-specific control of gene expression. <i>Cell</i> , 2013 , 152, 1173-83	56.2	2988
260	Genome-wide analysis in vivo of translation with nucleotide resolution using ribosome profiling. <i>Science</i> , 2009 , 324, 218-23	33.3	2472
259	Global landscape of protein complexes in the yeast <i>Saccharomyces cerevisiae</i> . <i>Nature</i> , 2006 , 440, 637-43	50.4	2327
258	CRISPR-mediated modular RNA-guided regulation of transcription in eukaryotes. <i>Cell</i> , 2013 , 154, 442-51	56.2	2255
257	Functional and genomic analyses reveal an essential coordination between the unfolded protein response and ER-associated degradation. <i>Cell</i> , 2000 , 101, 249-58	56.2	1597
256	Genome-Scale CRISPR-Mediated Control of Gene Repression and Activation. <i>Cell</i> , 2014 , 159, 647-61	56.2	1556
255	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
254	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
253	Single-cell proteomic analysis of <i>S. cerevisiae</i> reveals the architecture of biological noise. <i>Nature</i> , 2006 , 441, 840-6	50.4	1193
252	Molecular chaperones and protein quality control. <i>Cell</i> , 2006 , 125, 443-51	56.2	1174
251	The Human Cell Atlas. <i>ELife</i> , 2017 , 6,	8.9	937
250	An ER-mitochondria tethering complex revealed by a synthetic biology screen. <i>Science</i> , 2009 , 325, 477-81	33.3	935
249	The translational landscape of mTOR signalling steers cancer initiation and metastasis. <i>Nature</i> , 2012 , 485, 55-61	50.4	903
248	Decay of endoplasmic reticulum-localized mRNAs during the unfolded protein response. <i>Science</i> , 2006 , 313, 104-7	33.3	887

247	A protein-tagging system for signal amplification in gene expression and fluorescence imaging. <i>Cell</i> , 2014 , 159, 635-46	56.2	874
246	Oxidative protein folding in eukaryotes: mechanisms and consequences. <i>Journal of Cell Biology</i> , 2004 , 164, 341-6	7.3	810
245	Quantifying absolute protein synthesis rates reveals principles underlying allocation of cellular resources. <i>Cell</i> , 2014 , 157, 624-35	56.2	802
244	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
243	Functional dissection of protein complexes involved in yeast chromosome biology using a genetic interaction map. <i>Nature</i> , 2007 , 446, 806-10	50.4	731
242	Exploration of the function and organization of the yeast early secretory pathway through an epistatic miniarray profile. <i>Cell</i> , 2005 , 123, 507-19	56.2	706
241	Regulated Ire1-dependent decay of messenger RNAs in mammalian cells. <i>Journal of Cell Biology</i> , 2009 , 186, 323-31	7.3	691
240	CRISPR interference (CRISPRi) for sequence-specific control of gene expression. <i>Nature Protocols</i> , 2013 , 8, 2180-96	18.8	677
239	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
238	Conformational variations in an infectious protein determine prion strain differences. <i>Nature</i> , 2004 , 428, 323-8	50.4	665
237	Engineering complex synthetic transcriptional programs with CRISPR RNA scaffolds. <i>Cell</i> , 2015 , 160, 339-50	56.2	648
236	Cotranscriptional set2 methylation of histone H3 lysine 36 recruits a repressive Rpd3 complex. <i>Cell</i> , 2005 , 123, 593-605	56.2	621
235	Toward a comprehensive atlas of the physical interactome of <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 439-50	7.6	610
234	Nascent transcript sequencing visualizes transcription at nucleotide resolution. <i>Nature</i> , 2011 , 469, 368-73	50.4	571
233	Genome-wide probing of RNA structure reveals active unfolding of mRNA structures in vivo. <i>Nature</i> , 2014 , 505, 701-5	50.4	560
232	Ribosome profiling provides evidence that large noncoding RNAs do not encode proteins. <i>Cell</i> , 2013 , 154, 240-51	56.2	537
231	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
230	Comprehensive characterization of genes required for protein folding in the endoplasmic reticulum. <i>Science</i> , 2009 , 323, 1693-7	33.3	517

229	The physical basis of how prion conformations determine strain phenotypes. <i>Nature</i> , 2006 , 442, 585-9	50.4	497
228	Road to ruin: targeting proteins for degradation in the endoplasmic reticulum. <i>Science</i> , 2011 , 334, 1086-90	39.3	476
227	The anti-Shine-Dalgarno sequence drives translational pausing and codon choice in bacteria. <i>Nature</i> , 2012 , 484, 538-41	50.4	464
226	Orm family proteins mediate sphingolipid homeostasis. <i>Nature</i> , 2010 , 463, 1048-53	50.4	450
225	Mechanism of prion propagation: amyloid growth occurs by monomer addition. <i>PLoS Biology</i> , 2004 , 2, e321	9.7	436
224	Decoding human cytomegalovirus. <i>Science</i> , 2012 , 338, 1088-93	33.3	430
223	Ribosome profiling reveals pervasive translation outside of annotated protein-coding genes. <i>Cell Reports</i> , 2014 , 8, 1365-79	10.6	416
222	Biotechnology. A prudent path forward for genomic engineering and germline gene modification. <i>Science</i> , 2015 , 348, 36-8	33.3	413
221	CRISPRi-based genome-scale identification of functional long noncoding RNA loci in human cells. <i>Science</i> , 2017 , 355,	33.3	404
220	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
219	Proto-genes and de novo gene birth. <i>Nature</i> , 2012 , 487, 370-4	50.4	379
218	High-resolution view of the yeast meiotic program revealed by ribosome profiling. <i>Science</i> , 2012 , 335, 552-7	33.3	378
217	Ero1p: a novel and ubiquitous protein with an essential role in oxidative protein folding in the endoplasmic reticulum. <i>Molecular Cell</i> , 1998 , 1, 171-82	17.6	376
216	A comprehensive strategy enabling high-resolution functional analysis of the yeast genome. <i>Nature Methods</i> , 2008 , 5, 711-8	21.6	376
215	Reprogramming human T cell function and specificity with non-viral genome targeting. <i>Nature</i> , 2018 , 559, 405-409	50.4	367
214	A Comprehensive, CRISPR-based Functional Analysis of Essential Genes in Bacteria. <i>Cell</i> , 2016 , 165, 1493-1506	51.0	367
213	Characterization of the active intermediate of a GroEL-GroES-mediated protein folding reaction. <i>Cell</i> , 1996 , 84, 481-90	56.2	363
212	The GET complex mediates insertion of tail-anchored proteins into the ER membrane. <i>Cell</i> , 2008 , 134, 634-45	56.2	351

211	A luminal surveillance complex that selects misfolded glycoproteins for ER-associated degradation. <i>Cell</i> , 2006 , 126, 349-59	56.2	347
210	The FAD- and O(2)-dependent reaction cycle of Ero1-mediated oxidative protein folding in the endoplasmic reticulum. <i>Molecular Cell</i> , 2002 , 10, 983-94	17.6	344
209	Biochemical basis of oxidative protein folding in the endoplasmic reticulum. <i>Science</i> , 2000 , 290, 1571-4	33.3	344
208	Compact and highly active next-generation libraries for CRISPR-mediated gene repression and activation. <i>ELife</i> , 2016 , 5,	8.9	343
207	A critical role for amino-terminal glutamine/asparagine repeats in the formation and propagation of a yeast prion. <i>Cell</i> , 1998 , 93, 1241-52	56.2	338
206	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
205	Selective ribosome profiling reveals the cotranslational chaperone action of trigger factor in vivo. <i>Cell</i> , 2011 , 147, 1295-308	56.2	326
204	The structural basis of yeast prion strain variants. <i>Nature</i> , 2007 , 449, 233-7	50.4	295
203	Emerging principles of conformation-based prion inheritance. <i>Annual Review of Biochemistry</i> , 2004 , 73, 617-56	29.1	294
202	Molecular basis of infrared detection by snakes. <i>Nature</i> , 2010 , 464, 1006-11	50.4	287
201	Immunogenetics. Dynamic profiling of the protein life cycle in response to pathogens. <i>Science</i> , 2015 , 347, 1259038	33.3	284
200	Conservation and rewiring of functional modules revealed by an epistasis map in fission yeast. <i>Science</i> , 2008 , 322, 405-10	33.3	281
199	CRISPR Interference Efficiently Induces Specific and Reversible Gene Silencing in Human iPSCs. <i>Cell Stem Cell</i> , 2016 , 18, 541-53	18	271
198	Multiple Gln/Asn-rich prion domains confer susceptibility to induction of the yeast [PSI(+)] prion. <i>Cell</i> , 2001 , 106, 183-94	56.2	270
197	A systematic mammalian genetic interaction map reveals pathways underlying ricin susceptibility. <i>Cell</i> , 2013 , 152, 909-22	56.2	264
196	The action of molecular chaperones in the early secretory pathway. <i>Annual Review of Genetics</i> , 2001 , 35, 149-91	14.5	256
195	A strategy for extracting and analyzing large-scale quantitative epistatic interaction data. <i>Genome Biology</i> , 2006 , 7, R63	18.3	245
194	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

193	Molecular basis of a yeast prion species barrier. <i>Cell</i> , 2000 , 100, 277-88	56.2	244
192	Ribosome profiling reveals pervasive and regulated stop codon readthrough in <i>Drosophila melanogaster</i> . <i>ELife</i> , 2013 , 2, e01179	8.9	244
191	Nucleosomes impede Cas9 access to DNA in vivo and in vitro. <i>ELife</i> , 2016 , 5,	8.9	243
190	Principles of ER cotranslational translocation revealed by proximity-specific ribosome profiling. <i>Science</i> , 2014 , 346, 1257521	33.3	238
189	Deadly conformations--protein misfolding in prion disease. <i>Cell</i> , 1997 , 89, 499-510	56.2	237
188	Targeting and plasticity of mitochondrial proteins revealed by proximity-specific ribosome profiling. <i>Science</i> , 2014 , 346, 748-51	33.3	231
187	Promoter of lncRNA Gene PVT1 Is a Tumor-Suppressor DNA Boundary Element. <i>Cell</i> , 2018 , 173, 1398-1413	37.2	226
186	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
185	Single-cell analysis of long non-coding RNAs in the developing human neocortex. <i>Genome Biology</i> , 2016 , 17, 67	18.3	224
184	Small-molecule aggregates inhibit amyloid polymerization. <i>Nature Chemical Biology</i> , 2008 , 4, 197-9	11.7	223
183	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
182	Functional organization of the <i>S. cerevisiae</i> phosphorylation network. <i>Cell</i> , 2009 , 136, 952-63	56.2	211
181	A pause sequence enriched at translation start sites drives transcription dynamics in vivo. <i>Science</i> , 2014 , 344, 1042-7	33.3	209
180	Versatile protein tagging in cells with split fluorescent protein. <i>Nature Communications</i> , 2016 , 7, 11046	17.4	206
179	Amyloid structure: conformational diversity and consequences. <i>Annual Review of Biochemistry</i> , 2011 , 80, 557-85	29.1	205
178	A genetic interaction map of RNA-processing factors reveals links between Sem1/Dss1-containing complexes and mRNA export and splicing. <i>Molecular Cell</i> , 2008 , 32, 735-46	17.6	205
177	A molecular caliper mechanism for determining very long-chain fatty acid length. <i>Cell</i> , 2007 , 130, 663-77	56.2	196
176	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

175	Efficient catalysis of disulphide bond rearrangements by protein disulphide isomerase. <i>Nature</i> , 1993 , 365, 185-8	50.4	195
174	Defining the glycan destruction signal for endoplasmic reticulum-associated degradation. <i>Molecular Cell</i> , 2008 , 32, 870-7	17.6	193
173	DMS-MaPseq for genome-wide or targeted RNA structure probing in vivo. <i>Nature Methods</i> , 2017 , 14, 75-82	21.6	192
172	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, 741-51	17.6	186
171	Translation from unconventional 5Rstart sites drives tumour initiation. <i>Nature</i> , 2017 , 541, 494-499	50.4	185
170	High-throughput, quantitative analyses of genetic interactions in E. coli. <i>Nature Methods</i> , 2008 , 5, 781-7	21.6	181
169	Protein synthesis. Rqc2p and 60S ribosomal subunits mediate mRNA-independent elongation of nascent chains. <i>Science</i> , 2015 , 347, 75-8	33.3	180
168	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
167	Uniform nomenclature for the mitochondrial contact site and cristae organizing system. <i>Journal of Cell Biology</i> , 2014 , 204, 1083-6	7.3	177
166	Differential scales of protein quality control. <i>Cell</i> , 2014 , 157, 52-64	56.2	172
165	Membranes in balance: mechanisms of sphingolipid homeostasis. <i>Molecular Cell</i> , 2010 , 40, 267-79	17.6	170
164	MULTI-seq: sample multiplexing for single-cell RNA sequencing using lipid-tagged indices. <i>Nature Methods</i> , 2019 , 16, 619-626	21.6	169
163	Pervasive functional translation of noncanonical human open reading frames. <i>Science</i> , 2020 , 367, 1140-1146	33.3	168
162	Mechanism of cross-species prion transmission: an infectious conformation compatible with two highly divergent yeast prion proteins. <i>Cell</i> , 2005 , 121, 49-62	56.2	164
161	Pharmacological dimerization and activation of the exchange factor eIF2B antagonizes the integrated stress response. <i>ELife</i> , 2015 , 4, e07314	8.9	160
160	Dissection and design of yeast prions. <i>PLoS Biology</i> , 2004 , 2, E86	9.7	158
159	Ganglion-specific splicing of TRPV1 underlies infrared sensation in vampire bats. <i>Nature</i> , 2011 , 476, 88-91	50.4	156
158	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

157	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, 584-91	17.6	141
156	Molecular recording of mammalian embryogenesis. <i>Nature</i> , 2019 , 570, 77-82	50.4	140
155	Evidence for the prion hypothesis: induction of the yeast [PSI ⁺] factor by in vitro- converted Sup35 protein. <i>Science</i> , 2000 , 289, 595-9	33.3	137
154	Mapping the Genetic Landscape of Human Cells. <i>Cell</i> , 2018 , 174, 953-967.e22	56.2	136
153	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
152	Conformational diversity in a yeast prion dictates its seeding specificity. <i>Nature</i> , 2001 , 410, 223-7	50.4	133
151	Inducible and multiplex gene regulation using CRISPR-Cpf1-based transcription factors. <i>Nature Methods</i> , 2017 , 14, 1163-1166	21.6	132
150	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
149	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
148	Directed evolution of substrate-optimized GroEL/S chaperonins. <i>Cell</i> , 2002 , 111, 1027-39	56.2	121
147	High-throughput genetic interaction mapping in the fission yeast <i>Schizosaccharomyces pombe</i> . <i>Nature Methods</i> , 2007 , 4, 861-6	21.6	120
146	The SND proteins constitute an alternative targeting route to the endoplasmic reticulum. <i>Nature</i> , 2016 , 540, 134-138	50.4	120
145	Cellular noise regulons underlie fluctuations in <i>Saccharomyces cerevisiae</i> . <i>Molecular Cell</i> , 2012 , 45, 483-93.6	17.6	117
144	Therapy-Induced Evolution of Human Lung Cancer Revealed by Single-Cell RNA Sequencing. <i>Cell</i> , 2020 , 182, 1232-1251.e22	56.2	116
143	Backup without redundancy: genetic interactions reveal the cost of duplicate gene loss. <i>Molecular Systems Biology</i> , 2007 , 3, 86	12.2	115
142	The mTOR Complex Controls HIV Latency. <i>Cell Host and Microbe</i> , 2016 , 20, 785-797	23.4	115
141	Defining the physiological role of SRP in protein-targeting efficiency and specificity. <i>Science</i> , 2018 , 359, 689-692	33.3	108
140	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

139	The coding and noncoding architecture of the <i>Caulobacter crescentus</i> genome. <i>PLoS Genetics</i> , 2014 , 10, e1004463	6	101
138	A general lack of compensation for gene dosage in yeast. <i>Molecular Systems Biology</i> , 2010 , 6, 368	12.2	99
137	Mec1/Tel1 phosphorylation of the INO80 chromatin remodeling complex influences DNA damage checkpoint responses. <i>Cell</i> , 2007 , 130, 499-511	56.2	98
136	Ribosome Profiling: Global Views of Translation. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019 , 11,	10.2	94
135	Regulation of mRNA translation during mitosis. <i>ELife</i> , 2015 , 4,	8.9	92
134	The ER membrane protein complex interacts cotranslationally to enable biogenesis of multipass membrane proteins. <i>ELife</i> , 2018 , 7,	8.9	92
133	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
132	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
131	Plastid: nucleotide-resolution analysis of next-generation sequencing and genomics data. <i>BMC Genomics</i> , 2016 , 17, 958	4.5	90
130	Generation of prion transmission barriers by mutational control of amyloid conformations. <i>Nature</i> , 2003 , 424, 948-51	50.4	89
129	The helicase Ded1p controls use of near-cognate translation initiation codons in 5RUTRs. <i>Nature</i> , 2018 , 559, 130-134	50.4	87
128	Combinatorial single-cell CRISPR screens by direct guide RNA capture and targeted sequencing. <i>Nature Biotechnology</i> , 2020 , 38, 954-961	44.5	85
127	Probing the Global Cellular Responses to Lipotoxicity Caused by Saturated Fatty Acids. <i>Molecular Cell</i> , 2019 , 74, 32-44.e8	17.6	84
126	Release of both native and non-native proteins from a cis-only GroEL ternary complex. <i>Nature</i> , 1996 , 383, 96-9	50.4	84
125	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
124	Rapid creation and quantitative monitoring of high coverage shRNA libraries. <i>Nature Methods</i> , 2009 , 6, 443-5	21.6	82
123	Operon mRNAs are organized into ORF-centric structures that predict translation efficiency. <i>ELife</i> , 2017 , 6,	8.9	82
122	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

121	Genome-wide programmable transcriptional memory by CRISPR-based epigenome editing. <i>Cell</i> , 2021 , 184, 2503-2519.e17	56.2	80
120	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
119	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
118	A kinetic explanation for the rearrangement pathway of BPTI folding. <i>Nature Structural and Molecular Biology</i> , 1995 , 2, 1123-30	17.6	75
117	Ligand-binding domains of nuclear receptors facilitate tight control of split CRISPR activity. <i>Nature Communications</i> , 2016 , 7, 12009	17.4	73
116	CAT-tailing as a fail-safe mechanism for efficient degradation of stalled nascent polypeptides. <i>Science</i> , 2017 , 357, 414-417	33.3	69
115	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
114	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, 876-84	5.4	65
113	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
112	Exploring genetic interaction manifolds constructed from rich single-cell phenotypes. <i>Science</i> , 2019 , 365, 786-793	33.3	64
111	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, 5836-41	11.5	64
110	Construction, verification and experimental use of two epitope-tagged collections of budding yeast strains. <i>Comparative and Functional Genomics</i> , 2005 , 6, 2-16		64
109	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
108	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
107	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
106	Functional genomics platform for pooled screening and generation of mammalian genetic interaction maps. <i>Nature Protocols</i> , 2014 , 9, 1825-47	18.8	58
105	Genetic influences on translation in yeast. <i>PLoS Genetics</i> , 2014 , 10, e1004692	6	58
104	Automated identification of pathways from quantitative genetic interaction data. <i>Molecular Systems Biology</i> , 2010 , 6, 379	12.2	57

103	Origins and kinetic consequences of diversity in Sup35 yeast prion fibers. <i>Nature Structural Biology</i> , 2002 , 9, 389-96		56
102	Paradoxical resistance of multiple myeloma to proteasome inhibitors by decreased levels of 19S proteasomal subunits. <i>ELife</i> , 2015 , 4, e08153	8.9	54
101	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
100	A developmentally regulated translational control pathway establishes the meiotic chromosome segregation pattern. <i>Genes and Development</i> , 2013 , 27, 2147-63	12.6	53
99	Single-cell lineages reveal the rates, routes, and drivers of metastasis in cancer xenografts. <i>Science</i> , 2021 , 371,	33.3	51
98	Titrating gene expression using libraries of systematically attenuated CRISPR guide RNAs. <i>Nature Biotechnology</i> , 2020 , 38, 355-364	44.5	50
97	The utility of prions. <i>Developmental Cell</i> , 2002 , 2, 143-51	10.2	50
96	Global cellular response to chemotherapy-induced apoptosis. <i>ELife</i> , 2013 , 2, e01236	8.9	48
95	Enhanced prime editing systems by manipulating cellular determinants of editing outcomes. <i>Cell</i> , 2021 , 184, 5635-5652.e29	56.2	48
94	Native elongating transcript sequencing (NET-seq). <i>Current Protocols in Molecular Biology</i> , 2012 , Chapter 4, Unit 4.14.1-17	2.9	47
93	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
92	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
91	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, 18079-84	11.5	44
90	Targeting RAS-driven human cancer cells with antibodies to upregulated and essential cell-surface proteins. <i>ELife</i> , 2018 , 7,	8.9	44
89	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
88	CRISPR Approaches to Small Molecule Target Identification. <i>ACS Chemical Biology</i> , 2018 , 13, 366-375	4.9	41
87	Unraveling the mechanism of cell death induced by chemical fibrils. <i>Nature Chemical Biology</i> , 2014 , 10, 969-76	11.7	40
86	An efficient protein transformation protocol for introducing prions into yeast. <i>Methods in Enzymology</i> , 2006 , 412, 185-200	1.7	40

85	CRISPRi-based radiation modifier screen identifies long non-coding RNA therapeutic targets in glioma. <i>Genome Biology</i> , 2020 , 21, 83	18.3	39
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22	OpenCell: proteome-scale endogenous tagging enables the cartography of human cellular organization		4
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