Nicholas T Ingolia

List of Publications by Year
in descending order

65 papers	19,492 citations	70961 41 h-index	114278 63 g-index
86 all docs	86 docs citations	86 times ranked	23121 citing authors

#	Article	IF	Citations
1	Double stranded DNA breaks and genome editing trigger loss of ribosomal protein RPS27A. FEBS Journal, 2022, 289, 3101-3114.	2.2	13
2	Plasmid and Sequencing Library Preparation for CRISPRi Barcoded Expression Reporter Sequencing (CiBER-seq) in Saccharomyces cerevisiae. Bio-protocol, 2022, 12, e4376.	0.2	1
3	Analyzing the Composition and Organization of Ribonucleoprotein Complexes by APEX-Seq. Methods in Molecular Biology, 2022, 2428, 277-289.	0.4	4
4	Ribosome stalling during selenoprotein translation exposes a ferroptosis vulnerability. Nature Chemical Biology, 2022, 18, 751-761.	3.9	47
5	Standardized annotation of translated open reading frames. Nature Biotechnology, 2022, 40, 994-999.	9.4	86
6	Dual targeting of DDX3 and eIF4A by the translation inhibitor rocaglamide A. Cell Chemical Biology, 2021, 28, 475-486.e8.	2.5	37
7	A genome-scale CRISPR interference guide library enables comprehensive phenotypic profiling in yeast. BMC Genomics, 2021, 22, 205.	1.2	22
8	Dynamic post-transcriptional regulation by Mrn1 links cell wall homeostasis to mitochondrial structure and function. PLoS Genetics, 2021, 17, e1009521.	1.5	7
9	Phosphorylation of mRNA-Binding Proteins Puf1 and Puf2 by TORC2-Activated Protein Kinase Ypk1 Alleviates Their Repressive Effects. Membranes, 2021, 11, 500.	1.4	3
10	eIF4A inhibitors PatA and RocA stack the deck against translation. Structure, 2021, 29, 638-639.	1.6	1
11	The N-terminal domain of SARS-CoV-2Ânsp1 plays key roles in suppression of cellular gene expression and preservation of viral gene expression. Cell Reports, 2021, 37, 109841.	2.9	78
12	Low-bias ncRNA libraries using ordered two-template relay: Serial template jumping by a modified retroelement reverse transcriptase. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	27
13	Dysregulated mRNA Translation in the G2019S LRRK2 and LRRK2 Knock-Out Mouse Brains. ENeuro, 2021, 8, ENEURO.0310-21.2021.	0.9	6
14	Robust T cell activation requires an eIF3-driven burst in T cell receptor translation. ELife, 2021, 10, .	2.8	14
15	A methodology for discovering novel brain-relevant peptides: Combination of ribosome profiling and peptidomics. Neuroscience Research, 2020, 151, 31-37.	1.0	10
16	Defects in mRNA Translation in LRRK2-Mutant hiPSC-Derived Dopaminergic Neurons Lead to Dysregulated Calcium Homeostasis. Cell Stem Cell, 2020, 27, 633-645.e7.	5.2	38
17	Ribosomal protein S7 ubiquitination during ER stress in yeast is associated with selective mRNA translation and stress outcome. Scientific Reports, 2020, 10, 19669.	1.6	21
18	CiBER-seq dissects genetic networks by quantitative CRISPRi profiling of expression phenotypes. Science, 2020, 370, .	6.0	19

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19	Ribosome Profiling: Global Views of Translation. Cold Spring Harbor Perspectives in Biology, 2019, 11, a032698.	2.3	205
20	Proximity RNA Labeling by APEX-Seq Reveals the Organization of Translation Initiation Complexes and Repressive RNA Granules. Molecular Cell, 2019, 75, 875-887.e5.	4.5	153
21	MYC-Driven Small-Cell Lung Cancer is Metabolically Distinct and Vulnerable to Arginine Depletion. Clinical Cancer Research, 2019, 25, 5107-5121.	3.2	117
22	An Accessible Continuous-Culture Turbidostat for Pooled Analysis of Complex Libraries. ACS Synthetic Biology, 2019, 8, 844-856.	1.9	29
23	The Translation Inhibitor Rocaglamide Targets a Bimolecular Cavity between eIF4A and Polypurine RNA. Molecular Cell, 2019, 73, 738-748.e9.	4.5	128
24	Ribosomal protein RPL26 is the principal target of UFMylation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 1299-1308.	3.3	126
25	Repression of ferritin light chain translation by human eIF3. ELife, 2019, 8, .	2.8	28
26	Slowed decay of mRNAs enhances platelet specific translation. Blood, 2017, 129, e38-e48.	0.6	68
27	Transcriptome-wide measurement of translation by ribosome profiling. Methods, 2017, 126, 112-129.	1.9	361
28	The Growing Toolbox for Protein Synthesis Studies. Trends in Biochemical Sciences, 2017, 42, 612-624.	3.7	104
29	Ubiquitination of stalled ribosome triggers ribosome-associated quality control. Nature Communications, 2017, 8, 159.	5.8	249
30	Tracking the Missing Footprints of Idle Ribosomes. Cell Systems, 2017, 4, 583-584.	2.9	2
31	Post-Translational Dosage Compensation Buffers Genetic Perturbations to Stoichiometry of Protein Complexes. PLoS Genetics, 2017, 13, e1006554.	1.5	67
32	Global analysis of gene expression reveals mRNA superinduction is required for the inducible immune response to a bacterial pathogen. ELife, 2017, 6, .	2.8	41
33	eIF4B stimulates translation of long mRNAs with structured 5â€² UTRs and low closed-loop potential but weak dependence on eIF4G. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 10464-10472.	3.3	86
34	Starting too soon: upstream reading frames repress downstream translation. EMBO Journal, 2016, 35, 699-700.	3.5	9
35	Dynamic Regulation of a Ribosome Rescue Pathway in Erythroid Cells and Platelets. Cell Reports, 2016, 17, 1-10.	2.9	117
36	Seeing translation. Science, 2016, 352, 1391-1392.	6.0	19

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37	Rocaglates convert DEAD-box protein eIF4A into a sequence-selective translational repressor. Nature, 2016, 534, 558-561.	13.7	235
38	Ribosome Footprint Profiling of Translation throughout the Genome. Cell, 2016, 165, 22-33.	13.5	348
39	Differences in codon bias and GC content contribute to the balanced expression of TLR7 and TLR9. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1362-71.	3.3	102
40	The small molecule ISRIB reverses the effects of eIF2α phosphorylation on translation and stress granule assembly. ELife, 2015, 4, .	2.8	464
41	A Regression-Based Analysis of Ribosome-Profiling Data Reveals a Conserved Complexity to Mammalian Translation. Molecular Cell, 2015, 60, 816-827.	4.5	200
42	Neuronal UCP1 expression suggests a mechanism for local thermogenesis during hibernation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 1607-1612.	3.3	38
43	Genome-wide analysis of translational efficiency reveals distinct but overlapping functions of yeast DEAD-box RNA helicases Ded1 and eIF4A. Genome Research, 2015, 25, 1196-1205.	2.4	143
44	Integrated Transcriptome and Proteome Analyses Reveal Organ-Specific Proteome Deterioration in Old Rats. Cell Systems, 2015, 1, 224-237.	2.9	176
45	Cell-fate determination by ubiquitin-dependent regulation of translation. Nature, 2015, 525, 523-527.	13.7	145
46	Ribosome Profiling as a Tool to Decipher Viral Complexity. Annual Review of Virology, 2015, 2, 335-349.	3.0	26
47	Ribosome Profiling Reveals Pervasive Translation Outside of Annotated Protein-Coding Genes. Cell Reports, 2014, 8, 1365-1379.	2.9	591
48	Extensive stage-regulation of translation revealed by ribosome profiling of Trypanosoma brucei. BMC Genomics, 2014, 15, 911.	1.2	121
49	Causal signals between codon bias, <scp>mRNA</scp> structure, and the efficiency of translation and elongation. Molecular Systems Biology, 2014, 10, 770.	3.2	231
50	A Bicistronic MAVS Transcript Highlights a Class of Truncated Variants in Antiviral Immunity. Cell, 2014, 156, 800-811.	13.5	125
51	Ribosome profiling: new views of translation, from single codons to genome scale. Nature Reviews Genetics, 2014, 15, 205-213.	7.7	543
52	PTEN Is a Potent Suppressor of Small Cell Lung Cancer. Molecular Cancer Research, 2014, 12, 654-659.	1.5	100
53	Identification of Long-Lived Proteins Reveals Exceptional Stability of Essential Cellular Structures. Cell, 2013, 154, 971-982.	13.5	469
54	Genome€Wide Annotation and Quantitation of Translation by Ribosome Profiling. Current Protocols in Molecular Biology, 2013, 103, Unit 4.18.	2.9	55

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55	Ribosome Profiling Provides Evidence that Large Noncoding RNAs Do Not Encode Proteins. Cell, 2013, 154, 240-251.	13.5	678
56	Aneuploid yeast strains exhibit defects in cell growth and passage through START. Molecular Biology of the Cell, 2013, 24, 1274-1289.	0.9	79
57	Observation of dually decoded regions of the human genome using ribosome profiling data. Genome Research, 2012, 22, 2219-2229.	2.4	169
58	Decoding Human Cytomegalovirus. Science, 2012, 338, 1088-1093.	6.0	546
59	The ribosome profiling strategy for monitoring translation in vivo by deep sequencing of ribosome-protected mRNA fragments. Nature Protocols, 2012, 7, 1534-1550.	5.5	1,045
60	High-Resolution View of the Yeast Meiotic Program Revealed by Ribosome Profiling. Science, 2012, 335, 552-557.	6.0	496
61	The translational landscape of mTOR signalling steers cancer initiation and metastasis. Nature, 2012, 485, 55-61.	13.7	1,114
62	Ribosome Profiling of Mouse Embryonic Stem Cells Reveals the Complexity and Dynamics of Mammalian Proteomes. Cell, 2011, 147, 789-802.	13.5	1,904
63	Mammalian microRNAs predominantly act to decrease target mRNA levels. Nature, 2010, 466, 835-840.	13.7	3,513
64	Genome-Wide Translational Profiling by Ribosome Footprinting. Methods in Enzymology, 2010, 470, 119-142.	0.4	159
65	Genome-Wide Analysis in Vivo of Translation with Nucleotide Resolution Using Ribosome Profiling. Science, 2009, 324, 218-223.	6.0	3,283