

Nicholas T Ingolia

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4021376/publications.pdf>

Version: 2024-02-01

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	Mammalian microRNAs predominantly act to decrease target mRNA levels. <i>Nature</i> , 2010, 466, 835-840.	13.7	3,513
2	Genome-Wide Analysis in Vivo of Translation with Nucleotide Resolution Using Ribosome Profiling. <i>Science</i> , 2009, 324, 218-223.	6.0	3,283
3	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
4	The translational landscape of mTOR signalling steers cancer initiation and metastasis. <i>Nature</i> , 2012, 485, 55-61.	13.7	1,114
5	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
6	Ribosome Profiling Provides Evidence that Large Noncoding RNAs Do Not Encode Proteins. <i>Cell</i> , 2013, 154, 240-251.	13.5	678
7	Ribosome Profiling Reveals Pervasive Translation Outside of Annotated Protein-Coding Genes. <i>Cell Reports</i> , 2014, 8, 1365-1379.	2.9	591
8	Decoding Human Cytomegalovirus. <i>Science</i> , 2012, 338, 1088-1093.	6.0	546
9	Ribosome profiling: new views of translation, from single codons to genome scale. <i>Nature Reviews Genetics</i> , 2014, 15, 205-213.	7.7	543
10	High-Resolution View of the Yeast Meiotic Program Revealed by Ribosome Profiling. <i>Science</i> , 2012, 335, 552-557.	6.0	496
11	Identification of Long-Lived Proteins Reveals Exceptional Stability of Essential Cellular Structures. <i>Cell</i> , 2013, 154, 971-982.	13.5	469
12	The small molecule ISRIB reverses the effects of eIF2 γ phosphorylation on translation and stress granule assembly. <i>ELife</i> , 2015, 4, .	2.8	464
13	Transcriptome-wide measurement of translation by ribosome profiling. <i>Methods</i> , 2017, 126, 112-129.	1.9	361
14	Ribosome Footprint Profiling of Translation throughout the Genome. <i>Cell</i> , 2016, 165, 22-33.	13.5	348
15	Ubiquitination of stalled ribosome triggers ribosome-associated quality control. <i>Nature Communications</i> , 2017, 8, 159.	5.8	249
16	Rocaglates convert DEAD-box protein eIF4A into a sequence-selective translational repressor. <i>Nature</i> , 2016, 534, 558-561.	13.7	235
17	Causal signals between codon bias, $\langle scp \rangle$ mRNA $\langle scp \rangle$ structure, and the efficiency of translation and elongation. <i>Molecular Systems Biology</i> , 2014, 10, 770.	3.2	231
18	Ribosome Profiling: Global Views of Translation. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019, 11, a032698.	2.3	205

#	ARTICLE	IF	CITATIONS
19	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
20	Integrated Transcriptome and Proteome Analyses Reveal Organ-Specific Proteome Deterioration in Old Rats. <i>Cell Systems</i> , 2015, 1, 224-237.	2.9	176
21	Observation of dually decoded regions of the human genome using ribosome profiling data. <i>Genome Research</i> , 2012, 22, 2219-2229.	2.4	169
22	Genome-Wide Translational Profiling by Ribosome Footprinting. <i>Methods in Enzymology</i> , 2010, 470, 119-142.	0.4	159
23	Proximity RNA Labeling by APEX-Seq Reveals the Organization of Translation Initiation Complexes and Repressive RNA Granules. <i>Molecular Cell</i> , 2019, 75, 875-887.e5.	4.5	153
24	Cell-fate determination by ubiquitin-dependent regulation of translation. <i>Nature</i> , 2015, 525, 523-527.	13.7	145
25	Genome-wide analysis of translational efficiency reveals distinct but overlapping functions of yeast DEAD-box RNA helicases Ded1 and eIF4A. <i>Genome Research</i> , 2015, 25, 1196-1205.	2.4	143
26	The Translation Inhibitor Rocaglamide Targets a Bimolecular Cavity between eIF4A and Polypurine RNA. <i>Molecular Cell</i> , 2019, 73, 738-748.e9.	4.5	128
27	Ribosomal protein RPL26 is the principal target of UFMylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 1299-1308.	3.3	126
28	A Bicistronic MAVS Transcript Highlights a Class of Truncated Variants in Antiviral Immunity. <i>Cell</i> , 2014, 156, 800-811.	13.5	125
29	Extensive stage-regulation of translation revealed by ribosome profiling of <i>Trypanosoma brucei</i> . <i>BMC Genomics</i> , 2014, 15, 911.	1.2	121
30	Dynamic Regulation of a Ribosome Rescue Pathway in Erythroid Cells and Platelets. <i>Cell Reports</i> , 2016, 17, 1-10.	2.9	117
31	MYC-Driven Small-Cell Lung Cancer is Metabolically Distinct and Vulnerable to Arginine Depletion. <i>Clinical Cancer Research</i> , 2019, 25, 5107-5121.	3.2	117
32	The Growing Toolbox for Protein Synthesis Studies. <i>Trends in Biochemical Sciences</i> , 2017, 42, 612-624.	3.7	104
33	Differences in codon bias and GC content contribute to the balanced expression of TLR7 and TLR9. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1362-71.	3.3	102
34	PTEN Is a Potent Suppressor of Small Cell Lung Cancer. <i>Molecular Cancer Research</i> , 2014, 12, 654-659.	1.5	100
35	eIF4B stimulates translation of long mRNAs with structured 5' UTRs and low closed-loop potential but weak dependence on eIF4G. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10464-10472.	3.3	86
36	Standardized annotation of translated open reading frames. <i>Nature Biotechnology</i> , 2022, 40, 994-999.	9.4	86

#	ARTICLE	IF	CITATIONS
37	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
38	The N-terminal domain of SARS-CoV-2 Nsp1 plays key roles in suppression of cellular gene expression and preservation of viral gene expression. <i>Cell Reports</i> , 2021, 37, 109841.	2.9	78
39	Slowed decay of mRNAs enhances platelet specific translation. <i>Blood</i> , 2017, 129, e38-e48.	0.6	68
40	Post-Translational Dosage Compensation Buffers Genetic Perturbations to Stoichiometry of Protein Complexes. <i>PLoS Genetics</i> , 2017, 13, e1006554.	1.5	67
41	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
42	Ribosome stalling during selenoprotein translation exposes a ferroptosis vulnerability. <i>Nature Chemical Biology</i> , 2022, 18, 751-761.	3.9	47
43	Global analysis of gene expression reveals mRNA superinduction is required for the inducible immune response to a bacterial pathogen. <i>ELife</i> , 2017, 6, .	2.8	41
44	Neuronal UCP1 expression suggests a mechanism for local thermogenesis during hibernation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1607-1612.	3.3	38
45	Defects in mRNA Translation in LRRK2-Mutant hiPSC-Derived Dopaminergic Neurons Lead to Dysregulated Calcium Homeostasis. <i>Cell Stem Cell</i> , 2020, 27, 633-645.e7.	5.2	38
46	Dual targeting of DDX3 and eIF4A by the translation inhibitor rocaglamide A. <i>Cell Chemical Biology</i> , 2021, 28, 475-486.e8.	2.5	37
47	An Accessible Continuous-Culture Turbidostat for Pooled Analysis of Complex Libraries. <i>ACS Synthetic Biology</i> , 2019, 8, 844-856.	1.9	29
48	Repression of ferritin light chain translation by human eIF3. <i>ELife</i> , 2019, 8, .	2.8	28
49	Low-bias ncRNA libraries using ordered two-template relay: Serial template jumping by a modified retroelement reverse transcriptase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	27
50	Ribosome Profiling as a Tool to Decipher Viral Complexity. <i>Annual Review of Virology</i> , 2015, 2, 335-349.	3.0	26
51	A genome-scale CRISPR interference guide library enables comprehensive phenotypic profiling in yeast. <i>BMC Genomics</i> , 2021, 22, 205.	1.2	22
52	Ribosomal protein S7 ubiquitination during ER stress in yeast is associated with selective mRNA translation and stress outcome. <i>Scientific Reports</i> , 2020, 10, 19669.	1.6	21
53	Seeing translation. <i>Science</i> , 2016, 352, 1391-1392.	6.0	19
54	CiBER-seq dissects genetic networks by quantitative CRISPRi profiling of expression phenotypes. <i>Science</i> , 2020, 370, .	6.0	19

#	ARTICLE	IF	CITATIONS
55	Robust T cell activation requires an eIF3-driven burst in T cell receptor translation. <i>ELife</i> , 2021, 10, .	2.8	14
56	Double stranded DNA breaks and genome editing trigger loss of ribosomal protein RPS27A. <i>FEBS Journal</i> , 2022, 289, 3101-3114.	2.2	13
57	A methodology for discovering novel brain-relevant peptides: Combination of ribosome profiling and peptidomics. <i>Neuroscience Research</i> , 2020, 151, 31-37.	1.0	10
58	Starting too soon: upstream reading frames repress downstream translation. <i>EMBO Journal</i> , 2016, 35, 699-700.	3.5	9
59	Dynamic post-transcriptional regulation by Mrn1 links cell wall homeostasis to mitochondrial structure and function. <i>PLoS Genetics</i> , 2021, 17, e1009521.	1.5	7
60	Dysregulated mRNA Translation in the G2019S LRRK2 and LRRK2 Knock-Out Mouse Brains. <i>ENeuro</i> , 2021, 8, ENEURO.0310-21.2021.	0.9	6
61	Analyzing the Composition and Organization of Ribonucleoprotein Complexes by APEX-Seq. <i>Methods in Molecular Biology</i> , 2022, 2428, 277-289.	0.4	4
62	Phosphorylation of mRNA-Binding Proteins Puf1 and Puf2 by TORC2-Activated Protein Kinase Ypk1 Alleviates Their Repressive Effects. <i>Membranes</i> , 2021, 11, 500.	1.4	3
63	Tracking the Missing Footprints of Idle Ribosomes. <i>Cell Systems</i> , 2017, 4, 583-584.	2.9	2
64	eIF4A inhibitors PatA and RocA stack the deck against translation. <i>Structure</i> , 2021, 29, 638-639.	1.6	1
65	Plasmid and Sequencing Library Preparation for CRISPRi Barcoded Expression Reporter Sequencing (CiBER-seq) in <i>Saccharomyces cerevisiae</i> . <i>Bio-protocol</i> , 2022, 12, e4376.	0.2	1