

# Vic Narry Kim

## List of Publications by Year in descending order

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65  
papers

29,207  
citations

46984

47  
h-index

106281

65  
g-index

69  
all docs

69  
docs citations

69  
times ranked

33328  
citing authors

#	ARTICLE	IF	CITATIONS
1	The nuclear RNase III Drosha initiates microRNA processing. <i>Nature</i> , 2003, 425, 415-419.	13.7	4,463
2	Regulation of microRNA biogenesis. <i>Nature Reviews Molecular Cell Biology</i> , 2014, 15, 509-524.	16.1	4,396
3	Biogenesis of small RNAs in animals. <i>Nature Reviews Molecular Cell Biology</i> , 2009, 10, 126-139.	16.1	2,885
4	MicroRNA biogenesis: coordinated cropping and dicing. <i>Nature Reviews Molecular Cell Biology</i> , 2005, 6, 376-385.	16.1	2,256
5	MicroRNA maturation: stepwise processing and subcellular localization. <i>EMBO Journal</i> , 2002, 21, 4663-4670.	3.5	1,898
6	The Architecture of SARS-CoV-2 Transcriptome. <i>Cell</i> , 2020, 181, 914-921.e10.	13.5	1,759
7	Messenger-RNA-binding proteins and the messages they carry. <i>Nature Reviews Molecular Cell Biology</i> , 2002, 3, 195-205.	16.1	1,245
8	Human embryonic stem cells express a unique set of microRNAs. <i>Developmental Biology</i> , 2004, 270, 488-498.	0.9	914
9	Lin28 Mediates the Terminal Uridylation of let-7 Precursor MicroRNA. <i>Molecular Cell</i> , 2008, 32, 276-284.	4.5	885
10	Genomics of microRNA. <i>Trends in Genetics</i> , 2006, 22, 165-173.	2.9	835
11	TUT4 in Concert with Lin28 Suppresses MicroRNA Biogenesis through Pre-MicroRNA Uridylation. <i>Cell</i> , 2009, 138, 696-708.	13.5	730
12	miR-29 miRNAs activate p53 by targeting p85 $\beta$ and CDC42. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 23-29.	3.6	597
13	Dicer recognizes the 5' end of RNA for efficient and accurate processing. <i>Nature</i> , 2011, 475, 201-205.	13.7	444
14	TAIL-seq: Genome-wide Determination of Poly(A) Tail Length and 3' End Modifications. <i>Molecular Cell</i> , 2014, 53, 1044-1052.	4.5	402
15	Re-evaluation of the roles of <i>DROSHA</i> , <i>Exportin 5</i> , and <i>DICER</i> in microRNA biogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1881-9.	3.3	367
16	Functional Anatomy of the Human Microprocessor. <i>Cell</i> , 2015, 161, 1374-1387.	13.5	315
17	Small RNAs: classification, biogenesis, and function. <i>Molecules and Cells</i> , 2005, 19, 1-15.	1.0	289
18	Emerging Roles of RNA Modification: m6A and U-Tail. <i>Cell</i> , 2014, 158, 980-987.	13.5	272

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19	Mono-Uridylation of Pre-MicroRNA as a Key Step in the Biogenesis of Group II let-7 MicroRNAs. <i>Cell</i> , 2012, 151, 521-532.	13.5	266
20	Uridylation by TUT4 and TUT7 Marks mRNA for Degradation. <i>Cell</i> , 2014, 159, 1365-1376.	13.5	243
21	Small RNAs just got bigger: Piwi-interacting RNAs (piRNAs) in mammalian testes. <i>Genes and Development</i> , 2006, 20, 1993-1997.	2.7	234
22	MicroRNA precursors in motion: exportin-5 mediates their nuclear export. <i>Trends in Cell Biology</i> , 2004, 14, 156-159.	3.6	228
23	Characterization of DGCR8/Pasha, the essential cofactor for Drosha in primary miRNA processing. <i>Nucleic Acids Research</i> , 2006, 34, 4622-4629.	6.5	224
24	LIN28A Is a Suppressor of ER-Associated Translation in Embryonic Stem Cells. <i>Cell</i> , 2012, 151, 765-777.	13.5	208
25	Structure of Human DROSHA. <i>Cell</i> , 2016, 164, 81-90.	13.5	187
26	PKR Senses Nuclear and Mitochondrial Signals by Interacting with Endogenous Double-Stranded RNAs. <i>Molecular Cell</i> , 2018, 71, 1051-1063.e6.	4.5	156
27	PABP Cooperates with the CCR4-NOT Complex to Promote mRNA Deadenylation and Block Precocious Decay. <i>Molecular Cell</i> , 2018, 70, 1081-1088.e5.	4.5	154
28	Modifications of Small RNAs and Their Associated Proteins. <i>Cell</i> , 2010, 143, 703-709.	13.5	151
29	mTAIL-seq reveals dynamic poly(A) tail regulation in oocyte-to-embryo development. <i>Genes and Development</i> , 2016, 30, 1671-1682.	2.7	146
30	Regulation of Poly(A) Tail and Translation during the Somatic Cell Cycle. <i>Molecular Cell</i> , 2016, 62, 462-471.	4.5	144
31	Mixed tailing by TENT4A and TENT4B shields mRNA from rapid deadenylation. <i>Science</i> , 2018, 361, 701-704.	6.0	112
32	The SARS-CoV-2 RNA interactome. <i>Molecular Cell</i> , 2021, 81, 2838-2850.e6.	4.5	109
33	PKR is activated by cellular dsRNAs during mitosis and acts as a mitotic regulator. <i>Genes and Development</i> , 2014, 28, 1310-1322.	2.7	107
34	Genome-wide Mapping of DROSHA Cleavage Sites on Primary MicroRNAs and Noncanonical Substrates. <i>Molecular Cell</i> , 2017, 66, 258-269.e5.	4.5	106
35	<sc>TUT</sc> 7 controls the fate of precursor micro <sc>RNA</sc> s by using three different uridylation mechanisms. <i>EMBO Journal</i> , 2015, 34, 1801-1815.	3.5	97
36	Stress-activated miR-204 governs senescent phenotypes of chondrocytes to promote osteoarthritis development. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	96

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37	Deletion of Human tarbp2 Reveals Cellular MicroRNA Targets and Cell-Cycle Function of TRBP. Cell Reports, 2014, 9, 1061-1074.	2.9	95
38	Adenylation of Maternally Inherited MicroRNAs by Wispy. Molecular Cell, 2014, 56, 696-707.	4.5	87
39	Terminal Uridyltransferases Execute Programmed Clearance of Maternal Transcriptome in Vertebrate Embryos. Molecular Cell, 2018, 70, 72-82.e7.	4.5	87
40	A tale of non-canonical tails: gene regulation by post-transcriptional RNA tailing. Nature Reviews Molecular Cell Biology, 2020, 21, 542-556.	16.1	83
41	Sorting Out Small RNAs. Cell, 2008, 133, 25-26.	13.5	73
42	Bias-minimized quantification of microRNA reveals widespread alternative processing and 3' end modification. Nucleic Acids Research, 2019, 47, 2630-2640.	6.5	72
43	Single-molecule approach to immunoprecipitated protein complexes: insights into miRNA uridylation. EMBO Reports, 2011, 12, 690-696.	2.0	70
44	Molecular Basis for the Single-Nucleotide Precision of Primary microRNA Processing. Molecular Cell, 2019, 73, 505-518.e5.	4.5	66
45	PARN and TOE1 Constitute a 3' End Maturation Module for Nuclear Non-coding RNAs. Cell Reports, 2018, 23, 888-898.	2.9	55
46	Quantification of purified endogenous miRNAs with high sensitivity and specificity. Nature Communications, 2020, 11, 6033.	5.8	55
47	The regulatory impact of RNA-binding proteins on microRNA targeting. Nature Communications, 2021, 12, 5057.	5.8	54
48	A Mechanism for microRNA Arm Switching Regulated by Uridylation. Molecular Cell, 2020, 78, 1224-1236.e5.	4.5	52
49	RNA Interference in Functional Genomics and Medicine. Journal of Korean Medical Science, 2003, 18, 309.	1.1	48
50	Viral hijacking of the TENT4/ZCCHC14 complex protects viral RNAs via mixed tailing. Nature Structural and Molecular Biology, 2020, 27, 581-588.	3.6	42
51	A quantitative map of human primary microRNA processing sites. Molecular Cell, 2021, 81, 3422-3439.e11.	4.5	42
52	fCLIP-seq for transcriptomic footprinting of dsRNA-binding proteins: Lessons from DROSHA. Methods, 2019, 152, 3-11.	1.9	34
53	Chemical RNA digestion enables robust RNA-binding site mapping at single amino acid resolution. Nature Structural and Molecular Biology, 2020, 27, 678-682.	3.6	32
54	L1 retrotransposons exploit RNA m6A modification as an evolutionary driving force. Nature Communications, 2021, 12, 880.	5.8	32

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55	ERH facilitates microRNA maturation through the interaction with the N-terminus of DGCR8. <i>Nucleic Acids Research</i> , 2020, 48, 11097-11112.	6.5	29
56	Coordinate regulation of the senescent state by selective autophagy. <i>Developmental Cell</i> , 2021, 56, 1512-1525.e7.	3.1	29
57	Deuterium-Free, Three-Plexed Peptide Diethylation for Highly Accurate Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2019, 18, 1078-1087.	1.8	17
58	RNA demethylation by FTO stabilizes the FOXJ1 mRNA for proper motile ciliogenesis. <i>Developmental Cell</i> , 2021, 56, 1118-1130.e6.	3.1	14
59	Photoactivatable ribonucleosides mark base-specific RNA-binding sites. <i>Nature Communications</i> , 2021, 12, 6026.	5.8	14
60	Cell cycle micromanagement in embryonic stem cells. <i>Nature Genetics</i> , 2008, 40, 1391-1392.	9.4	13
61	U-tail as a guardian against invading RNAs. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 903-905.	3.6	11
62	FAX-RIC enables robust profiling of dynamic RNP complex formation in multicellular organisms in vivo. <i>Nucleic Acids Research</i> , 2021, 49, e28-e28.	6.5	11
63	MeCP2 Caught Moonlighting as a Suppressor of MicroRNA Processing. <i>Developmental Cell</i> , 2014, 28, 477-478.	3.1	8
64	Telomeres reformed with non-telomeric sequences in mouse embryonic stem cells. <i>Nature Communications</i> , 2021, 12, 1097.	5.8	3
65	MS1-Level Proteome Quantification Platform Allowing Maximally Increased Multiplexity for SILAC and In Vitro Chemical Labeling. <i>Analytical Chemistry</i> , 2020, 92, 4980-4989.	3.2	2