

# Vic Narry Kim

## List of Publications by Citations

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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.

65  
papers

23,343  
citations

41  
h-index

69  
g-index

69  
ext. papers

26,741  
ext. citations

24.2  
avg, IF

7.58  
L-index

#	Paper	IF	Citations
65	The nuclear RNase III Drosha initiates microRNA processing. <i>Nature</i> , <b>2003</b> , 425, 415-9	50.4	3928
64	Regulation of microRNA biogenesis. <i>Nature Reviews Molecular Cell Biology</i> , <b>2014</b> , 15, 509-24	48.7	3285
63	Biogenesis of small RNAs in animals. <i>Nature Reviews Molecular Cell Biology</i> , <b>2009</b> , 10, 126-39	48.7	2542
62	MicroRNA biogenesis: coordinated cropping and dicing. <i>Nature Reviews Molecular Cell Biology</i> , <b>2005</b> , 6, 376-85	48.7	1968
61	MicroRNA maturation: stepwise processing and subcellular localization. <i>EMBO Journal</i> , <b>2002</b> , 21, 4663-70	3	1620
60	Messenger-RNA-binding proteins and the messages they carry. <i>Nature Reviews Molecular Cell Biology</i> , <b>2002</b> , 3, 195-205	48.7	1095
59	The Architecture of SARS-CoV-2 Transcriptome. <i>Cell</i> , <b>2020</b> , 181, 914-921.e10	56.2	1035
58	Human embryonic stem cells express a unique set of microRNAs. <i>Developmental Biology</i> , <b>2004</b> , 270, 488-98	3	824
57	Lin28 mediates the terminal uridylation of let-7 precursor MicroRNA. <i>Molecular Cell</i> , <b>2008</b> , 32, 276-84	17.6	766
56	Genomics of microRNA. <i>Trends in Genetics</i> , <b>2006</b> , 22, 165-73	8.5	753
55	TUT4 in concert with Lin28 suppresses microRNA biogenesis through pre-microRNA uridylation. <i>Cell</i> , <b>2009</b> , 138, 696-708	56.2	628
54	miR-29 miRNAs activate p53 by targeting p85 alpha and CDC42. <i>Nature Structural and Molecular Biology</i> , <b>2009</b> , 16, 23-9	17.6	541
53	Dicer recognizes the 5Tend of RNA for efficient and accurate processing. <i>Nature</i> , <b>2011</b> , 475, 201-5	50.4	348
52	Re-evaluation of the roles of DROSHA, Exportin 5, and DICER in microRNA biogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, E1881-9	11.5	268
51	TAIL-seq: genome-wide determination of poly(A) tail length and 3Tend modifications. <i>Molecular Cell</i> , <b>2014</b> , 53, 1044-52	17.6	262
50	Small RNAs: classification, biogenesis, and function. <i>Molecules and Cells</i> , <b>2005</b> , 19, 1-15	3.5	246
49	Mono-uridylation of pre-microRNA as a key step in the biogenesis of group II let-7 microRNAs. <i>Cell</i> , <b>2012</b> , 151, 521-32	56.2	224

48	Functional Anatomy of the Human Microprocessor. <i>Cell</i> , <b>2015</b> , 161, 1374-87	56.2	219
47	Characterization of DGCR8/Pasha, the essential cofactor for Drosha in primary miRNA processing. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, 4622-9	20.1	204
46	MicroRNA precursors in motion: exportin-5 mediates their nuclear export. <i>Trends in Cell Biology</i> , <b>2004</b> , 14, 156-9	18.3	199
45	Emerging roles of RNA modification: m(6)A and U-tail. <i>Cell</i> , <b>2014</b> , 158, 980-987	56.2	186
44	Small RNAs just got bigger: Piwi-interacting RNAs (piRNAs) in mammalian testes. <i>Genes and Development</i> , <b>2006</b> , 20, 1993-7	12.6	185
43	Uridylation by TUT4 and TUT7 marks mRNA for degradation. <i>Cell</i> , <b>2014</b> , 159, 1365-76	56.2	171
42	LIN28A is a suppressor of ER-associated translation in embryonic stem cells. <i>Cell</i> , <b>2012</b> , 151, 765-777	56.2	171
41	Modifications of small RNAs and their associated proteins. <i>Cell</i> , <b>2010</b> , 143, 703-9	56.2	137
40	Structure of Human DROSHA. <i>Cell</i> , <b>2016</b> , 164, 81-90	56.2	130
39	Regulation of Poly(A) Tail and Translation during the Somatic Cell Cycle. <i>Molecular Cell</i> , <b>2016</b> , 62, 462-471	17.6	103
38	PABP Cooperates with the CCR4-NOT Complex to Promote mRNA Deadenylation and Block Precocious Decay. <i>Molecular Cell</i> , <b>2018</b> , 70, 1081-1088.e5	17.6	92
37	mTAIL-seq reveals dynamic poly(A) tail regulation in oocyte-to-embryo development. <i>Genes and Development</i> , <b>2016</b> , 30, 1671-82	12.6	90
36	PKR is activated by cellular dsRNAs during mitosis and acts as a mitotic regulator. <i>Genes and Development</i> , <b>2014</b> , 28, 1310-22	12.6	76
35	TUT7 controls the fate of precursor microRNAs by using three different uridylation mechanisms. <i>EMBO Journal</i> , <b>2015</b> , 34, 1801-15	13	75
34	Deletion of human tarbp2 reveals cellular microRNA targets and cell-cycle function of TRBP. <i>Cell Reports</i> , <b>2014</b> , 9, 1061-74	10.6	72
33	Genome-wide Mapping of DROSHA Cleavage Sites on Primary MicroRNAs and Noncanonical Substrates. <i>Molecular Cell</i> , <b>2017</b> , 66, 258-269.e5	17.6	67
32	PKR Senses Nuclear and Mitochondrial Signals by Interacting with Endogenous Double-Stranded RNAs. <i>Molecular Cell</i> , <b>2018</b> , 71, 1051-1063.e6	17.6	66
31	Adenylation of maternally inherited microRNAs by Wispy. <i>Molecular Cell</i> , <b>2014</b> , 56, 696-707	17.6	65

30	Sorting out small RNAs. <i>Cell</i> , <b>2008</b> , 133, 25-6	56.2	62
29	Mixed tailing by TENT4A and TENT4B shields mRNA from rapid deadenylation. <i>Science</i> , <b>2018</b> , 361, 701-704.3	35.3	61
28	Single-molecule approach to immunoprecipitated protein complexes: insights into miRNA uridylation. <i>EMBO Reports</i> , <b>2011</b> , 12, 690-6	6.5	60
27	Terminal Uridyltransferases Execute Programmed Clearance of Maternal Transcriptome in Vertebrate Embryos. <i>Molecular Cell</i> , <b>2018</b> , 70, 72-82.e7	17.6	47
26	Stress-activated miR-204 governs senescent phenotypes of chondrocytes to promote osteoarthritis development. <i>Science Translational Medicine</i> , <b>2019</b> , 11,	17.5	45
25	The architecture of SARS-CoV-2 transcriptome		41
24	RNA interference in functional genomics and medicine. <i>Journal of Korean Medical Science</i> , <b>2003</b> , 18, 309-18	18	40
23	Bias-minimized quantification of microRNA reveals widespread alternative processing and 3Tend modification. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 2630-2640	20.1	37
22	PARN and TOE1 Constitute a 3Tend Maturation Module for Nuclear Non-coding RNAs. <i>Cell Reports</i> , <b>2018</b> , 23, 888-898	10.6	34
21	Molecular Basis for the Single-Nucleotide Precision of Primary microRNA Processing. <i>Molecular Cell</i> , <b>2019</b> , 73, 505-518.e5	17.6	32
20	The SARS-CoV-2 RNA interactome. <i>Molecular Cell</i> , <b>2021</b> , 81, 2838-2850.e6	17.6	28
19	A tale of non-canonical tails: gene regulation by post-transcriptional RNA tailing. <i>Nature Reviews Molecular Cell Biology</i> , <b>2020</b> , 21, 542-556	48.7	27
18	fCLIP-seq for transcriptomic footprinting of dsRNA-binding proteins: Lessons from DROSHA. <i>Methods</i> , <b>2019</b> , 152, 3-11	4.6	23
17	The regulatory impact of RNA-binding proteins on microRNA targeting. <i>Nature Communications</i> , <b>2021</b> , 12, 5057	17.4	22
16	A Mechanism for microRNA Arm Switching Regulated by Uridylation. <i>Molecular Cell</i> , <b>2020</b> , 78, 1224-1236.e5	17.5	19
15	Viral hijacking of the TENT4-ZCCHC14 complex protects viral RNAs via mixed tailing. <i>Nature Structural and Molecular Biology</i> , <b>2020</b> , 27, 581-588	17.6	16
14	Chemical RNA digestion enables robust RNA-binding site mapping at single amino acid resolution. <i>Nature Structural and Molecular Biology</i> , <b>2020</b> , 27, 678-682	17.6	12
13	Quantification of purified endogenous miRNAs with high sensitivity and specificity. <i>Nature Communications</i> , <b>2020</b> , 11, 6033	17.4	11

12	ERH facilitates microRNA maturation through the interaction with the N-terminus of DGCR8. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, 11097-11112	20.1	11
11	L1 retrotransposons exploit RNA mA modification as an evolutionary driving force. <i>Nature Communications</i> , <b>2021</b> , 12, 880	17.4	11
10	Coordinate regulation of the senescent state by selective autophagy. <i>Developmental Cell</i> , <b>2021</b> , 56, 1512-1525.e7	15.25	10
9	Deuterium-Free, Three-Plexed Peptide Diethylation for Highly Accurate Quantitative Proteomics. <i>Journal of Proteome Research</i> , <b>2019</b> , 18, 1078-1087	5.6	9
8	U-tail as a guardian against invading RNAs. <i>Nature Structural and Molecular Biology</i> , <b>2018</b> , 25, 903-905	17.6	9
7	A quantitative map of human primary microRNA processing sites. <i>Molecular Cell</i> , <b>2021</b> , 81, 3422-3439.e11	17.6	8
6	MeCP2 caught moonlighting as a suppressor of MicroRNA processing. <i>Developmental Cell</i> , <b>2014</b> , 28, 477-482	10.2	7
5	RNA demethylation by FTO stabilizes the FOXJ1 mRNA for proper motile ciliogenesis. <i>Developmental Cell</i> , <b>2021</b> , 56, 1118-1130.e6	10.2	4
4	FAX-RIC enables robust profiling of dynamic RNP complex formation in multicellular organisms in vivo. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, e28	20.1	3
3	Photoactivatable ribonucleosides mark base-specific RNA-binding sites. <i>Nature Communications</i> , <b>2021</b> , 12, 6026	17.4	2
2	MS1-Level Proteome Quantification Platform Allowing Maximally Increased Multiplexity for SILAC and Chemical Labeling. <i>Analytical Chemistry</i> , <b>2020</b> , 92, 4980-4989	7.8	1
1	Telomeres reforged with non-telomeric sequences in mouse embryonic stem cells. <i>Nature Communications</i> , <b>2021</b> , 12, 1097	17.4	1