

Ryan A Flynn

List of Publications by Year in Descending Order

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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.

61
papers

12,568
citations

39
h-index

71
g-index

71
ext. papers

15,326
ext. citations

25.7
avg, IF

6.2
L-index

#	Paper	IF	Citations
61	Loquacious modulates flaviviral RNA replication in mosquito cells.. <i>PLoS Pathogens</i> , 2022 , 18, e1010163	7.6	0
60	The CD22-IGF2R interaction is a therapeutic target for microglial lysosome dysfunction in Niemann-Pick type C. <i>Science Translational Medicine</i> , 2021 , 13, eabg2919	17.5	2
59	Discovery and functional interrogation of SARS-CoV-2 RNA-host protein interactions. <i>Cell</i> , 2021 , 184, 2394-2411.e16	56.2	39
58	Small RNAs are modified with N-glycans and displayed on the surface of living cells. <i>Cell</i> , 2021 , 184, 3109-3124.e20	38.1	2
57	Diverse functional elements in RNA predicted transcriptome-wide by orthogonal RNA structure probing. <i>Nucleic Acids Research</i> , 2021 , 49, 11868-11882	20.1	1
56	fSHAPE, fSHAPE-eCLIP, and SHAPE-eCLIP probe transcript regions that interact with specific proteins. <i>STAR Protocols</i> , 2021 , 2, 100762	1.4	0
55	Progenitor identification and SARS-CoV-2 infection in human distal lung organoids. <i>Nature</i> , 2020 , 588, 670-675	50.4	103
54	A memory of eS25 loss drives resistance phenotypes. <i>Nucleic Acids Research</i> , 2020 , 48, 7279-7297	20.1	2
53	RNA helicase DDX21 mediates nucleotide stress responses in neural crest and melanoma cells. <i>Nature Cell Biology</i> , 2020 , 22, 372-379	23.4	19
52	DNA-PKcs has KU-dependent function in rRNA processing and haematopoiesis. <i>Nature</i> , 2020 , 579, 291-296	36.4	29
51	Proteomic analysis of young and old mouse hematopoietic stem cells and their progenitors reveals post-transcriptional regulation in stem cells. <i>ELife</i> , 2020 , 9,	8.9	6
50	Progenitor identification and SARS-CoV-2 infection in long-term human distal lung organoid cultures 2020 ,		17
49	Systematic discovery and functional interrogation of SARS-CoV-2 viral RNA-host protein interactions during infection 2020 ,		12
48	Footprinting SHAPE-eCLIP Reveals Transcriptome-wide Hydrogen Bonds at RNA-Protein Interfaces. <i>Molecular Cell</i> , 2020 , 80, 903-914.e8	17.6	12
47	HiChIRP reveals RNA-associated chromosome conformation. <i>Nature Methods</i> , 2019 , 16, 489-492	21.6	40
46	An RNA-centric dissection of host complexes controlling flavivirus infection. <i>Nature Microbiology</i> , 2019 , 4, 2369-2382	26.6	51
45	The novel lncRNA is pro-neurogenic and mutated in human neurodevelopmental disorders. <i>ELife</i> , 2019 , 8,	8.9	39

44	Functional significance of U2AF1 S34F mutations in lung adenocarcinomas. <i>Nature Communications</i> , 2019 , 10, 5712	17.4	15
43	Tissue-selective effects of nucleolar stress and rDNA damage in developmental disorders. <i>Nature</i> , 2018 , 554, 112-117	50.4	79
42	Retraction Note: DDX5 and its associated lncRNA Rmrp modulate T17 cell effector functions. <i>Nature</i> , 2018 , 562, 150	50.4	9
41	The Mammalian Ribo-interactome Reveals Ribosome Functional Diversity and Heterogeneity. <i>Cell</i> , 2017 , 169, 1051-1065.e18	56.2	210
40	Comparative Analysis Reveals Furoyl in Vivo Selective Hydroxyl Acylation Analyzed by Primer Extension Reagents Form Stable Ribosyl Ester Adducts. <i>Biochemistry</i> , 2017 , 56, 1811-1814	3.2	4
39	Inhibition of NGLY1 Inactivates the Transcription Factor Nrf1 and Potentiates Proteasome Inhibitor Cytotoxicity. <i>ACS Central Science</i> , 2017 , 3, 1143-1155	16.8	84
38	Enhancer connectome in primary human cells identifies target genes of disease-associated DNA elements. <i>Nature Genetics</i> , 2017 , 49, 1602-1612	36.3	253
37	Comparison of SHAPE reagents for mapping RNA structures inside living cells. <i>Rna</i> , 2017 , 23, 169-174	5.8	48
36	HiChIP: efficient and sensitive analysis of protein-directed genome architecture. <i>Nature Methods</i> , 2016 , 13, 919-922	21.6	505
35	Transcriptome-wide interrogation of RNA secondary structure in living cells with icSHAPE. <i>Nature Protocols</i> , 2016 , 11, 273-90	18.8	92
34	7SK-BAF axis controls pervasive transcription at enhancers. <i>Nature Structural and Molecular Biology</i> , 2016 , 23, 231-8	17.6	60
33	Novel Gene Expression Profile of Women with Intrinsic Skin Youthfulness by Whole Transcriptome Sequencing. <i>PLoS ONE</i> , 2016 , 11, e0165913	3.7	6
32	Medulloblastoma-associated DDX3 variant selectively alters the translational response to stress. <i>Oncotarget</i> , 2016 , 7, 28169-82	3.3	44
31	Stress from Nucleotide Depletion Activates the Transcriptional Regulator HEXIM1 to Suppress Melanoma. <i>Molecular Cell</i> , 2016 , 62, 34-46	17.6	52
30	irCLIP platform for efficient characterization of protein-RNA interactions. <i>Nature Methods</i> , 2016 , 13, 489-92	21.6	151
29	RNA Duplex Map in Living Cells Reveals Higher-Order Transcriptome Structure. <i>Cell</i> , 2016 , 165, 1267-1275	56.2	368
28	An inducible long noncoding RNA amplifies DNA damage signaling. <i>Nature Genetics</i> , 2016 , 48, 1370-1376	36.3	143
27	Systematic discovery of Xist RNA binding proteins. <i>Cell</i> , 2015 , 161, 404-16	56.2	662

26	Intrinsic retroviral reactivation in human preimplantation embryos and pluripotent cells. <i>Nature</i> , 2015 , 522, 221-5	50.4	339
25	Structural imprints in vivo decode RNA regulatory mechanisms. <i>Nature</i> , 2015 , 519, 486-90	50.4	454
24	Leukemia-Associated Cohesin Mutants Dominantly Enforce Stem Cell Programs and Impair Human Hematopoietic Progenitor Differentiation. <i>Cell Stem Cell</i> , 2015 , 17, 675-688	18	127
23	RNA helicase DDX21 coordinates transcription and ribosomal RNA processing. <i>Nature</i> , 2015 , 518, 249-53	50.4	167
22	DDX5 and its associated lncRNA Rmrp modulate TH17 cell effector functions. <i>Nature</i> , 2015 , 528, 517-22	50.4	130
21	Dissecting noncoding and pathogen RNA-protein interactomes. <i>Rna</i> , 2015 , 21, 135-43	5.8	61
20	Landscape and variation of RNA secondary structure across the human transcriptome. <i>Nature</i> , 2014 , 505, 706-9	50.4	390
19	m(6)A RNA modification controls cell fate transition in mammalian embryonic stem cells. <i>Cell Stem Cell</i> , 2014 , 15, 707-19	18	675
18	Long noncoding RNAs in cell-fate programming and reprogramming. <i>Cell Stem Cell</i> , 2014 , 14, 752-61	18	362
17	Abstract 158: Identification of BMP-Responsive Long Noncoding RNAs in Pluripotent Cells. <i>Plastic and Reconstructive Surgery</i> , 2014 , 133, 174	2.7	16
16	RNA structural analysis by evolving SHAPE chemistry. <i>Wiley Interdisciplinary Reviews RNA</i> , 2014 , 5, 867-81	10.3	44
15	Essential role of lncRNA binding for WDR5 maintenance of active chromatin and embryonic stem cell pluripotency. <i>ELife</i> , 2014 , 3, e02046	8.9	136
14	Control of somatic tissue differentiation by the long non-coding RNA TINCR. <i>Nature</i> , 2013 , 493, 231-5	50.4	665
13	RNA SHAPE analysis in living cells. <i>Nature Chemical Biology</i> , 2013 , 9, 18-20	11.7	288
12	Transcriptional profiling of long non-coding RNAs and novel transcribed regions across a diverse panel of archived human cancers. <i>Genome Biology</i> , 2012 , 13, R75	18.3	195
11	Active chromatin and noncoding RNAs: an intimate relationship. <i>Current Opinion in Genetics and Development</i> , 2012 , 22, 172-8	4.9	42
10	A unique chromatin signature uncovers early developmental enhancers in humans. <i>Nature</i> , 2011 , 470, 279-83	50.4	1545
9	A long noncoding RNA maintains active chromatin to coordinate homeotic gene expression. <i>Nature</i> , 2011 , 472, 120-4	50.4	1502

8	Antisense RNA polymerase II divergent transcripts are P-TEFb dependent and substrates for the RNA exosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 10460-5	11.5	141
7	c-Myc regulates transcriptional pause release. <i>Cell</i> , 2010 , 141, 432-45	56.2	930
6	Phosphotyrosine signaling analysis of site-specific mutations on EGFRvIII identifies determinants governing glioblastoma cell growth. <i>Molecular BioSystems</i> , 2010 , 6, 1227-37		36
5	Divergent transcription from active promoters. <i>Science</i> , 2008 , 322, 1849-51	33.3	695
4	Quantitative analysis of EGFRvIII cellular signaling networks reveals a combinatorial therapeutic strategy for glioblastoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 12867-72	11.5	328
3	Diagnosis, treatment, and management of breast cancer in previously augmented women. <i>Breast Journal</i> , 2006 , 12, 343-8	1.2	35
2	Zika Virus Infection Prevents Host mRNA Nuclear Export by Disrupting UPF1 Function		1
1	Mammalian Y RNAs are modified at discrete guanosine residues with N-glycans		3