

Gene W Yeo

List of Publications by Year in descending order

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Version: 2024-02-01

230
papers

32,292
citations

4955

84
h-index

5249

165
g-index

277
all docs

277
docs citations

277
times ranked

40991
citing authors

#	ARTICLE	IF	CITATIONS
1	Maximum Entropy Modeling of Short Sequence Motifs with Applications to RNA Splicing Signals. <i>Journal of Computational Biology</i> , 2004, 11, 377-394.	0.8	1,714
2	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	13.7	1,252
3	A Model for Neural Development and Treatment of Rett Syndrome Using Human Induced Pluripotent Stem Cells. <i>Cell</i> , 2010, 143, 527-539.	13.5	1,175
4	Robust transcriptome-wide discovery of RNA-binding protein binding sites with enhanced CLIP (eCLIP). <i>Nature Methods</i> , 2016, 13, 508-514.	9.0	1,092
5	Long pre-mRNA depletion and RNA missplicing contribute to neuronal vulnerability from loss of TDP-43. <i>Nature Neuroscience</i> , 2011, 14, 459-468.	7.1	1,050
6	Divergent Transcription from Active Promoters. <i>Science</i> , 2008, 322, 1849-1851.	6.0	801
7	L1 retrotransposition in human neural progenitor cells. <i>Nature</i> , 2009, 460, 1127-1131.	13.7	750
8	Context-Dependent and Disease-Specific Diversity in Protein Interactions within Stress Granules. <i>Cell</i> , 2018, 172, 590-604.e13.	13.5	672
9	A large-scale binding and functional map of human RNA-binding proteins. <i>Nature</i> , 2020, 583, 711-719.	13.7	667
10	Divergent roles of ALS-linked proteins FUS/TLS and TDP-43 intersect in processing long pre-mRNAs. <i>Nature Neuroscience</i> , 2012, 15, 1488-1497.	7.1	628
11	Systematic Identification and Analysis of Exonic Splicing Silencers. <i>Cell</i> , 2004, 119, 831-845.	13.5	606
12	Wnt-mediated activation of NeuroD1 and retro-elements during adult neurogenesis. <i>Nature Neuroscience</i> , 2009, 12, 1097-1105.	7.1	584
13	L1 retrotransposition in neurons is modulated by MeCP2. <i>Nature</i> , 2010, 468, 443-446.	13.7	572
14	An RNA code for the FOX2 splicing regulator revealed by mapping RNA-protein interactions in stem cells. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 130-137.	3.6	536
15	Complex Oscillatory Waves Emerging from Cortical Organoids Model Early Human Brain Network Development. <i>Cell Stem Cell</i> , 2019, 25, 558-569.e7.	5.2	520
16	Targeted degradation of sense and antisense <i>C9orf72</i> RNA foci as therapy for ALS and frontotemporal degeneration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E4530-9.	3.3	508
17	Variation in alternative splicing across human tissues. <i>Genome Biology</i> , 2004, 5, R74.	13.9	486
18	Programmable RNA Tracking in Live Cells with CRISPR/Cas9. <i>Cell</i> , 2016, 165, 488-496.	13.5	455

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19	Genome-wide Analysis of PTB-RNA Interactions Reveals a Strategy Used by the General Splicing Repressor to Modulate Exon Inclusion or Skipping. <i>Molecular Cell</i> , 2009, 36, 996-1006.	4.5	429
20	Integrative Genome-wide Analysis Reveals Cooperative Regulation of Alternative Splicing by hnRNP Proteins. <i>Cell Reports</i> , 2012, 1, 167-178.	2.9	420
21	Sequence, Structure, and Context Preferences of Human RNA Binding Proteins. <i>Molecular Cell</i> , 2018, 70, 854-867.e9.	4.5	408
22	NONCODING RNAs IN THE MAMMALIAN CENTRAL NERVOUS SYSTEM. <i>Annual Review of Neuroscience</i> , 2006, 29, 77-103.	5.0	401
23	How RNA-Binding Proteins Interact with RNA: Molecules and Mechanisms. <i>Molecular Cell</i> , 2020, 78, 9-29.	4.5	396
24	ALS-linked TDP-43 mutations produce aberrant RNA splicing and adult-onset motor neuron disease without aggregation or loss of nuclear TDP-43. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E736-45.	3.3	370
25	Pairing beyond the Seed Supports MicroRNA Targeting Specificity. <i>Molecular Cell</i> , 2016, 64, 320-333.	4.5	344
26	The Clothes Make the mRNA: Past and Present Trends in mRNP Fashion. <i>Annual Review of Biochemistry</i> , 2015, 84, 325-354.	5.0	322
27	Rbfox proteins regulate alternative mRNA splicing through evolutionarily conserved RNA bridges. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1434-1442.	3.6	313
28	RNA sequence analysis defines Dicer's role in mouse embryonic stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 18097-18102.	3.3	303
29	Emergence and rapid transmission of SARS-CoV-2 B.1.1.7 in the United States. <i>Cell</i> , 2021, 184, 2587-2594.e7.	13.5	285
30	Comprehensive discovery of endogenous Argonaute binding sites in <i>Caenorhabditis elegans</i> . <i>Nature Structural and Molecular Biology</i> , 2010, 17, 173-179.	3.6	279
31	The EJC Factor eIF4AIII Modulates Synaptic Strength and Neuronal Protein Expression. <i>Cell</i> , 2007, 130, 179-191.	13.5	278
32	Transcriptional Signature and Memory Retention of Human-Induced Pluripotent Stem Cells. <i>PLoS ONE</i> , 2009, 4, e7076.	1.1	276
33	LIN28 Binds Messenger RNAs at GGAGA Motifs and Regulates Splicing Factor Abundance. <i>Molecular Cell</i> , 2012, 48, 195-206.	4.5	267
34	Identification and analysis of alternative splicing events conserved in human and mouse. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 2850-2855.	3.3	263
35	Genome-wide Analysis Reveals SR Protein Cooperation and Competition in Regulated Splicing. <i>Molecular Cell</i> , 2013, 50, 223-235.	4.5	261
36	Plant-Derived Flavanol (-)Epicatechin Enhances Angiogenesis and Retention of Spatial Memory in Mice. <i>Journal of Neuroscience</i> , 2007, 27, 5869-5878.	1.7	256

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37	RESCUE-ESE identifies candidate exonic splicing enhancers in vertebrate exons. <i>Nucleic Acids Research</i> , 2004, 32, W187-W190.	6.5	251
38	Circadian Oscillations of Protein-Coding and Regulatory RNAs in a Highly Dynamic Mammalian Liver Epigenome. <i>Cell Metabolism</i> , 2012, 16, 833-845.	7.2	230
39	The Ro60 autoantigen binds endogenous retroelements and regulates inflammatory gene expression. <i>Science</i> , 2015, 350, 455-459.	6.0	225
40	Pervasive Chromatin-RNA Binding Protein Interactions Enable RNA-Based Regulation of Transcription. <i>Cell</i> , 2019, 178, 107-121.e18.	13.5	224
41	Differential L1 regulation in pluripotent stem cells of humans and apes. <i>Nature</i> , 2013, 503, 525-529.	13.7	220
42	Base editing: advances and therapeutic opportunities. <i>Nature Reviews Drug Discovery</i> , 2020, 19, 839-859.	21.5	218
43	Elimination of Toxic Microsatellite Repeat Expansion RNA by RNA-Targeting Cas9. <i>Cell</i> , 2017, 170, 899-912.e10.	13.5	213
44	Variation in sequence and organization of splicing regulatory elements in vertebrate genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 15700-15705.	3.3	208
45	The PIWI proteins SMEDWI-2 and SMEDWI-3 are required for stem cell function and piRNA expression in planarians. <i>Rna</i> , 2008, 14, 1174-1186.	1.6	207
46	Th17 Lymphocytes Induce Neuronal Cell Death in a Human iPSC-Based Model of Parkinson's Disease. <i>Cell Stem Cell</i> , 2018, 23, 123-131.e6.	5.2	206
47	ALS-causative mutations in FUS/TLS confer gain and loss of function by altered association with SMN and U1-snRNP. <i>Nature Communications</i> , 2015, 6, 6171.	5.8	205
48	Short poly(A) tails are a conserved feature of highly expressed genes. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 1057-1063.	3.6	200
49	Early transcriptional and epigenetic regulation of CD8+ T cell differentiation revealed by single-cell RNA sequencing. <i>Nature Immunology</i> , 2017, 18, 422-432.	7.0	194
50	Identification of Novel Long Noncoding RNAs Underlying Vertebrate Cardiovascular Development. <i>Circulation</i> , 2015, 131, 1278-1290.	1.6	185
51	A Combinatorial Code for Splicing Silencing: UAGG and GGGG Motifs. <i>PLoS Biology</i> , 2005, 3, e158.	2.6	177
52	Disruption of RNA Metabolism in Neurological Diseases and Emerging Therapeutic Interventions. <i>Neuron</i> , 2019, 102, 294-320.	3.8	176
53	Early specification of CD8+ T lymphocyte fates during adaptive immunity revealed by single-cell gene-expression analyses. <i>Nature Immunology</i> , 2014, 15, 365-372.	7.0	175
54	Genetic mutations in RNA-binding proteins and their roles in ALS. <i>Human Genetics</i> , 2017, 136, 1193-1214.	1.8	168

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55	NEAT1 scaffolds RNA-binding proteins and the Microprocessor to globally enhance pri-miRNA processing. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 816-824.	3.6	165
56	Small-Molecule Modulation of TDP-43 Recruitment to Stress Granules Prevents Persistent TDP-43 Accumulation in ALS/FTD. <i>Neuron</i> , 2019, 103, 802-819.e11.	3.8	161
57	Widespread RNA editing dysregulation in brains from autistic individuals. <i>Nature Neuroscience</i> , 2019, 22, 25-36.	7.1	161
58	Context-dependent functional compensation between Ythdf m ⁶ A reader proteins. <i>Genes and Development</i> , 2020, 34, 1373-1391.	2.7	158
59	SONAR Discovers RNA-Binding Proteins from Analysis of Large-Scale Protein-Protein Interactomes. <i>Molecular Cell</i> , 2016, 64, 282-293.	4.5	155
60	Single-Cell Alternative Splicing Analysis with Expedition Reveals Splicing Dynamics during Neuron Differentiation. <i>Molecular Cell</i> , 2017, 67, 148-161.e5.	4.5	155
61	Misregulated RNA processing in amyotrophic lateral sclerosis. <i>Brain Research</i> , 2012, 1462, 3-15.	1.1	150
62	Advances and challenges in the detection of transcriptome-wide protein-RNA interactions. <i>Wiley Interdisciplinary Reviews RNA</i> , 2018, 9, e1436.	3.2	150
63	Direct RNA sequencing enables m ⁶ A detection in endogenous transcript isoforms at base-specific resolution. <i>Rna</i> , 2020, 26, 19-28.	1.6	150
64	Heterogenous Populations of Tissue-Resident CD8+ T Cells Are Generated in Response to Infection and Malignancy. <i>Immunity</i> , 2020, 52, 808-824.e7.	6.6	149
65	iPSCORE: A Resource of 222 iPSC Lines Enabling Functional Characterization of Genetic Variation across a Variety of Cell Types. <i>Stem Cell Reports</i> , 2017, 8, 1086-1100.	2.3	147
66	Distinct and shared functions of ALS-associated proteins TDP-43, FUS and TAF15 revealed by multisystem analyses. <i>Nature Communications</i> , 2016, 7, 12143.	5.8	137
67	Protein-RNA Networks Regulated by Normal and ALS-Associated Mutant HNRNPA2B1 in the Nervous System. <i>Neuron</i> , 2016, 92, 780-795.	3.8	137
68	Predicting the functional states of human iPSC-derived neurons with single-cell RNA-seq and electrophysiology. <i>Molecular Psychiatry</i> , 2016, 21, 1573-1588.	4.1	136
69	Principles of RNA processing from analysis of enhanced CLIP maps for 150 RNA binding proteins. <i>Genome Biology</i> , 2020, 21, 90.	3.8	136
70	High-Resolution Profiling and Analysis of Viral and Host Small RNAs during Human Cytomegalovirus Infection. <i>Journal of Virology</i> , 2012, 86, 226-235.	1.5	134
71	Nonclassical splicing mutations in the coding and noncoding regions of the ATM Gene: Maximum entropy estimates of splice junction strengths. <i>Human Mutation</i> , 2004, 23, 67-76.	1.1	133
72	LIN-28 co-transcriptionally binds primary let-7 to regulate miRNA maturation in <i>Caenorhabditis elegans</i> . <i>Nature Structural and Molecular Biology</i> , 2011, 18, 302-308.	3.6	129

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73	Pseudotemporal Ordering of Single Cells Reveals Metabolic Control of Postnatal \hat{I}^2 Cell Proliferation. <i>Cell Metabolism</i> , 2017, 25, 1160-1175.e11.	7.2	128
74	Heterogeneity and clonal relationships of adaptive immune cells in ulcerative colitis revealed by single-cell analyses. <i>Science Immunology</i> , 2020, 5, .	5.6	127
75	Early precursors and molecular determinants of tissue-resident memory CD8 ⁺ T lymphocytes revealed by single-cell RNA sequencing. <i>Science Immunology</i> , 2020, 5, .	5.6	124
76	Interaction Landscape of Inherited Polymorphisms with Somatic Events in Cancer. <i>Cancer Discovery</i> , 2017, 7, 410-423.	7.7	121
77	Discovery and Analysis of Evolutionarily Conserved Intronic Splicing Regulatory Elements. <i>PLoS Genetics</i> , 2007, 3, e85.	1.5	120
78	Enhanced CLIP Uncovers IMP Protein-RNA Targets in Human Pluripotent Stem Cells Important for Cell Adhesion and Survival. <i>Cell Reports</i> , 2016, 15, 666-679.	2.9	118
79	Resources for the Comprehensive Discovery of Functional RNA Elements. <i>Molecular Cell</i> , 2016, 61, 903-913.	4.5	118
80	Alternative Splicing Events Identified in Human Embryonic Stem Cells and Neural Progenitors. <i>PLoS Computational Biology</i> , 2007, 3, e196.	1.5	116
81	Systematic Discovery of RNA Binding Proteins that Regulate MicroRNA Levels. <i>Molecular Cell</i> , 2018, 69, 1005-1016.e7.	4.5	107
82	Transcriptome-wide profiles of circular RNA and RNA-binding protein interactions reveal effects on circular RNA biogenesis and cancer pathway expression. <i>Genome Medicine</i> , 2020, 12, 112.	3.6	106
83	Musashi-2 attenuates AHR signalling to expand human haematopoietic stem cells. <i>Nature</i> , 2016, 532, 508-511.	13.7	101
84	RNA-binding proteins in neurodegeneration: Seq and you shall receive. <i>Trends in Neurosciences</i> , 2015, 38, 226-236.	4.2	97
85	Regulation of RNA editing by RNA-binding proteins in human cells. <i>Communications Biology</i> , 2019, 2, 19.	2.0	97
86	Reintroduction of the archaic variant of <i>NOVA1</i> in cortical organoids alters neurodevelopment. <i>Science</i> , 2021, 371, .	6.0	96
87	A regulator of Dscam mutually exclusive splicing fidelity. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 1134-1140.	3.6	90
88	Determination of tag density required for digital transcriptome analysis: Application to an androgen-sensitive prostate cancer model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 20179-20184.	3.3	90
89	Target Discrimination in Nonsense-Mediated mRNA Decay Requires Upf1 ATPase Activity. <i>Molecular Cell</i> , 2015, 59, 413-425.	4.5	89
90	PPAR- \hat{I} is repressed in Huntington's disease, is required for normal neuronal function and can be targeted therapeutically. <i>Nature Medicine</i> , 2016, 22, 37-45.	15.2	88

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91	G4C2 Repeat RNA Initiates a POM121-Mediated Reduction in Specific Nucleoporins in C9orf72 ALS/FTD. <i>Neuron</i> , 2020, 107, 1124-1140.e11.	3.8	88
92	Inhibition of YTHDF2 triggers proteotoxic cell death in MYC-driven breast cancer. <i>Molecular Cell</i> , 2021, 81, 3048-3064.e9.	4.5	86
93	A Gene Regulatory Network Cooperatively Controlled by Pdx1 and Sox9 Governs Lineage Allocation of Foregut Progenitor Cells. <i>Cell Reports</i> , 2015, 13, 326-336.	2.9	82
94	A Small RNA-Catalytic Argonaute Pathway Tunes Germline Transcript Levels to Ensure Embryonic Divisions. <i>Cell</i> , 2016, 165, 396-409.	13.5	82
95	The RNA Helicase DDX6 Controls Cellular Plasticity by Modulating P-Body Homeostasis. <i>Cell Stem Cell</i> , 2019, 25, 622-638.e13.	5.2	82
96	Robust, Cost-Effective Profiling of RNA Binding Protein Targets with Single-end Enhanced Crosslinking and Immunoprecipitation (seCLIP). <i>Methods in Molecular Biology</i> , 2017, 1648, 177-200.	0.4	78
97	Robust single-cell discovery of RNA targets of RNA-binding proteins and ribosomes. <i>Nature Methods</i> , 2021, 18, 507-519.	9.0	77
98	Hippocampus-dependent learning is associated with adult neurogenesis in MRL/MpJ mice. <i>Hippocampus</i> , 2009, 19, 658-669.	0.9	75
99	Pseudouridine synthases modify human pre-mRNA co-transcriptionally and affect pre-mRNA processing. <i>Molecular Cell</i> , 2022, 82, 645-659.e9.	4.5	75
100	MicroRNA-101 Regulates Multiple Developmental Programs to Constrain Excitation in Adult Neural Networks. <i>Neuron</i> , 2016, 92, 1337-1351.	3.8	73
101	Inference of Splicing Regulatory Activities by Sequence Neighborhood Analysis. <i>PLoS Genetics</i> , 2006, 2, e191.	1.5	71
102	Transcriptome-pathology correlation identifies interplay between TDP-43 and the expression of its kinase CK1E in sporadic ALS. <i>Acta Neuropathologica</i> , 2018, 136, 405-423.	3.9	69
103	Evidence for premature aging due to oxidative stress in iPSCs from Cockayne syndrome. <i>Human Molecular Genetics</i> , 2012, 21, 3825-3834.	1.4	67
104	Biallelic mutations in the 3' exonuclease TOE1 cause pontocerebellar hypoplasia and uncover a role in snRNA processing. <i>Nature Genetics</i> , 2017, 49, 457-464.	9.4	66
105	Overriding FUS autoregulation in mice triggers gain-of-toxic dysfunctions in RNA metabolism and autophagy-lysosome axis. <i>ELife</i> , 2019, 8, .	2.8	65
106	The dsRBP and Inactive Editor ADR-1 Utilizes dsRNA Binding to Regulate A-to-I RNA Editing across the <i>C. elegans</i> Transcriptome. <i>Cell Reports</i> , 2014, 6, 599-607.	2.9	64
107	High-Throughput and Cost-Effective Characterization of Induced Pluripotent Stem Cells. <i>Stem Cell Reports</i> , 2017, 8, 1101-1111.	2.3	64
108	Human Cytomegalovirus Infection of Human Embryonic Stem Cell-Derived Primitive Neural Stem Cells Is Restricted at Several Steps but Leads to the Persistence of Viral DNA. <i>Journal of Virology</i> , 2014, 88, 4021-4039.	1.5	63

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109	RBP-Maps enables robust generation of splicing regulatory maps. <i>Rna</i> , 2019, 25, 193-204.	1.6	63
110	Intracellular mRNA Regulation with Self-Assembled Locked Nucleic Acid Polymer Nanoparticles. <i>Journal of the American Chemical Society</i> , 2014, 136, 7615-7618.	6.6	62
111	Dysregulation of RBFOX2 Is an Early Event in Cardiac Pathogenesis of Diabetes. <i>Cell Reports</i> , 2016, 15, 2200-2213.	2.9	60
112	Pooled CRISPR screens with imaging on microwell arrays reveals stress granule-regulatory factors. <i>Nature Methods</i> , 2020, 17, 636-642.	9.0	60
113	Coordinate Nodal and BMP inhibition directs Baf60c-dependent cardiomyocyte commitment. <i>Genes and Development</i> , 2013, 27, 2332-2344.	2.7	54
114	Reactivation of Fetal Splicing Programs in Diabetic Hearts Is Mediated by Protein Kinase C Signaling. <i>Journal of Biological Chemistry</i> , 2013, 288, 35372-35386.	1.6	54
115	A Distinct MicroRNA Signature for Definitive Endoderm Derived From Human Embryonic Stem Cells. <i>Stem Cells and Development</i> , 2010, 19, 797-807.	1.1	51
116	Large-scale tethered function assays identify factors that regulate mRNA stability and translation. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 989-1000.	3.6	51
117	Active Protein Neddylation or Ubiquitylation Is Dispensable for Stress Granule Dynamics. <i>Cell Reports</i> , 2019, 27, 1356-1363.e3.	2.9	48
118	RNA-targeting CRISPR systems from metagenomic discovery to transcriptomic engineering. <i>Nature Cell Biology</i> , 2020, 22, 143-150.	4.6	48
119	Genome-Wide Approaches to Dissect the Roles of RNA Binding Proteins in Translational Control: Implications for Neurological Diseases. <i>Frontiers in Neuroscience</i> , 2012, 6, 144.	1.4	47
120	Deep sequencing identifies new and regulated microRNAs in <i>Schmidtea mediterranea</i> . <i>Rna</i> , 2009, 15, 1483-1491.	1.6	46
121	Rbfox2 function in RNA metabolism is impaired in hypoplastic left heart syndrome patient hearts. <i>Scientific Reports</i> , 2016, 6, 30896.	1.6	45
122	AMPK regulation of Raptor and TSC2 mediate metformin effects on transcriptional control of anabolism and inflammation. <i>Genes and Development</i> , 2020, 34, 1330-1344.	2.7	45
123	Longitudinal assessment of tumor development using cancer avatars derived from genetically engineered pluripotent stem cells. <i>Nature Communications</i> , 2020, 11, 550.	5.8	45
124	Integrin Activation Controls Regulatory T Cell-Mediated Peripheral Tolerance. <i>Journal of Immunology</i> , 2018, 200, 4012-4023.	0.4	44
125	Zmat3 Is a Key Splicing Regulator in the p53 Tumor Suppression Program. <i>Molecular Cell</i> , 2020, 80, 452-469.e9.	4.5	44
126	Suppression of Endothelial AGO1 Promotes Adipose Tissue Browning and Improves Metabolic Dysfunction. <i>Circulation</i> , 2020, 142, 365-379.	1.6	44

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127	Functional Genomic Analysis of the let-7 Regulatory Network in <i>Caenorhabditis elegans</i> . <i>PLoS Genetics</i> , 2013, 9, e1003353.	1.5	43
128	A multi-scale map of cell structure fusing protein images and interactions. <i>Nature</i> , 2021, 600, 536-542.	13.7	43
129	RNA-binding protein CPEB1 remodels host and viral RNA landscapes. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 1101-1110.	3.6	40
130	Nol12 is a multifunctional RNA binding protein at the nexus of RNA and DNA metabolism. <i>Nucleic Acids Research</i> , 2017, 45, 12509-12528.	6.5	40
131	Regulation of Asymmetric Division and CD8+ T Lymphocyte Fate Specification by Protein Kinase C η and Protein Kinase C δ . <i>Journal of Immunology</i> , 2015, 194, 2249-2259.	0.4	38
132	Allele-specific binding of RNA-binding proteins reveals functional genetic variants in the RNA. <i>Nature Communications</i> , 2019, 10, 1338.	5.8	38
133	Huntington's disease mice and human brain tissue exhibit increased G3BP1 granules and TDP43 mislocalization. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	38
134	Genomic analysis of the molecular neuropathology of tuberous sclerosis using a human stem cell model. <i>Genome Medicine</i> , 2016, 8, 94.	3.6	37
135	CRISPR/Cas9-mediated integration enables TAG-eCLIP of endogenously tagged RNA binding proteins. <i>Methods</i> , 2017, 118-119, 50-59.	1.9	37
136	Patch-Seq Protocol to Analyze the Electrophysiology, Morphology and Transcriptome of Whole Single Neurons Derived From Human Pluripotent Stem Cells. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 261.	1.4	37
137	An in vivo genome-wide CRISPR screen identifies the RNA-binding protein Stauf2 as a key regulator of myeloid leukemia. <i>Nature Cancer</i> , 2020, 1, 410-422.	5.7	37
138	The sustained expression of Cas9 targeting toxic RNAs reverses disease phenotypes in mouse models of myotonic dystrophy type 1. <i>Nature Biomedical Engineering</i> , 2021, 5, 157-168.	11.6	37
139	Illuminating RNA biology through imaging. <i>Nature Cell Biology</i> , 2022, 24, 815-824.	4.6	34
140	Immunoglobulin light chain (IgL) genes in zebrafish: Genomic configurations and inversional rearrangements between (V)J(C) gene clusters. <i>Developmental and Comparative Immunology</i> , 2008, 32, 421-434.	1.0	33
141	Retrotransposon long interspersed nucleotide element-1 (LINE-1) is activated during salamander limb regeneration. <i>Development Growth and Differentiation</i> , 2012, 54, 673-685.	0.6	33
142	Applications of Cas9 as an RNA-programmed RNA-binding protein. <i>BioEssays</i> , 2015, 37, 732-739.	1.2	33
143	Loss of LUC7L2 and U1 snRNP subunits shifts energy metabolism from glycolysis to OXPHOS. <i>Molecular Cell</i> , 2021, 81, 1905-1919.e12.	4.5	33
144	Tethered Function Assays as Tools to Elucidate the Molecular Roles of RNA-Binding Proteins. <i>Advances in Experimental Medicine and Biology</i> , 2016, 907, 61-88.	0.8	32

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145	Emergence of an early SARS-CoV-2 epidemic in the United States. <i>Cell</i> , 2021, 184, 4939-4952.e15.	13.5	31
146	The <i>C. elegans</i> neural editome reveals an ADAR target mRNA required for proper chemotaxis. <i>ELife</i> , 2017, 6, .	2.8	31
147	The Calcineurin Variant CnA ²¹ Controls Mouse Embryonic Stem Cell Differentiation by Directing mTORC2 Membrane Localization and Activation. <i>Cell Chemical Biology</i> , 2016, 23, 1372-1382.	2.5	30
148	S-nitrosylated TDP-43 triggers aggregation, cell-to-cell spread, and neurotoxicity in hiPSCs and in vivo models of ALS/FTD. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	28
149	An important class of intron retention events in human erythroblasts is regulated by cryptic exons proposed to function as splicing decoys. <i>Rna</i> , 2018, 24, 1255-1265.	1.6	27
150	Genome-wide approaches in the study of microRNA biology. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2011, 3, 491-512.	6.6	26
151	Self-Transfecting Micellar RNA: Modulating Nanoparticle Cell Interactions via High Density Display of Small Molecule Ligands on Micelle Coronas. <i>Bioconjugate Chemistry</i> , 2018, 29, 126-135.	1.8	26
152	Transcriptome-wide identification of RNA-binding protein binding sites using seCLIP-seq. <i>Nature Protocols</i> , 2022, 17, 1223-1265.	5.5	26
153	Evaluation of Engineered CRISPR-Cas-Mediated Systems for Site-Specific RNA Editing. <i>Cell Reports</i> , 2020, 33, 108350.	2.9	25
154	The long noncoding RNA Malat1 regulates CD8+ T cell differentiation by mediating epigenetic repression. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	25
155	The Period protein homolog LIN-42 negatively regulates microRNA biogenesis in <i>C. elegans</i> . <i>Developmental Biology</i> , 2014, 390, 126-135.	0.9	24
156	Variation in single-nucleotide sensitivity of eCLIP derived from reverse transcription conditions. <i>Methods</i> , 2017, 126, 29-37.	1.9	24
157	Pre-existing adaptive immunity to the RNA-editing enzyme Cas13d in humans. <i>Nature Medicine</i> , 2022, 28, 1372-1376.	15.2	24
158	Blurred Boundaries: The RNA Binding Protein Lin28A Is Also an Epigenetic Regulator. <i>Molecular Cell</i> , 2016, 61, 1-2.	4.5	23
159	Gain-of-function cardiomyopathic mutations in RBM20 rewire splicing regulation and re-distribute ribonucleoprotein granules within processing bodies. <i>Nature Communications</i> , 2021, 12, 6324.	5.8	23
160	A Novel Splice-Site Mutation in ALS2 Establishes the Diagnosis of Juvenile Amyotrophic Lateral Sclerosis in a Family with Early Onset Anarthria and Generalized Dystonias. <i>PLoS ONE</i> , 2014, 9, e113258.	1.1	22
161	A role for alternative splicing in circadian control of exocytosis and glucose homeostasis. <i>Genes and Development</i> , 2020, 34, 1089-1105.	2.7	22
162	Tissue-selective restriction of RNA editing of CaV1.3 by splicing factor SRSF9. <i>Nucleic Acids Research</i> , 2018, 46, 7323-7338.	6.5	21

#	ARTICLE	IF	CITATIONS
163	Peptide Brush Polymers for Efficient Delivery of a Gene Editing Protein to Stem Cells. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 15646-15649.	7.2	21
164	DDX5 promotes oncogene C3 and FABP1 expressions and drives intestinal inflammation and tumorigenesis. <i>Life Science Alliance</i> , 2020, 3, e202000772.	1.3	21
165	Footprinting SHAPE-eCLIP Reveals Transcriptome-wide Hydrogen Bonds at RNA-Protein Interfaces. <i>Molecular Cell</i> , 2020, 80, 903-914.e8.	4.5	20
166	Transcriptome-wide analysis of PGC-1 β binding RNAs identifies genes linked to glucagon metabolic action. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 22204-22213.	3.3	20
167	Repeat RNA expansion disorders of the nervous system: post-transcriptional mechanisms and therapeutic strategies. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2021, 56, 31-53.	2.3	20
168	A protein-RNA interaction atlas of the ribosome biogenesis factor AATF. <i>Scientific Reports</i> , 2019, 9, 11071.	1.6	19
169	The mRNA Decay Factor CAR-1/LSM14 Regulates Axon Regeneration via Mitochondrial Calcium Dynamics. <i>Current Biology</i> , 2020, 30, 865-876.e7.	1.8	19
170	Integrative RNA-omics Discovers <i>GNAS</i> Alternative Splicing as a Phenotypic Driver of Splicing Factor-Mutant Neoplasms. <i>Cancer Discovery</i> , 2022, 12, 836-855.	7.7	19
171	Persistent mRNA localization defects and cell death in ALS neurons caused by transient cellular stress. <i>Cell Reports</i> , 2021, 36, 109685.	2.9	18
172	Glial cells maintain synapses by inhibiting an activity-dependent retrograde protease signal. <i>PLoS Genetics</i> , 2019, 15, e1007948.	1.5	17
173	Multiple layers of molecular controls modulate self-renewal and neuronal lineage specification of embryonic stem cells. <i>Human Molecular Genetics</i> , 2008, 17, R67-R75.	1.4	16
174	Experimental and Computational Considerations in the Study of RNA-Binding Protein-RNA Interactions. <i>Advances in Experimental Medicine and Biology</i> , 2016, 907, 1-28.	0.8	15
175	Disruption in A-to-I Editing Levels Affects <i>C.Âelegans</i> Development More Than a Complete Lack of Editing. <i>Cell Reports</i> , 2019, 27, 1244-1253.e4.	2.9	15
176	A Transcriptome-wide Translational Program Defined by LIN28B Expression Level. <i>Molecular Cell</i> , 2019, 73, 304-313.e3.	4.5	15
177	Conserved metabolite regulation of stress granule assembly via AdoMet. <i>Journal of Cell Biology</i> , 2020, 219, .	2.3	14
178	Analysis of SARS-CoV-2 RNA Persistence across Indoor Surface Materials Reveals Best Practices for Environmental Monitoring Programs. <i>MSystems</i> , 2021, 6, e0113621.	1.7	14
179	Alternative Splicing of a Novel Inducible Exon Diversifies the CASK Guanylate Kinase Domain. <i>Journal of Nucleic Acids</i> , 2012, 2012, 1-15.	0.8	12
180	The ViReflow pipeline enables user friendly large scale viral consensus genome reconstruction. <i>Scientific Reports</i> , 2022, 12, 5077.	1.6	12

#	ARTICLE	IF	CITATIONS
181	Handwashing and Detergent Treatment Greatly Reduce SARS-CoV-2 Viral Load on Halloween Candy Handled by COVID-19 Patients. <i>MSystems</i> , 2020, 5, .	1.7	11
182	ADAR and hnRNPC deficiency synergize in activating endogenous dsRNA-induced type I IFN responses. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	11
183	Aberrant NOVA1 function disrupts alternative splicing in early stages of amyotrophic lateral sclerosis. <i>Acta Neuropathologica</i> , 2022, 144, 413-435.	3.9	11
184	Nxf1 Natural Variant E610G Is a Semi-dominant Suppressor of IAP-Induced RNA Processing Defects. <i>PLoS Genetics</i> , 2015, 11, e1005123.	1.5	10
185	Alternative Splicing in Stem Cell Self-Renewal and Differentiation. <i>Advances in Experimental Medicine and Biology</i> , 2010, 695, 92-104.	0.8	10
186	The Host-Microbiome Response to Hyperbaric Oxygen Therapy in Ulcerative Colitis Patients. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2022, 14, 35-53.	2.3	10
187	Nuclear and cytoplasmic poly(A) binding proteins (PABPs) favor distinct transcripts and isoforms. <i>Nucleic Acids Research</i> , 2022, 50, 4685-4702.	6.5	9
188	Non-microRNA binding competitively inhibits LIN28 regulation. <i>Cell Reports</i> , 2021, 36, 109517.	2.9	8
189	MECP2-related pathways are dysregulated in a cortical organoid model of myotonic dystrophy. <i>Science Translational Medicine</i> , 2022, 14, .	5.8	8
190	Splicing regulators: targets and drugs. <i>Genome Biology</i> , 2005, 6, 240.	13.9	7
191	Comprehensive Identification of miRNA Target Sites in Live Animals. <i>Methods in Molecular Biology</i> , 2011, 732, 169-185.	0.4	7
192	Reply to: "CD8+ T cell diversification by asymmetric cell division". <i>Nature Immunology</i> , 2015, 16, 893-894.	7.0	7
193	Peptide Brush Polymers for Efficient Delivery of a Gene Editing Protein to Stem Cells. <i>Angewandte Chemie</i> , 2019, 131, 15793-15796.	1.6	6
194	RNA binding protein DDX5 directs tuft cell specification and function to regulate microbial repertoire and disease susceptibility in the intestine. <i>Gut</i> , 2022, 71, 1790-1802.	6.1	6
195	Crosstalk between CRISPR-Cas9 and the human transcriptome. <i>Nature Communications</i> , 2022, 13, 1125.	5.8	6
196	Zika Virus Is Transmitted in Neural Progenitor Cells via Cell-to-Cell Spread, and Infection Is Inhibited by the Autophagy Inducer Trehalose. <i>Journal of Virology</i> , 2021, 95, .	1.5	5
197	A CRISPR RNA-binding protein screen reveals regulators of RUNX1 isoform generation. <i>Blood Advances</i> , 2021, 5, 1310-1323.	2.5	5
198	SARS-CoV-2 Distribution in Residential Housing Suggests Contact Deposition and Correlates with <i>Rothia</i> sp.. <i>MSystems</i> , 2022, 7, e0141121.	1.7	5

#	ARTICLE	IF	CITATIONS
199	RNA-Seq Analysis of Gene Expression and Alternative Splicing by Double-Random Priming Strategy. <i>Methods in Molecular Biology</i> , 2011, 729, 247-255.	0.4	4
200	Global analysis of RNA-binding proteins identifies a positive feedback loop between LARP1 and MYC that promotes tumorigenesis. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, 147.	2.4	4
201	Identification of the global miR-130a targetome reveals a role for TBL1XR1 in hematopoietic stem cell self-renewal and t(8;21) AML. <i>Cell Reports</i> , 2022, 38, 110481.	2.9	4
202	Implementation of Practical Surface SARS-CoV-2 Surveillance in School Settings. <i>MSystems</i> , 2022, 7, .	1.7	4
203	Making the cut in the dark genome. <i>Science</i> , 2016, 354, 705-706.	6.0	3
204	The <i>Thermus thermophilus</i> DEAD-box protein Hera is a general RNA binding protein and plays a key role in tRNA metabolism. <i>Rna</i> , 2020, 26, 1557-1574.	1.6	3
205	APEX Proximity Labeling of Stress Granule Proteins. <i>Methods in Molecular Biology</i> , 2022, 2428, 381-399.	0.4	3
206	The splicing factor RBM17 drives leukemic stem cell maintenance by evading nonsense-mediated decay of pro-leukemic factors. <i>Nature Communications</i> , 2022, 13, .	5.8	3
207	Regulatory network of microRNAs in RAW 264.7 macrophage cells. , 2010, 2010, 6198-201.		2
208	Discovery and Functional Interrogation of the Virus and Host RNA Interactome of SARS-Cov-2 Proteins. <i>SSRN Electronic Journal</i> , 0, , .	0.4	2
209	Contextâ€dependent and Diseaseâ€specific Diversity in Stress Granules Formed from Preâ€existing Protein Interactions. <i>FASEB Journal</i> , 2018, 32, 252.3.	0.2	2
210	Motoneuron expression profiling identifies an association between an axonal splice variant of HDGF-related protein 3 and peripheral myelination. <i>Journal of Biological Chemistry</i> , 2020, 295, 12233-12246.	1.6	1
211	fSHAPE, fSHAPE-eCLIP, and SHAPE-eCLIP probe transcript regions that interact with specific proteins. <i>STAR Protocols</i> , 2021, 2, 100762.	0.5	1
212	Integrative genomeâ€wide analysis reveals cooperative regulation of alternative splicing by hnRNP proteins. <i>FASEB Journal</i> , 2012, 26, 748.1.	0.2	1
213	Abstract 3558: The role of miRNA in PAX3-FKHR positive rhabdomyosarcoma. , 2014, , .		1
214	SINGLE CELL ANALYSIS, WHAT IS IN THE FUTURE?. , 2018, , .		1
215	Sentinel Cards Provide Practical SARS-CoV-2 Monitoring in School Settings. <i>MSystems</i> , 2022, 7, .	1.7	1
216	Musashi-2 posttranscriptionally attenuates aryl hydrocarbon receptor signaling to expand human hematopoietic stem cells. <i>Experimental Hematology</i> , 2015, 43, S90.	0.2	0

#	ARTICLE	IF	CITATIONS
217	From Protein-RNA Predictions toward a Peptide-RNA Code. <i>Molecular Cell</i> , 2016, 64, 437-438.	4.5	0
218	Analysis of Single Cells on a Pseudotime Scale along Postnatal Pancreatic Beta Cell Development. , 2017, , .		0
219	MEDLI-44. MUSASHI-1 IS A MASTER REGULATOR OF ABERRANT TRANSLATION IN GROUP 3 MEDULLOBLASTOMA. <i>Neuro-Oncology</i> , 2019, 21, ii112-ii113.	0.6	0
220	TMOD-28. AUTHENTIC HUMAN GLIOMA MODELING USING GENETICALLY ENGINEERED INDUCED PLURIPOTENT STEM CELLS. <i>Neuro-Oncology</i> , 2019, 21, vi268-vi269.	0.6	0
221	OTEH-9. scRNA sequencing of proneural GBM avatar model reveals acquisition of oncogenic transcriptional programming and infers a developmental path towards a genomically unstable state. <i>Neuro-Oncology Advances</i> , 2021, 3, ii12-ii12.	0.4	0
222	Discovery and Analysis of Evolutionarily Conserved Intronic Splicing Regulatory Elements in Mammalian Genomes. <i>PLoS Genetics</i> , 2005, preprint, e85.	1.5	0
223	The small RNA complement of salamander limb regeneration. <i>FASEB Journal</i> , 2012, 26, 952.5.	0.2	0
224	Discrete LIN28 binding sites in mature messenger RNA sequences reveals regulation of a network of splicing factors and downstream alternative splicing patterns. <i>FASEB Journal</i> , 2012, 26, 951.4.	0.2	0
225	Intron Retention Mechanisms That Regulate SF3B1 and Mitoferrin Gene Expression during Late Erythropoiesis. <i>Blood</i> , 2016, 128, 1200-1200.	0.6	0
226	Active Protein Neddylaton or Ubiquitylation is Dispensable for Stress Granule Dynamics. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
227	Vascular Modulation of Adipose function: Role of Endothelial Argonaute 1. <i>FASEB Journal</i> , 2019, 33, 527.12.	0.2	0
228	Abstract LB-187: Enhanced mapping of N6-methyladenosine (m6A) RNA modification sites with m6A-eCLIP. , 2020, , .		0
229	Adaptation of enhanced crosslinking and immunoprecipitation (eCLIP) for the high-throughput, high-resolution mapping of N6-methyladenosine modifications. <i>FASEB Journal</i> , 2020, 34, 1-1.	0.2	0
230	Antibody-Oligonucleotide Conjugation Using a SPAAC Copper-Free Method Compatible with 10 ⁴ -Genomics™ Single-Cell RNA-Seq. <i>Methods in Molecular Biology</i> , 2022, 2463, 67-80.	0.4	0