

# 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	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
2	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
3	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
4	APEX Proximity Labeling of Stress Granule Proteins. <i>Methods in Molecular Biology</i> , 2022, 2428, 381-399.	0.4	3
5	Antibody-Oligonucleotide Conjugation Using a SPAAC Copper-Free Method Compatible with 10 <sup>5</sup> -Genomics™ Single-Cell RNA-Seq. <i>Methods in Molecular Biology</i> , 2022, 2463, 67-80.	0.4	0
6	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
7	Crosstalk between CRISPR-Cas9 and the human transcriptome. <i>Nature Communications</i> , 2022, 13, 1125.	5.8	6
8	The ViReflow pipeline enables user friendly large scale viral consensus genome reconstruction. <i>Scientific Reports</i> , 2022, 12, 5077.	1.6	12
9	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
10	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
11	Transcriptome-wide identification of RNA-binding protein binding sites using seCLIP-seq. <i>Nature Protocols</i> , 2022, 17, 1223-1265.	5.5	26
12	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
13	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
14	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
15	Sentinel Cards Provide Practical SARS-CoV-2 Monitoring in School Settings. <i>MSystems</i> , 2022, 7, .	1.7	1
16	Illuminating RNA biology through imaging. <i>Nature Cell Biology</i> , 2022, 24, 815-824.	4.6	34
17	Implementation of Practical Surface SARS-CoV-2 Surveillance in School Settings. <i>MSystems</i> , 2022, 7, .	1.7	4
18	Pre-existing adaptive immunity to the RNA-editing enzyme Cas13d in humans. <i>Nature Medicine</i> , 2022, 28, 1372-1376.	15.2	24

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19	MECP2-related pathways are dysregulated in a cortical organoid model of myotonic dystrophy. <i>Science Translational Medicine</i> , 2022, 14, .	5.8	8
20	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
21	Aberrant NOVA1 function disrupts alternative splicing in early stages of amyotrophic lateral sclerosis. <i>Acta Neuropathologica</i> , 2022, 144, 413-435.	3.9	11
22	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
23	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
24	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
25	Reintroduction of the archaic variant of <i>NOVA1</i> in cortical organoids alters neurodevelopment. <i>Science</i> , 2021, 371, .	6.0	96
26	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
27	A CRISPR RNA-binding protein screen reveals regulators of RUNX1 isoform generation. <i>Blood Advances</i> , 2021, 5, 1310-1323.	2.5	5
28	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
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	Robust single-cell discovery of RNA targets of RNA-binding proteins and ribosomes. <i>Nature Methods</i> , 2021, 18, 507-519.	9.0	77
31	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
32	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
33	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
34	Inhibition of YTHDF2 triggers proteotoxic cell death in MYC-driven breast cancer. <i>Molecular Cell</i> , 2021, 81, 3048-3064.e9.	4.5	86
35	Non-microRNA binding competitively inhibits LIN28 regulation. <i>Cell Reports</i> , 2021, 36, 109517.	2.9	8
36	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

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37	fSHAPE, fSHAPE-eCLIP, and SHAPE-eCLIP probe transcript regions that interact with specific proteins. STAR Protocols, 2021, 2, 100762.	0.5	1
38	Emergence of an early SARS-CoV-2 epidemic in the United States. Cell, 2021, 184, 4939-4952.e15.	13.5	31
39	Gain-of-function cardiomyopathic mutations in RBM20 rewire splicing regulation and re-distribute ribonucleoprotein granules within processing bodies. Nature Communications, 2021, 12, 6324.	5.8	23
40	Analysis of SARS-CoV-2 RNA Persistence across Indoor Surface Materials Reveals Best Practices for Environmental Monitoring Programs. MSystems, 2021, 6, e0113621.	1.7	14
41	A multi-scale map of cell structure fusing protein images and interactions. Nature, 2021, 600, 536-542.	13.7	43
42	Direct RNA sequencing enables m <sup>6</sup> A detection in endogenous transcript isoforms at base-specific resolution. Rna, 2020, 26, 19-28.	1.6	150
43	Base editing: advances and therapeutic opportunities. Nature Reviews Drug Discovery, 2020, 19, 839-859.	21.5	218
44	G4C2 Repeat RNA Initiates a POM121-Mediated Reduction in Specific Nucleoporins in C9orf72 ALS/FTD. Neuron, 2020, 107, 1124-1140.e11.	3.8	88
45	The <i>Thermus thermophilus</i> DEAD-box protein Hera is a general RNA binding protein and plays a key role in tRNA metabolism. Rna, 2020, 26, 1557-1574.	1.6	3
46	Footprinting SHAPE-eCLIP Reveals Transcriptome-wide Hydrogen Bonds at RNA-Protein Interfaces. Molecular Cell, 2020, 80, 903-914.e8.	4.5	20
47	Handwashing and Detergent Treatment Greatly Reduce SARS-CoV-2 Viral Load on Halloween Candy Handled by COVID-19 Patients. MSystems, 2020, 5, .	1.7	11
48	Transcriptome-wide profiles of circular RNA and RNA-binding protein interactions reveal effects on circular RNA biogenesis and cancer pathway expression. Genome Medicine, 2020, 12, 112.	3.6	106
49	Motoneuron expression profiling identifies an association between an axonal splice variant of HDGF-related protein 3 and peripheral myelination. Journal of Biological Chemistry, 2020, 295, 12233-12246.	1.6	1
50	A large-scale binding and functional map of human RNA-binding proteins. Nature, 2020, 583, 711-719.	13.7	667
51	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	13.7	1,252
52	Transcriptome-wide analysis of PGC-1 $\alpha$ binding RNAs identifies genes linked to glucagon metabolic action. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 22204-22213.	3.3	20
53	AMPK regulation of Raptor and TSC2 mediate metformin effects on transcriptional control of anabolism and inflammation. Genes and Development, 2020, 34, 1330-1344.	2.7	45
54	Large-scale tethered function assays identify factors that regulate mRNA stability and translation. Nature Structural and Molecular Biology, 2020, 27, 989-1000.	3.6	51

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55	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
56	Evaluation of Engineered CRISPR-Cas-Mediated Systems for Site-Specific RNA Editing. <i>Cell Reports</i> , 2020, 33, 108350.	2.9	25
57	Zmat3 Is a Key Splicing Regulator in the p53 Tumor Suppression Program. <i>Molecular Cell</i> , 2020, 80, 452-469.e9.	4.5	44
58	An in vivo genome-wide CRISPR screen identifies the RNA-binding protein Staufen2 as a key regulator of myeloid leukemia. <i>Nature Cancer</i> , 2020, 1, 410-422.	5.7	37
59	Pooled CRISPR screens with imaging on microarray reveals stress granule-regulatory factors. <i>Nature Methods</i> , 2020, 17, 636-642.	9.0	60
60	Suppression of Endothelial AGO1 Promotes Adipose Tissue Browning and Improves Metabolic Dysfunction. <i>Circulation</i> , 2020, 142, 365-379.	1.6	44
61	Early precursors and molecular determinants of tissue-resident memory CD8 <sup>+</sup> T lymphocytes revealed by single-cell RNA sequencing. <i>Science Immunology</i> , 2020, 5, .	5.6	124
62	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
63	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
64	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
65	How RNA-Binding Proteins Interact with RNA: Molecules and Mechanisms. <i>Molecular Cell</i> , 2020, 78, 9-29.	4.5	396
66	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
67	Heterogenous Populations of Tissue-Resident CD8 <sup>+</sup> T Cells Are Generated in Response to Infection and Malignancy. <i>Immunity</i> , 2020, 52, 808-824.e7.	6.6	149
68	RNA-targeting CRISPR systems from metagenomic discovery to transcriptomic engineering. <i>Nature Cell Biology</i> , 2020, 22, 143-150.	4.6	48
69	Conserved metabolite regulation of stress granule assembly via AdoMet. <i>Journal of Cell Biology</i> , 2020, 219, .	2.3	14
70	Context-dependent functional compensation between Ythdf m <sup>6</sup> A reader proteins. <i>Genes and Development</i> , 2020, 34, 1373-1391.	2.7	158
71	DDX5 promotes oncogene C3 and FABP1 expressions and drives intestinal inflammation and tumorigenesis. <i>Life Science Alliance</i> , 2020, 3, e202000772.	1.3	21
72	Abstract LB-187: Enhanced mapping of N6-methyladenosine (m6A) RNA modification sites with m6A-eCLIP. , 2020, , .		0

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73	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
74	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
75	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
76	A protein-RNA interaction atlas of the ribosome biogenesis factor AATF. <i>Scientific Reports</i> , 2019, 9, 11071.	1.6	19
77	MEDU-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
78	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
79	Pervasive Chromatin-RNA Binding Protein Interactions Enable RNA-Based Regulation of Transcription. <i>Cell</i> , 2019, 178, 107-121.e18.	13.5	224
80	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
81	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
82	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
83	Disruption of RNA Metabolism in Neurological Diseases and Emerging Therapeutic Interventions. <i>Neuron</i> , 2019, 102, 294-320.	3.8	176
84	Active Protein Neddylation or Ubiquitylation Is Dispensable for Stress Granule Dynamics. <i>Cell Reports</i> , 2019, 27, 1356-1363.e3.	2.9	48
85	Allele-specific binding of RNA-binding proteins reveals functional genetic variants in the RNA. <i>Nature Communications</i> , 2019, 10, 1338.	5.8	38
86	Glial cells maintain synapses by inhibiting an activity-dependent retrograde protease signal. <i>PLoS Genetics</i> , 2019, 15, e1007948.	1.5	17
87	TMOD-28. AUTHENTIC HUMAN GLIOMA MODELING USING GENETICALLY ENGINEERED INDUCED PLURIPOTENT STEM CELLS. <i>Neuro-Oncology</i> , 2019, 21, vi268-vi269.	0.6	0
88	Widespread RNA editing dysregulation in brains from autistic individuals. <i>Nature Neuroscience</i> , 2019, 22, 25-36.	7.1	161
89	Regulation of RNA editing by RNA-binding proteins in human cells. <i>Communications Biology</i> , 2019, 2, 19.	2.0	97
90	RBP-Maps enables robust generation of splicing regulatory maps. <i>Rna</i> , 2019, 25, 193-204.	1.6	63

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91	A Transcriptome-wide Translational Program Defined by LIN28B Expression Level. <i>Molecular Cell</i> , 2019, 73, 304-313.e3.	4.5	15
92	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
93	Vascular Modulation of Adipose function: Role of Endothelial Argonaute 1. <i>FASEB Journal</i> , 2019, 33, 527.12.	0.2	0
94	Context-Dependent and Disease-Specific Diversity in Protein Interactions within Stress Granules. <i>Cell</i> , 2018, 172, 590-604.e13.	13.5	672
95	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
96	Integrin Activation Controls Regulatory T Cell-Mediated Peripheral Tolerance. <i>Journal of Immunology</i> , 2018, 200, 4012-4023.	0.4	44
97	Systematic Discovery of RNA Binding Proteins that Regulate MicroRNA Levels. <i>Molecular Cell</i> , 2018, 69, 1005-1016.e7.	4.5	107
98	Advances and challenges in the detection of transcriptome-wide protein-RNA interactions. <i>Wiley Interdisciplinary Reviews RNA</i> , 2018, 9, e1436.	3.2	150
99	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
100	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
101	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
102	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
103	Sequence, Structure, and Context Preferences of Human RNA Binding Proteins. <i>Molecular Cell</i> , 2018, 70, 854-867.e9.	4.5	408
104	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
105	Context-dependent and Disease-specific Diversity in Stress Granules Formed from Pre-existing Protein Interactions. <i>FASEB Journal</i> , 2018, 32, 252.3.	0.2	2
106	SINGLE CELL ANALYSIS, WHAT IS IN THE FUTURE?. , 2018, , .		1
107	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
108	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

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109	Interaction Landscape of Inherited Polymorphisms with Somatic Events in Cancer. <i>Cancer Discovery</i> , 2017, 7, 410-423.	7.7	121
110	High-Throughput and Cost-Effective Characterization of Induced Pluripotent Stem Cells. <i>Stem Cell Reports</i> , 2017, 8, 1101-1111.	2.3	64
111	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
112	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
113	CRISPR/Cas9-mediated integration enables TAG-eCLIP of endogenously tagged RNA binding proteins. <i>Methods</i> , 2017, 118-119, 50-59.	1.9	37
114	Analysis of Single Cells on a Pseudotime Scale along Postnatal Pancreatic Beta Cell Development. , 2017, , .		0
115	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
116	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
117	Genetic mutations in RNA-binding proteins and their roles in ALS. <i>Human Genetics</i> , 2017, 136, 1193-1214.	1.8	168
118	Elimination of Toxic Microsatellite Repeat Expansion RNA by RNA-Targeting Cas9. <i>Cell</i> , 2017, 170, 899-912.e10.	13.5	213
119	Variation in single-nucleotide sensitivity of eCLIP derived from reverse transcription conditions. <i>Methods</i> , 2017, 126, 29-37.	1.9	24
120	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
121	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
122	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
123	The <i>C. elegans</i> neural editome reveals an ADAR target mRNA required for proper chemotaxis. <i>ELife</i> , 2017, 6, .	2.8	31
124	MicroRNA-101 Regulates Multiple Developmental Programs to Constrain Excitation in Adult Neural Networks. <i>Neuron</i> , 2016, 92, 1337-1351.	3.8	73
125	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
126	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



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127	Musashi-2 attenuates AHR signalling to expand human haematopoietic stem cells. <i>Nature</i> , 2016, 532, 508-511.	13.7	101
128	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
129	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
130	SONAR Discovers RNA-Binding Proteins from Analysis of Large-Scale Protein-Protein Interactomes. <i>Molecular Cell</i> , 2016, 64, 282-293.	4.5	155
131	Pairing beyond the Seed Supports MicroRNA Targeting Specificity. <i>Molecular Cell</i> , 2016, 64, 320-333.	4.5	344
132	The Calcineurin Variant CnA $\hat{2}$ 1 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
133	Making the cut in the dark genome. <i>Science</i> , 2016, 354, 705-706.	6.0	3
134	RNA-binding protein CPEB1 remodels host and viral RNA landscapes. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 1101-1110.	3.6	40
135	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
136	From Protein-RNA Predictions toward a Peptide-RNA Code. <i>Molecular Cell</i> , 2016, 64, 437-438.	4.5	0
137	Rbfox2 function in RNA metabolism is impaired in hypoplastic left heart syndrome patient hearts. <i>Scientific Reports</i> , 2016, 6, 30896.	1.6	45
138	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
139	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
140	Dysregulation of RBFOX2 Is an Early Event in Cardiac Pathogenesis of Diabetes. <i>Cell Reports</i> , 2016, 15, 2200-2213.	2.9	60
141	PPAR- $\hat{1}$ 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
142	Programmable RNA Tracking in Live Cells with CRISPR/Cas9. <i>Cell</i> , 2016, 165, 488-496.	13.5	455
143	Resources for the Comprehensive Discovery of Functional RNA Elements. <i>Molecular Cell</i> , 2016, 61, 903-913.	4.5	118
144	A Small RNA-Catalytic Argonaute Pathway Tunes Germline Transcript Levels to Ensure Embryonic Divisions. <i>Cell</i> , 2016, 165, 396-409.	13.5	82

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145	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
146	Blurred Boundaries: The RNA Binding Protein Lin28A Is Also an Epigenetic Regulator. <i>Molecular Cell</i> , 2016, 61, 1-2.	4.5	23
147	Intron Retention Mechanisms That Regulate SF3B1 and Mitoferrin Gene Expression during Late Erythropoiesis. <i>Blood</i> , 2016, 128, 1200-1200.	0.6	0
148	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
149	Regulation of Asymmetric Division and CD8+ T Lymphocyte Fate Specification by Protein Kinase C $\eta$ and Protein Kinase C $\delta$ . <i>Journal of Immunology</i> , 2015, 194, 2249-2259.	0.4	38
150	Identification of Novel Long Noncoding RNAs Underlying Vertebrate Cardiovascular Development. <i>Circulation</i> , 2015, 131, 1278-1290.	1.6	185
151	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
152	Applications of Cas9 as an RNA-programmed RNA-binding protein. <i>BioEssays</i> , 2015, 37, 732-739.	1.2	33
153	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
154	RNA-binding proteins in neurodegeneration: Seq and you shall receive. <i>Trends in Neurosciences</i> , 2015, 38, 226-236.	4.2	97
155	Target Discrimination in Nonsense-Mediated mRNA Decay Requires Upf1 ATPase Activity. <i>Molecular Cell</i> , 2015, 59, 413-425.	4.5	89
156	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
157	Reply to: "CD8+ T cell diversification by asymmetric cell division". <i>Nature Immunology</i> , 2015, 16, 893-894.	7.0	7
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