List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Inherited retinal diseases: Linking genes, disease-causing variants, and relevant therapeutic modalities. Progress in Retinal and Eye Research, 2022, 89, 101029.	7.3	58
2	Landscape of adenosine-to-inosine RNA recoding across human tissues. Nature Communications, 2022, 13, 1184.	5.8	46
3	PO-675-08 A-G RNA EDITING AS A MEDIATOR OF ATRIAL FIBRILLATION. Heart Rhythm, 2022, 19, S342.	0.3	О
4	RNA editing contributes to epitranscriptome diversity in chronic lymphocytic leukemia. Leukemia, 2021, 35, 1053-1063.	3.3	17
5	RNA editing of the 5-HT2C receptor in the central nucleus of the amygdala is involved in resilience behavior. Translational Psychiatry, 2021, 11, 137.	2.4	6
6	Systematic identification of A-to-I RNA editing in zebrafish development and adult organs. Nucleic Acids Research, 2021, 49, 4325-4337.	6.5	21
7	Deciphering the principles of the RNA editing code via large-scale systematic probing. Molecular Cell, 2021, 81, 2374-2387.e3.	4.5	20
8	The New RNA-Editing Era – Ethical Considerations. Trends in Genetics, 2021, 37, 685-687.	2.9	4
9	Detection of A-to-I Hyper-edited RNA Sequences. Methods in Molecular Biology, 2021, 2181, 213-227.	0.4	3
10	ALU A-to-I RNA Editing: Millions of Sites and Many Open Questions. Methods in Molecular Biology, 2021, 2181, 149-162.	0.4	11
11	Global quantification exposes abundant low-level off-target activity by base editors. Genome Research, 2021, 31, 2354-2361.	2.4	14
12	A Parkinson's disease Circ <scp>RNA</scp> s Resource reveals a link between circ <scp>SLC</scp> 8A1 and oxidative stress. EMBO Molecular Medicine, 2020, 12, e11942.	3.3	93
13	Major Dysregulated Gene Sets and Increased RNA Editing in PolyI:C Treated Mice May Contribute to the Emergence of Major Neurodevelopmental Disorders. Biological Psychiatry, 2020, 87, S304.	0.7	0
14	Increased RNA editing in maternal immune activation model of neurodevelopmental disease. Nature Communications, 2020, 11, 5236.	5.8	24
15	The cell line A-to-I RNA editing catalogue. Nucleic Acids Research, 2020, 48, 5849-5858.	6.5	47
16	Purifying selection of long dsRNA is the first line of defense against false activation of innate immunity. Genome Biology, 2020, 21, 26.	3.8	31
17	Biallelic DMXL2 mutations impair autophagy and cause Ohtahara syndrome with progressive course. Brain, 2019, 142, 3876-3891.	3.7	23
18	Genome-wide quantification of ADAR adenosine-to-inosine RNA editing activity. Nature Methods, 2019, 16, 1131-1138.	9.0	126

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19	Adenosine-to-Inosine RNA Editing Within Corticolimbic Brain Regions Is Regulated in Response to Chronic Social Defeat Stress in Mice. Frontiers in Psychiatry, 2019, 10, 277.	1.3	15
20	Specific inhibition of splicing factor activity by decoy RNA oligonucleotides. Nature Communications, 2019, 10, 1590.	5.8	70
21	RNA editing is abundant and correlates with task performance in a social bumblebee. Nature Communications, 2019, 10, 1605.	5.8	57
22	Loss of ADAR1 in tumours overcomes resistance to immune checkpoint blockade. Nature, 2019, 565, 43-48.	13.7	449
23	Computational approaches for detection and quantification of A-to-I RNA-editing. Methods, 2019, 156, 25-31.	1.9	28
24	A-to-I RNA editing — immune protector and transcriptome diversifier. Nature Reviews Genetics, 2018, 19, 473-490.	7.7	402
25	Increased RNA Editing May Provide a Source for Autoantigens in Systemic Lupus Erythematosus. Cell Reports, 2018, 23, 50-57.	2.9	91
26	Human cancer tissues exhibit reduced A-to-I editing of miRNAs coupled with elevated editing of their targets. Nucleic Acids Research, 2018, 46, 71-82.	6.5	138
27	Whole-genome sequencing reveals principles of brain retrotransposition in neurodevelopmental disorders. Cell Research, 2018, 28, 187-203.	5.7	46
28	Decreased A-to-I RNA editing as a source of keratinocytes' dsRNA in psoriasis. Rna, 2018, 24, 828-840.	1.6	34
29	Identification of ADAR1 adenosine deaminase dependency in a subset of cancer cells. Nature Communications, 2018, 9, 5450.	5.8	157
30	A-to-I RNA Editing: An Overlooked Source of Cancer Mutations. Cancer Cell, 2018, 33, 789-790.	7.7	36
31	ROP: dumpster diving in RNA-sequencing to find the source of 1 trillion reads across diverse adult human tissues. Genome Biology, 2018, 19, 36.	3.8	42
32	<scp>RNA</scp> editing of Filamin A pre― <scp>mRNA</scp> regulates vascular contraction and diastolic blood pressure. EMBO Journal, 2018, 37, .	3.5	86
33	Control and automation of multilayered integrated microfluidic device fabrication. Lab on A Chip, 2017, 17, 557-566.	3.1	17
34	Abnormalities in A-to-I RNA editing patterns in CNS injuries correlate with dynamic changes in cell type composition. Scientific Reports, 2017, 7, 43421.	1.6	40
35	A-to-I RNA Editing in the Earliest-Diverging Eumetazoan Phyla. Molecular Biology and Evolution, 2017, 34, 1890-1901.	3.5	45
36	Trade-off between Transcriptome Plasticity and Genome Evolution in Cephalopods. Cell, 2017, 169, 191-202.e11.	13.5	268

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37	Integrating networks and comparative genomics reveals retroelement proliferation dynamics in hominid genomes. Science Advances, 2017, 3, e1701256.	4.7	16
38	RNA editing by ADAR1 leads to context-dependent transcriptome-wide changes in RNA secondary structure. Nature Communications, 2017, 8, 1440.	5.8	77
39	Dynamic hyper-editing underlies temperature adaptation in Drosophila. PLoS Genetics, 2017, 13, e1006931.	1.5	51
40	Massive A-to-I RNA editing is common across the Metazoa and correlates with dsRNA abundance. Genome Biology, 2017, 18, 185.	3.8	118
41	Promoting RNA editing by ADAR attraction. Genome Biology, 2017, 18, 196.	3.8	2
42	Extensive RNA editing and splicing increase immune self-representation diversity in medullary thymic epithelial cells. Genome Biology, 2016, 17, 219.	3.8	67
43	A novel homozygous splice site mutation in NALCN identified in siblings with cachexia, strabismus, severe intellectual disability, epilepsy and abnormal respiratory rhythm. European Journal of Medical Genetics, 2016, 59, 204-209.	0.7	28
44	Clustered mutations in hominid genome evolution are consistent with APOBEC3G enzymatic activity. Genome Research, 2016, 26, 579-587.	2.4	14
45	Expanding preconception carrier screening for the Jewish population using high throughput microfluidics technology and next generation sequencing. BMC Medical Genomics, 2016, 9, 24.	0.7	2
46	Transcriptome, genetic editing, and microRNA divergence substantiate sympatric speciation of blind mole rat, <i>Spalax</i> . Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7584-7589.	3.3	25
47	Activation-Induced Cytidine Deaminase Links Ovulation-Induced Inflammation and Serous Carcinogenesis. Neoplasia, 2016, 18, 90-99.	2.3	23
48	Reduced levels of protein recoding by A-to-I RNA editing in Alzheimer's disease. Rna, 2016, 22, 290-302.	1.6	122
49	DNA Editing of LTR Retrotransposons Reveals the Impact of APOBECs on Vertebrate Genomes. Molecular Biology and Evolution, 2016, 33, 554-567.	3.5	29
50	DNA Editing by APOBECs: A Genomic Preserver and Transformer. Trends in Genetics, 2016, 32, 16-28.	2.9	64
51	The majority of transcripts in the squid nervous system are extensively recoded by A-to-I RNA editing. ELife, 2015, 4, .	2.8	124
52	Fmrp Interacts with Adar and Regulates RNA Editing, Synaptic Density and Locomotor Activity in Zebrafish. PLoS Genetics, 2015, 11, e1005702.	1.5	76
53	Elevated RNA Editing Activity Is a Major Contributor to Transcriptomic Diversity in Tumors. Cell Reports, 2015, 13, 267-276.	2.9	262
54	m <sup>6</sup> A mRNA methylation facilitates resolution of naÃ⁻ve pluripotency toward differentiation. Science, 2015, 347, 1002-1006.	6.0	1,288

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55	Analysis of Intron Sequences Reveals Hallmarks of Circular RNA Biogenesis in Animals. Cell Reports, 2015, 10, 170-177.	2.9	918
56	Does RNA editing compensate for Alu invasion of the primate genome?. BioEssays, 2015, 37, 175-181.	1.2	17
57	DNA and RNA editing of retrotransposons accelerate mammalian genome evolution. Annals of the New York Academy of Sciences, 2015, 1341, 115-125.	1.8	15
58	Identification of recurrent regulated alternative splicing events across human solid tumors. Nucleic Acids Research, 2015, 43, 5130-5144.	6.5	137
59	Novel mutation in TSPAN12 leads to autosomal recessive inheritance of congenital vitreoretinal disease with intraâ€familial phenotypic variability. American Journal of Medical Genetics, Part A, 2014, 164, 2996-3002.	0.7	17
60	Positive correlation between ADAR expression and its targets suggests a complex regulation mediated by RNA editing in the human brain. RNA Biology, 2014, 11, 1447-1456.	1.5	14
61	A genome-wide map of hyper-edited RNA reveals numerous new sites. Nature Communications, 2014, 5, 4726.	5.8	193
62	A-to-I RNA editing occurs at over a hundred million genomic sites, located in a majority of human genes. Genome Research, 2014, 24, 365-376.	2.4	492
63	Genome-wide analysis of Alu editability. Nucleic Acids Research, 2014, 42, 6876-6884.	6.5	99
64	Characterizing of functional human coding RNA editing from evolutionary, structural, and dynamic perspectives. Proteins: Structure, Function and Bioinformatics, 2014, 82, 3117-3131.	1.5	15
65	Genome-wide adaptive complexes to underground stresses in blind mole rats Spalax. Nature Communications, 2014, 5, 3966.	5.8	124
66	Mammalian conserved ADAR targets comprise only a small fragment of the human editosome. Genome Biology, 2014, 15, R5.	13.9	152
67	Human housekeeping genes, revisited. Trends in Genetics, 2013, 29, 569-574.	2.9	1,091
68	Differential inhibition of LINE1 and LINE2 retrotransposition by vertebrate AID/APOBEC proteins. Retrovirology, 2013, 10, 156.	0.9	25
69	Activity-Dependent A-to-I RNA Editing in Rat Cortical Neurons. Genetics, 2012, 192, 281-287.	1.2	36
70	Large-scale DNA editing of retrotransposons accelerates mammalian genome evolution. Nature Communications, 2011, 2, 519.	5.8	43
71	Identification of Widespread Ultra-Edited Human RNAs. PLoS Genetics, 2011, 7, e1002317.	1.5	79
72	Age-related gene-specific changes of A-to-I mRNA editing in the human brain. Mechanisms of Ageing and Development, 2010, 131, 445-447.	2.2	40

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73	Consistent levels of A-to-I RNA editing across individuals in coding sequences and non-conserved Alu repeats. BMC Genomics, 2010, 11, 608.	1.2	33
74	Adenosine-to-inosine RNA editing shapes transcriptome diversity in primates. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 12174-12179.	3.3	155
75	A Survey of Genomic Traces Reveals a Common Sequencing Error, RNA Editing, and DNA Editing. PLoS Genetics, 2010, 6, e1000954.	1.5	40
76	Sequence based identification of RNA editing sites. RNA Biology, 2010, 7, 248-252.	1.5	35
77	Evidence for large diversity in the human transcriptome created by Alu RNA editing. Nucleic Acids Research, 2009, 37, 6905-6915.	6.5	58
78	Efficiency of complex production in changing environment. BMC Systems Biology, 2009, 3, 3.	3.0	9
79	Genome-Wide Identification of Human RNA Editing Sites by Parallel DNA Capturing and Sequencing. Science, 2009, 324, 1210-1213.	6.0	483
80	Intronic Alus Influence Alternative Splicing. PLoS Genetics, 2008, 4, e1000204.	1.5	129
81	Altered adenosine-to-inosine RNA editing in human cancer. Genome Research, 2007, 17, 1586-1595.	2.4	292
82	RNA-editing-mediated exon evolution. Genome Biology, 2007, 8, R29.	13.9	174
83	RNA editing level in the mouse is determined by the genomic repeat repertoire. Rna, 2006, 12, 1802-1809.	1.6	135
84	Algorithmic approaches for identification of RNA editing sites. Briefings in Functional Genomics & Proteomics, 2006, 5, 43-45.	3.8	13
85	Connectivity and expression in protein networks: Proteins in a complex are uniformly expressed. Physical Review E, 2006, 73, 031909.	0.8	14
86	Letter from the editor: adenosineâ€ŧoâ€inosine RNA editing in Alu repeats in the human genome. EMBO Reports, 2005, 6, 831-835.	2.0	51
87	From genome to antivirals: SARS as a test tube. Drug Discovery Today, 2005, 10, 345-352.	3.2	16
88	Is abundant A-to-I RNA editing primate-specific?. Trends in Genetics, 2005, 21, 77-81.	2.9	125
89	Is there any sense in antisense editing?. Trends in Genetics, 2005, 21, 544-547.	2.9	42
90	Evidence for abundant transcription of non-coding regions in the Saccharomyces cerevisiae genome. BMC Genomics, 2005, 6, 93.	1.2	23

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91	Identification of RNA editing sites in the SNP database. Nucleic Acids Research, 2005, 33, 4612-4617.	6.5	48
92	Evolutionarily conserved human targets of adenosine to inosine RNA editing. Nucleic Acids Research, 2005, 33, 1162-1168.	6.5	177
93	Systematic identification of abundant A-to-I editing sites in the human transcriptome. Nature Biotechnology, 2004, 22, 1001-1005.	9.4	740
94	Evolution of multicellularity in Metazoa: comparative analysis of the subcellular localization of proteins in Saccharomyces, Drosophila and Caenorhabditis. Cell Biology International, 2004, 28, 171-178.	1.4	11
95	The importance of alternative splicing in the drug discovery process. Targets, 2003, 2, 109-114.	0.3	8
96	Characterization of the nodulation plasmid encoded chemoreceptor gene mcpG from Rhizobium leguminosarum. BMC Microbiology, 2003, 3, 1.	1.3	24
97	Cloaked similarity between HIV-1 and SARS-CoV suggests an anti-SARS strategy. BMC Microbiology, 2003, 3, 20.	1.3	69
98	Human housekeeping genes are compact. Trends in Genetics, 2003, 19, 362-365.	2.9	612
99	Widespread occurrence of antisense transcription in the human genome. Nature Biotechnology, 2003, 21, 379-386.	9.4	607
100	Preferential Attachment in the Protein Network Evolution. Physical Review Letters, 2003, 91, 138701.	2.9	183
101	A-to-I Editing of ALU Repeats. , 0, , 255-279.		0