

# Yuki Kato

## List of Publications by Year in descending order

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Version: 2024-02-01

14  
papers

323  
citations

1163117

8  
h-index

1058476

14  
g-index

15  
all docs

15  
docs citations

15  
times ranked

229  
citing authors

#	ARTICLE	IF	CITATIONS
1	Prediction of RNA secondary structure including pseudoknots for long sequences. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	36
2	Age-dependent decline in remyelination capacity is mediated by apelinâ€‘APJ signaling. <i>Nature Aging</i> , 2021, 1, 284-294.	11.6	18
3	RNA editing at a limited number of sites is sufficient to prevent MDA5 activation in the mouse brain. <i>PLoS Genetics</i> , 2021, 17, e1009516.	3.5	42
4	Dimethylarginine dimethylaminohydrolase 1 as a novel regulator of oligodendrocyte differentiation in the central nervous system remyelination. <i>Glia</i> , 2021, 69, 2591-2604.	4.9	4
5	Mutations in the adenosine deaminase ADAR1 that prevent endogenous Z-RNA binding induce Aicardi-GoutiÃ‘res-syndrome-like encephalopathy. <i>Immunity</i> , 2021, 54, 1976-1988.e7.	14.3	56
6	An Aicardi-GoutiÃ‘res Syndromeâ€‘Causative Point Mutation in <i>Adar1</i> Gene Invokes Multiorgan Inflammation and Late-Onset Encephalopathy in Mice. <i>Journal of Immunology</i> , 2021, 207, 3016-3027.	0.8	11
7	ADAR1 Regulates Early T Cell Development via MDA5-Dependent and -Independent Pathways. <i>Journal of Immunology</i> , 2020, 204, 2156-2168.	0.8	17
8	A comparative analysis of ADAR mutant mice reveals site-specific regulation of RNA editing. <i>Rna</i> , 2020, 26, 454-469.	3.5	38
9	Bivartect: accurate and memory-saving breakpoint detection by direct read comparison. <i>Bioinformatics</i> , 2020, 36, 2725-2730.	4.1	3
10	ADAR-mediated RNA editing is required for thymic self-tolerance and inhibition of autoimmunity. <i>EMBO Reports</i> , 2018, 19, .	4.5	47
11	Myotube-derived factor promotes oligodendrocyte precursor cell proliferation. <i>Biochemical and Biophysical Research Communications</i> , 2018, 500, 609-613.	2.1	3
12	An accessibility-incorporated method for accurate prediction of RNA-RNA interactions from sequence data. <i>Bioinformatics</i> , 2017, 33, 202-209.	4.1	7
13	Alignment-free comparative genomic screen for structured RNAs using coarse-grained secondary structure dot plots. <i>BMC Genomics</i> , 2017, 18, 935.	2.8	1
14	DAFS: simultaneous aligning and folding of RNA sequences via dual decomposition. <i>Bioinformatics</i> , 2012, 28, 3218-3224.	4.1	40