

Marc Parisien

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

9,189
citations

201575

27
h-index

149623

56
g-index

62
all docs

62
docs citations

62
times ranked

10456
citing authors

#	ARTICLE	IF	CITATIONS
1	N6-methyladenosine-dependent regulation of messenger RNA stability. <i>Nature</i> , 2014, 505, 117-120.	13.7	3,138
2	N6-methyladenosine-dependent RNA structural switches regulate RNA-protein interactions. <i>Nature</i> , 2015, 518, 560-564.	13.7	1,482
3	The MC-Fold and MC-Sym pipeline infers RNA structure from sequence data. <i>Nature</i> , 2008, 452, 51-55.	13.7	726
4	N 6-methyladenosine alters RNA structure to regulate binding of a low-complexity protein. <i>Nucleic Acids Research</i> , 2017, 45, 6051-6063.	6.5	586
5	Probing <i>N</i> ⁶ -methyladenosine RNA modification status at single nucleotide resolution in mRNA and long noncoding RNA. <i>Rna</i> , 2013, 19, 1848-1856.	1.6	421
6	Regulation of Co-transcriptional Pre-mRNA Splicing by m6A through the Low-Complexity Protein hnRNPG. <i>Molecular Cell</i> , 2019, 76, 70-81.e9.	4.5	248
7	Angiogenin-Cleaved tRNA Halves Interact with Cytochrome <i>c</i> , Protecting Cells from Apoptosis during Osmotic Stress. <i>Molecular and Cellular Biology</i> , 2014, 34, 2450-2463.	1.1	236
8	Genome-wide Identification and Quantitative Analysis of Cleaved tRNA Fragments Induced by Cellular Stress. <i>Journal of Biological Chemistry</i> , 2012, 287, 42708-42725.	1.6	181
9	Staufen1 regulates diverse classes of mammalian transcripts. <i>EMBO Journal</i> , 2007, 26, 2670-2681.	3.5	174
10	N6-Methyladenosine Modification in a Long Noncoding RNA Hairpin Predisposes Its Conformation to Protein Binding. <i>Journal of Molecular Biology</i> , 2016, 428, 822-833.	2.0	164
11	Quantitative H2S-mediated protein sulfhydration reveals metabolic reprogramming during the integrated stress response. <i>ELife</i> , 2015, 4, e10067.	2.8	154
12	New metrics for comparing and assessing discrepancies between RNA 3D structures and models. <i>Rna</i> , 2009, 15, 1875-1885.	1.6	138
13	miR-183 cluster scales mechanical pain sensitivity by regulating basal and neuropathic pain genes. <i>Science</i> , 2017, 356, 1168-1171.	6.0	124
14	Single cell transcriptomics of primate sensory neurons identifies cell types associated with chronic pain. <i>Nature Communications</i> , 2021, 12, 1510.	5.8	121
15	Acute inflammatory response via neutrophil activation protects against the development of chronic pain. <i>Science Translational Medicine</i> , 2022, 14, eabj9954.	5.8	115
16	Queuosine modification protects cognate tRNAs against ribonuclease cleavage. <i>Rna</i> , 2018, 24, 1305-1313.	1.6	92
17	Effect of Human Genetic Variability on Gene Expression in Dorsal Root Ganglia and Association with Pain Phenotypes. <i>Cell Reports</i> , 2017, 19, 1940-1952.	2.9	83
18	Human pain genetics database: a resource dedicated to human pain genetics research. <i>Pain</i> , 2018, 159, 749-763.	2.0	80

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19	Diversity of human tRNA genes from the 1000-genomes project. <i>RNA Biology</i> , 2013, 10, 1853-1867.	1.5	79
20	The Cap-Binding Translation Initiation Factor, eIF4E, Binds a Pseudoknot in a Viral Cap-Independent Translation Element. <i>Structure</i> , 2011, 19, 868-880.	1.6	69
21	Genetic studies of human neuropathic pain conditions: a review. <i>Pain</i> , 2018, 159, 583-594.	2.0	64
22	Single-cell RNA sequencing reveals time- and sex-specific responses of mouse spinal cord microglia to peripheral nerve injury and links ApoE to chronic pain. <i>Nature Communications</i> , 2022, 13, 843.	5.8	62
23	RNA Structure Determination Using SAXS Data. <i>Journal of Physical Chemistry B</i> , 2010, 114, 10039-10048.	1.2	58
24	Genetic pathway analysis reveals a major role for extracellular matrix organization in inflammatory and neuropathic pain. <i>Pain</i> , 2019, 160, 932-944.	2.0	53
25	Microbiome characterization by high-throughput transfer RNA sequencing and modification analysis. <i>Nature Communications</i> , 2018, 9, 5353.	5.8	48
26	Genome-wide association reveals contribution of MRAS to painful temporomandibular disorder in males. <i>Pain</i> , 2019, 160, 579-591.	2.0	37
27	Theoretical modeling of multiprotein complexes by iSPOT: Integration of small-angle X-ray scattering, hydroxyl radical footprinting, and computational docking. <i>Journal of Structural Biology</i> , 2016, 196, 340-349.	1.3	34
28	COMT gene locus. <i>Pain</i> , 2015, 156, 2072-2083.	2.0	28
29	Discovery of a Redox Thiol Switch: Implications for Cellular Energy Metabolism. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 852-870.	2.5	28
30	Long-term male-specific chronic pain via telomere- and p53-mediated spinal cord cellular senescence. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	25
31	NMR structure of a 4 Å— 4 nucleotide RNA internal loop from an R2 retrotransposon: Identification of a three purine-purine sheared pair motif and comparison to MC-SYM predictions. <i>Rna</i> , 2011, 17, 1664-1677.	1.6	24
32	Determining RNA three-dimensional structures using low-resolution data. <i>Journal of Structural Biology</i> , 2012, 179, 252-260.	1.3	24
33	Genome-wide analysis identifies impaired axonogenesis in chronic overlapping pain conditions. <i>Brain</i> , 2022, 145, 1111-1123.	3.7	24
34	Rationalization and prediction of selective decoding of pseudouridine-modified nonsense and sense codons. <i>Rna</i> , 2012, 18, 355-367.	1.6	23
35	Discovering RNA-Protein Interactome by Using Chemical Context Profiling of the RNA-Protein Interface. <i>Cell Reports</i> , 2013, 3, 1703-1713.	2.9	23
36	Sex- and age-specific genetic analysis of chronic back pain. <i>Pain</i> , 2021, 162, 1176-1187.	2.0	21

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37	Alternative Splicing of the Delta-Opioid Receptor Gene Suggests Existence of New Functional Isoforms. <i>Molecular Neurobiology</i> , 2019, 56, 2855-2869.	1.9	20
38	NK cell recruitment limits tissue damage during an enteric helminth infection. <i>Mucosal Immunology</i> , 2020, 13, 357-370.	2.7	20
39	A new catalog of protein β -sheets. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 545-558.	1.5	18
40	Ranking the factors that contribute to protein β -sheet folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 824-829.	1.5	17
41	A genetic polymorphism that is associated with mitochondrial energy metabolism increases risk of fibromyalgia. <i>Pain</i> , 2020, 161, 2860-2871.	2.0	17
42	The dichotomous role of epiregulin in pain. <i>Pain</i> , 2020, 161, 1052-1064.	2.0	17
43	On Docking, Scoring and Assessing Protein-DNA Complexes in a Rigid-Body Framework. <i>PLoS ONE</i> , 2012, 7, e32647.	1.1	13
44	A functional polymorphism in the ATP-Binding Cassette B1 transporter predicts pharmacologic response to combination of nortriptyline and morphine in neuropathic pain patients. <i>Pain</i> , 2020, 161, 619-629.	2.0	13
45	Anatomical selectivity in overlap of chronic facial and bodily pain. <i>Pain Reports</i> , 2019, 4, e729.	1.4	12
46	A study in scarlet: MC1R as the main predictor of red hair and exemplar of the flip-flop effect. <i>Human Molecular Genetics</i> , 2019, 28, 2093-2106.	1.4	11
47	RKB: a Semantic Web knowledge base for RNA. <i>Journal of Biomedical Semantics</i> , 2010, 1, S2.	0.9	5
48	Alternative Splicing of Opioid Receptor Genes Shows a Conserved Pattern for 6TM Receptor Variants. <i>Cellular and Molecular Neurobiology</i> , 2021, 41, 1039-1055.	1.7	5
49	Multi-ethnic GWAS and meta-analysis of sleep quality identify MPP6 as a novel gene that functions in sleep center neurons. <i>Sleep</i> , 2021, 44, .	0.6	5
50	Profound analgesia is associated with a truncated peptide resulting from tissue specific alternative splicing of DRG CA8-204 regulated by an exon-level cis-eQTL. <i>PLoS Genetics</i> , 2019, 15, e1008226.	1.5	4
51	Identifying genetic determinants of inflammatory pain in mice using a large-scale gene-targeted screen. <i>Pain</i> , 2022, 163, 1139-1157.	2.0	4
52	Identification of two distinct intracellular localization signals in STT3-B. <i>Archives of Biochemistry and Biophysics</i> , 2006, 445, 108-114.	1.4	3
53	Post-concussion symptoms and chronic pain after mild traumatic brain injury are modulated by multiple locus effect in the <i>BDNF</i> gene through the expression of antisense: A pilot prospective control study. <i>Canadian Journal of Pain</i> , 2017, 1, 112-126.	0.6	2
54	Extracellular matrix mediated plasticity in neuropathic pain. <i>Journal of Pain</i> , 2018, 19, S15.	0.7	2

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55	Reversion mutation of cDNA CA8-204 minigene construct produces a truncated functional peptide that regulates calcium release in vitro and produces profound analgesia in vivo. Mammalian Genome, 2020, 31, 287-294.	1.0	1