

# Marc Parisien

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

56  
papers

5,933  
citations

24  
h-index

62  
g-index

62  
ext. papers

7,804  
ext. citations

10.1  
avg, IF

5.75  
L-index

#	Paper	IF	Citations
56	N6-methyladenosine-dependent regulation of messenger RNA stability. <i>Nature</i> , <b>2014</b> , 505, 117-20	50.4	1949
55	N(6)-methyladenosine-dependent RNA structural switches regulate RNA-protein interactions. <i>Nature</i> , <b>2015</b> , 518, 560-4	50.4	988
54	The MC-Fold and MC-Sym pipeline infers RNA structure from sequence data. <i>Nature</i> , <b>2008</b> , 452, 51-5	50.4	596
53	N6-methyladenosine alters RNA structure to regulate binding of a low-complexity protein. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, 6051-6063	20.1	339
52	Probing N6-methyladenosine RNA modification status at single nucleotide resolution in mRNA and long noncoding RNA. <i>Rna</i> , <b>2013</b> , 19, 1848-56	5.8	320
51	Angiogenin-cleaved tRNA halves interact with cytochrome c, protecting cells from apoptosis during osmotic stress. <i>Molecular and Cellular Biology</i> , <b>2014</b> , 34, 2450-63	4.8	172
50	Staufen1 regulates diverse classes of mammalian transcripts. <i>EMBO Journal</i> , <b>2007</b> , 26, 2670-81	13	157
49	Genome-wide identification and quantitative analysis of cleaved tRNA fragments induced by cellular stress. <i>Journal of Biological Chemistry</i> , <b>2012</b> , 287, 42708-25	5.4	150
48	Regulation of Co-transcriptional Pre-mRNA Splicing by mA through the Low-Complexity Protein hnRNPG. <i>Molecular Cell</i> , <b>2019</b> , 76, 70-81.e9	17.6	124
47	N(6)-Methyladenosine Modification in a Long Noncoding RNA Hairpin Predisposes Its Conformation to Protein Binding. <i>Journal of Molecular Biology</i> , <b>2016</b> , 428, 822-833	6.5	122
46	Quantitative H2S-mediated protein sulphydration reveals metabolic reprogramming during the integrated stress response. <i>ELife</i> , <b>2015</b> , 4, e10067	8.9	113
45	New metrics for comparing and assessing discrepancies between RNA 3D structures and models. <i>Rna</i> , <b>2009</b> , 15, 1875-85	5.8	102
44	miR-183 cluster scales mechanical pain sensitivity by regulating basal and neuropathic pain genes. <i>Science</i> , <b>2017</b> , 356, 1168-1171	33.3	80
43	Diversity of human tRNA genes from the 1000-genomes project. <i>RNA Biology</i> , <b>2013</b> , 10, 1853-67	4.8	62
42	Queuosine modification protects cognate tRNAs against ribonuclease cleavage. <i>Rna</i> , <b>2018</b> , 24, 1305-1313	3.8	56
41	The cap-binding translation initiation factor, eIF4E, binds a pseudoknot in a viral cap-independent translation element. <i>Structure</i> , <b>2011</b> , 19, 868-80	5.2	53
40	RNA structure determination using SAXS data. <i>Journal of Physical Chemistry B</i> , <b>2010</b> , 114, 10039-48	3.4	46

39	Genetic studies of human neuropathic pain conditions: a review. <i>Pain</i> , <b>2018</b> , 159, 583-594	8	38
38	Human pain genetics database: a resource dedicated to human pain genetics research. <i>Pain</i> , <b>2018</b> , 159, 749-763	8	37
37	Single cell transcriptomics of primate sensory neurons identifies cell types associated with chronic pain. <i>Nature Communications</i> , <b>2021</b> , 12, 1510	17.4	35
36	Effect of Human Genetic Variability on Gene Expression in Dorsal Root Ganglia and Association with Pain Phenotypes. <i>Cell Reports</i> , <b>2017</b> , 19, 1940-1952	10.6	34
35	Genetic pathway analysis reveals a major role for extracellular matrix organization in inflammatory and neuropathic pain. <i>Pain</i> , <b>2019</b> , 160, 932-944	8	31
34	Microbiome characterization by high-throughput transfer RNA sequencing and modification analysis. <i>Nature Communications</i> , <b>2018</b> , 9, 5353	17.4	31
33	Genome-wide association reveals contribution of MRAS to painful temporomandibular disorder in males. <i>Pain</i> , <b>2019</b> , 160, 579-591	8	26
32	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> , <b>2016</b> , 196, 340-349	3.4	24
31	Discovering RNA-protein interactome by using chemical context profiling of the RNA-protein interface. <i>Cell Reports</i> , <b>2013</b> , 3, 1703-13	10.6	22
30	NMR structure of a 4 x 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> , <b>2011</b> , 17, 1664-77	5.8	21
29	COMT gene locus: new functional variants. <i>Pain</i> , <b>2015</b> , 156, 2072-2083	8	20
28	Determining RNA three-dimensional structures using low-resolution data. <i>Journal of Structural Biology</i> , <b>2012</b> , 179, 252-60	3.4	20
27	Rationalization and prediction of selective decoding of pseudouridine-modified nonsense and sense codons. <i>Rna</i> , <b>2012</b> , 18, 355-67	5.8	20
26	Discovery of a Redox Thiol Switch: Implications for Cellular Energy Metabolism. <i>Molecular and Cellular Proteomics</i> , <b>2020</b> , 19, 852-870	7.6	16
25	Ranking the factors that contribute to protein beta-sheet folding. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2007</b> , 68, 824-9	4.2	16
24	A new catalog of protein beta-sheets. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2005</b> , 61, 545-58	4.2	16
23	Alternative Splicing of the Delta-Opioid Receptor Gene Suggests Existence of New Functional Isoforms. <i>Molecular Neurobiology</i> , <b>2019</b> , 56, 2855-2869	6.2	13
22	NK cell recruitment limits tissue damage during an enteric helminth infection. <i>Mucosal Immunology</i> , <b>2020</b> , 13, 357-370	9.2	11

21	On docking, scoring and assessing protein-DNA complexes in a rigid-body framework. <i>PLoS ONE</i> , <b>2012</b> , 7, e32647	3.7	8
20	The dichotomous role of epiregulin in pain. <i>Pain</i> , <b>2020</b> , 161, 1052-1064	8	7
19	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> , <b>2020</b> , 161, 619-629	8	7
18	Anatomical selectivity in overlap of chronic facial and bodily pain. <i>Pain Reports</i> , <b>2019</b> , 4, e729	3.5	7
17	Sex- and age-specific genetic analysis of chronic back pain. <i>Pain</i> , <b>2021</b> , 162, 1176-1187	8	6
16	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> , <b>2022</b> , 13, 843	17.4	5
15	RKB: a Semantic Web knowledge base for RNA. <i>Journal of Biomedical Semantics</i> , <b>2010</b> , 1 Suppl 1, S2	2.2	4
14	A genetic polymorphism that is associated with mitochondrial energy metabolism increases risk of fibromyalgia. <i>Pain</i> , <b>2020</b> , 161, 2860-2871	8	4
13	A study in scarlet: MC1R as the main predictor of red hair and exemplar of the flip-flop effect. <i>Human Molecular Genetics</i> , <b>2019</b> , 28, 2093-2106	5.6	4
12	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> , <b>2019</b> , 15, e1008226	6	3
11	Identification of two distinct intracellular localization signals in STT3-B. <i>Archives of Biochemistry and Biophysics</i> , <b>2006</b> , 445, 108-14	4.1	3
10	Single cell transcriptomics of primate sensory neurons identifies cell types associated with human chronic pain		3
9	Post-concussion symptoms and chronic pain after mild traumatic brain injury are modulated by multiple locus effect in the gene through the expression of antisense: A pilot prospective control study.. <i>Canadian Journal of Pain</i> , <b>2017</b> , 1, 112-126	1.5	2
8	Genome-wide analysis identifies significant contribution of brain-expressed genes in chronic, but not acute, back pain		2
7	Discovery of a redox-thiol switch regulating cellular energy metabolism		2
6	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. <i>Mammalian Genome</i> , <b>2020</b> , 31, 287-294	3.2	1
5	Alternative Splicing of Opioid Receptor Genes Shows a Conserved Pattern for 6TM Receptor Variants. <i>Cellular and Molecular Neurobiology</i> , <b>2021</b> , 41, 1039-1055	4.6	1
4	Direct reprogramming of the intestinal epithelium by parasitic helminths subverts type 2 immunity		1

- 3 Acute inflammatory response via neutrophil activation protects against the development of chronic pain.. *Science Translational Medicine*, **2022**, 14, eabj9954 17.5 1
- 2 Identifying genetic determinants of inflammatory pain in mice using a large-scale gene-targeted screen.. *Pain*, **2022**, 163, 1139-1157 8 0
- 1 Predict RNA 2D and 3D Structure over the Internet Using MC-Tools **2014**, 633-666