

Marc Parisien

List of Publications by Year in Descending Order

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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	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	17.4	5
55	Identifying genetic determinants of inflammatory pain in mice using a large-scale gene-targeted screen.. <i>Pain</i> , 2022 , 163, 1139-1157	8	0
54	Acute inflammatory response via neutrophil activation protects against the development of chronic pain.. <i>Science Translational Medicine</i> , 2022 , 14, eabj9954	17.5	1
53	Sex- and age-specific genetic analysis of chronic back pain. <i>Pain</i> , 2021 , 162, 1176-1187	8	6
52	Single cell transcriptomics of primate sensory neurons identifies cell types associated with chronic pain. <i>Nature Communications</i> , 2021 , 12, 1510	17.4	35
51	Alternative Splicing of Opioid Receptor Genes Shows a Conserved Pattern for 6TM Receptor Variants. <i>Cellular and Molecular Neurobiology</i> , 2021 , 41, 1039-1055	4.6	1
50	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> , 2020 , 31, 287-294	3.2	1
49	Discovery of a Redox Thiol Switch: Implications for Cellular Energy Metabolism. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 852-870	7.6	16
48	The dichotomous role of epiregulin in pain. <i>Pain</i> , 2020 , 161, 1052-1064	8	7
47	NK cell recruitment limits tissue damage during an enteric helminth infection. <i>Mucosal Immunology</i> , 2020 , 13, 357-370	9.2	11
46	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	8	7
45	A genetic polymorphism that is associated with mitochondrial energy metabolism increases risk of fibromyalgia. <i>Pain</i> , 2020 , 161, 2860-2871	8	4
44	Regulation of Co-transcriptional Pre-mRNA Splicing by mA through the Low-Complexity Protein hnRNPG. <i>Molecular Cell</i> , 2019 , 76, 70-81.e9	17.6	124
43	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	6	3
42	Alternative Splicing of the Delta-Opioid Receptor Gene Suggests Existence of New Functional Isoforms. <i>Molecular Neurobiology</i> , 2019 , 56, 2855-2869	6.2	13
41	Anatomical selectivity in overlap of chronic facial and bodily pain. <i>Pain Reports</i> , 2019 , 4, e729	3.5	7
40	Genome-wide association reveals contribution of MRAS to painful temporomandibular disorder in males. <i>Pain</i> , 2019 , 160, 579-591	8	26

39	Genetic pathway analysis reveals a major role for extracellular matrix organization in inflammatory and neuropathic pain. <i>Pain</i> , 2019 , 160, 932-944	8	31
38	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	5.6	4
37	Human pain genetics database: a resource dedicated to human pain genetics research. <i>Pain</i> , 2018 , 159, 749-763	8	37
36	Genetic studies of human neuropathic pain conditions: a review. <i>Pain</i> , 2018 , 159, 583-594	8	38
35	Microbiome characterization by high-throughput transfer RNA sequencing and modification analysis. <i>Nature Communications</i> , 2018 , 9, 5353	17.4	31
34	Queuosine modification protects cognate tRNAs against ribonuclease cleavage. <i>Rna</i> , 2018 , 24, 1305-1313	3.8	56
33	N6-methyladenosine alters RNA structure to regulate binding of a low-complexity protein. <i>Nucleic Acids Research</i> , 2017 , 45, 6051-6063	20.1	339
32	miR-183 cluster scales mechanical pain sensitivity by regulating basal and neuropathic pain genes. <i>Science</i> , 2017 , 356, 1168-1171	33.3	80
31	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> , 2017 , 1, 112-126	1.5	2
30	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	10.6	34
29	N(6)-Methyladenosine Modification in a Long Noncoding RNA Hairpin Predisposes Its Conformation to Protein Binding. <i>Journal of Molecular Biology</i> , 2016 , 428, 822-833	6.5	122
28	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	3.4	24
27	N(6)-methyladenosine-dependent RNA structural switches regulate RNA-protein interactions. <i>Nature</i> , 2015 , 518, 560-4	50.4	988
26	COMT gene locus: new functional variants. <i>Pain</i> , 2015 , 156, 2072-2083	8	20
25	Quantitative H2S-mediated protein sulfhydrylation reveals metabolic reprogramming during the integrated stress response. <i>ELife</i> , 2015 , 4, e10067	8.9	113
24	Predict RNA 2D and 3D Structure over the Internet Using MC-Tools 2014 , 633-666		
23	N6-methyladenosine-dependent regulation of messenger RNA stability. <i>Nature</i> , 2014 , 505, 117-20	50.4	1949
22	Angiogenin-cleaved tRNA halves interact with cytochrome c, protecting cells from apoptosis during osmotic stress. <i>Molecular and Cellular Biology</i> , 2014 , 34, 2450-63	4.8	172

21	Discovering RNA-protein interactome by using chemical context profiling of the RNA-protein interface. <i>Cell Reports</i> , 2013 , 3, 1703-13	10.6	22
20	Probing N6-methyladenosine RNA modification status at single nucleotide resolution in mRNA and long noncoding RNA. <i>Rna</i> , 2013 , 19, 1848-56	5.8	320
19	Diversity of human tRNA genes from the 1000-genomes project. <i>RNA Biology</i> , 2013 , 10, 1853-67	4.8	62
18	Determining RNA three-dimensional structures using low-resolution data. <i>Journal of Structural Biology</i> , 2012 , 179, 252-60	3.4	20
17	On docking, scoring and assessing protein-DNA complexes in a rigid-body framework. <i>PLoS ONE</i> , 2012 , 7, e32647	3.7	8
16	Rationalization and prediction of selective decoding of pseudouridine-modified nonsense and sense codons. <i>Rna</i> , 2012 , 18, 355-67	5.8	20
15	Genome-wide identification and quantitative analysis of cleaved tRNA fragments induced by cellular stress. <i>Journal of Biological Chemistry</i> , 2012 , 287, 42708-25	5.4	150
14	The cap-binding translation initiation factor, eIF4E, binds a pseudoknot in a viral cap-independent translation element. <i>Structure</i> , 2011 , 19, 868-80	5.2	53
13	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> , 2011 , 17, 1664-77	5.8	21
12	RNA structure determination using SAXS data. <i>Journal of Physical Chemistry B</i> , 2010 , 114, 10039-48	3.4	46
11	RKB: a Semantic Web knowledge base for RNA. <i>Journal of Biomedical Semantics</i> , 2010 , 1 Suppl 1, S2	2.2	4
10	New metrics for comparing and assessing discrepancies between RNA 3D structures and models. <i>Rna</i> , 2009 , 15, 1875-85	5.8	102
9	The MC-Fold and MC-Sym pipeline infers RNA structure from sequence data. <i>Nature</i> , 2008 , 452, 51-5	50.4	596
8	Ranking the factors that contribute to protein beta-sheet folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 68, 824-9	4.2	16
7	Staufen1 regulates diverse classes of mammalian transcripts. <i>EMBO Journal</i> , 2007 , 26, 2670-81	13	157
6	Identification of two distinct intracellular localization signals in STT3-B. <i>Archives of Biochemistry and Biophysics</i> , 2006 , 445, 108-14	4.1	3
5	A new catalog of protein beta-sheets. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61, 545-58	4.2	16
4	Genome-wide analysis identifies significant contribution of brain-expressed genes in chronic, but not acute, back pain		2

- 3 Single cell transcriptomics of primate sensory neurons identifies cell types associated with human chronic pain 3
- 2 Discovery of a redox-thiol switch regulating cellular energy metabolism 2
- 1 Direct reprogramming of the intestinal epithelium by parasitic helminths subverts type 2 immunity 1