

Maja Jagodic

List of Publications by Year in descending order

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Version: 2024-02-01

72
papers

6,895
citations

172457

29
h-index

91884

69
g-index

85
all docs

85
docs citations

85
times ranked

12563
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. <i>Nature</i> , 2011, 476, 214-219. | 27.8 | 2,400 |
| 2 | Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. <i>Nature Genetics</i> , 2013, 45, 1353-1360. | 21.4 | 1,213 |
| 3 | Multiple sclerosis genomic map implicates peripheral immune cells and microglia in susceptibility. <i>Science</i> , 2019, 365, . | 12.6 | 710 |
| 4 | An evaluation of analysis pipelines for DNA methylation profiling using the Illumina HumanMethylation450 BeadChip platform. <i>Epigenetics</i> , 2013, 8, 333-346. | 2.7 | 192 |
| 5 | Combined sequence-based and genetic mapping analysis of complex traits in outbred rats. <i>Nature Genetics</i> , 2013, 45, 767-775. | 21.4 | 176 |
| 6 | Competitive repopulation of an empty microglial niche yields functionally distinct subsets of microglia-like cells. <i>Nature Communications</i> , 2018, 9, 4845. | 12.8 | 148 |
| 7 | DNA methylation as a mediator of HLA-DRB1*15:01 and a protective variant in multiple sclerosis. <i>Nature Communications</i> , 2018, 9, 2397. | 12.8 | 147 |
| 8 | Therapeutic efficacy of dimethyl fumarate in relapsing-remitting multiple sclerosis associates with ROS pathway in monocytes. <i>Nature Communications</i> , 2019, 10, 3081. | 12.8 | 97 |
| 9 | Circulating miR-150 in CSF is a novel candidate biomarker for multiple sclerosis. <i>Neurology: Neuroimmunology and NeuroInflammation</i> , 2016, 3, e219. | 6.0 | 92 |
| 10 | Microglial autophagy-associated phagocytosis is essential for recovery from neuroinflammation. <i>Science Immunology</i> , 2020, 5, . | 11.9 | 89 |
| 11 | Functional genomics analysis of vitamin D effects on CD4+ T cells in vivo in experimental autoimmune encephalomyelitis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1678-E1687. | 7.1 | 81 |
| 12 | Local Delivery of miR-21 Stabilizes Fibrous Caps in Vulnerable Atherosclerotic Lesions. <i>Molecular Therapy</i> , 2018, 26, 1040-1055. | 8.2 | 75 |
| 13 | Efficacy of vitamin D in treating multiple sclerosis-like neuroinflammation depends on developmental stage. <i>Experimental Neurology</i> , 2013, 249, 39-48. | 4.1 | 66 |
| 14 | BAFF-secreting neutrophils drive plasma cell responses during emergency granulopoiesis. <i>Journal of Experimental Medicine</i> , 2016, 213, 1537-1553. | 8.5 | 66 |
| 15 | Fatal demyelinating disease is induced by monocyte-derived macrophages in the absence of TGF- β 2 signaling. <i>Nature Immunology</i> , 2018, 19, 1-7. | 14.5 | 62 |
| 16 | Identification of MS-specific serum miRNAs in an international multicenter study. <i>Neurology: Neuroimmunology and NeuroInflammation</i> , 2018, 5, e491. | 6.0 | 59 |
| 17 | Small non-coding RNAs as important players, biomarkers and therapeutic targets in multiple sclerosis: A comprehensive overview. <i>Journal of Autoimmunity</i> , 2019, 101, 17-25. | 6.5 | 58 |
| 18 | Smoking induces DNA methylation changes in Multiple Sclerosis patients with exposure-response relationship. <i>Scientific Reports</i> , 2017, 7, 14589. | 3.3 | 55 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 19 | A Role for <i>VAV1</i> in Experimental Autoimmune Encephalomyelitis and Multiple Sclerosis. <i>Science Translational Medicine</i> , 2009, 1, 10ra21. | 12.4 | 52 |
| 20 | DNA methylation mediates genotype and smoking interaction in the development of anti-citrullinated peptide antibody-positive rheumatoid arthritis. <i>Arthritis Research and Therapy</i> , 2017, 19, 71. | 3.5 | 48 |
| 21 | Tobacco smoking induces changes in true DNA methylation, hydroxymethylation and gene expression in bronchoalveolar lavage cells. <i>EBioMedicine</i> , 2019, 46, 290-304. | 6.1 | 48 |
| 22 | Human skin long noncoding RNA WAKMAR1 regulates wound healing by enhancing keratinocyte migration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 9443-9452. | 7.1 | 48 |
| 23 | Combining evidence from four immune cell types identifies DNA methylation patterns that implicate functionally distinct pathways during Multiple Sclerosis progression. <i>EBioMedicine</i> , 2019, 43, 411-423. | 6.1 | 45 |
| 24 | An Advanced Intercross Line Resolves <i>Eae18</i> into Two Narrow Quantitative Trait Loci Syntenic to Multiple Sclerosis Candidate Loci. <i>Journal of Immunology</i> , 2004, 173, 1366-1373. | 0.8 | 44 |
| 25 | Next-Generation Sequencing Identifies MicroRNAs that Associate with Pathogenic Autoimmune Neuroinflammation in Rats. <i>Journal of Immunology</i> , 2013, 190, 4066-4075. | 0.8 | 44 |
| 26 | Impact of genetic risk loci for multiple sclerosis on expression of proximal genes in patients. <i>Human Molecular Genetics</i> , 2018, 27, 912-928. | 2.9 | 41 |
| 27 | The multiple sclerosis risk gene <i>IL22RA2</i> contributes to a more severe murine autoimmune neuroinflammation. <i>Genes and Immunity</i> , 2014, 15, 457-465. | 4.1 | 39 |
| 28 | Acute treatment with valproic acid and l-thyroxine ameliorates clinical signs of experimental autoimmune encephalomyelitis and prevents brain pathology in DA rats. <i>Neurobiology of Disease</i> , 2014, 71, 220-233. | 4.4 | 34 |
| 29 | Genome-Wide Screen for MicroRNAs Reveals a Role for miR-203 in Melanoma Metastasis. <i>Journal of Investigative Dermatology</i> , 2018, 138, 882-892. | 0.7 | 34 |
| 30 | Hypermethylation of <i>MIR21</i> in CD4+ T cells from patients with relapsing-remitting multiple sclerosis associates with lower miRNA-21 levels and concomitant up-regulation of its target genes. <i>Multiple Sclerosis Journal</i> , 2018, 24, 1288-1300. | 3.0 | 33 |
| 31 | <i>Gsta4</i> controls apoptosis of differentiating adult oligodendrocytes during homeostasis and remyelination via the mitochondria-associated Fas-Casp8-Bid-axis. <i>Nature Communications</i> , 2020, 11, 4071. | 12.8 | 31 |
| 32 | Epigenetic research in multiple sclerosis: progress, challenges, and opportunities. <i>Physiological Genomics</i> , 2017, 49, 447-461. | 2.3 | 30 |
| 33 | Congenetic mapping confirms a locus on rat chromosome 10 conferring strong protection against myelin oligodendrocyte glycoprotein-induced experimental autoimmune encephalomyelitis. <i>Immunogenetics</i> , 2001, 53, 410-415. | 2.4 | 29 |
| 34 | C-type lectin receptors Mcl and Mincle control development of multiple sclerosis-like neuroinflammation. <i>Journal of Clinical Investigation</i> , 2020, 130, 838-852. | 8.2 | 27 |
| 35 | Usability of human Infinium MethylationEPIC BeadChip for mouse DNA methylation studies. <i>BMC Bioinformatics</i> , 2017, 18, 486. | 2.6 | 25 |
| 36 | Resolution of a 16.8-Mb Autoimmunity-Regulating Rat Chromosome 4 Region into Multiple Encephalomyelitis Quantitative Trait Loci and Evidence for Epistasis. <i>Journal of Immunology</i> , 2005, 174, 918-924. | 0.8 | 24 |

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|----|--|-----|-----------|
| 37 | Neuronal methylome reveals CREB-associated neuro-axonal impairment in multiple sclerosis. <i>Clinical Epigenetics</i> , 2019, 11, 86. | 4.1 | 24 |
| 38 | STATegra: Multi-Omics Data Integration – A Conceptual Scheme With a Bioinformatics Pipeline. <i>Frontiers in Genetics</i> , 2021, 12, 620453. | 2.3 | 24 |
| 39 | Characterization of Multiple Sclerosis candidate gene expression kinetics in rat experimental autoimmune encephalomyelitis. <i>Journal of Neuroimmunology</i> , 2009, 210, 30-39. | 2.3 | 22 |
| 40 | Different epigenetic clocks reflect distinct pathophysiological features of multiple sclerosis. <i>Epigenomics</i> , 2019, 11, 1429-1439. | 2.1 | 22 |
| 41 | Genomic imprinting: A missing piece of the Multiple Sclerosis puzzle?. <i>International Journal of Biochemistry and Cell Biology</i> , 2015, 67, 49-57. | 2.8 | 21 |
| 42 | Epigenetic insights into multiple sclerosis disease progression. <i>Journal of Internal Medicine</i> , 2020, 288, 82-102. | 6.0 | 21 |
| 43 | Multiple loci comprising immune-related genes regulate experimental neuroinflammation. <i>Genes and Immunity</i> , 2010, 11, 21-36. | 4.1 | 20 |
| 44 | Comparison of EM-seq and PBAT methylome library methods for low-input DNA. <i>Epigenetics</i> , 2022, 17, 1195-1204. | 2.7 | 19 |
| 45 | Rat bone marrow-derived dendritic cells generated with GM-CSF/IL-4 or FLT3L exhibit distinct phenotypical and functional characteristics. <i>Journal of Leukocyte Biology</i> , 2016, 99, 437-446. | 3.3 | 18 |
| 46 | Parent-of-Origin Effects Implicate Epigenetic Regulation of Experimental Autoimmune Encephalomyelitis and Identify Imprinted Dlk1 as a Novel Risk Gene. <i>PLoS Genetics</i> , 2014, 10, e1004265. | 3.5 | 16 |
| 47 | Natural Polymorphisms in Tap2 Influence Negative Selection and CD4 ⁺ CD8 Lineage Commitment in the Rat. <i>PLoS Genetics</i> , 2014, 10, e1004151. | 3.5 | 16 |
| 48 | Changes in methylation within the STK32B promoter are associated with an increased risk for generalized anxiety disorder in adolescents. <i>Journal of Psychiatric Research</i> , 2018, 102, 44-51. | 3.1 | 16 |
| 49 | VAV1 regulates experimental autoimmune arthritis and is associated with anti-CCP negative rheumatoid arthritis. <i>Genes and Immunity</i> , 2017, 18, 48-56. | 4.1 | 15 |
| 50 | Small noncoding RNA profiling across cellular and biofluid compartments and their implications for multiple sclerosis immunopathology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, . | 7.1 | 15 |
| 51 | Non-parametric combination analysis of multiple data types enables detection of novel regulatory mechanisms in T cells of multiple sclerosis patients. <i>Scientific Reports</i> , 2019, 9, 11996. | 3.3 | 13 |
| 52 | IL-22 Binding Protein Promotes the Disease Process in Multiple Sclerosis. <i>Journal of Immunology</i> , 2019, 203, 888-898. | 0.8 | 13 |
| 53 | GeneSetCluster: a tool for summarizing and integrating gene-set analysis results. <i>BMC Bioinformatics</i> , 2020, 21, 443. | 2.6 | 13 |
| 54 | Longitudinal DNA methylation changes at MET may alter HGF/c-MET signalling in adolescents at risk for depression. <i>Epigenetics</i> , 2020, 15, 646-663. | 2.7 | 12 |

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|----|--|------|-----------|
| 55 | Methylome and transcriptome signature of bronchoalveolar cells from multiple sclerosis patients in relation to smoking. <i>Multiple Sclerosis Journal</i> , 2021, 27, 1014-1026. | 3.0 | 12 |
| 56 | Combining genetic mapping with genome-wide expression in experimental autoimmune encephalomyelitis highlights a gene network enriched for T cell functions and candidate genes regulating autoimmunity. <i>Human Molecular Genetics</i> , 2013, 22, 4952-4966. | 2.9 | 11 |
| 57 | Anti-MOG antibodies are under polygenic regulation with the most significant control coming from the C-type lectin-like gene locus. <i>Genes and Immunity</i> , 2013, 14, 409-419. | 4.1 | 11 |
| 58 | Combined-cross analysis of genome-wide linkage scans for experimental autoimmune encephalomyelitis in rat. <i>Genomics</i> , 2006, 88, 737-744. | 2.9 | 10 |
| 59 | miR-31 regulates energy metabolism and is suppressed in T cells from patients with Sjögren's syndrome. <i>European Journal of Immunology</i> , 2019, 49, 313-322. | 2.9 | 10 |
| 60 | DNA methylation changes in glial cells of the normal-appearing white matter in Multiple Sclerosis patients. <i>Epigenetics</i> , 2022, 17, 1311-1330. | 2.7 | 10 |
| 61 | MOG-induced experimental autoimmune encephalomyelitis in the rat species triggers anti-neurofascin antibody response that is genetically regulated. <i>Journal of Neuroinflammation</i> , 2015, 12, 194. | 7.2 | 8 |
| 62 | IL-22 binding protein regulates murine skin inflammation. <i>Experimental Dermatology</i> , 2017, 26, 444-446. | 2.9 | 7 |
| 63 | Effect of Vitamin D on Experimental Autoimmune Neuroinflammation Is Dependent on Haplotypes Comprising Naturally Occurring Allelic Variants of CIITA (Mhc2ta). <i>Frontiers in Neurology</i> , 2020, 11, 600401. | 2.4 | 6 |
| 64 | A validated generally applicable approach using the systematic assessment of disease modules by GWAS reveals a multi-omic module strongly associated with risk factors in multiple sclerosis. <i>BMC Genomics</i> , 2021, 22, 631. | 2.8 | 5 |
| 65 | Translational utility of experimental autoimmune encephalomyelitis: recent developments. <i>Journal of Inflammation Research</i> , 2015, 8, 211. | 3.5 | 4 |
| 66 | Deep characterization of paired chromatin and transcriptomes in four immune cell types from multiple sclerosis patients. <i>Epigenomics</i> , 2021, 13, 1607-1618. | 2.1 | 4 |
| 67 | MicroRNAs as promising novel biomarkers and potential drug targets for inflammatory neurological diseases. <i>Journal of the Neurological Sciences</i> , 2015, 356, 3-4. | 0.6 | 3 |
| 68 | Epigenetics and multiple sclerosis. , 2017, , 185-213. | | 2 |
| 69 | A Silent Exonic SNP in Kdm3a Affects Nucleic Acids Structure but Does Not Regulate Experimental Autoimmune Encephalomyelitis. <i>PLoS ONE</i> , 2013, 8, e81912. | 2.5 | 1 |
| 70 | Nurture your scientific curiosity early in your research career. <i>Nature Genetics</i> , 2013, 45, 116-118. | 21.4 | 0 |
| 71 | Positional Gene Cloning in Experimental Populations. <i>Methods in Molecular Biology</i> , 2014, 1304, 3-24. | 0.9 | 0 |
| 72 | DNA Methylation in Multiple Sclerosis. <i>RNA Technologies</i> , 2019, , 181-214. | 0.3 | 0 |