

# Sergio Baranzini

## List of Publications by Year in descending order

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185  
papers

21,396  
citations

22099

59  
h-index

10127

140  
g-index

206  
all docs

206  
docs citations

206  
times ranked

25221  
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.	13.7	2,400
2	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. <i>Nature Genetics</i> , 2013, 45, 1353-1360.	9.4	1,213
3	Multiple sclerosis. <i>Lancet, The</i> , 2018, 391, 1622-1636.	6.3	1,204
4	The Influence of the Proinflammatory Cytokine, Osteopontin, on Autoimmune Demyelinating Disease. <i>Science</i> , 2001, 294, 1731-1735.	6.0	807
5	Meta-analysis of genome scans and replication identify CD6, IRF8 and TNFRSF1A as new multiple sclerosis susceptibility loci. <i>Nature Genetics</i> , 2009, 41, 776-782.	9.4	729
6	Multiple sclerosis genomic map implicates peripheral immune cells and microglia in susceptibility. <i>Science</i> , 2019, 365, .	6.0	710
7	Gut bacteria from multiple sclerosis patients modulate human T cells and exacerbate symptoms in mouse models. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 10713-10718.	3.3	709
8	Gut microbiota from multiple sclerosis patients enables spontaneous autoimmune encephalomyelitis in mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 10719-10724.	3.3	666
9	Dysregulation of the Wnt pathway inhibits timely myelination and remyelination in the mammalian CNS. <i>Genes and Development</i> , 2009, 23, 1571-1585.	2.7	537
10	Incidental MRI anomalies suggestive of multiple sclerosis. <i>Neurology</i> , 2009, 72, 800-805.	1.5	509
11	Proteomic analysis of active multiple sclerosis lesions reveals therapeutic targets. <i>Nature</i> , 2008, 451, 1076-1081.	13.7	472
12	Genome, epigenome and RNA sequences of monozygotic twins discordant for multiple sclerosis. <i>Nature</i> , 2010, 464, 1351-1356.	13.7	463
13	Genome-wide association analysis of susceptibility and clinical phenotype in multiple sclerosis. <i>Human Molecular Genetics</i> , 2009, 18, 767-778.	1.4	419
14	Pathway and network-based analysis of genome-wide association studies in multiple sclerosis. <i>Human Molecular Genetics</i> , 2009, 18, 2078-2090.	1.4	371
15	Systematic integration of biomedical knowledge prioritizes drugs for repurposing. <i>ELife</i> , 2017, 6, .	2.8	333
16	Long-term evolution of multiple sclerosis disability in the treatment era. <i>Annals of Neurology</i> , 2016, 80, 499-510.	2.8	331
17	Class II HLA interactions modulate genetic risk for multiple sclerosis. <i>Nature Genetics</i> , 2015, 47, 1107-1113.	9.4	312
18	Mapping Multiple Sclerosis Susceptibility to the HLA-DR Locus in African Americans. <i>American Journal of Human Genetics</i> , 2004, 74, 160-167.	2.6	311

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19	Axin2 as regulatory and therapeutic target in newborn brain injury and remyelination. <i>Nature Neuroscience</i> , 2011, 14, 1009-1016.	7.1	307
20	The genetics of multiple sclerosis: SNPs to pathways to pathogenesis. <i>Nature Reviews Genetics</i> , 2008, 9, 516-526.	7.7	294
21	Myelin Regeneration: A Recapitulation of Development?. <i>Annual Review of Neuroscience</i> , 2011, 34, 21-43.	5.0	282
22	Heterogeneity at the HLA-DRB1 locus and risk for multiple sclerosis. <i>Human Molecular Genetics</i> , 2006, 15, 2813-2824.	1.4	279
23	Astrocyte-encoded positional cues maintain sensorimotor circuit integrity. <i>Nature</i> , 2014, 509, 189-194.	13.7	266
24	Silent progression in disease activity-free relapsing multiple sclerosis. <i>Annals of Neurology</i> , 2019, 85, 653-666.	2.8	265
25	Recirculating Intestinal IgA-Producing Cells Regulate Neuroinflammation via IL-10. <i>Cell</i> , 2019, 176, 610-624.e18.	13.5	241
26	The genetics of multiple sclerosis: an update review. <i>Immunological Reviews</i> , 2012, 248, 87-103.	2.8	230
27	Rituximab Efficiently Depletes Increased CD20-Expressing T Cells in Multiple Sclerosis Patients. <i>Journal of Immunology</i> , 2014, 193, 580-586.	0.4	223
28	Differential Micro RNA Expression in PBMC from Multiple Sclerosis Patients. <i>PLoS ONE</i> , 2009, 4, e6309.	1.1	222
29	B cell repertoire diversity and clonal expansion in multiple sclerosis brain lesions. <i>Journal of Immunology</i> , 1999, 163, 5133-44.	0.4	217
30	Modules, networks and systems medicine for understanding disease and aiding diagnosis. <i>Genome Medicine</i> , 2014, 6, 82.	3.6	169
31	Peroxisome proliferator-activated receptor (PPAR) expression in T cells mediates gender differences in development of T cell-mediated autoimmunity. <i>Journal of Experimental Medicine</i> , 2007, 204, 321-330.	4.2	167
32	The Genetics of Multiple Sclerosis: From 0 to 200 in 50 Years. <i>Trends in Genetics</i> , 2017, 33, 960-970.	2.9	165
33	Hippocampal demyelination and memory dysfunction are associated with increased levels of the neuronal microRNA miR-124 and reduced AMPA receptors. <i>Annals of Neurology</i> , 2013, 73, 637-645.	2.8	164
34	Genome-Wide Pharmacogenomic Analysis of the Response to Interferon Beta Therapy in Multiple Sclerosis. <i>Archives of Neurology</i> , 2008, 65, 337-44.	4.9	154
35	Genotype-Phenotype correlations in multiple sclerosis: HLA genes influence disease severity inferred by 1HMR spectroscopy and MRI measures. <i>Brain</i> , 2009, 132, 250-259.	3.7	154
36	Janus-like opposing roles of CD47 in autoimmune brain inflammation in humans and mice. <i>Journal of Experimental Medicine</i> , 2012, 209, 1325-1334.	4.2	147

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37	Transcriptional Analysis of Multiple Sclerosis Brain Lesions Reveals a Complex Pattern of Cytokine Expression. <i>Journal of Immunology</i> , 2000, 165, 6576-6582.	0.4	145
38	Transcription-Based Prediction of Response to IFN $\beta$ Using Supervised Computational Methods. <i>PLoS Biology</i> , 2004, 3, e2.	2.6	144
39	The genetics of autoimmune diseases: a networked perspective. <i>Current Opinion in Immunology</i> , 2009, 21, 596-605.	2.4	133
40	Gut microbiota-specific IgA B cells traffic to the CNS in active multiple sclerosis. <i>Science Immunology</i> , 2020, 5, .	5.6	132
41	Aberrant oligodendroglial-vascular interactions disrupt the blood-brain barrier, triggering CNS inflammation. <i>Nature Neuroscience</i> , 2019, 22, 709-718.	7.1	131
42	Gut microbiome analysis in neuromyelitis optica reveals overabundance of <i>Clostridium perfringens</i> . <i>Annals of Neurology</i> , 2016, 80, 443-447.	2.8	125
43	Multiple sclerosis: Genomic rewards. <i>Journal of Neuroimmunology</i> , 2001, 113, 171-184.	1.1	123
44	Genetic variation influences glutamate concentrations in brains of patients with multiple sclerosis. <i>Brain</i> , 2010, 133, 2603-2611.	3.7	123
45	Heterogeneous Network Edge Prediction: A Data Integration Approach to Prioritize Disease-Associated Genes. <i>PLoS Computational Biology</i> , 2015, 11, e1004259.	1.5	120
46	A pathogenic and clonally expanded B cell transcriptome in active multiple sclerosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 22932-22943.	3.3	119
47	Multiple sclerosis genetics "is the glass half full, or half empty?". <i>Nature Reviews Neurology</i> , 2010, 6, 429-437.	4.9	115
48	Low-Frequency and Rare-Coding Variation Contributes to Multiple Sclerosis Risk. <i>Cell</i> , 2018, 175, 1679-1687.e7.	13.5	115
49	Abrogation of T cell quiescence characterizes patients at high risk for multiple sclerosis after the initial neurological event. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 11839-11844.	3.3	105
50	Uncoupling the Roles of <i>HLA-DRB1</i> and <i>HLA-DRB5</i> Genes in Multiple Sclerosis. <i>Journal of Immunology</i> , 2008, 181, 5473-5480.	0.4	105
51	Systems biology and its application to the understanding of neurological diseases. <i>Annals of Neurology</i> , 2009, 65, 124-139.	2.8	99
52	Parallel states of pathological Wnt signaling in neonatal brain injury and colon cancer. <i>Nature Neuroscience</i> , 2014, 17, 506-512.	7.1	98
53	Blood RNA profiling in a large cohort of multiple sclerosis patients and healthy controls. <i>Human Molecular Genetics</i> , 2013, 22, 4194-4205.	1.4	81
54	The HLA locus and multiple sclerosis in Spain. Role in disease susceptibility, clinical course and response to interferon- $\beta$ . <i>Journal of Neuroimmunology</i> , 2002, 130, 194-201.	1.1	78

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55	Pharmacogenomic analysis of interferon receptor polymorphisms in multiple sclerosis. <i>Genes and Immunity</i> , 2003, 4, 147-152.	2.2	77
56	The Role of the Gut Microbiome in Multiple Sclerosis Risk and Progression: Towards Characterization of the "MS Microbiome". <i>Neurotherapeutics</i> , 2018, 15, 126-134.	2.1	75
57	Disease-modifying therapies alter gut microbial composition in MS. <i>Neurology: Neuroimmunology and NeuroInflammation</i> , 2019, 6, e517.	3.1	75
58	A validated gene regulatory network and GWAS identifies early regulators of T cell-associated diseases. <i>Science Translational Medicine</i> , 2015, 7, 313ra178.	5.8	66
59	Association of HLA Genetic Risk Burden With Disease Phenotypes in Multiple Sclerosis. <i>JAMA Neurology</i> , 2016, 73, 795.	4.5	64
60	Modeling the cumulative genetic risk for multiple sclerosis from genome-wide association data. <i>Genome Medicine</i> , 2011, 3, 3.	3.6	63
61	The molecular signature of therapeutic mesenchymal stem cells exposes the architecture of the hematopoietic stem cell niche synapse. <i>BMC Genomics</i> , 2007, 8, 65.	1.2	61
62	Expression profiling of Aldh1l1 precursors in the developing spinal cord reveals glial lineage-specific genes and direct Sox9-Nfe2l1 interactions. <i>Glia</i> , 2013, 61, 1518-1532.	2.5	61
63	Manitoba-oculo-tricho-anal (MOTA) syndrome is caused by mutations in FREM1. <i>Journal of Medical Genetics</i> , 2011, 48, 375-382.	1.5	60
64	Osteopontin polymorphisms and disease course in multiple sclerosis. <i>Genes and Immunity</i> , 2003, 4, 312-315.	2.2	59
65	Multiple Sclerosis-Associated Changes in the Composition and Immune Functions of Spore-Forming Bacteria. <i>MSystems</i> , 2018, 3, .	1.7	56
66	The Gut Microbiome in Neuromyelitis Optica. <i>Neurotherapeutics</i> , 2018, 15, 92-101.	2.1	54
67	Integrating biomedical research and electronic health records to create knowledge-based biologically meaningful machine-readable embeddings. <i>Nature Communications</i> , 2019, 10, 3045.	5.8	54
68	Precision medicine in chronic disease management: The multiple sclerosis screen. <i>Annals of Neurology</i> , 2014, 76, 633-642.	2.8	53
69	A genome-wide association study of brain lesion distribution in multiple sclerosis. <i>Brain</i> , 2013, 136, 1012-1024.	3.7	52
70	Blood miRNA expression pattern is a possible risk marker for natalizumab-associated progressive multifocal leukoencephalopathy in multiple sclerosis patients. <i>Multiple Sclerosis Journal</i> , 2014, 20, 1851-1859.	1.4	50
71	The autoimmune disease-associated transcription factors EOMES and TBX21 are dysregulated in multiple sclerosis and define a molecular subtype of disease. <i>Clinical Immunology</i> , 2014, 151, 16-24.	1.4	49
72	Selective Estrogen Receptor Modulators Enhance CNS Remyelination Independent of Estrogen Receptors. <i>Journal of Neuroscience</i> , 2019, 39, 2184-2194.	1.7	49

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73	Revealing the genetic basis of multiple sclerosis: are we there yet?. <i>Current Opinion in Genetics and Development</i> , 2011, 21, 317-324.	1.5	46
74	Genetics of multiple sclerosis. <i>Current Opinion in Neurology</i> , 2012, 25, 239-245.	1.8	46
75	IFN- $\gamma$ orchestrates mesenchymal stem cell plasticity through the signal transducer and activator of transcription 1 and 3 and mammalian target of rapamycin pathways. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 1667-1676.	1.5	46
76	microRNA and exosome profiling in multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2020, 26, 599-604.	1.4	46
77	Genome-Wide Network Analysis Reveals the Global Properties of IFN- $\gamma$ Immediate Transcriptional Effects in Humans. <i>Journal of Immunology</i> , 2007, 178, 5076-5085.	0.4	43
78	Data integration and systems biology approaches for biomarker discovery: Challenges and opportunities for multiple sclerosis. <i>Journal of Neuroimmunology</i> , 2012, 248, 58-65.	1.1	42
79	Changes in matrix metalloproteinases and their inhibitors during interferon-beta treatment in multiple sclerosis. <i>Clinical Immunology</i> , 2009, 130, 145-150.	1.4	41
80	Tob1 plays a critical role in the activation of encephalitogenic T cells in CNS autoimmunity. <i>Journal of Experimental Medicine</i> , 2013, 210, 1301-1309.	4.2	40
81	Genome sequencing uncovers phenocopies in primary progressive multiple sclerosis. <i>Annals of Neurology</i> , 2018, 84, 51-63.	2.8	38
82	Biolink Model: A universal schema for knowledge graphs in clinical, biomedical, and translational science. <i>Clinical and Translational Science</i> , 2022, 15, 1848-1855.	1.5	38
83	Modular Transcriptional Activity Characterizes the Initiation and Progression of Autoimmune Encephalomyelitis. <i>Journal of Immunology</i> , 2005, 174, 7412-7422.	0.4	37
84	iCTNet: A Cytoscape plugin to produce and analyze integrative complex traits networks. <i>BMC Bioinformatics</i> , 2011, 12, 380.	1.2	36
85	Mapping gene activity in complex disorders: Integration of expression and genomic scans for multiple sclerosis. <i>Journal of Neuroimmunology</i> , 2005, 167, 157-169.	1.1	34
86	In depth comparison of an individual's DNA and its lymphoblastoid cell line using whole genome sequencing. <i>BMC Genomics</i> , 2012, 13, 477.	1.2	34
87	Longitudinal system-based analysis of transcriptional responses to type I interferons. <i>Physiological Genomics</i> , 2009, 38, 362-371.	1.0	32
88	Genetic associations with brain cortical thickness in multiple sclerosis. <i>Genes, Brain and Behavior</i> , 2015, 14, 217-227.	1.1	31
89	The autoimmune risk gene ZMIZ1 is a vitamin D responsive marker of a molecular phenotype of multiple sclerosis. <i>Journal of Autoimmunity</i> , 2017, 78, 57-69.	3.0	31
90	The relative contributions of obesity, vitamin D, leptin, and adiponectin to multiple sclerosis risk: A Mendelian randomization mediation analysis. <i>Multiple Sclerosis Journal</i> , 2021, 27, 1994-2000.	1.4	31

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91	Early complement genes are associated with visual system degeneration in multiple sclerosis. <i>Brain</i> , 2019, 142, 2722-2736.	3.7	30
92	Childhood obesity and multiple sclerosis: A Mendelian randomization study. <i>Multiple Sclerosis Journal</i> , 2021, 27, 2150-2158.	1.4	30
93	PINBPA: Cytoscape app for network analysis of GWAS data. <i>Bioinformatics</i> , 2015, 31, 262-264.	1.8	29
94	Opposite Roles of NMDA Receptors in Relapsing and Primary Progressive Multiple Sclerosis. <i>PLoS ONE</i> , 2013, 8, e67357.	1.1	29
95	A gene pathway analysis highlights the role of cellular adhesion molecules in multiple sclerosis susceptibility. <i>Genes and Immunity</i> , 2014, 15, 126-132.	2.2	26
96	Analysis of antibody gene rearrangement, usage, and specificity in chronic focal encephalitis. <i>Neurology</i> , 2002, 58, 709-716.	1.5	25
97	Response to Comment on "The Influence of the Proinflammatory Cytokine, Osteopontin, on Autoimmune Demyelinating Disease". <i>Science</i> , 2003, 299, 1845b-1845.	6.0	25
98	Role of antiproliferative gene <i>Tob1</i> in the immune system. <i>Clinical and Experimental Neuroimmunology</i> , 2014, 5, 132-136.	0.5	24
99	NR1H3 p.Arg415Gln Is Not Associated to Multiple Sclerosis Risk. <i>Neuron</i> , 2016, 92, 333-335.	3.8	24
100	Household paired design reduces variance and increases power in multi-city gut microbiome study in multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2021, 27, 366-379.	1.4	24
101	Functional Energetics of CD4+ Cellular Immunity in Monoclonal Antibody-Associated Progressive Multifocal Leukoencephalopathy in Autoimmune Disorders. <i>PLoS ONE</i> , 2011, 6, e18506.	1.1	23
102	Levels of brain-derived neurotrophic factor in patients with multiple sclerosis. <i>Annals of Clinical and Translational Neurology</i> , 2020, 7, 2251-2261.	1.7	23
103	Naive CD4 T-cell activation identifies MS patients having rapid transition to progressive MS. <i>Neurology</i> , 2014, 82, 681-690.	1.5	22
104	Classification of neurological diseases using multi-dimensional CSF analysis. <i>Brain</i> , 2021, 144, 2625-2634.	3.7	22
105	Embedding electronic health records onto a knowledge network recognizes prodromal features of multiple sclerosis and predicts diagnosis. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2022, 29, 424-434.	2.2	22
106	Gene Expression Profiling in Neurological Disorders: Toward a Systems-Level Understanding of the Brain. <i>NeuroMolecular Medicine</i> , 2005, 6, 031-052.	1.8	21
107	Harnessing electronic medical records to advance research on multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2019, 25, 408-418.	1.4	21
108	Gene expression analysis reveals altered brain transcription of glutamate receptors and inflammatory genes in a patient with chronic focal (Rasmussen's) encephalitis. <i>Journal of Neuroimmunology</i> , 2002, 128, 9-15.	1.1	20

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109	Quantitative Longitudinal Analysis of T Cell Receptor Repertoire Expression in HIV-Infected Patients on Antiretroviral and Interleukin-2 Therapy. <i>AIDS Research and Human Retroviruses</i> , 2007, 23, 741-747.	0.5	20
110	Sequencing of the IL6 gene in a case-control study of cerebral palsy in children. <i>BMC Medical Genetics</i> , 2013, 14, 126.	2.1	20
111	Prognostic biomarkers of IFN $\beta$ therapy in multiple sclerosis patients. <i>Multiple Sclerosis Journal</i> , 2015, 21, 894-904.	1.4	20
112	Meta-analysis of genome-wide association studies reveals genetic overlap between Hodgkin lymphoma and multiple sclerosis. <i>International Journal of Epidemiology</i> , 2016, 45, 728-740.	0.9	20
113	Increased Transcriptional Activity of Milk-Related Genes following the Active Phase of Experimental Autoimmune Encephalomyelitis and Multiple Sclerosis. <i>Journal of Immunology</i> , 2007, 179, 4074-4082.	0.4	19
114	Progress toward a universal biomedical data translator. <i>Clinical and Translational Science</i> , 2022, 15, 1838-1847.	1.5	17
115	Systems-based medicine approaches to understand and treat complex diseases. The example of multiple sclerosis. <i>Autoimmunity</i> , 2006, 39, 651-662.	1.2	16
116	Detection of identity by descent using next-generation whole genome sequencing data. <i>BMC Bioinformatics</i> , 2012, 13, 121.	1.2	16
117	Cell type-specific transcriptomics identifies neddylation as a novel therapeutic target in multiple sclerosis. <i>Brain</i> , 2021, 144, 450-461.	3.7	16
118	Genetic variation in the odorant receptors family 13 and the mhc loci influence mate selection in a multiple sclerosis dataset. <i>BMC Genomics</i> , 2010, 11, 626.	1.2	15
119	Polygenic risk score association with multiple sclerosis susceptibility and phenotype in Europeans. <i>Brain</i> , 2023, 146, 645-656.	3.7	15
120	A non-synonymous single-nucleotide polymorphism associated with multiple sclerosis risk affects the EVI5 interactome. <i>Human Molecular Genetics</i> , 2015, 24, ddv412.	1.4	14
121	Distinctive waves of innate immune response in the retina in experimental autoimmune encephalomyelitis. <i>JCI Insight</i> , 2021, 6, .	2.3	14
122	Specific hypomethylation programs underpin B cell activation in early multiple sclerosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	14
123	Large-scale gene-expression studies and the challenge of multiple sclerosis. <i>Genome Biology</i> , 2002, 3, reviews1027.1.	13.9	13
124	Dynamic regulation of alternative ATP-binding cassette transporter A1 transcripts. <i>Biochemical and Biophysical Research Communications</i> , 2003, 306, 463-468.	1.0	13
125	Protein network analysis reveals selectively vulnerable regions and biological processes in FTD. <i>Neurology: Genetics</i> , 2018, 4, e266.	0.9	12
126	A New Point Mutation (M313T) in the Thyroid Hormone Receptor $\beta$ Gene in a Patient with Resistance to Thyroid Hormone. <i>Thyroid</i> , 1997, 7, 43-44.	2.4	11



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127	A robust type I interferon gene signature from blood RNA defines quantitative but not qualitative differences between three major IFN $\alpha$ drugs in the treatment of multiple sclerosis. <i>Human Molecular Genetics</i> , 2015, 24, 3192-3205.	1.4	11
128	iCTNet2: integrating heterogeneous biological interactions to understand complex traits. <i>F1000Research</i> , 2015, 4, 485.	0.8	11
129	Interferon-beta affects mitochondrial activity in CD4 <sup>+</sup> lymphocytes: Implications for mechanism of action in multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2015, 21, 1262-1270.	1.4	10
130	Data characterizing the ZMIZ1 molecular phenotype of multiple sclerosis. <i>Data in Brief</i> , 2017, 11, 364-370.	0.5	10
131	Vitamin D Regulates MerTK-Dependent Phagocytosis in Human Myeloid Cells. <i>Journal of Immunology</i> , 2020, 205, 398-406.	0.4	10
132	Serum antibodies to phosphatidylcholine in MS. <i>Neurology: Neuroimmunology and NeuroInflammation</i> , 2020, 7, e765.	3.1	10
133	Knowledge Network Embedding of Transcriptomic Data from Spaceflown Mice Uncovers Signs and Symptoms Associated with Terrestrial Diseases. <i>Life</i> , 2021, 11, 42.	1.1	10
134	SARS-CoV-2 meta-interactome suggests disease-specific, autoimmune pathophysiologies and therapeutic targets. <i>F1000Research</i> , 2020, 9, 992.	0.8	10
135	MRI-derived g-ratio and lesion severity in newly diagnosed multiple sclerosis. <i>Brain Communications</i> , 2021, 3, fcab249.	1.5	10
136	Patient with an Xp21 contiguous gene deletion syndrome in association with agenesis of the corpus callosum. <i>American Journal of Medical Genetics Part A</i> , 1997, 70, 216-221.	2.4	9
137	Genomics and new targets for multiple sclerosis. <i>Pharmacogenomics</i> , 2005, 6, 151-161.	0.6	9
138	Genetic variation across RNA metabolism and cell death gene networks is implicated in the semantic variant of primary progressive aphasia. <i>Scientific Reports</i> , 2019, 9, 10854.	1.6	9
139	Genetic contribution to multiple sclerosis risk among Ashkenazi Jews. <i>BMC Medical Genetics</i> , 2015, 16, 55.	2.1	8
140	Immune cell-specific transcriptional profiling highlights distinct molecular pathways controlled by Tob1 upon experimental autoimmune encephalomyelitis. <i>Scientific Reports</i> , 2016, 6, 31603.	1.6	8
141	Mononuclear cell transcriptome changes associated with dimethyl fumarate in MS. <i>Neurology: Neuroimmunology and NeuroInflammation</i> , 2018, 5, e470.	3.1	8
142	iCTNet2: integrating heterogeneous biological interactions to understand complex traits. <i>F1000Research</i> , 2015, 4, 485.	0.8	8
143	iPINBPA: an integrative network-based functional module discovery tool for genome-wide association studies. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2015, , 255-66.	0.7	8
144	iPINBPA: AN INTEGRATIVE NETWORK-BASED FUNCTIONAL MODULE DISCOVERY TOOL FOR GENOME-WIDE ASSOCIATION STUDIES. , 2014, , .		7

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145	SNP imputation bias reduces effect size determination. <i>Frontiers in Genetics</i> , 2015, 6, 30.	1.1	7
146	Evidence for association of chromosome 10 open reading frame (C10orf27) gene polymorphisms and multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2008, 14, 412-414.	1.4	6
147	Assessing the Power of Exome Chips. <i>PLoS ONE</i> , 2015, 10, e0139642.	1.1	6
148	Direct Deletion Analysis in Two Duchenne Muscular Dystrophy Symptomatic Females Using Polymorphic Dinucleotide (CA) <sub>n</sub> Loci within the Dystrophin Gene. <i>BMB Reports</i> , 2003, 36, 179-184.	1.1	6
149	Deletion patterns in Argentine patients with Duchenne and Becker muscular dystrophy. <i>Neurological Research</i> , 1998, 20, 409-414.	0.6	5
150	Predictive modeling of therapy response in multiple sclerosis using gene expression data. , 2006, 2006, 5519-22.		5
151	Autoimmune Disorders. , 2013, , 822-838.		5
152	Insights into microbiome research 2: Experimental design, sample collection, and shipment. <i>Multiple Sclerosis Journal</i> , 2018, 24, 1419-1420.	1.4	5
153	Mendelian randomization study shows no causal effects of serum urate levels on the risk of MS. <i>Neurology: Neuroimmunology and NeuroInflammation</i> , 2021, 8, e920.	3.1	5
154	A biomedical open knowledge network harnesses the power of AI to understand deep human biology. <i>AI Magazine</i> , 2022, 43, 46-58.	1.4	5
155	FutureMS cohort profile: a Scottish multicentre inception cohort study of relapsing-remitting multiple sclerosis. <i>BMJ Open</i> , 2022, 12, e058506.	0.8	5
156	Longitudinal analysis of B cell repertoire and antibody gene rearrangements during early HIV infection. <i>Genes and Immunity</i> , 2005, 6, 66-69.	2.2	4
157	Carrier detection in Duchenne and Becker muscular dystrophy Argentine families. <i>Clinical Genetics</i> , 1998, 54, 503-511.	1.0	4
158	Transcriptional expression patterns triggered by chemically distinct neuroprotective molecules. <i>Neuroscience</i> , 2012, 226, 10-20.	1.1	4
159	New insights into the genetics of multiple sclerosis. <i>Journal of Rehabilitation Research and Development</i> , 2002, 39, 201-9.	1.6	4
160	Four new polymorphisms in the human dystrophin gene from an Argentinian population. , 1997, 20, 1451-1453.		3
161	Gene expression profiling in MS: a fulfilled promise?. <i>Multiple Sclerosis Journal</i> , 2013, 19, 1813-1814.	1.4	3
162	The microbiome and MS: The influence of the microbiota on MS risk and progression”Session chair summary. <i>Multiple Sclerosis Journal</i> , 2018, 24, 587-589.	1.4	3

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163	Insights into microbiome research 1: How to choose appropriate controls for a microbiome study in MS?. Multiple Sclerosis Journal, 2018, 24, 1278-1279.	1.4	3
164	Insights into microbiome research 6: The role of consortia in studying the role of microbes in health and disease. Multiple Sclerosis Journal, 2019, 25, 336-337.	1.4	3
165	Biological concepts of multiple sclerosis pathogenesis and relationship to treatment. , 2007, , 23-44.		3
166	Patient with an Xp21 contiguous gene deletion syndrome in association with agenesis of the corpus callosum. American Journal of Medical Genetics Part A, 1997, 70, 216-21.	2.4	2
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