

Sergio Baranzini

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.

180
papers

15,808
citations

53
h-index

125
g-index

206
ext. papers

19,126
ext. citations

9.9
avg, IF

6.25
L-index

#	Paper	IF	Citations
180	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. <i>Nature</i> , 2011 , 476, 214-9	50.4	1948
179	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. <i>Nature Genetics</i> , 2013 , 45, 1353-60	36.3	934
178	The influence of the proinflammatory cytokine, osteopontin, on autoimmune demyelinating disease. <i>Science</i> , 2001 , 294, 1731-5	33.3	729
177	Multiple sclerosis. <i>Lancet, The</i> , 2018 , 391, 1622-1636	40	698
176	Meta-analysis of genome scans and replication identify CD6, IRF8 and TNFRSF1A as new multiple sclerosis susceptibility loci. <i>Nature Genetics</i> , 2009 , 41, 776-82	36.3	621
175	Dysregulation of the Wnt pathway inhibits timely myelination and remyelination in the mammalian CNS. <i>Genes and Development</i> , 2009 , 23, 1571-85	12.6	459
174	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	11.5	453
173	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	11.5	441
172	Proteomic analysis of active multiple sclerosis lesions reveals therapeutic targets. <i>Nature</i> , 2008 , 451, 1076-81	50.4	406
171	Genome, epigenome and RNA sequences of monozygotic twins discordant for multiple sclerosis. <i>Nature</i> , 2010 , 464, 1351-6	50.4	390
170	Incidental MRI anomalies suggestive of multiple sclerosis: the radiologically isolated syndrome. <i>Neurology</i> , 2009 , 72, 800-5	6.5	361
169	Genome-wide association analysis of susceptibility and clinical phenotype in multiple sclerosis. <i>Human Molecular Genetics</i> , 2009 , 18, 767-78	5.6	357
168	Pathway and network-based analysis of genome-wide association studies in multiple sclerosis. <i>Human Molecular Genetics</i> , 2009 , 18, 2078-90	5.6	310
167	Multiple sclerosis genomic map implicates peripheral immune cells and microglia in susceptibility. <i>Science</i> , 2019 , 365,	33.3	309
166	Mapping multiple sclerosis susceptibility to the HLA-DR locus in African Americans. <i>American Journal of Human Genetics</i> , 2004 , 74, 160-7	11	274
165	Axin2 as regulatory and therapeutic target in newborn brain injury and remyelination. <i>Nature Neuroscience</i> , 2011 , 14, 1009-16	25.5	265
164	The genetics of multiple sclerosis: SNPs to pathways to pathogenesis. <i>Nature Reviews Genetics</i> , 2008 , 9, 516-26	30.1	259

163	Heterogeneity at the HLA-DRB1 locus and risk for multiple sclerosis. <i>Human Molecular Genetics</i> , 2006 , 15, 2813-24	5.6	246
162	Myelin regeneration: a recapitulation of development?. <i>Annual Review of Neuroscience</i> , 2011 , 34, 21-43	17	242
161	Long-term evolution of multiple sclerosis disability in the treatment era. <i>Annals of Neurology</i> , 2016 , 80, 499-510	9.4	229
160	Class II HLA interactions modulate genetic risk for multiple sclerosis. <i>Nature Genetics</i> , 2015 , 47, 1107-1113	13.3	215
159	B cell repertoire diversity and clonal expansion in multiple sclerosis brain lesions. <i>Journal of Immunology</i> , 1999 , 163, 5133-44	5.3	208
158	Astrocyte-encoded positional cues maintain sensorimotor circuit integrity. <i>Nature</i> , 2014 , 509, 189-94	50.4	202
157	The genetics of multiple sclerosis: an up-to-date review. <i>Immunological Reviews</i> , 2012 , 248, 87-103	11.3	192
156	Differential micro RNA expression in PBMC from multiple sclerosis patients. <i>PLoS ONE</i> , 2009 , 4, e6309	3.7	184
155	Rituximab efficiently depletes increased CD20-expressing T cells in multiple sclerosis patients. <i>Journal of Immunology</i> , 2014 , 193, 580-586	5.3	160
154	Systematic integration of biomedical knowledge prioritizes drugs for repurposing. <i>ELife</i> , 2017 , 6,	8.9	151
153	Peroxisome proliferator-activated receptor (PPAR)alpha expression in T cells mediates gender differences in development of T cell-mediated autoimmunity. <i>Journal of Experimental Medicine</i> , 2007 , 204, 321-30	16.6	139
152	Silent progression in disease activity-free relapsing multiple sclerosis. <i>Annals of Neurology</i> , 2019 , 85, 653-666	9.4	135
151	Genome-wide pharmacogenomic analysis of the response to interferon beta therapy in multiple sclerosis. <i>Archives of Neurology</i> , 2008 , 65, 337-44		135
150	Transcriptional analysis of multiple sclerosis brain lesions reveals a complex pattern of cytokine expression. <i>Journal of Immunology</i> , 2000 , 165, 6576-82	5.3	134
149	Recirculating Intestinal IgA-Producing Cells Regulate Neuroinflammation via IL-10. <i>Cell</i> , 2019 , 176, 610-624	34.1	133
148	Genotype-Phenotype correlations in multiple sclerosis: HLA genes influence disease severity inferred by 1HMR spectroscopy and MRI measures. <i>Brain</i> , 2009 , 132, 250-9	11.2	132
147	Modules, networks and systems medicine for understanding disease and aiding diagnosis. <i>Genome Medicine</i> , 2014 , 6, 82	14.4	126
146	Transcription-based prediction of response to IFNbeta using supervised computational methods. <i>PLoS Biology</i> , 2005 , 3, e2	9.7	122

145	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, 637-45	9.4	117
144	Multiple sclerosis: genomic rewards. <i>Journal of Neuroimmunology</i> , 2001 , 113, 171-84	3.5	111
143	The genetics of autoimmune diseases: a networked perspective. <i>Current Opinion in Immunology</i> , 2009 , 21, 596-605	7.8	110
142	Janus-like opposing roles of CD47 in autoimmune brain inflammation in humans and mice. <i>Journal of Experimental Medicine</i> , 2012 , 209, 1325-34	16.6	108
141	Genetic variation influences glutamate concentrations in brains of patients with multiple sclerosis. <i>Brain</i> , 2010 , 133, 2603-11	11.2	107
140	The Genetics of Multiple Sclerosis: From 0 to 200 in 50 Years. <i>Trends in Genetics</i> , 2017 , 33, 960-970	8.5	103
139	Multiple sclerosis genetics--is the glass half full, or half empty?. <i>Nature Reviews Neurology</i> , 2010 , 6, 429-37	10.7	103
138	Gut microbiome analysis in neuromyelitis optica reveals overabundance of <i>Clostridium perfringens</i> . <i>Annals of Neurology</i> , 2016 , 80, 443-7	9.4	95
137	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, 11839-44	11.5	83
136	Uncoupling the roles of HLA-DRB1 and HLA-DRB5 genes in multiple sclerosis. <i>Journal of Immunology</i> , 2008 , 181, 5473-80	5.3	83
135	Systems biology and its application to the understanding of neurological diseases. <i>Annals of Neurology</i> , 2009 , 65, 124-39	9.4	82
134	Parallel states of pathological Wnt signaling in neonatal brain injury and colon cancer. <i>Nature Neuroscience</i> , 2014 , 17, 506-12	25.5	76
133	Low-Frequency and Rare-Coding Variation Contributes to Multiple Sclerosis Risk. <i>Cell</i> , 2018 , 175, 1679-1687	16.7	72
132	Heterogeneous Network Edge Prediction: A Data Integration Approach to Prioritize Disease-Associated Genes. <i>PLoS Computational Biology</i> , 2015 , 11, e1004259	5	69
131	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	3.5	68
130	Pharmacogenomic analysis of interferon receptor polymorphisms in multiple sclerosis. <i>Genes and Immunity</i> , 2003 , 4, 147-52	4.4	68
129	Aberrant oligodendroglial-vascular interactions disrupt the blood-brain barrier, triggering CNS inflammation. <i>Nature Neuroscience</i> , 2019 , 22, 709-718	25.5	61
128	Blood RNA profiling in a large cohort of multiple sclerosis patients and healthy controls. <i>Human Molecular Genetics</i> , 2013 , 22, 4194-205	5.6	58

127	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	4.5	53
126	Osteopontin polymorphisms and disease course in multiple sclerosis. <i>Genes and Immunity</i> , 2003 , 4, 312-5	4.4	52
125	Modeling the cumulative genetic risk for multiple sclerosis from genome-wide association data. <i>Genome Medicine</i> , 2011 , 3, 3	14.4	48
124	Gut microbiota-specific IgA B cells traffic to the CNS in active multiple sclerosis. <i>Science Immunology</i> , 2020 , 5,	28	48
123	Manitoba-oculo-tricho-anal (MOTA) syndrome is caused by mutations in FREM1. <i>Journal of Medical Genetics</i> , 2011 , 48, 375-82	5.8	46
122	A validated gene regulatory network and GWAS identifies early regulators of T cell-associated diseases. <i>Science Translational Medicine</i> , 2015 , 7, 313ra178	17.5	45
121	A genome-wide association study of brain lesion distribution in multiple sclerosis. <i>Brain</i> , 2013 , 136, 1012-14	12.4	45
120	Revealing the genetic basis of multiple sclerosis: are we there yet?. <i>Current Opinion in Genetics and Development</i> , 2011 , 21, 317-24	4.9	44
119	Association of HLA Genetic Risk Burden With Disease Phenotypes in Multiple Sclerosis. <i>JAMA Neurology</i> , 2016 , 73, 795-802	17.2	43
118	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, 1851-5	5	43
117	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	11.5	43
116	Disease-modifying therapies alter gut microbial composition in MS. <i>Neurology: Neuroimmunology and NeuroInflammation</i> , 2019 , 6, e517	9.1	43
115	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, 1518-32	9	41
114	Genetics of multiple sclerosis: swimming in an ocean of data. <i>Current Opinion in Neurology</i> , 2012 , 25, 239-45	7.1	40
113	Genome-wide network analysis reveals the global properties of IFN-beta immediate transcriptional effects in humans. <i>Journal of Immunology</i> , 2007 , 178, 5076-85	5.3	39
112	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	6.4	39
111	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	9	37
110	Precision medicine in chronic disease management: The multiple sclerosis BioScreen. <i>Annals of Neurology</i> , 2014 , 76, 633-42	9.4	36

109	Changes in matrix metalloproteinases and their inhibitors during interferon-beta treatment in multiple sclerosis. <i>Clinical Immunology</i> , 2009 , 130, 145-50	9	36
108	Multiple Sclerosis-Associated Changes in the Composition and Immune Functions of Spore-Forming Bacteria. <i>MSystems</i> , 2018 , 3,	7.6	36
107	Modular transcriptional activity characterizes the initiation and progression of autoimmune encephalomyelitis. <i>Journal of Immunology</i> , 2005 , 174, 7412-22	5.3	33
106	Data integration and systems biology approaches for biomarker discovery: challenges and opportunities for multiple sclerosis. <i>Journal of Neuroimmunology</i> , 2012 , 248, 58-65	3.5	32
105	Tob1 plays a critical role in the activation of encephalitogenic T cells in CNS autoimmunity. <i>Journal of Experimental Medicine</i> , 2013 , 210, 1301-9	16.6	32
104	The Gut Microbiome in Neuromyelitis Optica. <i>Neurotherapeutics</i> , 2018 , 15, 92-101	6.4	31
103	IFN- β 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	11.5	31
102	iCTNet: a Cytoscape plugin to produce and analyze integrative complex traits networks. <i>BMC Bioinformatics</i> , 2011 , 12, 380	3.6	30
101	In depth comparison of an individual's DNA and its lymphoblastoid cell line using whole genome sequencing. <i>BMC Genomics</i> , 2012 , 13, 477	4.5	29
100	Mapping gene activity in complex disorders: Integration of expression and genomic scans for multiple sclerosis. <i>Journal of Neuroimmunology</i> , 2005 , 167, 157-69	3.5	28
99	Genetic associations with brain cortical thickness in multiple sclerosis. <i>Genes, Brain and Behavior</i> , 2015 , 14, 217-27	3.6	25
98	PINBPA: cytoscape app for network analysis of GWAS data. <i>Bioinformatics</i> , 2015 , 31, 262-4	7.2	25
97	Longitudinal system-based analysis of transcriptional responses to type I interferons. <i>Physiological Genomics</i> , 2009 , 38, 362-71	3.6	25
96	Opposite roles of NMDA receptors in relapsing and primary progressive multiple sclerosis. <i>PLoS ONE</i> , 2013 , 8, e67357	3.7	25
95	Selective Estrogen Receptor Modulators Enhance CNS Remyelination Independent of Estrogen Receptors. <i>Journal of Neuroscience</i> , 2019 , 39, 2184-2194	6.6	24
94	A gene pathway analysis highlights the role of cellular adhesion molecules in multiple sclerosis susceptibility. <i>Genes and Immunity</i> , 2014 , 15, 126-32	4.4	23
93	Comment on "The influence of the proinflammatory cytokine, osteopontin, on autoimmune demyelinating disease". <i>Science</i> , 2003 , 299, 1845; author reply 1845	33.3	22
92	Genome sequencing uncovers phenocopies in primary progressive multiple sclerosis. <i>Annals of Neurology</i> , 2018 , 84, 51-63	9.4	21

91	Analysis of antibody gene rearrangement, usage, and specificity in chronic focal encephalitis. <i>Neurology</i> , 2002 , 58, 709-16	6.5	21
90	Integrating biomedical research and electronic health records to create knowledge-based biologically meaningful machine-readable embeddings. <i>Nature Communications</i> , 2019 , 10, 3045	17.4	20
89	NR1H3 p.Arg415Gln Is Not Associated to Multiple Sclerosis Risk. <i>Neuron</i> , 2016 , 92, 333-335	13.9	19
88	Functional energetics of CD4+ cellular immunity in monoclonal antibody-associated progressive multifocal leukoencephalopathy in autoimmune disorders. <i>PLoS ONE</i> , 2011 , 6, e18506	3.7	19
87	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	3.5	19
86	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	15.5	18
85	Gene expression profiling in neurological disorders: toward a systems-level understanding of the brain. <i>NeuroMolecular Medicine</i> , 2004 , 6, 31-51	4.6	18
84	Naive CD4 T-cell activation identifies MS patients having rapid transition to progressive MS. <i>Neurology</i> , 2014 , 82, 681-90	6.5	17
83	The role of antiproliferative gene Tob1 in the immune system. <i>Clinical and Experimental Neuroimmunology</i> , 2014 , 5, 132-136	0.4	16
82	Detection of identity by descent using next-generation whole genome sequencing data. <i>BMC Bioinformatics</i> , 2012 , 13, 121	3.6	16
81	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, 4074-82	5.3	16
80	Meta-analysis of genome-wide association studies reveals genetic overlap between Hodgkin lymphoma and multiple sclerosis. <i>International Journal of Epidemiology</i> , 2016 , 45, 728-40	7.8	16
79	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	15
78	Systems-based medicine approaches to understand and treat complex diseases. The example of multiple sclerosis. <i>Autoimmunity</i> , 2006 , 39, 651-62	3	15
77	Harnessing electronic medical records to advance research on multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2019 , 25, 408-418	5	15
76	A non-synonymous single-nucleotide polymorphism associated with multiple sclerosis risk affects the EVI5 interactome. <i>Human Molecular Genetics</i> , 2015 , 24, 7151-8	5.6	14
75	Prognostic biomarkers of IFN β therapy in multiple sclerosis patients. <i>Multiple Sclerosis Journal</i> , 2015 , 21, 894-904	5	13
74	microRNA and exosome profiling in multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2020 , 26, 599-604	5	13

73	Early complement genes are associated with visual system degeneration in multiple sclerosis. <i>Brain</i> , 2019 , 142, 2722-2736	11.2	13
72	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	4.5	13
71	Dynamic regulation of alternative ATP-binding cassette transporter A1 transcripts. <i>Biochemical and Biophysical Research Communications</i> , 2003 , 306, 463-8	3.4	13
70	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, 43-4	6.2	10
69	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		8
68	Genomics and new targets for multiple sclerosis. <i>Pharmacogenomics</i> , 2005 , 6, 151-61	2.6	8
67	Large-scale gene-expression studies and the challenge of multiple sclerosis. <i>Genome Biology</i> , 2002 , 3, reviews1027	18.3	8
66	Childhood obesity and multiple sclerosis: A Mendelian randomization study. <i>Multiple Sclerosis Journal</i> , 2021 , 27, 2150-2158	5	8
65	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 ¹⁻³		8
64	A robust type I interferon gene signature from blood RNA defines quantitative but not qualitative differences between three major IFN β drugs in the treatment of multiple sclerosis. <i>Human Molecular Genetics</i> , 2015 , 24, 3192-205	5.6	7
63	Genetic contribution to multiple sclerosis risk among Ashkenazi Jews. <i>BMC Medical Genetics</i> , 2015 , 16, 55	2.1	7
62	Interferon-beta affects mitochondrial activity in CD4+ lymphocytes: Implications for mechanism of action in multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2015 , 21, 1262-70	5	7
61	iCTNet2: integrating heterogeneous biological interactions to understand complex traits. <i>F1000Research</i> , 2015 , 4, 485	3.6	7
60	Immune cell-specific transcriptional profiling highlights distinct molecular pathways controlled by Tob1 upon experimental autoimmune encephalomyelitis. <i>Scientific Reports</i> , 2016 , 6, 31603	4.9	7
59	Protein network analysis reveals selectively vulnerable regions and biological processes in FTD. <i>Neurology: Genetics</i> , 2018 , 4, e266	3.8	7
58	Assessing the Power of Exome Chips. <i>PLoS ONE</i> , 2015 , 10, e0139642	3.7	6
57	iCTNet2: integrating heterogeneous biological interactions to understand complex traits. <i>F1000Research</i> , 2015 , 4, 485	3.6	6
56	Direct deletion analysis in two Duchenne muscular dystrophy symptomatic females using polymorphic dinucleotide (CA) _n loci within the dystrophin gene. <i>BMB Reports</i> , 2003 , 36, 179-84	5.5	6

55	Classification of neurological diseases using multi-dimensional CSF analysis. <i>Brain</i> , 2021 , 144, 2625-2634	11.2	6
54	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	4.9	5
53	Evidence for association of chromosome 10 open reading frame (C10orf27) gene polymorphisms and multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2008 , 14, 412-4	5	5
52	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, 741-7	1.6	5
51	Deletion patterns in Argentine patients with Duchenne and Becker muscular dystrophy. <i>Neurological Research</i> , 1998 , 20, 409-414	2.7	5
50	SARS-CoV-2 meta-interactome suggests disease-specific, autoimmune pathophysiologies and therapeutic targets. <i>F1000Research</i> , 2020 , 9, 992	3.6	5
49	Cell type-specific transcriptomics identifies neddylation as a novel therapeutic target in multiple sclerosis. <i>Brain</i> , 2021 , 144, 450-461	11.2	5
48	FutureMS Cohort Profile: A Scottish Multi-Centre Inception Cohort Study of Relapsing-Remitting Multiple Sclerosis		5
47	Household paired design reduces variance and increases power in multi-city gut microbiome study in multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2020 , 1352458520924594	5	5
46	SNP imputation bias reduces effect size determination. <i>Frontiers in Genetics</i> , 2015 , 6, 30	4.5	4
45	Levels of brain-derived neurotrophic factor in patients with multiple sclerosis. <i>Annals of Clinical and Translational Neurology</i> , 2020 , 7, 2251-2261	5.3	4
44	Vitamin D Regulates MerTK-Dependent Phagocytosis in Human Myeloid Cells. <i>Journal of Immunology</i> , 2020 , 205, 398-406	5.3	4
43	Mononuclear cell transcriptome changes associated with dimethyl fumarate in MS. <i>Neurology: Neuroimmunology and NeuroInflammation</i> , 2018 , 5, e470	9.1	4
42	Transcriptional expression patterns triggered by chemically distinct neuroprotective molecules. <i>Neuroscience</i> , 2012 , 226, 10-20	3.9	4
41	Predictive modeling of therapy response in multiple sclerosis using gene expression data. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society</i> , 2006 , 2006, 5519-22		4
40	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> , 2021 ,	8.6	4
39	Distinctive waves of innate immune response in the retina in experimental autoimmune encephalomyelitis. <i>JCI Insight</i> , 2021 , 6,	9.9	4
38	Knowledge Network Embedding of Transcriptomic Data from Spaceflown Mice Uncovers Signs and Symptoms Associated with Terrestrial Diseases. <i>Life</i> , 2021 , 11,	3	4

37	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	5	4
36	Insights into microbiome research 2: Experimental design, sample collection, and shipment. <i>Multiple Sclerosis Journal</i> , 2018 , 24, 1419-1420	5	4
35	New insights into the genetics of multiple sclerosis. <i>Journal of Rehabilitation Research and Development</i> , 2002 , 39, 201-9		4
34	Biolink Model: A universal schema for knowledge graphs in clinical, biomedical, and translational science. <i>Clinical and Translational Science</i> ,	4.9	4
33	Data characterizing the ZMIZ1 molecular phenotype of multiple sclerosis. <i>Data in Brief</i> , 2017 , 11, 364-370.2		3
32	Serum antibodies to phosphatidylcholine in MS. <i>Neurology: Neuroimmunology and NeuroInflammation</i> , 2020 , 7,	9.1	3
31	Insights into microbiome research 1: How to choose appropriate controls for a microbiome study in MS?. <i>Multiple Sclerosis Journal</i> , 2018 , 24, 1278-1279	5	3
30	Autoimmune Disorders 2013 , 822-838		3
29	Four new polymorphisms in the human dystrophin gene from an Argentinian population. <i>Muscle and Nerve</i> , 1997 , 20, 1451-3	3.4	3
28	Carrier detection in Duchenne and Becker muscular dystrophy Argentine families. <i>Clinical Genetics</i> , 1998 , 54, 503-11	4	3
27	Longitudinal analysis of B cell repertoire and antibody gene rearrangements during early HIV infection. <i>Genes and Immunity</i> , 2005 , 6, 66-9	4.4	3
26	Rephetio: Repurposing drugs on a hetnet [project]		3
25	Biological concepts of multiple sclerosis pathogenesis and relationship to treatment 2007 , 23-44		3
24	Insights into microbiome research 6: The role of consortia in studying the role of microbes in health and disease. <i>Multiple Sclerosis Journal</i> , 2019 , 25, 336-337	5	2
23	Rephetio: Repurposing drugs on a hetnet [proposal]		2
22	Renaming heterogeneous networks to a more concise and catchy term 2015 ,		2
21	Mendelian randomization study shows no causal effects of serum urate levels on the risk of MS. <i>Neurology: Neuroimmunology and NeuroInflammation</i> , 2021 , 8,	9.1	2
20	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, 216-21		2

19	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,	11.5	2
18	Whole genome sequences of 2 octogenarians with sustained cognitive abilities. <i>Neurobiology of Aging</i> , 2015 , 36, 1435-8	5.6	1
17	MRI-derived g-ratio and lesion severity in newly diagnosed multiple sclerosis. <i>Brain Communications</i> , 2021 , 3, fcab249	4.5	1
16	Gene expression profiling in neurological and neuroinflammatory diseases 2008 , 115-130		1
15	Systematic integration of biomedical knowledge prioritizes drugs for repurposing		1
14	Patient with an Xp21 contiguous gene deletion syndrome in association with agenesis of the corpus callosum 1997 , 70, 216		1
13	A biomedical open knowledge network harnesses the power of AI to understand deep human biology. <i>AI Magazine</i> , 2022 , 43, 46-58	6.1	1
12	Progress Toward a Universal Biomedical Data Translator. <i>Clinical and Translational Science</i> ,	4.9	1
11	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	5	0
10	Insights into microbiome research 4: The computational analysis. <i>Multiple Sclerosis Journal</i> , 2019 , 25, 21-22	5	
9	Insights into microbiome research 5: Mapping is first but function must come next. <i>Multiple Sclerosis Journal</i> , 2019 , 25, 193-195	5	
8	The era of GWAS is over - Commentary. <i>Multiple Sclerosis Journal</i> , 2018 , 24, 260-261	5	
7	ID: 144. <i>Cytokine</i> , 2015 , 76, 93	4	
6	The genetics of multiple sclerosis35-45		
5	10 Advanced data mining and predictive modelling at the core of personalised medicine. <i>Studies in Multidisciplinarity</i> , 2005 , 165-192		
4	A framework and mechanistically focused, in silico method for enabling rational translational research. <i>Summit on Translational Bioinformatics</i> , 2008 , 2008, 46-50		
3	Peroxisome proliferator-activated receptor (PPAR) expression in T cells mediates gender differences in development of T cell-mediated autoimmunity. <i>Journal of Cell Biology</i> , 2007 , 176, i9-i9	7.3	
2	Meta-Analysis of Hodgkin Lymphoma and Asthma Genome-Wide Association Scans reveals common variants in GATA3. <i>Blood</i> , 2014 , 124, 135-135	2.2	

- 1 Insights into microbiome research 3: Who's there versus what are they doing?. *Multiple Sclerosis Journal*, **2018**, 24, 1541-1542

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