Sergio Baranzini

List of Publications by Year
in descending order

185 papers	21,396 citations	22132 59 h-index	10152 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. Nature, 2011, 476, 214-219.	13.7	2,400
2	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. Nature Genetics, 2013, 45, 1353-1360.	9.4	1,213
3	Multiple sclerosis. Lancet, The, 2018, 391, 1622-1636.	6.3	1,204
4	The Influence of the Proinflammatory Cytokine, Osteopontin, on Autoimmune Demyelinating Disease. Science, 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. Nature Genetics, 2009, 41, 776-782.	9.4	729
6	Multiple sclerosis genomic map implicates peripheral immune cells and microglia in susceptibility. Science, 2019, 365, .	6.0	710
7	Gut bacteria from multiple sclerosis patients modulate human T cells and exacerbate symptoms in mouse models. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 10713-10718.	3.3	709
8	Gut microbiota from multiple sclerosis patients enables spontaneous autoimmune encephalomyelitis in mice. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 10719-10724.	3.3	666
9	Dysregulation of the Wnt pathway inhibits timely myelination and remyelination in the mammalian CNS. Genes and Development, 2009, 23, 1571-1585.	2.7	537
10	Incidental MRI anomalies suggestive of multiple sclerosis. Neurology, 2009, 72, 800-805.	1.5	509
11	Proteomic analysis of active multiple sclerosis lesions reveals therapeutic targets. Nature, 2008, 451, 1076-1081.	13.7	472
12	Genome, epigenome and RNA sequences of monozygotic twins discordant for multiple sclerosis. Nature, 2010, 464, 1351-1356.	13.7	463
13	Genome-wide association analysis of susceptibility and clinical phenotype in multiple sclerosis. Human Molecular Genetics, 2009, 18, 767-778.	1.4	419
14	Pathway and network-based analysis of genome-wide association studies in multiple sclerosis. Human Molecular Genetics, 2009, 18, 2078-2090.	1.4	371
15	Systematic integration of biomedical knowledge prioritizes drugs for repurposing. ELife, 2017, 6, .	2.8	333
16	Longâ€term evolution of multiple sclerosis disability in the treatment era. Annals of Neurology, 2016, 80, 499-510.	2.8	331
17	Class II HLA interactions modulate genetic risk for multiple sclerosis. Nature Genetics, 2015, 47, 1107-1113.	9.4	312
18	Mapping Multiple Sclerosis Susceptibility to the HLA-DR Locus in African Americans. American Journal of Human Genetics, 2004, 74, 160-167.	2.6	311

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19	Axin2 as regulatory and therapeutic target in newborn brain injury and remyelination. Nature Neuroscience, 2011, 14, 1009-1016.	7.1	307
20	The genetics of multiple sclerosis: SNPs to pathways to pathogenesis. Nature Reviews Genetics, 2008, 9, 516-526.	7.7	294
21	Myelin Regeneration: A Recapitulation of Development?. Annual Review of Neuroscience, 2011, 34, 21-43.	5.0	282
22	Heterogeneity at the HLA-DRB1 locus and risk for multiple sclerosis. Human Molecular Genetics, 2006, 15, 2813-2824.	1.4	279
23	Astrocyte-encoded positional cues maintain sensorimotor circuit integrity. Nature, 2014, 509, 189-194.	13.7	266
24	Silent progression in disease activityâ€“free relapsing multiple sclerosis. Annals of Neurology, 2019, 85, 653-666.	2.8	265
25	Recirculating Intestinal IgA-Producing Cells Regulate Neuroinflammation via IL-10. Cell, 2019, 176, 610-624.e18.	13.5	241
26	The genetics of multiple sclerosis: an upâ€toâ€date review. Immunological Reviews, 2012, 248, 87-103.	2.8	230
27	Rituximab Efficiently Depletes Increased CD20-Expressing T Cells in Multiple Sclerosis Patients. Journal of Immunology, 2014, 193, 580-586.	0.4	223
28	Differential Micro RNA Expression in PBMC from Multiple Sclerosis Patients. PLoS ONE, 2009, 4, e6309.	1.1	222
29	B cell repertoire diversity and clonal expansion in multiple sclerosis brain lesions. Journal of Immunology, 1999, 163, 5133-44.	0.4	217
30	Modules, networks and systems medicine for understanding disease and aiding diagnosis. Genome Medicine, 2014, 6, 82.	3.6	169
31	Peroxisome proliferatorâ€“activated receptor (PPAR)Î± expression in T cells mediates gender differences in development of T cellâ€“mediated autoimmunity. Journal of Experimental Medicine, 2007, 204, 321-330.	4.2	167
32	The Genetics of Multiple Sclerosis: From 0 to 200 in 50 Years. Trends in Genetics, 2017, 33, 960-970.	2.9	165
33	Hippocampal demyelination and memory dysfunction are associated with increased levels of the neuronal microRNA miRâ€124 and reduced AMPA receptors. Annals of Neurology, 2013, 73, 637-645.	2.8	164
34	Genome-Wide Pharmacogenomic Analysis of the Response to Interferon Beta Therapy in Multiple Sclerosis. Archives of Neurology, 2008, 65, 337-44.	4.9	154
35	Genotypeâ€“Phenotype correlations in multiple sclerosis: HLA genes influence disease severity inferred by 1HMR spectroscopy and MRI measures. Brain, 2009, 132, 250-259.	3.7	154
36	Janus-like opposing roles of CD47 in autoimmune brain inflammation in humans and mice. Journal of Experimental Medicine, 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. Journal of Immunology, 2000, 165, 6576-6582.	0.4	145
38	Transcription-Based Prediction of Response to IFNÎ² Using Supervised Computational Methods. PLoS Biology, 2004, 3, e2.	2.6	144
39	The genetics of autoimmune diseases: a networked perspective. Current Opinion in Immunology, 2009, 21, 596-605.	2.4	133
40	Gut microbiotaâ€“specific IgA ⁺ B cells traffic to the CNS in active multiple sclerosis. Science Immunology, 2020, 5, .	5.6	132
41	Aberrant oligodendroglialâ€“vascular interactions disrupt the bloodâ€“brain barrier, triggering CNS inflammation. Nature Neuroscience, 2019, 22, 709-718.	7.1	131
42	Gut microbiome analysis in neuromyelitis optica reveals overabundance of Clostridium perfringens. Annals of Neurology, 2016, 80, 443-447.	2.8	125
43	Multiple sclerosis: Genomic rewards. Journal of Neuroimmunology, 2001, 113, 171-184.	1.1	123
44	Genetic variation influences glutamate concentrations in brains of patients with multiple sclerosis. Brain, 2010, 133, 2603-2611.	3.7	123
45	Heterogeneous Network Edge Prediction: A Data Integration Approach to Prioritize Disease-Associated Genes. PLoS Computational Biology, 2015, 11, e1004259.	1.5	120
46	A pathogenic and clonally expanded B cell transcriptome in active multiple sclerosis. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 22932-22943.	3.3	119
47	Multiple sclerosis geneticsâ€”is the glass half full, or half empty?. Nature Reviews Neurology, 2010, 6, 429-437.	4.9	115
48	Low-Frequency and Rare-Coding Variation Contributes to Multiple Sclerosis Risk. Cell, 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. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 11839-11844.	3.3	105
50	Uncoupling the Roles of HLA-DRB1 and HLA-DRB5 Genes in Multiple Sclerosis. Journal of Immunology, 2008, 181, 5473-5480.	0.4	105
51	Systems biology and its application to the understanding of neurological diseases. Annals of Neurology, 2009, 65, 124-139.	2.8	99
52	Parallel states of pathological Wnt signaling in neonatal brain injury and colon cancer. Nature Neuroscience, 2014, 17, 506-512.	7.1	98
53	Blood RNA profiling in a large cohort of multiple sclerosis patients and healthy controls. Human Molecular Genetics, 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-Î². Journal of Neuroimmunology, 2002, 130, 194-201.	1.1	78

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55	Pharmacogenomic analysis of interferon receptor polymorphisms in multiple sclerosis. Genes and Immunity, 2003, 4, 147-152.	2.2	77
56	The Role of the Gut Microbiome in Multiple Sclerosis Risk and Progression: Towards Characterization of the â€œMS Microbiomeâ€. Neurotherapeutics, 2018, 15, 126-134.	2.1	75
57	Disease-modifying therapies alter gut microbial composition in MS. Neurology: Neuroimmunology and NeuroInflammation, 2019, 6, e517.	3.1	75
58	A validated gene regulatory network and GWAS identifies early regulators of T cellâ€“associated diseases. Science Translational Medicine, 2015, 7, 313ra178.	5.8	66
59	Association of HLA Genetic Risk Burden With Disease Phenotypes in Multiple Sclerosis. JAMA Neurology, 2016, 73, 795.	4.5	64
60	Modeling the cumulative genetic risk for multiple sclerosis from genome-wide association data. Genome Medicine, 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. BMC Genomics, 2007, 8, 65.	1.2	61
62	Expression profiling of Aldh1l1â€precursors in the developing spinal cord reveals glial lineageâ€specific genes and direct Sox9â€Nfe2l1 interactions. Glia, 2013, 61, 1518-1532.	2.5	61
63	Manitoba-oculo-tricho-anal (MOTA) syndrome is caused by mutations in FREM1. Journal of Medical Genetics, 2011, 48, 375-382.	1.5	60
64	Osteopontin polymorphisms and disease course in multiple sclerosis. Genes and Immunity, 2003, 4, 312-315.	2.2	59
65	Multiple Sclerosis-Associated Changes in the Composition and Immune Functions of Spore-Forming Bacteria. MSystems, 2018, 3, .	1.7	56
66	The Gut Microbiome in Neuromyelitis Optica. Neurotherapeutics, 2018, 15, 92-101.	2.1	54
67	Integrating biomedical research and electronic health records to create knowledge-based biologically meaningful machine-readable embeddings. Nature Communications, 2019, 10, 3045.	5.8	54
68	Precision medicine in chronic disease management: The multiple sclerosis <scp>B</scp>io<scp>S</scp>creen. Annals of Neurology, 2014, 76, 633-642.	2.8	53
69	A genome-wide association study of brain lesion distribution in multiple sclerosis. Brain, 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. Multiple Sclerosis Journal, 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. Clinical Immunology, 2014, 151, 16-24.	1.4	49
72	Selective Estrogen Receptor Modulators Enhance CNS Remyelination Independent of Estrogen Receptors. Journal of Neuroscience, 2019, 39, 2184-2194.	1.7	49

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73	Revealing the genetic basis of multiple sclerosis: are we there yet?. Current Opinion in Genetics and Development, 2011, 21, 317-324.	1.5	46
74	Genetics of multiple sclerosis. Current Opinion in Neurology, 2012, 25, 239-245.	1.8	46
75	IFN-Î³ orchestrates mesenchymal stem cell plasticity through the signal transducer and activator of transcription 1 and 3 and mammalian target of rapamycin pathways. Journal of Allergy and Clinical Immunology, 2017, 139, 1667-1676.	1.5	46
76	microRNA and exosome profiling in multiple sclerosis. Multiple Sclerosis Journal, 2020, 26, 599-604.	1.4	46
77	Genome-Wide Network Analysis Reveals the Global Properties of IFN-Î² Immediate Transcriptional Effects in Humans. Journal of Immunology, 2007, 178, 5076-5085.	0.4	43
78	Data integration and systems biology approaches for biomarker discovery: Challenges and opportunities for multiple sclerosis. Journal of Neuroimmunology, 2012, 248, 58-65.	1.1	42
79	Changes in matrix metalloproteinases and their inhibitors during interferon-beta treatment in multiple sclerosis. Clinical Immunology, 2009, 130, 145-150.	1.4	41
80	Tob1 plays a critical role in the activation of encephalitogenic T cells in CNS autoimmunity. Journal of Experimental Medicine, 2013, 210, 1301-1309.	4.2	40
81	Genome sequencing uncovers phenocopies in primary progressive multiple sclerosis. Annals of Neurology, 2018, 84, 51-63.	2.8	38
82	Biolink Model: A universal schema for knowledge graphs in clinical, biomedical, and translational science. Clinical and Translational Science, 2022, 15, 1848-1855.	1.5	38
83	Modular Transcriptional Activity Characterizes the Initiation and Progression of Autoimmune Encephalomyelitis. Journal of Immunology, 2005, 174, 7412-7422.	0.4	37
84	iCTNet: A Cytoscape plugin to produce and analyze integrative complex traits networks. BMC Bioinformatics, 2011, 12, 380.	1.2	36
85	Mapping gene activity in complex disorders: Integration of expression and genomic scans for multiple sclerosis. Journal of Neuroimmunology, 2005, 167, 157-169.	1.1	34
86	In depth comparison of an individualâ€™s DNA and its lymphoblastoid cell line using whole genome sequencing. BMC Genomics, 2012, 13, 477.	1.2	34
87	Longitudinal system-based analysis of transcriptional responses to type I interferons. Physiological Genomics, 2009, 38, 362-371.	1.0	32
88	Genetic associations with brain cortical thickness inÂmultiple sclerosis. Genes, Brain and Behavior, 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. Journal of Autoimmunity, 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. Multiple Sclerosis Journal, 2021, 27, 1994-2000.	1.4	31

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91	Early complement genes are associated with visual system degeneration in multiple sclerosis. Brain, 2019, 142, 2722-2736.	3.7	30
92	Childhood obesity and multiple sclerosis: A Mendelian randomization study. Multiple Sclerosis Journal, 2021, 27, 2150-2158.	1.4	30
93	PINBPA: Cytoscape app for network analysis of GWAS data. Bioinformatics, 2015, 31, 262-264.	1.8	29
94	Opposite Roles of NMDA Receptors in Relapsing and Primary Progressive Multiple Sclerosis. PLoS ONE, 2013, 8, e67357.	1.1	29
95	A gene pathway analysis highlights the role of cellular adhesion molecules in multiple sclerosis susceptibility. Genes and Immunity, 2014, 15, 126-132.	2.2	26
96	Analysis of antibody gene rearrangement, usage, and specificity in chronic focal encephalitis. Neurology, 2002, 58, 709-716.	1.5	25
97	Response to Comment on "The Influence of the Proinflammatory Cytokine, Osteopontin, on Autoimmune Demyelinating Disease". Science, 2003, 299, 1845b-1845.	6.0	25
98	Role of antiproliferative gene Tob1 in the immune system. Clinical and Experimental Neuroimmunology, 2014, 5, 132-136.	0.5	24
99	NR1H3 p.Arg415Gln Is Not Associated to Multiple Sclerosis Risk. Neuron, 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. Multiple Sclerosis Journal, 2021, 27, 366-379.	1.4	24
101	Functional Energetics of CD4+-Cellular Immunity in Monoclonal Antibody-Associated Progressive Multifocal Leukoencephalopathy in Autoimmune Disorders. PLoS ONE, 2011, 6, e18506.	1.1	23
102	Levels of brainâ€derived neurotrophic factor in patients with multiple sclerosis. Annals of Clinical and Translational Neurology, 2020, 7, 2251-2261.	1.7	23
103	Naive CD4 T-cell activation identifies MS patients having rapid transition to progressive MS. Neurology, 2014, 82, 681-690.	1.5	22
104	Classification of neurological diseases using multi-dimensional CSF analysis. Brain, 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. Journal of the American Medical Informatics Association: JAMIA, 2022, 29, 424-434.	2.2	22
106	Gene Expression Profiling in Neurological Disorders: Toward a Systems-Level Understanding of the Brain. NeuroMolecular Medicine, 2005, 6, 031-052.	1.8	21
107	Harnessing electronic medical records to advance research on multiple sclerosis. Multiple Sclerosis Journal, 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. Journal of Neuroimmunology, 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. AIDS Research and Human Retroviruses, 2007, 23, 741-747.	0.5	20
110	Sequencing of the IL6 gene in a caseâ€“control study of cerebral palsy in children. BMC Medical Genetics, 2013, 14, 126.	2.1	20
111	Prognostic biomarkers of IFNb therapy in multiple sclerosis patients. Multiple Sclerosis Journal, 2015, 21, 894-904.	1.4	20
112	Meta-analysis of genome-wide association studies reveals genetic overlap between Hodgkin lymphoma and multiple sclerosis. International Journal of Epidemiology, 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. Journal of Immunology, 2007, 179, 4074-4082.	0.4	19
114	Progress toward a universal biomedical data translator. Clinical and Translational Science, 2022, 15, 1838-1847.	1.5	17
115	Systems-based medicine approaches to understand and treat complex diseases. The example of multiple sclerosis. Autoimmunity, 2006, 39, 651-662.	1.2	16
116	Detection of identity by descent using next-generation whole genome sequencing data. BMC Bioinformatics, 2012, 13, 121.	1.2	16
117	Cell type-specific transcriptomics identifies neddylation as a novel therapeutic target in multiple sclerosis. Brain, 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. BMC Genomics, 2010, 11, 626.	1.2	15
119	Polygenic risk score association with multiple sclerosis susceptibility and phenotype in Europeans. Brain, 2023, 146, 645-656.	3.7	15
120	A non-synonymous single-nucleotide polymorphism associated with multiple sclerosis risk affects the EVI5 interactome. Human Molecular Genetics, 2015, 24, ddv412.	1.4	14
121	Distinctive waves of innate immune response in the retina in experimental autoimmune encephalomyelitis. JCI Insight, 2021, 6, .	2.3	14
122	Specific hypomethylation programs underpin B cell activation in early multiple sclerosis. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	14
123	Large-scale gene-expression studies and the challenge of multiple sclerosis. Genome Biology, 2002, 3, reviews1027.1.	13.9	13
124	Dynamic regulation of alternative ATP-binding cassette transporter A1 transcripts. Biochemical and Biophysical Research Communications, 2003, 306, 463-468.	1.0	13
125	Protein network analysis reveals selectively vulnerable regions and biological processes in FTD. Neurology: Genetics, 2018, 4, e266.	0.9	12
126	A New Point Mutation (M313T) in the Thyroid Hormone Receptor Î² Gene in a Patient with Resistance to Thyroid Hormone. Thyroid, 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 IFNÂ drugs in the treatment of multiple sclerosis. Human Molecular Genetics, 2015, 24, 3192-3205.	1.4	11
128	iCTNet2: integrating heterogeneous biological interactions to understand complex traits. F1000Research, 2015, 4, 485.	0.8	11
129	Interferon-beta affects mitochondrial activity in CD4⁺ lymphocytes: Implications for mechanism of action in multiple sclerosis. Multiple Sclerosis Journal, 2015, 21, 1262-1270.	1.4	10
130	Data characterizing the ZMIZ1 molecular phenotype of multiple sclerosis. Data in Brief, 2017, 11, 364-370.	0.5	10
131	Vitamin D Regulates MerTK-Dependent Phagocytosis in Human Myeloid Cells. Journal of Immunology, 2020, 205, 398-406.	0.4	10
132	Serum antibodies to phosphatidylcholine in MS. Neurology: Neuroimmunology and NeuroInflammation, 2020, 7, e765.	3.1	10
133	Knowledge Network Embedding of Transcriptomic Data from Spaceflown Mice Uncovers Signs and Symptoms Associated with Terrestrial Diseases. Life, 2021, 11, 42.	1.1	10
134	SARS-CoV-2 meta-interactome suggests disease-specific, autoimmune pathophysiologies and therapeutic targets. F1000Research, 2020, 9, 992.	0.8	10
135	MRI-derived g-ratio and lesion severity in newly diagnosed multiple sclerosis. Brain Communications, 2021, 3, fcab249.	1.5	10
136	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, 216-221.	2.4	9
137	Genomics and new targets for multiple sclerosis. Pharmacogenomics, 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. Scientific Reports, 2019, 9, 10854.	1.6	9
139	Genetic contribution to multiple sclerosis risk among Ashkenazi Jews. BMC Medical Genetics, 2015, 16, 55.	2.1	8
140	Immune cell-specific transcriptional profiling highlights distinct molecular pathways controlled by Tob1 upon experimental autoimmune encephalomyelitis. Scientific Reports, 2016, 6, 31603.	1.6	8
141	Mononuclear cell transcriptome changes associated with dimethyl fumarate in MS. Neurology: Neuroimmunology and NeuroInflammation, 2018, 5, e470.	3.1	8
142	iCTNet2: integrating heterogeneous biological interactions to understand complex traits. F1000Research, 2015, 4, 485.	0.8	8
143	iPINBPA: an integrative network-based functional module discovery tool for genome-wide association studies. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 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. Frontiers in Genetics, 2015, 6, 30.	1.1	7
146	Evidence for association of chromosome 10 open reading frame (C10orf27) gene polymorphisms and multiple sclerosis. Multiple Sclerosis Journal, 2008, 14, 412-414.	1.4	6
147	Assessing the Power of Exome Chips. PLoS ONE, 2015, 10, e0139642.	1.1	6
148	Direct Deletion Analysis in Two Duchenne Muscular Dystrophy Symptomatic Females Using Polymorphic Dinucleotide (CA)_n Loci within the Dystrophin Gene. BMB Reports, 2003, 36, 179-184.	1.1	6
149	Deletion patterns in Argentine patients with Duchenne and Becker muscular dystrophy. Neurological Research, 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. Multiple Sclerosis Journal, 2018, 24, 1419-1420.	1.4	5
153	Mendelian randomization study shows no causal effects of serum urate levels on the risk of MS. Neurology: Neuroimmunology and NeuroInflammation, 2021, 8, e920.	3.1	5
154	A biomedical open knowledge network harnesses the power of AI to understand deep human biology. AI Magazine, 2022, 43, 46-58.	1.4	5
155	FutureMS cohort profile: a Scottish multicentre inception cohort study of relapsing-remitting multiple sclerosis. BMJ Open, 2022, 12, e058506.	0.8	5
156	Longitudinal analysis of B cell repertoire and antibody gene rearrangements during early HIV infection. Genes and Immunity, 2005, 6, 66-69.	2.2	4
157	Carrier detection in Duchenne and Becker muscular dystrophy Argentine families. Clinical Genetics, 1998, 54, 503-511.	1.0	4
158	Transcriptional expression patterns triggered by chemically distinct neuroprotective molecules. Neuroscience, 2012, 226, 10-20.	1.1	4
159	New insights into the genetics of multiple sclerosis. Journal of Rehabilitation Research and Development, 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?. Multiple Sclerosis Journal, 2013, 19, 1813-1814.	1.4	3
162	The microbiome and MS: The influence of the microbiota on MS risk and progressionâ€"Session chair summary. Multiple Sclerosis Journal, 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
167	Peroxisome proliferatorâ€“activated receptor (PPAR)Î± expression in T cells mediates gender differences in development of T cellâ€“mediated autoimmunity. Journal of Experimental Medicine, 2007, 204, 693-693.	4.2	1
168	Peroxisome Poliferator-activated Receptor-Î± (PPARÎ±) Expression in T Cells Mediates Gender Differences in Development of T Cell-mediated Autoimmunity. Clinical Immunology, 2007, 123, S74.	1.4	1
169	Whole genome sequences of 2 octogenarians with sustained cognitive abilities. Neurobiology of Aging, 2015, 36, 1435-1438.	1.5	1
170	Patient with an Xp21 contiguous gene deletion syndrome in association with agenesis of the corpus callosum. , 1997, 70, 216.		1
171	Gene expression profiling in neurological and neuroinflammatory diseases. , 2008, , 115-130.		1
172	Meta-Analysis of Hodgkin Lymphoma and Asthma Genome-Wide Association Scans reveals common variants in GATA3. Blood, 2014, 124, 135-135.	0.6	1
173	10 Advanced data mining and predictive modelling at the core of personalised medicine. Studies in Multidisciplinarity, 2005, , 165-192.	0.0	0
174	Uncoupling the roles of HLA-DRB1 and HLA-DRB5 genes in multiple sclerosis. Journal of Immunology, 2009, 182, 2551.1-2551.	0.4	0
175	The genetics of multiple sclerosis. , 0, , 35-45.		0
176	Genome-wide RNA expression profiling in human grey and white matter tissue reveals a role for PSA-NCAM dysregulation in MS pathogenesis. Journal of Neuroimmunology, 2014, 275, 180-181.	1.1	0
177	Decreased miR-219 expression in MS: Clinical implications?. Journal of Neuroimmunology, 2014, 275, 111.	1.1	0
178	ID: 144. Cytokine, 2015, 76, 93.	1.4	0
179	The era of GWAS is over â€“ Commentary. Multiple Sclerosis Journal, 2018, 24, 260-261.	1.4	0
180	Insights into microbiome research 3: Whoâ€™s there versus what are they doing?. Multiple Sclerosis Journal, 2018, 24, 1541-1542.	1.4	0

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181	Insights into microbiome research 4: The computational analysis. Multiple Sclerosis Journal, 2019, 25, 21-22.	1.4	0
182	Insights into microbiome research 5: Mapping is first but function must come next. Multiple Sclerosis Journal, 2019, 25, 193-195.	1.4	0
183	Peroxisome proliferatorâ€“activated receptor (PPAR)Î± expression in T cells mediates gender differences in development of T cellâ€“mediated autoimmunity. Journal of Cell Biology, 2007, 176, i9-i9.	2.3	0
184	A framework and mechanistically focused, in silico method for enabling rational translational research. Summit on Translational Bioinformatics, 2008, 2008, 46-50.	0.7	0
185	Predictive modeling of therapy response in multiple sclerosis using gene expression data. Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 2006, , .	0.5	0