Sergio Baranzini

List of Publications by Year
in descending order

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	Polygenic risk score association with multiple sclerosis susceptibility and phenotype in Europeans. Brain, 2023, 146, 645-656.	3.7	15
2	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
3	A biomedical open knowledge network harnesses the power of AI to understand deep human biology. AI Magazine, 2022, 43, 46-58.	1.4	5
4	Progress toward a universal biomedical data translator. Clinical and Translational Science, 2022, 15, 1838-1847.	1.5	17
5	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
6	FutureMS cohort profile: a Scottish multicentre inception cohort study of relapsing-remitting multiple sclerosis. BMJ Open, 2022, 12, e058506.	0.8	5
7	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
8	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
9	Knowledge Network Embedding of Transcriptomic Data from Spaceflown Mice Uncovers Signs and Symptoms Associated with Terrestrial Diseases. Life, 2021, 11, 42.	1.1	10
10	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
11	Childhood obesity and multiple sclerosis: A Mendelian randomization study. Multiple Sclerosis Journal, 2021, 27, 2150-2158.	1.4	30
12	Classification of neurological diseases using multi-dimensional CSF analysis. Brain, 2021, 144, 2625-2634.	3.7	22
13	Distinctive waves of innate immune response in the retina in experimental autoimmune encephalomyelitis. JCI Insight, 2021, 6, .	2.3	14
14	Cell type-specific transcriptomics identifies neddylation as a novel therapeutic target in multiple sclerosis. Brain, 2021, 144, 450-461.	3.7	16
15	MRI-derived g-ratio and lesion severity in newly diagnosed multiple sclerosis. Brain Communications, 2021, 3, fcab249.	1.5	10
16	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
17	Gut microbiotaâ€“specific IgA ⁺ B cells traffic to the CNS in active multiple sclerosis. Science Immunology, 2020, 5, .	5.6	132
18	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

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19	Levels of brainâ€derived neurotrophic factor in patients with multiple sclerosis. Annals of Clinical and Translational Neurology, 2020, 7, 2251-2261.	1.7	23
20	Vitamin D Regulates MerTK-Dependent Phagocytosis in Human Myeloid Cells. Journal of Immunology, 2020, 205, 398-406.	0.4	10
21	Serum antibodies to phosphatidylcholine in MS. Neurology: Neuroimmunology and NeuroInflammation, 2020, 7, e765.	3.1	10
22	microRNA and exosome profiling in multiple sclerosis. Multiple Sclerosis Journal, 2020, 26, 599-604.	1.4	46
23	SARS-CoV-2 meta-interactome suggests disease-specific, autoimmune pathophysiologies and therapeutic targets. F1000Research, 2020, 9, 992.	0.8	10
24	Integrating biomedical research and electronic health records to create knowledge-based biologically meaningful machine-readable embeddings. Nature Communications, 2019, 10, 3045.	5.8	54
25	Early complement genes are associated with visual system degeneration in multiple sclerosis. Brain, 2019, 142, 2722-2736.	3.7	30
26	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
27	Multiple sclerosis genomic map implicates peripheral immune cells and microglia in susceptibility. Science, 2019, 365, .	6.0	710
28	Insights into microbiome research 4: The computational analysis. Multiple Sclerosis Journal, 2019, 25, 21-22.	1.4	0
29	Selective Estrogen Receptor Modulators Enhance CNS Remyelination Independent of Estrogen Receptors. Journal of Neuroscience, 2019, 39, 2184-2194.	1.7	49
30	Insights into microbiome research 5: Mapping is first but function must come next. Multiple Sclerosis Journal, 2019, 25, 193-195.	1.4	0
31	Aberrant oligodendroglialâ€“vascular interactions disrupt the bloodâ€“brain barrier, triggering CNS inflammation. Nature Neuroscience, 2019, 22, 709-718.	7.1	131
32	Silent progression in disease activityâ€“free relapsing multiple sclerosis. Annals of Neurology, 2019, 85, 653-666.	2.8	265
33	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
34	Disease-modifying therapies alter gut microbial composition in MS. Neurology: Neuroimmunology and NeuroInflammation, 2019, 6, e517.	3.1	75
35	Recirculating Intestinal IgA-Producing Cells Regulate Neuroinflammation via IL-10. Cell, 2019, 176, 610-624.e18.	13.5	241
36	Harnessing electronic medical records to advance research on multiple sclerosis. Multiple Sclerosis Journal, 2019, 25, 408-418.	1.4	21

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37	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
38	The Gut Microbiome in Neuromyelitis Optica. Neurotherapeutics, 2018, 15, 92-101.	2.1	54
39	The era of GWAS is over â€“ Commentary. Multiple Sclerosis Journal, 2018, 24, 260-261.	1.4	0
40	Multiple sclerosis. Lancet, The, 2018, 391, 1622-1636.	6.3	1,204
41	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
42	Multiple Sclerosis-Associated Changes in the Composition and Immune Functions of Spore-Forming Bacteria. MSystems, 2018, 3, .	1.7	56
43	Insights into microbiome research 2: Experimental design, sample collection, and shipment. Multiple Sclerosis Journal, 2018, 24, 1419-1420.	1.4	5
44	Protein network analysis reveals selectively vulnerable regions and biological processes in FTD. Neurology: Genetics, 2018, 4, e266.	0.9	12
45	Insights into microbiome research 3: Whoâ€™s there versus what are they doing?. Multiple Sclerosis Journal, 2018, 24, 1541-1542.	1.4	0
46	Low-Frequency and Rare-Coding Variation Contributes to Multiple Sclerosis Risk. Cell, 2018, 175, 1679-1687.e7.	13.5	115
47	Mononuclear cell transcriptome changes associated with dimethyl fumarate in MS. Neurology: Neuroimmunology and NeuroInflammation, 2018, 5, e470.	3.1	8
48	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
49	Genome sequencing uncovers phenocopies in primary progressive multiple sclerosis. Annals of Neurology, 2018, 84, 51-63.	2.8	38
50	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
51	Data characterizing the ZMIZ1 molecular phenotype of multiple sclerosis. Data in Brief, 2017, 11, 364-370.	0.5	10
52	The Genetics of Multiple Sclerosis: From 0 to 200 in 50 Years. Trends in Genetics, 2017, 33, 960-970.	2.9	165
53	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
54	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

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55	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
56	Systematic integration of biomedical knowledge prioritizes drugs for repurposing. ELife, 2017, 6, .	2.8	333
57	Immune cell-specific transcriptional profiling highlights distinct molecular pathways controlled by Tob1 upon experimental autoimmune encephalomyelitis. Scientific Reports, 2016, 6, 31603.	1.6	8
58	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
59	Longâ€term evolution of multiple sclerosis disability in the treatment era. Annals of Neurology, 2016, 80, 499-510.	2.8	331
60	Gut microbiome analysis in neuromyelitis optica reveals overabundance of Clostridium perfringens. Annals of Neurology, 2016, 80, 443-447.	2.8	125
61	NR1H3 p.Arg415Gln Is Not Associated to Multiple Sclerosis Risk. Neuron, 2016, 92, 333-335.	3.8	24
62	Association of HLA Genetic Risk Burden With Disease Phenotypes in Multiple Sclerosis. JAMA Neurology, 2016, 73, 795.	4.5	64
63	ID: 144. Cytokine, 2015, 76, 93.	1.4	0
64	Assessing the Power of Exome Chips. PLoS ONE, 2015, 10, e0139642.	1.1	6
65	Genetic associations with brain cortical thickness inÂmultiple sclerosis. Genes, Brain and Behavior, 2015, 14, 217-227.	1.1	31
66	SNP imputation bias reduces effect size determination. Frontiers in Genetics, 2015, 6, 30.	1.1	7
67	Whole genome sequences of 2 octogenarians with sustained cognitive abilities. Neurobiology of Aging, 2015, 36, 1435-1438.	1.5	1
68	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
69	A non-synonymous single-nucleotide polymorphism associated with multiple sclerosis risk affects the EVI5 interactome. Human Molecular Genetics, 2015, 24, ddv412.	1.4	14
70	Genetic contribution to multiple sclerosis risk among Ashkenazi Jews. BMC Medical Genetics, 2015, 16, 55.	2.1	8
71	Class II HLA interactions modulate genetic risk for multiple sclerosis. Nature Genetics, 2015, 47, 1107-1113.	9.4	312
72	A validated gene regulatory network and GWAS identifies early regulators of T cellâ€“associated diseases. Science Translational Medicine, 2015, 7, 313ra178.	5.8	66

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73	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
74	Prognostic biomarkers of IFNb therapy in multiple sclerosis patients. Multiple Sclerosis Journal, 2015, 21, 894-904.	1.4	20
75	PINBPA: Cytoscape app for network analysis of GWAS data. Bioinformatics, 2015, 31, 262-264.	1.8	29
76	iCTNet2: integrating heterogeneous biological interactions to understand complex traits. F1000Research, 2015, 4, 485.	0.8	11
77	iCTNet2: integrating heterogeneous biological interactions to understand complex traits. F1000Research, 2015, 4, 485.	0.8	8
78	Heterogeneous Network Edge Prediction: A Data Integration Approach to Prioritize Disease-Associated Genes. PLoS Computational Biology, 2015, 11, e1004259.	1.5	120
79	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
80	iPINBPA: AN INTEGRATIVE NETWORK-BASED FUNCTIONAL MODULE DISCOVERY TOOL FOR GENOME-WIDE ASSOCIATION STUDIES. , 2014, , .		7
81	Modules, networks and systems medicine for understanding disease and aiding diagnosis. Genome Medicine, 2014, 6, 82.	3.6	169
82	Naive CD4 T-cell activation identifies MS patients having rapid transition to progressive MS. Neurology, 2014, 82, 681-690.	1.5	22
83	Role of antiproliferative gene Tob1 in the immune system. Clinical and Experimental Neuroimmunology, 2014, 5, 132-136.	0.5	24
84	Parallel states of pathological Wnt signaling in neonatal brain injury and colon cancer. Nature Neuroscience, 2014, 17, 506-512.	7.1	98
85	Astrocyte-encoded positional cues maintain sensorimotor circuit integrity. Nature, 2014, 509, 189-194.	13.7	266
86	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
87	Rituximab Efficiently Depletes Increased CD20-Expressing T Cells in Multiple Sclerosis Patients. Journal of Immunology, 2014, 193, 580-586.	0.4	223
88	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
89	Decreased miR-219 expression in MS: Clinical implications?. Journal of Neuroimmunology, 2014, 275, 111.	1.1	0
90	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

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91	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
92	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
93	Meta-Analysis of Hodgkin Lymphoma and Asthma Genome-Wide Association Scans reveals common variants in GATA3. Blood, 2014, 124, 135-135.	0.6	1
94	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. Nature Genetics, 2013, 45, 1353-1360.	9.4	1,213
95	A genome-wide association study of brain lesion distribution in multiple sclerosis. Brain, 2013, 136, 1012-1024.	3.7	52
96	Blood RNA profiling in a large cohort of multiple sclerosis patients and healthy controls. Human Molecular Genetics, 2013, 22, 4194-4205.	1.4	81
97	Sequencing of the IL6 gene in a caseâ€“control study of cerebral palsy in children. BMC Medical Genetics, 2013, 14, 126.	2.1	20
98	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
99	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
100	Gene expression profiling in MS: a fulfilled promise?. Multiple Sclerosis Journal, 2013, 19, 1813-1814.	1.4	3
101	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
102	Autoimmune Disorders. , 2013, , 822-838.		5
103	Opposite Roles of NMDA Receptors in Relapsing and Primary Progressive Multiple Sclerosis. PLoS ONE, 2013, 8, e67357.	1.1	29
104	Genetics of multiple sclerosis. Current Opinion in Neurology, 2012, 25, 239-245.	1.8	46
105	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
106	Detection of identity by descent using next-generation whole genome sequencing data. BMC Bioinformatics, 2012, 13, 121.	1.2	16
107	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
108	Transcriptional expression patterns triggered by chemically distinct neuroprotective molecules. Neuroscience, 2012, 226, 10-20.	1.1	4

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109	The genetics of multiple sclerosis: an upâ€toâ€date review. Immunological Reviews, 2012, 248, 87-103.	2.8	230
110	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
111	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. Nature, 2011, 476, 214-219.	13.7	2,400
112	Axin2 as regulatory and therapeutic target in newborn brain injury and remyelination. Nature Neuroscience, 2011, 14, 1009-1016.	7.1	307
113	Modeling the cumulative genetic risk for multiple sclerosis from genome-wide association data. Genome Medicine, 2011, 3, 3.	3.6	63
114	Myelin Regeneration: A Recapitulation of Development?. Annual Review of Neuroscience, 2011, 34, 21-43.	5.0	282
115	Revealing the genetic basis of multiple sclerosis: are we there yet?. Current Opinion in Genetics and Development, 2011, 21, 317-324.	1.5	46
116	Manitoba-oculo-tricho-anal (MOTA) syndrome is caused by mutations in FREM1. Journal of Medical Genetics, 2011, 48, 375-382.	1.5	60
117	Functional Energetics of CD4+-Cellular Immunity in Monoclonal Antibody-Associated Progressive Multifocal Leukoencephalopathy in Autoimmune Disorders. PLoS ONE, 2011, 6, e18506.	1.1	23
118	iCTNet: A Cytoscape plugin to produce and analyze integrative complex traits networks. BMC Bioinformatics, 2011, 12, 380.	1.2	36
119	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
120	Genome, epigenome and RNA sequences of monozygotic twins discordant for multiple sclerosis. Nature, 2010, 464, 1351-1356.	13.7	463
121	Genetic variation influences glutamate concentrations in brains of patients with multiple sclerosis. Brain, 2010, 133, 2603-2611.	3.7	123
122	Multiple sclerosis geneticsâ€”is the glass half full, or half empty?. Nature Reviews Neurology, 2010, 6, 429-437.	4.9	115
123	Incidental MRI anomalies suggestive of multiple sclerosis. Neurology, 2009, 72, 800-805.	1.5	509
124	Pathway and network-based analysis of genome-wide association studies in multiple sclerosis. Human Molecular Genetics, 2009, 18, 2078-2090.	1.4	371
125	Uncoupling the roles of HLA-DRB1 and HLA-DRB5 genes in multiple sclerosis. Journal of Immunology, 2009, 182, 2551.1-2551.	0.4	0
126	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

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127	Longitudinal system-based analysis of transcriptional responses to type I interferons. Physiological Genomics, 2009, 38, 362-371.	1.0	32
128	Dysregulation of the Wnt pathway inhibits timely myelination and remyelination in the mammalian CNS. Genes and Development, 2009, 23, 1571-1585.	2.7	537
129	Changes in matrix metalloproteinases and their inhibitors during interferon-beta treatment in multiple sclerosis. Clinical Immunology, 2009, 130, 145-150.	1.4	41
130	Systems biology and its application to the understanding of neurological diseases. Annals of Neurology, 2009, 65, 124-139.	2.8	99
131	The genetics of autoimmune diseases: a networked perspective. Current Opinion in Immunology, 2009, 21, 596-605.	2.4	133
132	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
133	Genome-wide association analysis of susceptibility and clinical phenotype in multiple sclerosis. Human Molecular Genetics, 2009, 18, 767-778.	1.4	419
134	Differential Micro RNA Expression in PBMC from Multiple Sclerosis Patients. PLoS ONE, 2009, 4, e6309.	1.1	222
135	Proteomic analysis of active multiple sclerosis lesions reveals therapeutic targets. Nature, 2008, 451, 1076-1081.	13.7	472
136	The genetics of multiple sclerosis: SNPs to pathways to pathogenesis. Nature Reviews Genetics, 2008, 9, 516-526.	7.7	294
137	Genome-Wide Pharmacogenomic Analysis of the Response to Interferon Beta Therapy in Multiple Sclerosis. Archives of Neurology, 2008, 65, 337-44.	4.9	154
138	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
139	Uncoupling the Roles of HLA-DRB1 and HLA-DRB5 Genes in Multiple Sclerosis. Journal of Immunology, 2008, 181, 5473-5480.	0.4	105
140	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
141	Gene expression profiling in neurological and neuroinflammatory diseases. , 2008, , 115-130.		1
142	A framework and mechanistically focused, in silico method for enabling rational translational research. Summit on Translational Bioinformatics, 2008, 2008, 46-50.	0.7	0
143	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
144	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

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145	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
146	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
147	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
148	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
149	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
150	Biological concepts of multiple sclerosis pathogenesis and relationship to treatment. , 2007, , 23-44.		3
151	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
152	Systems-based medicine approaches to understand and treat complex diseases. The example of multiple sclerosis. Autoimmunity, 2006, 39, 651-662.	1.2	16
153	Heterogeneity at the HLA-DRB1 locus and risk for multiple sclerosis. Human Molecular Genetics, 2006, 15, 2813-2824.	1.4	279
154	Predictive modeling of therapy response in multiple sclerosis using gene expression data. , 2006, 2006, 5519-22.		5
155	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
156	Gene Expression Profiling in Neurological Disorders: Toward a Systems-Level Understanding of the Brain. NeuroMolecular Medicine, 2005, 6, 031-052.	1.8	21
157	Longitudinal analysis of B cell repertoire and antibody gene rearrangements during early HIV infection. Genes and Immunity, 2005, 6, 66-69.	2.2	4
158	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
159	Modular Transcriptional Activity Characterizes the Initiation and Progression of Autoimmune Encephalomyelitis. Journal of Immunology, 2005, 174, 7412-7422.	0.4	37
160	Genomics and new targets for multiple sclerosis. Pharmacogenomics, 2005, 6, 151-161.	0.6	9
161	10 Advanced data mining and predictive modelling at the core of personalised medicine. Studies in Multidisciplinarity, 2005, , 165-192.	0.0	0
162	Transcription-Based Prediction of Response to IFNÎ² Using Supervised Computational Methods. PLoS Biology, 2004, 3, e2.	2.6	144

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163	Mapping Multiple Sclerosis Susceptibility to the HLA-DR Locus in African Americans. American Journal of Human Genetics, 2004, 74, 160-167.	2.6	311
164	Pharmacogenomic analysis of interferon receptor polymorphisms in multiple sclerosis. Genes and Immunity, 2003, 4, 147-152.	2.2	77
165	Osteopontin polymorphisms and disease course in multiple sclerosis. Genes and Immunity, 2003, 4, 312-315.	2.2	59
166	Dynamic regulation of alternative ATP-binding cassette transporter A1 transcripts. Biochemical and Biophysical Research Communications, 2003, 306, 463-468.	1.0	13
167	Response to Comment on "The Influence of the Proinflammatory Cytokine, Osteopontin, on Autoimmune Demyelinating Disease". Science, 2003, 299, 1845b-1845.	6.0	25
168	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
169	Analysis of antibody gene rearrangement, usage, and specificity in chronic focal encephalitis. Neurology, 2002, 58, 709-716.	1.5	25
170	Large-scale gene-expression studies and the challenge of multiple sclerosis. Genome Biology, 2002, 3, reviews1027.1.	13.9	13
171	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
172	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
173	New insights into the genetics of multiple sclerosis. Journal of Rehabilitation Research and Development, 2002, 39, 201-9.	1.6	4
174	The Influence of the Proinflammatory Cytokine, Osteopontin, on Autoimmune Demyelinating Disease. Science, 2001, 294, 1731-1735.	6.0	807
175	Multiple sclerosis: Genomic rewards. Journal of Neuroimmunology, 2001, 113, 171-184.	1.1	123
176	Transcriptional Analysis of Multiple Sclerosis Brain Lesions Reveals a Complex Pattern of Cytokine Expression. Journal of Immunology, 2000, 165, 6576-6582.	0.4	145
177	B cell repertoire diversity and clonal expansion in multiple sclerosis brain lesions. Journal of Immunology, 1999, 163, 5133-44.	0.4	217
178	Deletion patterns in Argentine patients with Duchenne and Becker muscular dystrophy. Neurological Research, 1998, 20, 409-414.	0.6	5
179	Carrier detection in Duchenne and Becker muscular dystrophy Argentine families. Clinical Genetics, 1998, 54, 503-511.	1.0	4
180	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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181	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
182	Four new polymorphisms in the human dystrophin gene from an Argentinian population. , 1997, 20, 1451-1453.		3
183	Patient with an Xp21 contiguous gene deletion syndrome in association with agenesis of the corpus callosum. , 1997, 70, 216.		1
184	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
185	The genetics of multiple sclerosis. , 0, , 35-45.		0