

manuela sironi

List of Publications by Year in Descending Order

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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.

145
papers

5,080
citations

39
h-index

66
g-index

151
ext. papers

6,355
ext. citations

6.7
avg, IF

5.69
L-index

#	Paper	IF	Citations
145	Dating the Emergence of Human Endemic Coronaviruses. <i>Viruses</i> , 2022 , 14, 1095	6.2	2
144	Genetic Variability of Human Cytomegalovirus Clinical Isolates Correlates With Altered Expression of Natural Killer Cell-Activating Ligands and IFN- γ <i>Frontiers in Immunology</i> , 2021 , 12, 532484	8.4	2
143	Adaptation of the endemic coronaviruses HCoV-OC43 and HCoV-229E to the human host. <i>Virus Evolution</i> , 2021 , 7, veab061	3.7	2
142	Alternation between taxonomically divergent hosts is not the major determinant of flavivirus evolution. <i>Virus Evolution</i> , 2021 , 7, veab040	3.7	
141	Kinetochore proteins and microtubule-destabilizing factors are fast evolving in eutherian mammals. <i>Molecular Ecology</i> , 2021 , 30, 1505-1515	5.7	4
140	One year into the pandemic: Short-term evolution of SARS-CoV-2 and emergence of new lineages. <i>Infection, Genetics and Evolution</i> , 2021 , 92, 104869	4.5	18
139	2021 Taxonomic update of phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. <i>Archives of Virology</i> , 2021 , 166, 3513-3566	2.6	10
138	The substitution spectra of coronavirus genomes. <i>Briefings in Bioinformatics</i> , 2021 ,	13.4	3
137	Possible European Origin of Circulating Varicella Zoster Virus Strains. <i>Journal of Infectious Diseases</i> , 2020 , 221, 1286-1294	7	6
136	Intrinsically disordered regions are abundant in simplexvirus proteomes and display signatures of positive selection. <i>Virus Evolution</i> , 2020 , 6, veaa028	3.7	6
135	Coding potential and sequence conservation of SARS-CoV-2 and related animal viruses. <i>Infection, Genetics and Evolution</i> , 2020 , 83, 104353	4.5	51
134	Past and ongoing adaptation of human cytomegalovirus to its host. <i>PLoS Pathogens</i> , 2020 , 16, e1008476	7.6	9
133	SARS-CoV-2 and COVID-19: A genetic, epidemiological, and evolutionary perspective. <i>Infection, Genetics and Evolution</i> , 2020 , 84, 104384	4.5	78
132	Evolutionary analysis of exogenous and integrated HHV-6A/HHV-6B populations. <i>Virus Evolution</i> , 2020 , 6, veaa035	3.7	1
131	Evolution and Genetic Diversity of Primate Cytomegaloviruses. <i>Microorganisms</i> , 2020 , 8,	4.9	2
130	Computational Inference of Selection Underlying the Evolution of the Novel Coronavirus, Severe Acute Respiratory Syndrome Coronavirus 2. <i>Journal of Virology</i> , 2020 , 94,	6.6	89
129	Population structure of Lassa Mammarenavirus in West Africa. <i>Viruses</i> , 2020 , 12,	6.2	4

128	Recent Out-of-Africa Migration of Human Herpes Simplex Viruses. <i>Molecular Biology and Evolution</i> , 2020 , 37, 1259-1271	8.3	10
127	Recombination and Positive Selection Differentially Shaped the Diversity of Subgenera. <i>Viruses</i> , 2020 , 12,	6.2	8
126	Antigenic variation of SARS-CoV-2 in response to immune pressure. <i>Molecular Ecology</i> , 2020 , 30, 3548	5.7	12
125	You Will Never Walk Alone: Codispersal of JC Polyomavirus with Human Populations. <i>Molecular Biology and Evolution</i> , 2020 , 37, 442-454	8.3	3
124	Taxonomy of the order Bunyavirales: second update 2018. <i>Archives of Virology</i> , 2019 , 164, 927-941	2.6	76
123	Taxonomy of the order Bunyavirales: update 2019. <i>Archives of Virology</i> , 2019 , 164, 1949-1965	2.6	148
122	Phylogenies in ART: HIV reservoirs, HIV latency and drug resistance. <i>Current Opinion in Pharmacology</i> , 2019 , 48, 24-32	5.1	20
121	The influence of DCDC2 risk genetic variants on reading: Testing main and haplotypic effects. <i>Neuropsychologia</i> , 2019 , 130, 52-58	3.2	6
120	The chameleonic genetics of Lassa virus. <i>Lancet Infectious Diseases</i> , 2019 , 19, 1276-1277	25.5	
119	A complex evolutionary relationship between HHV-6A and HHV-6B. <i>Virus Evolution</i> , 2019 , 5, vez043	3.7	1
118	ICTV Virus Taxonomy Profile: Arenaviridae. <i>Journal of General Virology</i> , 2019 , 100, 1200-1201	4.9	31
117	Mode and tempo of human hepatitis virus evolution. <i>Computational and Structural Biotechnology Journal</i> , 2019 , 17, 1384-1395	6.8	5
116	Retraction to: A complex evolutionary relationship between HHV-6A and HHV-6B. <i>Virus Evolution</i> , 2019 , 5, vez054	3.7	
115	Arenavirus genomics: novel insights into viral diversity, origin, and evolution. <i>Current Opinion in Virology</i> , 2019 , 34, 18-28	7.5	18
114	Ancient Evolution of Mammarenaviruses: Adaptation via Changes in the L Protein and No Evidence for Host-Virus Codivergence. <i>Genome Biology and Evolution</i> , 2018 , 10, 863-874	3.9	14
113	Origin and dispersal of Hepatitis E virus. <i>Emerging Microbes and Infections</i> , 2018 , 7, 11	18.9	34
112	Genetic susceptibility to infectious diseases: Current status and future perspectives from genome-wide approaches. <i>Infection, Genetics and Evolution</i> , 2018 , 66, 286-307	4.5	25
111	Strategy of Human Cytomegalovirus To Escape Interferon Beta-Induced APOBEC3G Editing Activity. <i>Journal of Virology</i> , 2018 , 92,	6.6	12

110	Evolutionary Analysis Provides Insight Into the Origin and Adaptation of HCV. <i>Frontiers in Microbiology</i> , 2018 , 9, 854	5.7	8
109	Evolutionary rates of mammalian telomere-stability genes correlate with karyotype features and female germline expression. <i>Nucleic Acids Research</i> , 2018 , 46, 7153-7168	20.1	5
108	Genetic conflicts with Plasmodium parasites and functional constraints shape the evolution of erythrocyte cytoskeletal proteins. <i>Scientific Reports</i> , 2018 , 8, 14682	4.9	1
107	The Diversity of Mammalian Hemoproteins and Microbial Heme Scavengers Is Shaped by an Arms Race for Iron Piracy. <i>Frontiers in Immunology</i> , 2018 , 9, 2086	8.4	5
106	Multiple Selected Changes May Modulate the Molecular Interaction between RH5 and Primate Basigin. <i>MBio</i> , 2018 , 9,	7.8	2
105	Analysis of Reptarenavirus genomes indicates different selective forces acting on the S and L segments and recent expansion of common genotypes. <i>Infection, Genetics and Evolution</i> , 2018 , 64, 212-218	4.5	3
104	Susceptibility to type 2 diabetes may be modulated by haplotypes in G6PC2, a target of positive selection. <i>BMC Evolutionary Biology</i> , 2017 , 17, 43	3	9
103	A common genetic variant in FOXP2 is associated with language-based learning (dis)abilities: Evidence from two Italian independent samples. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2017 , 174, 578-586	3.5	13
102	TLR3 Mutations in Adult Patients With Herpes Simplex Virus and Varicella-Zoster Virus Encephalitis. <i>Journal of Infectious Diseases</i> , 2017 , 215, 1430-1434	7	36
101	REST, a master regulator of neurogenesis, evolved under strong positive selection in humans and in non human primates. <i>Scientific Reports</i> , 2017 , 7, 9530	4.9	15
100	Distinct selective forces and Neanderthal introgression shaped genetic diversity at genes involved in neurodevelopmental disorders. <i>Scientific Reports</i> , 2017 , 7, 6116	4.9	7
99	Evolutionary analysis of Old World arenaviruses reveals a major adaptive contribution of the viral polymerase. <i>Molecular Ecology</i> , 2017 , 26, 5173-5188	5.7	7
98	Molecular Evolution of Human Coronavirus Genomes. <i>Trends in Microbiology</i> , 2017 , 25, 35-48	12.4	405
97	A 6-amino acid insertion/deletion polymorphism in the mucin domain of TIM-1 confers protections against HIV-1 infection. <i>Microbes and Infection</i> , 2017 , 19, 69-74	9.3	7
96	Positive Selection Drives Evolution at the Host-Filovirus Interaction Surface. <i>Molecular Biology and Evolution</i> , 2016 , 33, 2836-2847	8.3	13
95	Extensive Positive Selection Drives the Evolution of Nonstructural Proteins in Lineage C Betacoronaviruses. <i>Journal of Virology</i> , 2016 , 90, 3627-39	6.6	47
94	Nonstructural Proteins Are Preferential Positive Selection Targets in Zika Virus and Related Flaviviruses. <i>PLoS Neglected Tropical Diseases</i> , 2016 , 10, e0004978	4.8	41
93	The mammalian complement system as an epitome of host-pathogen genetic conflicts. <i>Molecular Ecology</i> , 2016 , 25, 1324-39	5.7	10

92	The evolutionary history of genes involved in spoken and written language: beyond FOXP2. <i>Scientific Reports</i> , 2016 , 6, 22157	4.9	39
91	OASes and STING: adaptive evolution in concert. <i>Genome Biology and Evolution</i> , 2015 , 7, 1016-32	3.9	27
90	Evolutionary insights into host-pathogen interactions from mammalian sequence data. <i>Nature Reviews Genetics</i> , 2015 , 16, 224-36	30.1	139
89	Diverse selective regimes shape genetic diversity at ADAR genes and at their coding targets. <i>RNA Biology</i> , 2015 , 12, 149-61	4.8	7
88	Evolution of the rapidly mutating human salivary agglutinin gene (DMBT1) and population subsistence strategy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 5105-10	11.5	25
87	The heptad repeat region is a major selection target in MERS-CoV and related coronaviruses. <i>Scientific Reports</i> , 2015 , 5, 14480	4.9	40
86	Determining multiallelic complex copy number and sequence variation from high coverage exome sequencing data. <i>BMC Genomics</i> , 2015 , 16, 891	4.5	3
85	Variants in the CYP7B1 gene region do not affect natural resistance to HIV-1 infection. <i>Retrovirology</i> , 2015 , 12, 80	3.6	1
84	Positive selection underlies the species-specific binding of Plasmodium falciparum RH5 to human basigin. <i>Molecular Ecology</i> , 2015 , 24, 4711-22	5.7	11
83	Natural Selection at the Brush-Border: Adaptations to Carbohydrate Diets in Humans and Other Mammals. <i>Genome Biology and Evolution</i> , 2015 , 7, 2569-84	3.9	10
82	Evolutionary Analysis Identifies an MX2 Haplotype Associated with Natural Resistance to HIV-1 Infection. <i>AIDS Research and Human Retroviruses</i> , 2014 , 30, A24-A25	1.6	
81	The CCR5B2 allele is not a major predisposing factor for severe H1N1pdm09 infection. <i>BMC Research Notes</i> , 2014 , 7, 504	2.3	11
80	No association of IFI16 (interferon-inducible protein 16) variants with susceptibility to multiple sclerosis. <i>Journal of Neuroimmunology</i> , 2014 , 271, 49-52	3.5	1
79	Human genome variability, natural selection and infectious diseases. <i>Current Opinion in Immunology</i> , 2014 , 30, 9-16	7.8	49
78	RIG-I-like receptors evolved adaptively in mammals, with parallel evolution at LGP2 and RIG-I. <i>Journal of Molecular Biology</i> , 2014 , 426, 1351-65	6.5	23
77	Possible association between SNAP-25 single nucleotide polymorphisms and alterations of categorical fluency and functional MRI parameters in Alzheimer's disease. <i>Journal of Alzheimer's Disease</i> , 2014 , 42, 1015-28	4.3	26
76	A regulatory polymorphism in HAVCR2 modulates susceptibility to HIV-1 infection. <i>PLoS ONE</i> , 2014 , 9, e106442	3.7	9
75	Genetic adaptation of the human circadian clock to day-length latitudinal variations and relevance for affective disorders. <i>Genome Biology</i> , 2014 , 15, 499	18.3	22

74	An evolutionary analysis of antigen processing and presentation across different timescales reveals pervasive selection. <i>PLoS Genetics</i> , 2014 , 10, e1004189	6	31
73	Ancient and recent selective pressures shaped genetic diversity at AIM2-like nucleic acid sensors. <i>Genome Biology and Evolution</i> , 2014 , 6, 830-45	3.9	22
72	Evolutionary analysis identifies an MX2 haplotype associated with natural resistance to HIV-1 infection. <i>Molecular Biology and Evolution</i> , 2014 , 31, 2402-14	8.3	18
71	Albuminoid genes: evolving at the interface of dispensability and selection. <i>Genome Biology and Evolution</i> , 2014 , 6, 2983-97	3.9	8
70	ABO histo-blood group might modulate predisposition to Crohn's disease and affect disease behavior. <i>Journal of Crohn's and Colitis</i> , 2014 , 8, 489-94	1.5	19
69	Haptoglobin (HP) and Haptoglobin-related protein (HPR) copy number variation, natural selection, and trypanosomiasis. <i>Human Genetics</i> , 2014 , 133, 69-83	6.3	27
68	Crohn's disease loci are common targets of protozoa-driven selection. <i>Molecular Biology and Evolution</i> , 2013 , 30, 1077-87	8.3	19
67	A nonsense polymorphism (R392X) in TLR5 protects from obesity but predisposes to diabetes. <i>Journal of Immunology</i> , 2013 , 190, 3716-20	5.3	29
66	A 175 million year history of T cell regulatory molecules reveals widespread selection, with adaptive evolution of disease alleles. <i>Immunity</i> , 2013 , 38, 1129-41	32.3	26
65	Endoplasmic reticulum aminopeptidase 2 haplotypes play a role in modulating susceptibility to HIV infection. <i>Aids</i> , 2013 , 27, 1697-706	3.5	18
64	Pathogen-driven selection in the human genome. <i>International Journal of Evolutionary Biology</i> , 2013 , 2013, 204240		30
63	Long-standing balancing selection in the THBS4 gene: influence on sex-specific brain expression and gray matter volumes in Alzheimer disease. <i>Human Mutation</i> , 2013 , 34, 743-53	4.7	6
62	Evolutionary analysis of the contact system indicates that kininogen evolved adaptively in mammals and in human populations. <i>Molecular Biology and Evolution</i> , 2013 , 30, 1397-408	8.3	16
61	Identification of a new susceptibility variant for multiple sclerosis in OAS1 by population genetics analysis. <i>Human Genetics</i> , 2012 , 131, 87-97	6.3	17
60	A common polymorphism in TLR3 confers natural resistance to HIV-1 infection. <i>Journal of Immunology</i> , 2012 , 188, 818-23	5.3	87
59	Mammalian NPC1 genes may undergo positive selection and human polymorphisms associate with type 2 diabetes. <i>BMC Medicine</i> , 2012 , 10, 140	11.4	14
58	An evolutionary history of the selectin gene cluster in humans. <i>Heredity</i> , 2012 , 109, 117-26	3.6	4
57	Variants in SNAP25 are targets of natural selection and influence verbal performances in women. <i>Cellular and Molecular Life Sciences</i> , 2012 , 69, 1705-15	10.3	9

56	Evolutionary history of copy-number-variable locus for the low-affinity Fcγ receptor: mutation rate, autoimmune disease, and the legacy of helminth infection. <i>American Journal of Human Genetics</i> , 2012 , 90, 973-85	11	32
55	Genetic variability at the TREX1 locus is not associated with natural resistance to HIV-1 infection. <i>Aids</i> , 2012 , 26, 1443-5	3.5	5
54	A trans-specific polymorphism in ZC3HAV1 is maintained by long-standing balancing selection and may confer susceptibility to multiple sclerosis. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1599-613	8.3	19
53	A functional variant in ERAP1 predisposes to multiple sclerosis. <i>PLoS ONE</i> , 2012 , 7, e29931	3.7	41
52	A positively selected APOBEC3H haplotype is associated with natural resistance to HIV-1 infection. <i>Evolution; International Journal of Organic Evolution</i> , 2011 , 65, 3311-22	3.8	18
51	Balancing selection is common in the extended MHC region but most alleles with opposite risk profile for autoimmune diseases are neutrally evolving. <i>BMC Evolutionary Biology</i> , 2011 , 11, 171	3	21
50	Evolutionary genetic dissection of human interferons. <i>Journal of Experimental Medicine</i> , 2011 , 208, 2747-56	10.6	118
49	An evolutionary analysis of RAC2 identifies haplotypes associated with human autoimmune diseases. <i>Molecular Biology and Evolution</i> , 2011 , 28, 3319-29	8.3	15
48	Signatures of environmental genetic adaptation pinpoint pathogens as the main selective pressure through human evolution. <i>PLoS Genetics</i> , 2011 , 7, e1002355	6	349
47	GeCo++: a C++ library for genomic features computation and annotation in the presence of variants. <i>Bioinformatics</i> , 2011 , 27, 1313-5	7.2	20
46	Genetic diversity at endoplasmic reticulum aminopeptidases is maintained by balancing selection and is associated with natural resistance to HIV-1 infection. <i>Human Molecular Genetics</i> , 2010 , 19, 4705-14	5.6	67
45	Fine mapping of AHI1 as a schizophrenia susceptibility gene: from association to evolutionary evidence. <i>FASEB Journal</i> , 2010 , 24, 3066-82	0.9	32
44	Polymorphisms in the CPB2 gene are maintained by balancing selection and result in haplotype-preferential splicing of exon 7. <i>Molecular Biology and Evolution</i> , 2010 , 27, 1945-54	8.3	12
43	Genome-wide identification of susceptibility alleles for viral infections through a population genetics approach. <i>PLoS Genetics</i> , 2010 , 6, e1000849	6	50
42	Population genetics of IFIH1: ancient population structure, local selection, and implications for susceptibility to type 1 diabetes. <i>Molecular Biology and Evolution</i> , 2010 , 27, 2555-66	8.3	40
41	Genetic variability in the ACE gene region surrounding the Alu I/D polymorphism is maintained by balancing selection in human populations. <i>Pharmacogenetics and Genomics</i> , 2010 , 20, 131-4	1.9	6
40	Response to Wilson et al.. <i>American Journal of Human Genetics</i> , 2010 , 86, 493-495	11	78
39	Long-term balancing selection maintains trans-specific polymorphisms in the human TRIM5 gene. <i>Human Genetics</i> , 2010 , 128, 577-88	6.3	42

38	The role of protozoa-driven selection in shaping human genetic variability. <i>Trends in Genetics</i> , 2010 , 26, 95-9	8.5	29
37	The landscape of human genes involved in the immune response to parasitic worms. <i>BMC Evolutionary Biology</i> , 2010 , 10, 264	3	46
36	The hygiene hypothesis: an evolutionary perspective. <i>Microbes and Infection</i> , 2010 , 12, 421-7	9.3	63
35	Parasites represent a major selective force for interleukin genes and shape the genetic predisposition to autoimmune conditions. <i>Journal of Experimental Medicine</i> , 2009 , 206, 1395-408	16.6	189
34	Point mutations and a large intragenic deletion in SPG11 in complicated spastic paraplegia without thin corpus callosum. <i>Journal of Medical Genetics</i> , 2009 , 46, 345-51	5.8	26
33	A complex selection signature at the human AVPR1B gene. <i>BMC Evolutionary Biology</i> , 2009 , 9, 123	3	8
32	A population genetics study of the familial Mediterranean fever gene: evidence of balancing selection under an overdominance regime. <i>Genes and Immunity</i> , 2009 , 10, 678-86	4.4	16
31	Diverse evolutionary histories for beta-adrenoreceptor genes in humans. <i>American Journal of Human Genetics</i> , 2009 , 85, 64-75	11	30
30	Widespread balancing selection and pathogen-driven selection at blood group antigen genes. <i>Genome Research</i> , 2009 , 19, 199-212	9.7	122
29	Both selective and neutral processes drive GC content evolution in the human genome. <i>BMC Evolutionary Biology</i> , 2008 , 8, 99	3	39
28	The signature of long-standing balancing selection at the human defensin beta-1 promoter. <i>Genome Biology</i> , 2008 , 9, R143	18.3	53
27	A clinical, genetic, and biochemical characterization of SPG7 mutations in a large cohort of patients with hereditary spastic paraplegia. <i>Human Mutation</i> , 2008 , 29, 522-31	4.7	74
26	Intron size in mammals: complexity comes to terms with economy. <i>Trends in Genetics</i> , 2007 , 23, 20-4	8.5	32
25	A region in the dystrophin gene major hot spot harbors a cluster of deletion breakpoints and generates double-strand breaks in yeast. <i>FASEB Journal</i> , 2006 , 20, 1910-2	0.9	14
24	Gene function and expression level influence the insertion/fixation dynamics of distinct transposon families in mammalian introns. <i>Genome Biology</i> , 2006 , 7, R120	18.3	27
23	Both conserved and non-conserved regions of Spo11 are essential for meiotic recombination initiation in yeast. <i>Molecular Genetics and Genomics</i> , 2006 , 276, 313-21	3.1	10
22	Fixation of conserved sequences shapes human intron size and influences transposon-insertion dynamics. <i>Trends in Genetics</i> , 2005 , 21, 484-8	8.5	24
21	Mutation finding in patients with dysferlin deficiency and role of the dysferlin interacting proteins annexin A1 and A2 in muscular dystrophies. <i>Human Mutation</i> , 2005 , 26, 283	4.7	50

20	Silencers regulate both constitutive and alternative splicing events in mammals. <i>Cellular and Molecular Life Sciences</i> , 2005 , 62, 1579-604	10.3	50
19	Analysis of intronic conserved elements indicates that functional complexity might represent a major source of negative selection on non-coding sequences. <i>Human Molecular Genetics</i> , 2005 , 14, 2533-46	5.6	63
18	Silencer elements as possible inhibitors of pseudoexon splicing. <i>Nucleic Acids Research</i> , 2004 , 32, 1783-91	10.1	102
17	An intragenic deletion/inversion event in the DMD gene determines a novel exon creation and results in a BMD phenotype. <i>Human Genetics</i> , 2004 , 115, 13-8	6.3	16
16	Human skin-derived stem cells migrate throughout forebrain and differentiate into astrocytes after injection into adult mouse brain. <i>Journal of Neuroscience Research</i> , 2004 , 77, 475-86	4.4	119
15	Over-representation of exonic splicing enhancers in human intronless genes suggests multiple functions in mRNA processing. <i>Biochemical and Biophysical Research Communications</i> , 2004 , 322, 470-6	3.4	12
14	A CAV3 microdeletion differentially affects skeletal muscle and myocardium. <i>Neurology</i> , 2003 , 61, 1513-8	0.5	39
13	Trans-acting factors may cause dystrophin splicing misregulation in BMD skeletal muscles. <i>FEBS Letters</i> , 2003 , 537, 30-4	3.8	15
12	Two dystrophin proteins and transcripts in a mild dystrophinopathic patient. <i>Neuromuscular Disorders</i> , 2003 , 13, 13-6	2.9	3
11	Molecular analysis of LGMD-2B and MM patients: identification of novel DYSF mutations and possible founder effect in the Italian population. <i>Neuromuscular Disorders</i> , 2003 , 13, 788-95	2.9	32
10	Comparative analysis of vertebrate dystrophin loci indicate intron gigantism as a common feature. <i>Genome Research</i> , 2003 , 13, 764-72	9.7	15
9	The dystrophin gene is alternatively spliced throughout its coding sequence. <i>FEBS Letters</i> , 2002 , 517, 163-6	3.8	30
8	Analysis of splicing parameters in the dystrophin gene: relevance for physiological and pathogenetic splicing mechanisms. <i>Human Genetics</i> , 2001 , 109, 73-84	6.3	21
7	Intraarterial injection of muscle-derived CD34(+)Sca-1(+) stem cells restores dystrophin in mdx mice. <i>Journal of Cell Biology</i> , 2001 , 152, 335-48	7.3	232
6	Transcriptional activation of the non-muscle, full-length dystrophin isoforms in Duchenne muscular dystrophy skeletal muscle. <i>Journal of the Neurological Sciences</i> , 2001 , 186, 51-7	3.2	17
5	Chemotactic factors enhance myogenic cell migration across an endothelial monolayer. <i>Experimental Cell Research</i> , 2001 , 268, 36-44	4.2	49
4	Primary beta-sarcoglycanopathy manifesting as recurrent exercise-induced myoglobinuria. <i>Neuromuscular Disorders</i> , 2001 , 11, 389-94	2.9	27
3	Loss of Dp140 dystrophin isoform and intellectual impairment in Duchenne dystrophy. <i>Neurology</i> , 2000 , 55, 559-64	6.5	92

2	Loss of Dp140 regulatory sequences is associated with cognitive impairment in dystrophinopathies. <i>Neuromuscular Disorders</i> , 2000 , 10, 194-9	2.9	50
1	Absence of brain Dp140 isoform and cognitive impairment in Becker muscular dystrophy. <i>Lancet, The</i> , 1999 , 353, 897-8	40	21