

Curriculum vitae

Manuela Sironi, PhD

Personal Data: born November 30th, 1971 in Como, Italy. Citizenship: Italian.

ORCID: 0000-0002-2267-5266

SCOPUS ID: 7102892131

Researcher ID: AAH-5456-2019

Personal e-mail: manu.sir@gmail.com

Institutional e-mail: manuela.sironi@BP.LNF.IT

Telephone number: +39 339 5709734



Education and research experience:

2024-present: Associate Professor of Genetics, University of Milano-Bicocca

2006-present: Principal Investigator, Bioinformatics Unit., IRCCS E. Medea (Bosisio Parini, Italy).

2008-2020: Assistant Professor (University of Milan, Italy).

2007-2010: PhD in Molecular Medicine (University of Milan, Italy).

2005-2006: Researcher, Bioinformatics Lab, IRCCS E. Medea (Bosisio Parini, Italy).

2004: Visiting Scientist, Wadsworth Center, Molecular Genetics Program, Center for Medical Sciences, Albany, USA.

2001-2003: Specialty in Applied Genetics (University of Milan, Italy).

1998-2004: Researcher, Molecular Biology Unit, IRCCS E. Medea (Bosisio Parini, Italy).

1996-1998: Research fellowship, Department of Neurological Sciences, University of Milan, IRCCS Ospedale Maggiore Policlinico (Milano, Italy).

1995-1996: Research fellowship, Experimental Oncology, Istituto Nazionale per lo Studio e la Cura dei Tumori (Milano, Italy).

1995: Magna cum Laude Degree in Biological Sciences (Università degli Studi di Milano, Italy).

1990: High school graduation (60/60), Liceo Scientifico "P. Giovio", Como (Italy).

National Scientific qualifications (ASN):

2023: National Scientific Qualification to cover the role of Full Professor in Genetics (05/I1);

2022: National Scientific Qualification to cover the role of Associate Professor in Molecular Biology (05/E2);
National Scientific Qualification to cover the role of Associate Professor in Clinical and Medical Microbiology (06/A3).

2020: National Scientific Qualification to cover the role of Associate Professor in Microbiology (05/I2).

2018: National Scientific Qualification to cover the role of Associate Professor in Medical Genetics (06/A1).

2018: National Scientific Qualification to cover the role of Associate Professor in Health sciences and applied medical technologies (06/N1).

2017: National Scientific Qualification to cover the role of Associate Professor in Zoology and Anthropology (05/B1).

Language skills:

Italian: mother tongue.

English: fluent (written and spoken).

French: beginner (written and spoken).

Publications and bibliographic indexes:

Author of 181 publications in peer-reviewed international scientific journals (excluding conference proceedings): 26 first author, 99 last author.

Total citations: 7007 (Scopus), 10535 (Google Scholar).

H-index: 44 (Scopus), 52 (Google Scholar).

Editorial Boards:

2022-present: Co-Editor in Chief of Infection, Genetics and Evolution (Elsevier, IF=3.2).
2022-present: Editorial board of Viruses (MDPI, IF=5.8).
2020-present: Chief Editor of the Bioinformatic and Predictive Virology section (Frontiers in Virology, IF= not yet assigned).
2018-present: Senior Editor for Scientific Reports (Nature Publishing Group, IF=4.4).
2016-2021: Handling Editor for Infection, Genetics and Evolution (Elsevier).
2016-2018: Editorial Board of Scientific Reports (Nature Publishing Group).

Scientific boards:

2017-present: member of the *Arenaviridae* Study Group-International Committee on Taxonomy of Viruses (ICTV, <https://ictv.global/>).
2004-2020: Board member of the Neurology Residency Program, University of Milan.
2006-present: member of the Technical and Scientific Board, IRCCS E. Medea.

Committees/grant reviewing activity:

2023: Expert evaluator for the Fundação para a Ciência e a Tecnologia, I.P. (FCT), the Portuguese public funding agency for R&D [Experimental Biology panel].
2022: co-Chair of the Experimental Biology panel, Fundação para a Ciência e a Tecnologia, I.P. (FCT), the Portuguese public funding agency for R&D.
2021: Chair of the Experimental Biology panel, Fundação para a Ciência e a Tecnologia, I.P. (FCT), the Portuguese public funding agency for R&D.
2020: Expert evaluator for the Fundação para a Ciência e a Tecnologia, I.P. (FCT), the Portuguese public funding agency for R&D [Clinical Medicine panel].
2017: Expert evaluator for the Fundação para a Ciência e a Tecnologia, I.P. (FCT), the Portuguese public funding agency for R&D [Experimental Biology panel].
2015: Expert evaluator for the Fundação para a Ciência e a Tecnologia, I.P. (FCT), the Portuguese public funding agency for R&D [Experimental Biology panel].
2015: Expert evaluator for the European Research Commission, stage 1, H2020-BIOTEC.
2011: Expert evaluator for the European Research Commission, stage 1 and stage 2, FP7-HEALTH-2011-two stage [Topic 2.1.1-3 Large-scale genomics approaches to identify host determinants of infectious diseases].
Reviewer for the following agencies/programs: Swiss National Science Foundation, Cariplo Foundation (Italy), UEFISCDI EEA Grants, INCEPTION Program (France), ERINHA-ISIDORE Program (2022 Monkeypox Call).

Awarded Grants:

2023: PI, "An evolution-guided approach to study the interaction between MPXV and RIPK3, a central mediator of necroptosis", ISIDORE Program (A New Approach to Pandemic Preparedness & Responsiveness Research in Europe, Monkeypox Call).
2020-2021: PI, "Characterization of SARS-CoV-2 accessory proteins in terms of host adaptation, biochemical properties, and pharmacophore models-CORONA", Fondazione Cariplo.
2020-2021: collaborator, "Characterization of SARS-CoV-2 coding sequences and assessment of their role in COVID-19 pathogenesis", Regione Lombardia.
2010-2015: collaborator, "Role of pathogen-driven selection in shaping the predisposition to inflammatory bowel disease (IBD): identification of disease susceptibility alleles" The Broad Medical Research Program of The Broad Foundation [grant IBD-0294].
2012-2013: Unit PI, "Comparison between Caucasian and Chinese genetic profiles predicting the response to rostafuroxin" (funded by CVie Therapeutics Company Limited).

2008: PI, “A population genetics approach to the identification of disease alleles and its application to juvenile and perinatal stroke”, the Italian Ministry of Health (“Ricerca Finalizzata,[RF-IEM-2007-633627].

2000-present: PI, one project/year “Ricerca Corrente” [the Italian Ministry of Health].

Memberships:

Italian Society of Evolutionary Biology (SIBE)

Manuscript reviewer for:

Science, Trends in Genetics, Molecular Biology and Evolution, BMC Evolutionary Biology; Journal of Molecular Evolution, Journal of Medical Genetics, Gene, Human Genetics, American Journal of Human Genetics, PLoS Genetics, Molecular Ecology, PLoS Pathogens, PNAS, Nature Communications, Journal of Virology, Nature Ecology and Evolution.

Teaching:

2008-2013: Assistant Professor, Practical Neurology 4 (Postgenomics and bioinformatics, comparative genomics), 6 hours/year, Neurology Residency Program, University of Milan

2013/2014: Assistant Professor, Practical Neurology 4 (Postgenomics, bioinformatics, comparative genomics, population genetics), 6 hours/year, Neurology Residency Program, University of Milan

2014/2015: Assistant Professor, Practical Neurology 4 (Postgenomics, bioinformatics, comparative genomics, population genetics), 6 hours/year, Neurology Residency Program, University of Milan

2015/2016: Assistant Professor, Practical Neurology 4 (Postgenomics, bioinformatics, comparative genomics, population genetics), 4 hours/year, Neurology Residency Program, University of Milan

2016/2017: Assistant Professor, Practical Neurology 3 (Postgenomics, bioinformatics, comparative genomics, population genetics), 4 hours/year, Neurology Residency Program, University of Milan

2017/2018: Assistant Professor, Practical Neurology 3 (Postgenomics, bioinformatics, comparative genomics, population genetics), 4 hours/year, Neurology Residency Program, University of Milan

2018/2019: Assistant Professor, Practical Neurology 3 (Postgenomics, bioinformatics, comparative genomics, population genetics), 4 hours/year, Neurology Residency Program, University of Milan

Student tutoring/Jury member:

2005-2006: co-supervisor, Matteo Fumagalli, Master Degree in Biomedical Engineering, Politecnico di Milano.

2008-2010: co-supervisor, Matteo Fumagalli, PhD in Biomedical Engineering, Politecnico di Milano.

2009-2010: co-supervisor, Beatrice Montorfano, Master Degree in Biotechnology, Università di Milano Bicocca.

2010-2011: co-supervisor, Diego Forni, Master Degree in Biotechnology, Università di Milano Bicocca.

2014-2016: co-supervisor, Chiara Pontremoli, PhD in Molecular and Translational Medicine. Università degli Studi di Milano.

2020: jury member, Léa Picard, THESE de DOCTORAT DE L'UNIVERSITE DE LYON, l'Ecole Normale Supérieure de Lyon, Biologie Moléculaire, Intégrative et Cellulaire

2024: revision committee member, Tommaso Alfonsi PhD thesis, PhD in Information Technology, Politecnico di Milano.

Awards

Listed among the Top Italian Scientists (TIS) and the Top Italian Women Scientists (TIWS) (<https://topitalianscientists.org/>).

1996-1998: Research fellowship, Department of Neurological Sciences, University of Milan, IRCCS Ospedale Maggiore Policlinico (Milano, Italy).

Invited talks and event organization (last 10 years):

2016

Member of the Scientific Committee of MEEGID XIII, 13th International Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases, 10-13 May 2016, Institute of Tropical Medicine, Antwerp, Belgium

Invited Speaker at MEEGID XIII, 13th International Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases, 10-13 May 2016, Institute of Tropical Medicine, Antwerp, Belgium

Invited speaker at 8th congresso ICAR 2016, Italian Conference on AIDS and Antiviral Research- Università Milano-Bicocca, Milano, 6-8 Giugno 2016.

Invited speaker at the by the Italian Societies of Microbiology (SIM) and of Immunology, Clinical Immunology and Allergology (SIICA) (Novara, Novarello Congress Center, from 23 to 25 June 2016).

2017

Invited speaker at the 7th LCI-Symposium 2017 Evolution and Infection (Leibniz Center Infection), Leibniz, Germany.

2018

Keynote speaker at the Joint Spring Symposium 2018- Danish Society for Parasitology and Danish Society for Tropical Medicine & International Health- Copenhagen.

Member of the Scientific Committee of the 14th International Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases (MEEGID) - Sitges, Spain.

Invited speaker at the 14th International Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases- Sitges, Spain.

Invited seminar at INGM (Istituto Nazionale di Genetica Molecolare) [Seminar: "Zoonoses and the Red Queen (evolutionary genetics of zoonotic infections)"]

2019

Invited speaker at the Jacques Monod Conference - cjm5-2019 : Virus evolution on the mutualist - parasite continuum (Roscoff, France).

2020

Invited speaker- giornate virtuali del congresso della Società Italiana di Microbiologia-- 48th Virtual SIM 2020 (21-22 settembre 2020).

Invited speaker - XII PhD Meeting-- University of Milano-Bicocca

Invited seminar – Residency in Neurology, Università degli Studi di Milano [Evolutionary history and origin of SARS-CoV-2]

2021

Invited seminar for Séminaires d'Écologie et d'Évolution de Montpellier -- LabEx Centre Méditerranéen de l'Environnement et de la Biodiversité -- Center for Research on the Ecology and Evolution of Diseases (CREES)

2022

Invited speaker at the International Discussion Group on COVID Related Activities (hosted by

McGill university, McGill Genome Center, Montreal, Canada).

Invited speaker at XVI FISV Congress, 3R: Research, Resilience, Reprise -- Reggia di Portici (Naples), Italy (14-16 September 2022)

2023

Co-Chair of MEEGID XVI (16th International Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases, Elsevier), Dresden (14-17 November 2023)

Invited seminar, Department of Biosciences, University of Milan (24 November 2023)

2025

Co-Chair of MEEGID XVII (17th International Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases, Elsevier), to be held in Kolkata, India (18-21 November 2025)

Scientific dissemination activity:

Since 2014: active participation (interactive talks and activities) to the Researchers' Night (organized by IRCCS E. Medea)

2020: dissemination activity on COVID-19 (with the support of Cariplo Foundation). Target: local secondary schools (11 schools, more than 900 students reached).

List of publications

Journal articles (international, peer reviewed only):

- 1 Fassati A, Bardoni A, **Sironi M**, Wells DJ, Bresolin N, Scarlato G, Hatanaka M, Yamaoka S, Dickson G. Insertion of two independent enhancers in the long terminal repeat of a self-inactivating vector results in high-titer retroviral vectors with tissue-specific expression. *Hum Gene Ther*. 1998; 9(17):2459-68. doi: 10.1089/hum.1998.9.17-2459
- 2 Bardoni A, **Sironi M**, Felisari G, Comi GP, Bresolin N. Absence of brain Dp140 isoform and cognitive impairment in Becker muscular dystrophy. *Lancet*. 1999; 353(9156):897-8. doi: 10.1016/S0140-6736(98)05801-2
- 3 Bardoni A, Felisari G, **Sironi M**, Comi G, Lai M, Robotti M, Bresolin N. Loss of Dp140 regulatory sequences is associated with cognitive impairment in dystrophinopathies. *Neuromuscul Disord*. 2000; 10(3):194-9. doi: 10.1016/S0960-8966(99)00108-x
- 4 Felisari G, Martinelli Boneschi F, Bardoni A, **Sironi M**, Comi GP, Robotti M, Turconi AC, Lai M, Corrao G, Bresolin N. Loss of Dp140 dystrophin isoform and intellectual impairment in Duchenne dystrophy. *Neurology*. 2000; 55(4):559-64. doi: 10.1212/wnl.55.4.559.
- 5 **Sironi M**, Corti S, Locatelli F, Cagliani R, Comi GP. A novel splice site mutation (3157+1G>T) in the dystrophin gene causing total exon skipping and DMD phenotype. *Hum Mutat*. 2001; 17(3):239. doi: 10.1002/humu.18
- 6 Torrente Y, Tremblay JP, Pisati F, Belicchi M, Rossi B, **Sironi M**, Fortunato F, El Fahime M, D'Angelo MG, Caron NJ, Constantin G, Paulin D, Scarlato G, Bresolin N. Intraarterial injection of muscle-derived CD34(+)Sca-1(+) stem cells restores dystrophin in mdx mice. *J Cell Biol*. 2001; 152(2):335-48. doi: 10.1083/jcb.152.2.335
- 7 Cagliani R, Comi GP, Tancredi L, **Sironi M**, Fortunato F, Giorda R, Bardoni A, Moggio M, Prella A, Bresolin N, Scarlato G. Primary beta-sarcoglycanopathy manifesting as recurrent exercise-induced myoglobinuria. *Neuromuscul Disord*. 2001; 11(4):389-94. doi: 10.1016/S0960-8966(00)00207-8
- 8 **Sironi M**, Bardoni A, Felisari G, Cagliani R, Robotti M, Comi GP, Moggio M, Bresolin N. Transcriptional activation of the non-muscle, full-length dystrophin isoforms in Duchenne muscular dystrophy skeletal muscle. *J Neurol Sci*. 2001; 186(1-2):51-7. doi: 10.1016/S0022-510X(01)00502-0
- 9 Corti S, Salani S, Del Bo R, **Sironi M**, Strazzer S, D'Angelo MG, Comi GP, Bresolin N, Scarlato G. Chemotactic factors enhance myogenic cell migration across an endothelial monolayer. *Exp Cell Res*. 2001; 268(1):36-44. doi: 10.1006/excr.2001.5267
- 10 **Sironi M**, Pozzoli U, Cagliani R, Comi GP, Bardoni A, Bresolin N. Analysis of splicing parameters in the dystrophin gene: relevance for physiological and pathogenetic splicing mechanisms. *Hum Genet*. 2001; 109(1):73-84. doi: 10.1007/s004390100547

- 11 Pozzoli U, **Sironi M**, Cagliani R, Comi GP, Bardoni A, Bresolin N.
Comparative analysis of the human dystrophin and utrophin gene structures. *Genetics*. 2002; 160(2):793-8. doi: 10.1093/genetics/160.2.793
- 12 **Sironi M**, Cagliani R, Pozzoli U, Bardoni A, Comi GP, Giorda R, Bresolin N.
The dystrophin gene is alternatively spliced throughout its coding sequence. *FEBS Lett*. 2002; 517(1-3):163-6. doi: 10.1016/s0014-5793(02)02613-3
- 13 Torrente Y, Belicchi M, Pisati F, Pagano SF, Fortunato F, **Sironi M**, D'Angelo MG, Parati EA, Scarlato G, Bresolin N.
Alternative sources of neurons and glia from somatic stem cells. *Cell Transplant*. 2002; 11(1):25-34.
- 14 Cagliani R, Bardoni A, **Sironi M**, Fortunato F, Prella A, Felisari G, Bonaglia MC, D'Angelo MG, Moggio M, Bresolin N, Comi GP.
Two dystrophin proteins and transcripts in a mild dystrophinopathic patient. *Neuromuscul Disord*. 2003; 13(1):13-6. doi: 10.1016/s0960-8966(02)00192-x
- 15 **Sironi M**, Pozzoli U, Cagliani R, Giorda R, Comi GP, Bardoni A, Menozzi G, Bresolin N.
Relevance of sequence and structure elements for deletion events in the dystrophin gene major hot-spot. *Hum Genet*. 2003; 112(3):272-88. doi: 10.1007/s00439-002-0881-5
- 16 **Sironi M**, Cagliani R, Comi GP, Pozzoli U, Bardoni A, Giorda R, Bresolin N.
Trans-acting factors may cause dystrophin splicing misregulation in BMD skeletal muscles. *FEBS Lett*. 2003; 537(1-3):30-4. doi: 10.1016/s0014-5793(03)00066-8
- 17 Pozzoli U, Elgar G, Cagliani R, Riva L, Comi GP, Bresolin N, Bardoni A, **Sironi M**.
Comparative analysis of vertebrate dystrophin loci indicate intron gigantism as a common feature. *Genome Res*. 2003; 13(5):764-72. doi: 10.1101/gr.776503
- 18 Cagliani R, Fortunato F, Giorda R, Rodolico C, Bonaglia MC, **Sironi M**, D'Angelo MG, Prella A, Locatelli F, Toscano A, Bresolin N, Comi GP.
Molecular analysis of LGMD-2B and MM patients: identification of novel DYSF mutations and possible founder effect in the Italian population. *Neuromuscul Disord*. 2003; 13(10):788-95. doi: 10.1016/s0960-8966(03)00133-0
- 19 Cagliani R, Bresolin N, Prella A, Gallanti A, Fortunato F, **Sironi M**, Ciscato P, Fagiolari G, Bonato S, Galbiati S, Corti S, Lamperti C, Moggio M, Comi GP.
A CAV3 microdeletion differentially affects skeletal muscle and myocardium. *Neurology*. 2003; 61(11):1513-9. doi: 10.1212/01.wnl.0000097320.35982.03
- 20 Belicchi M, Pisati F, Lopa R, Porretti L, Fortunato F, **Sironi M**, Scalapogna M, Parati EA, Bresolin N, Torrente Y.
Human skin-derived stem cells migrate throughout forebrain and differentiate into astrocytes after injection into adult mouse brain. *J Neurosci Res*. 2004; 77(4):475-86. doi: 10.1002/jnr.20151.
- 21 Pozzoli U, Riva L, Menozzi G, Cagliani R, Comi GP, Bresolin N, Giorda R, **Sironi M**.
Over-representation of exonic splicing enhancers in human intronless genes suggests multiple functions in mRNA processing. *Biochem Biophys Res Commun*. 2004; 322(2):470-6. doi: 10.1016/j.bbrc.2004.07.144

- 22 Cagliani R, **Sironi M**, Ciafaloni E, Bardoni A, Fortunato F, Prella A, Serafini M, Bresolin N, Comi GP.
An intragenic deletion/inversion event in the DMD gene determines a novel exon creation and results in a BMD phenotype. *Hum Genet.* 2004; 115(1):13-8. doi: 10.1007/s00439-004-1118-6
- 23 **Sironi M**, Menozzi G, Riva L, Cagliani R, Comi GP, Bresolin N, Giorda R, Pozzoli U.
Silencer elements as possible inhibitors of pseudoexon splicing. *Nucleic Acids Res.* 2004; 32(5):1783-91. doi: 10.1093/nar/gkh341
- 24 Pozzoli U, **Sironi M**.
Silencers regulate both constitutive and alternative splicing events in mammals. *Cell Mol Life Sci.* 2005; 62(14):1579-604. Review. doi: 10.1007/s00018-005-5030-6
- 25 **Sironi M**, Menozzi G, Comi GP, Cagliani R, Bresolin N, Pozzoli U.
Analysis of intronic conserved elements indicates that functional complexity might represent a major source of negative selection on non-coding sequences. *Hum Mol Genet.* 2005; 14(17):2533-46. doi: 10.1093/hmg/ddi257
- 26 **Sironi M**, Menozzi G, Comi GP, Bresolin N, Cagliani R, Pozzoli U.
Fixation of conserved sequences shapes human intron size and influences transposon-insertion dynamics. *Trends Genet.* 2005; 21(9):484-8. doi: 10.1016/j.tig.2005.06.009
- 27 Cagliani R, Magri F, Toscano A, Merlini L, Fortunato F, Lamperti C, Rodolico C, Prella A, **Sironi M**, Aguenouz M, Ciscato P, Uncini A, Moggio M, Bresolin N, Comi GP.
Mutation finding in patients with dysferlin deficiency and role of the dysferlin interacting proteins annexin A1 and A2 in muscular dystrophies. *Hum Mutat.* 2005; 26(3):283. doi: 10.1002/humu.9364
- 28 **Sironi M**, Menozzi G, Comi GP, Cereda M, Cagliani R, Bresolin N, Pozzoli U.
Gene function and expression level influence the insertion/fixation dynamics of distinct transposon families in mammalian introns. *Genome Biol.* 2006; 7(12):R120. doi: 10.1186/gb-2006-7-12-r120
- 29 **Sironi M**, Pozzoli U, Comi GP, Riva S, Bordoni A, Bresolin N, Nag DK.
A region in the dystrophin gene major hot spot harbors a cluster of deletion breakpoints and generates double-strand breaks in yeast. *FASEB J.* 2006; 20(11):1910-2. doi: 10.1096/fj.05-5635fje
- 30 Nag DK, Pata JD, **Sironi M**, Flood DR, Hart AM.
Both conserved and non-conserved regions of Spo11 are essential for meiotic recombination initiation in yeast. *Mol Genet Genomics.* 2006; 276(4):313-21. doi: 10.1007/s00438-006-0143-7
- 31 Pozzoli U, Menozzi G, Comi GP, Cagliani R, Bresolin N, **Sironi M**.
Intron size in mammals: complexity comes to terms with economy. *Trends Genet.* 2007; 23(1):20-4. doi: 10.1016/j.tig.2006.10.003
- 32 Cagliani R, Fumagalli M, Riva S, Pozzoli U, Comi GP, Menozzi G, Bresolin N, **Sironi M**.
The signature of long-standing balancing selection at the human defensin beta-1 promoter. *Genome Biol.* 2008; 9(9):R143. doi: 10.1186/gb-2008-9-9-r143.
- 33 Pozzoli U, Menozzi G, Fumagalli M, Cereda M, Comi GP, Cagliani R, Bresolin N, **Sironi M**.
Both selective and neutral processes drive GC content evolution in the human genome. *BMC Evol Biol.* 2008; 8:99. doi: 10.1186/1471-2148-8-99.

- 34 Arnoldi A, Tonelli A, Crippa F, Villani G, Pacelli C, **Sironi M**, Pozzoli U, D'Angelo MG, Meola G, Martinuzzi A, Crimella C, Redaelli F, Panzeri C, Renieri A, Comi GP, Turconi AC, Bresolin N, Bassi MT.
A clinical, genetic, and biochemical characterization of SPG7 mutations in a large cohort of patients with hereditary spastic paraplegia. *Hum Mutat.* 2008; 29(4):522-31. doi: 10.1002/humu.20682.
- 35 Fumagalli M, Cagliani R, Pozzoli U, Riva S, Comi GP, Menozzi G, Bresolin N, **Sironi M**.
A population genetics study of the familial Mediterranean fever gene: evidence of balancing selection under an overdominance regime. *Genes Immun.* 2009; 10(8):678-86. doi: 10.1038/gene.2009.59.
- 36 Cagliani R, Fumagalli M, Pozzoli U, Riva S, Comi GP, Torri F, Macchiardi F, Bresolin N, **Sironi M**.
Diverse evolutionary histories for beta-adrenoreceptor genes in humans. *Am J Hum Genet.* 2009; 85(1):64-75. doi: 0.1016/j.ajhg.2009.06.005.
- 37 Cagliani R, Fumagalli M, Pozzoli U, Riva S, Cereda M, Comi GP, Pattini L, Bresolin N, **Sironi M**.
A complex selection signature at the human AVPR1B gene. *BMC Evol Biol.* 2009 Jun 1;9:123. doi: 10.1186/1471-2148-9-123.
- 38 Fumagalli M, Pozzoli U, Cagliani R, Comi GP, Riva S, Clerici M, Bresolin N, **Sironi M**.
Parasites represent a major selective force for interleukin genes and shape the genetic predisposition to autoimmune conditions. *J Exp Med.* 2009; 206(6):1395-408. doi: 10.1084/jem.20082779.
- 39 Crimella C, Arnoldi A, Crippa F, Mostacciuolo ML, Boaretto F, **Sironi M**, D'Angelo MG, Manzoni S, Piccinini L, Turconi AC, Toscano A, Musumeci O, Benedetti S, Fazio R, Bresolin N, Daga A, Martinuzzi A, Bassi MT.
Point mutations and a large intragenic deletion in SPG11 in complicated spastic paraplegia without thin corpus callosum. *J Med Genet.* 2009; 46(5):345-51. doi: 10.1136/jmg.2008.063321.
- 40 Fumagalli M, Cagliani R, Pozzoli U, Riva S, Comi GP, Menozzi G, Bresolin N, **Sironi M**.
Widespread balancing selection and pathogen-driven selection at blood group antigen genes. *Genome Res.* 2009; 19(2):199-212. doi:10.1101/gr.082768.108.
- 41 Fumagalli M, Pozzoli U, Cagliani R, Comi GP, Bresolin N, Clerici M, **Sironi M**.
Genome-wide identification of susceptibility alleles for viral infections through a population genetics approach. *PLoS Genet.* 2010; 6(2):e1000849. doi: 10.1371/journal.pgen.1000849.
- 42 Pozzoli U, Fumagalli M, Cagliani R, Comi GP, Bresolin N, Clerici M, **Sironi M**.
The role of protozoa-driven selection in shaping human genetic variability. *Trends Genet.* 2010; 26(3):95-9. doi: 10.1016/j.tig.2009.12.010.
- 43 Cagliani R, Fumagalli M, Riva S, Pozzoli U, Comi GP, Bresolin N, **Sironi M**.
Genetic variability in the ACE gene region surrounding the Alu I/D polymorphism is maintained by balancing selection in human populations. *Pharmacogenet Genomics.* 2010; 20(2):131-4. doi: 10.1097/FPC.0b013e3283333532.
- 44 Cagliani R, Riva S, Biasin M, Fumagalli M, Pozzoli U, Lo Caputo S, Mazzotta F, Piacentini L, Bresolin N, Clerici M, **Sironi M**.
Genetic diversity at endoplasmic reticulum aminopeptidases is maintained by balancing selection and is associated with natural resistance to HIV-1 infection. *Hum Mol Genet.* 2010; 19(23):4705-14. doi: 10.1093/hmg/ddq401.

- 45 Cagliani R, Fumagalli M, Biasin M, Piacentini L, Riva S, Pozzoli U, Bonaglia MC, Bresolin N, Clerici M, **Sironi M**.
Long-term balancing selection maintains trans-specific polymorphisms in the human TRIM5 gene. *Hum Genet.* 2010; 128(6):577-88. doi: 10.1007/s00439-010-0884-6.
- 46 Fumagalli M, Pozzoli U, Cagliani R, Comi GP, Bresolin N, Clerici M, **Sironi M**.
The landscape of human genes involved in the immune response to parasitic worms. *BMC Evol Biol.* 2010; 10:264. doi: 10.1186/1471-2148-10-264.
- 47 Fumagalli M, Cagliani R, Riva S, Pozzoli U, Biasin M, Piacentini L, Comi GP, Bresolin N, Clerici M, **Sironi M**.
Population genetics of IFIH1: ancient population structure, local selection, and implications for susceptibility to type 1 diabetes. *Mol Biol Evol.* 2010; 27(11):2555-66. doi: 10.1093/molbev/msq141.
- 48 Torri F, Akelai A, Lupoli S, **Sironi M**, Amann-Zalcenstein D, Fumagalli M, Dal Fiume C, Ben-Asher E, Kanyas K, Cagliani R, Cozzi P, Trombetti G, Strik Lievers L, Salvi E, Orro A, Beckmann JS, Lancet D, Kohn Y, Milanesi L, Ebstein RB, Lerer B, Macciardi F.
Fine mapping of AHI1 as a schizophrenia susceptibility gene: from association to evolutionary evidence. *FASEB J.* 2010; 24(8):3066-82. doi:10.1096/fj.09-152611.
- 49 Cagliani R, Fumagalli M, Riva S, Pozzoli U, Fracassetti M, Bresolin N, Comi GP, **Sironi M**.
Polymorphisms in the CPB2 gene are maintained by balancing selection and result in haplotype-preferential splicing of exon 7. *Mol Biol Evol.* 2010; 27(8):1945-54. doi: 10.1093/molbev/msq082.
- 50 **Sironi M**, Clerici M.
The hygiene hypothesis: an evolutionary perspective. *Microbes Infect.* 2010; 12(6):421-7. doi: 10.1016/j.micinf.2010.02.002. Review.
- 51 Manry J, Laval G, Patin E, Fornarino S, Itan Y, Fumagalli M, **Sironi M**, Tichit M, Bouchier C, Casanova JL, Barreiro LB, Quintana-Murci L.
Evolutionary genetic dissection of human interferons. *J Exp Med.* 2011; 208(13):2747-59. doi:10.1084/jem.20111680.
- 52 Fumagalli M, **Sironi M**, Pozzoli U, Ferrer-Admetlla A, Pattini L, Nielsen R.
Signatures of environmental genetic adaptation pinpoint pathogens as the main selective pressure through human evolution. *PLoS Genet.* 2011; 7(11):e1002355. doi: 10.1371/journal.pgen.1002355.
- 53 Cagliani R, Riva S, Fumagalli M, Biasin M, Caputo SL, Mazzotta F, Piacentini L, Pozzoli U, Bresolin N, Clerici M, **Sironi M**.
A positively selected APOBEC3H haplotype is associated with natural resistance to HIV-1 infection. *Evolution.* 2011; 65(11):3311-22. doi: 10.1111/j.1558-5646.2011.01368.x.
- 54 Cagliani R, Riva S, Pozzoli U, Fumagalli M, Comi GP, Bresolin N, Clerici M, **Sironi M**.
Balancing selection is common in the extended MHC region but most alleles with opposite risk profile for autoimmune diseases are neutrally evolving. *BMC Evol Biol.* 2011; 11:171. doi: 10.1186/1471-2148-11-171.
- 55 **Sironi M**, Guerini FR, Agliardi C, Biasin M, Cagliani R, Fumagalli M, Caputo D, Cassinotti A, Ardizzone S, Zanzottera M, Bolognesi E, Riva S, Kanari Y, Miyazawa M, Clerici M.

An evolutionary analysis of RAC2 identifies haplotypes associated with human autoimmune diseases. *Mol Biol Evol.* 2011; 28(12):3319-29. doi: 10.1093/molbev/msr164.

- 56 Cereda M, **Sironi M**, Cavalleri M, Pozzoli U.
GeCo++: a C++ library for genomic features computation and annotation in the presence of variants. *Bioinformatics.* 2011; 27(9):1313-5. doi: 10.1093/bioinformatics/btr123.
- 57 Cagliani R, Fumagalli M, Guerini FR, Riva S, Galimberti D, Comi GP, Agliardi C, Scarpini E, Pozzoli U, Forni D, Caputo D, Asselta R, Biasin M, Paraboschi EM, Bresolin N, Clerici M, **Sironi M**.
Identification of a new susceptibility variant for multiple sclerosis in OAS1 by population genetics analysis. *Hum Genet.* 2012; 131(1):87-97. doi: 10.1007/s00439-011-1053-2.
- 58 Al-Daghri NM, Cagliani R, Forni D, Alokail MS, Pozzoli U, Alkharfy KM, Sabico S, Clerici M, **Sironi M**.
Mammalian NPC1 genes may undergo positive selection and human polymorphisms associate with type 2 diabetes. *BMC Med.* 2012; 10:140. doi: 10.1186/1741-7015-10-140.
- 59 Machado LR, Hardwick RJ, Bowdrey J, Bogle H, Knowles TJ, **Sironi M**, Hollox EJ.
Evolutionary history of copy-number-variable locus for the low-affinity Fcγ receptor: mutation rate, autoimmune disease, and the legacy of helminth infection. *Am J Hum Genet.* 2012; 90(6):973-85. doi: 10.1016/j.ajhg.2012.04.018.
- 60 Fumagalli M, Fracassetti M, Cagliani R, Forni D, Pozzoli U, Comi GP, Marini F, Bresolin N, Clerici M, **Sironi M**.
An evolutionary history of the selectin gene cluster in humans. *Heredity (Edinb).* 2012; 109(2):117-26. doi:10.1038/hdy.2012.20.
- 61 **Sironi M**, Biasin M, Forni D, Cagliani R, De Luca M, Saulle I, Caputo SL, Mazzotta F, Macias J, Pineda JA, Caruz A, Clerici M.
Genetic variability at the TREX1 locus is not associated with natural resistance to HIV-1 infection. *AIDS.* 2012; 26(11):1443-5. doi: 10.1097/QAD.0b013e328354b3c2.
- 62 Cagliani R, Guerini FR, Fumagalli M, Riva S, Agliardi C, Galimberti D, Pozzoli U, Goris A, Dubois B, Fenoglio C, Forni D, Sanna S, Zara I, Pitzalis M, Zoledziewska M, Cucca F, Marini F, Comi GP, Scarpini E, Bresolin N, Clerici M, **Sironi M**.
A trans-specific polymorphism in ZC3HAV1 is maintained by long-standing balancing selection and may confer susceptibility to multiple sclerosis. *Mol Biol Evol.* 2012; 29(6):1599-613. doi: 10.1093/molbev/mss002.
- 63 Guerini FR, Cagliani R, Forni D, Agliardi C, Caputo D, Cassinotti A, Galimberti D, Fenoglio C, Biasin M, Asselta R, Scarpini E, Comi GP, Bresolin N, Clerici M, **Sironi M**.
A functional variant in ERAP1 predisposes to multiple sclerosis. *PLoS One.* 2012; 7(1):e29931. doi: 10.1371/journal.pone.0029931.
- 64 Cagliani R, Riva S, Marino C, Fumagalli M, D'Angelo MG, Riva V, Comi GP, Pozzoli U, Forni D, Cáceres M, Bresolin N, Clerici M, **Sironi M**.
Variants in SNAP25 are targets of natural selection and influence verbal performances in women. *Cell Mol Life Sci.* 2012; 69(10):1705-15. doi: 10.1007/s00018-011-0896-y.
- 65 **Sironi M**, Biasin M, Cagliani R, Forni D, De Luca M, Saulle I, Lo Caputo S, Mazzotta F, Macías J, Pineda JA, Caruz A, Clerici M.

- A common polymorphism in TLR3 confers natural resistance to HIV-1 infection. *J Immunol.* 2012; 188(2):818-23. doi: 10.4049/jimmunol.1102179
- 66 Biasin M, **Sironi M**, Saulle I, de Luca M, la Rosa F, Cagliani R, Forni D, Agliardi C, lo Caputo S, Mazzotta F, Trabattoni D, Macias J, Pineda JA, Caruz A, Clerici M.
Endoplasmic reticulum aminopeptidase 2 haplotypes play a role in modulating susceptibility to HIV infection. *AIDS.* 2013; 27(11):1697-706. doi: 10.1097/QAD.0b013e3283601cee
 - 67 Cagliani R, Guerini FR, Rubio-Acero R, Baglio F, Forni D, Agliardi C, Griffanti L, Fumagalli M, Pozzoli U, Riva S, Calabrese E, Sikora M, Casals F, Comi GP, Bresolin N, Cáceres M, Clerici M, **Sironi M**.
Long-standing balancing selection in the THBS4 gene: influence on sex-specific brain expression and gray matter volumes in Alzheimer disease. *Hum Mutat.* 2013; 34(5):743-53. doi: 10.1002/humu.22301.
 - 68 Cagliani R, Pozzoli U, Forni D, Cassinotti A, Fumagalli M, Giani M, Fichera M, Lombardini M, Ardizzone S, Asselta R, de Franchis R, Riva S, Biasin M, Comi GP, Bresolin N, Clerici M, **Sironi M**.
Crohn's disease loci are common targets of protozoa-driven selection. *Mol Biol Evol.* 2013; 30(5):1077-87. doi: 10.1093/molbev/mst020.
 - 69 Forni D, Cagliani R, Pozzoli U, Colleoni M, Riva S, Biasin M, Filippi G, DeGioia L, Gnudi F, Comi GP, Bresolin N, Clerici M, **Sironi M**.
A 175 million year history of T cell regulatory molecules reveals widespread selection, with adaptive evolution of disease alleles. *Immunity.* 2013; 38(6):1129-41. doi: 10.1016/j.immuni.2013.04.008.
 - 70 Cagliani R, **Sironi M**.
Pathogen-driven selection in the human genome. *Int J Evol Biol.* 2013; 2013:204240. doi: 10.1155/2013/204240. Review.
 - 71 Cagliani R, Forni D, Riva S, Pozzoli U, Colleoni M, Bresolin N, Clerici M, **Sironi M**.
Evolutionary analysis of the contact system indicates that kininogen evolved adaptively in mammals and in human populations. *Mol Biol Evol.* 2013; 30(6):1397-408. doi: 10.1093/molbev/mst054.
 - 72 Al-Daghri NM, Clerici M, Al-Attas O, Forni D, Alokail MS, Alkharfy KM, Sabico S, Mohammed AK, Cagliani R, **Sironi M**.
A nonsense polymorphism (R392X) in TLR5 protects from obesity but predisposes to diabetes. *J Immunol.* 2013; 190(7):3716-20. doi: 10.4049/jimmunol.1202936.
 - 73 **Sironi M**, Biasin M, Gnudi F, Cagliani R, Saulle I, Forni D, Rainone V, Trabattoni D, Garziano M, Mazzotta F, Real LM, Rivero-Juarez A, Caruz A, Caputo SL, Clerici M.
A Regulatory Polymorphism in HAVCR2 Modulates Susceptibility to HIV-1 Infection. *PLoS One.* 2014; 9(9):e106442. doi: 10.1371/journal.pone.0106442.
 - 74 **Sironi M**, Cagliani R, Pontremoli C, Rossi M, Migliorino G, Clerici M, Gori A.
The CCR5Δ32 allele is not a major predisposing factor for severe H1N1pdm09 infection. *BMC Res Notes.* 2014; 7:504. doi: 10.1186/1756-0500-7-504.
 - 75 Guerini FR, Agliardi C, **Sironi M**, Arosio B, Calabrese E, Zanzottera M, Bolognesi E, Ricci C, Costa AS, Galimberti D, Griffanti L, Bianchi A, Savazzi F, Mari D, Scarpini E, Baglio F, Nemni R, Clerici M.
Possible Association between SNAP-25 Single Nucleotide Polymorphisms and Alterations of Categorical Fluency and Functional MRI Parameters in Alzheimer's Disease. *J Alzheimers Dis.* 2014; 42(3):1015-28. doi: 10.3233/JAD-140057.

- 76 **Sironi M**, Biasin M, Cagliani R, Gnudi F, Saulle I, Ibba S, Filippi G, Yahyaei S, Tresoldi C, Riva S, Trabattoni D, De Gioia L, Lo Caputo S, Mazzotta F, Forni D, Pontremoli C, Pineda JA, Pozzoli U, Rivero-Juarez A, Caruz A, Clerici M.
Evolutionary Analysis Identifies an MX2 Haplotype Associated with Natural Resistance to HIV-1 Infection. *Mol Biol Evol.* 2014; 31(9):2402-14. doi:10.1093/molbev/msu193.
- 77 Hardwick RJ, Ménard A, **Sironi M**, Milet J, Garcia A, Sese C, Yang F, Fu B, Courtin D, Hollox EJ.
Haptoglobin (HP) and Haptoglobin-related protein (HPR) copy number variation, natural selection, and trypanosomiasis. *Hum Genet.* 2014; 133(1):69-83. doi: 10.1007/s00439-013-1352-x.
- 78 Fumagalli M, **Sironi M**.
Human genome variability, natural selection and infectious diseases. *Curr Opin Immunol.* 2014; 30C:9-16. doi: 10.1016/j.coi.2014.05.001. Review.
- 79 Guerini FR, Clerici M, Cagliani R, Malhotra S, Montalban X, Forni D, Agliardi C, Riva S, Caputo D, Galimberti D, Asselta R, Fenoglio C, Scarpini E, Comi GP, Bresolin N, Comabella M, **Sironi M**.
No association of IFI16 (interferon-inducible protein 16) variants with susceptibility to multiple sclerosis. *J Neuroimmunol.* 2014; 271(1-2):49-52. doi: 10.1016/j.jneuroim.2014.04.006.
- 80 Cagliani R, Forni D, Biasin M, Comabella M, Guerini FR, Riva S, Pozzoli U, Agliardi C, Caputo D, Malhotra S, Montalban X, Bresolin N, Clerici M, **Sironi M**.
Ancient and recent selective pressures shaped genetic diversity at AIM2-like nucleic acid sensors. *Genome Biol Evol.* 2014; 6(4):830-45. doi: 10.1093/gbe/evu066.
- 81 Forni D, Cagliani R, Tresoldi C, Pozzoli U, De Gioia L, Filippi G, Riva S, Menozzi G, Colleoni M, Biasin M, Lo Caputo S, Mazzotta F, Comi GP, Bresolin N, Clerici M, **Sironi M**.
An evolutionary analysis of antigen processing and presentation across different timescales reveals pervasive selection. *PLoS Genet.* 2014; 10(3):e1004189. doi: 10.1371/journal.pgen.1004189.
- 82 Forni D, Cleynen I, Ferrante M, Cassinotti A, Cagliani R, Ardizzone S, Vermeire S, Fichera M, Lombardini M, Maconi G, de Franchis R, Asselta R, Biasin M, Clerici M, **Sironi M**.
ABO histo-blood group might modulate predisposition to Crohn's disease and affect disease behavior. *J Crohns Colitis.* 2014; 8(6):489-94. doi: 10.1016/j.crohns.2013.10.014.
- 83 Cagliani R, Forni D, Tresoldi C, Pozzoli U, Filippi G, Rainone V, De Gioia L, Clerici M, **Sironi M**.
RIG-I-like receptors evolved adaptively in mammals, with parallel evolution at LGP2 and RIG-I. *J Mol Biol.* 2014; 426(6):1351-65. doi: 10.1016/j.jmb.2013.10.040.
- 84 Mozzi A, Forni D, Cagliani R, Pozzoli U, Vertemara J, Bresolin N, **Sironi M**.
Albuminoid genes: evolving at the interface of dispensability and selection. *Genome Biol Evol.* 2014; 6(11):2983-97. doi: 10.1093/gbe/evu235.
- 85 Forni D, Pozzoli U, Cagliani R, Tresoldi C, Menozzi G, Riva S, Guerini FR, Comi GP, Bolognesi E, Bresolin N, Clerici M, **Sironi M**.
Genetic adaptation of the human circadian clock to day-length latitudinal variations and relevance for affective disorders. *Genome Biol.* 2014; 15(10):499. doi: 10.1186/s13059-014-0499-7

- 86 Mozzi A, Pontremoli C, Forni D, Clerici M, Pozzoli U, Bresolin N, Cagliani R, **Sironi M**. OASes and STING: adaptive evolution in concert. *Genome Biol Evol* 2015; 16(4):224-36. doi: 10.1093/gbe/evv046
- 87 Forni D, Mozzi A, Pontremoli C, Vertemara J, Pozzoli U, Biasin M, Bresolin N, Clerici M, Cagliani R, **Sironi M**. Diverse selective regimes shape genetic diversity at ADAR genes and at their coding targets. *RNA Biology* 2015; 12(2):149-61. doi: 10.1080/15476286.2015.1017215
- 88 Polley S, Gomes S, Forni D, **Sironi M**, Balaskas T, Hains D, Yang F, Hollox EJ. Evolution of the rapidly-mutating human salivary agglutinin gene (DMBT1) and population subsistence strategy. *Proc Natl Acad Sci USA* 2015; 112(16):5105-10. doi: 10.1073/pnas.1416531112
- 89 **Sironi M**, Cagliani R, Forni D, Clerici M. Evolutionary insights into host–pathogen interactions from mammalian sequence data. *Nat Rev Genet* 2015; 16(4):224-36. doi: 10.1038/nrg3905. Review.
- 90 Pontremoli C, Mozzi A, Forni D, Cagliani R, Pozzoli U, Menozzi G, Vertemara J, Bresolin N, Clerici M, **Sironi M**. Natural selection at the brush-border: adaptations to carbohydrate diets in humans and other mammals. *Genome Biol Evol.* 2015; 7(9):2569-84. doi: 10.1093/gbe/evv166
- 91 Forni D, Pontremoli C, Cagliani R, Pozzoli U, Clerici M, **Sironi M**. Positive selection underlies the species-specific binding of Plasmodium falciparum RH5 to human basigin. *Mol Ecol.* 2015; 24(18):4711-22. doi: 10.1111/mec.13354
- 92 Diego Forni D, Filippi G, Cagliani R, De Gioia L, Pozzoli U, Al-Daghri N, Clerici M, **Sironi M**. The heptad repeat region is a major selection target in MERS-CoV and related coronaviruses. *Sci Rep,* 2015; 5:14480. doi: 10.1111/mec.13354
- 93 **Sironi M**, Biasin M, Pontremoli C, Cagliani R, Saulle I, Trabattoni D, Vichi F, Lo Caputo S, Mazzotta F, Aguilar-Jimenez W, Rugeles MT, Cedeno S, Sanchez J, Brander C, Clerici M. Variants in the CYP7B1 gene region do not affect natural resistance to HIV-1 infection. *Retrovirology.* 2015; 12(1):80. doi:10.1186/s12977-015-0206-0.
- 94 Forni D, Martin D, Abujaber R, Sharp AJ, **Sironi M**, Hollox EJ. Determining multiallelic complex copy number and sequence variation from high coverage exome sequencing data. *BMC Genomics.* 2015; 16(1):891. doi:10.1186/s12864-015-2123-y.
- 95 Forni D, Cagliani R, Mozzi A, Pozzoli U, Al-Daghri N, Clerici M, **Sironi M**. Extensive positive selection drives the evolution of non-structural proteins in lineage C Betacoronaviruses. *J Virol.* 2016; 90(7):3627-39. doi: 10.1128/JVI.02988-15.
- 96 Mozzi A, Forni D, Clerici M, Pozzoli U, Mascheretti S, Guerini FR, Riva S, Bresolin N, Cagliani R, **Sironi M**. The evolutionary history of genes involved in spoken and written language: beyond FOXP2. *Sci Rep.* 2016 ;6:22157. doi: 10.1038/srep22157.

- 97 Cagliani R, Forni D, Filippi G, Mozzi A, De Gioia L, Pontremoli C, Pozzoli U, Bresolin N, Clerici M, **Sironi M**. The mammalian complement system as an epitome of host-pathogen genetic conflicts. *Mol Ecol*. 2016; 25(6):1324-39. doi: 10.1111/mec.13558.
- 98 Biasin M, **Sironi M**, Saulle I, Pontremoli C, Garziano M, Cagliani R, Trabattoni D, Lo Caputo S, Vichi F, Mazzotta F, Forni D, Riva S, Aguilar-Jimenez W, Cedeño S, Sanchez J, Brander C, Zapata W, Rugeles MT, Clerici M.
A 6-amino acid insertion/deletion polymorphism in the mucin domain of TIM-1 confers protections against HIV-1 infection. *Microbes Infect*. 2016; 19(1):69-74 doi: 10.1016/j.micinf.2016.09.005.
- 99 **Sironi M**, Forni D, Clerici M, Cagliani R.
Nonstructural Proteins Are Preferential Positive Selection Targets in Zika Virus and Related Flaviviruses. *PLoS Negl Trop Dis*. 2016; 10(9):e0004978. doi: 10.1371/journal.pntd.0004978.
- 100 Pontremoli C, Forni D, Cagliani R, Filippi G, De Gioia L, Pozzoli U, Clerici M, **Sironi M**.
Positive Selection Drives Evolution at the Host-Filovirus Interaction Surface. *Mol Biol Evol*. 2016; 33(11):2836-2847. doi: 10.1093/molbev/msw158
- 101 **Sironi M**, Peri AM, Cagliani R, Forni D, Riva S, Biasin M, Clerici M, Gori A.
TLR3 Mutations in Adult Patients With Herpes Simplex Virus and Varicella-Zoster Virus Encephalitis. *J Infect Dis*. 2017; 215(9):1430-1434. doi:10.1093/infdis/jix166.
- 102 Mozzi A, Riva V, Forni D, **Sironi M**, Marino C, Molteni M, Riva S, Guerini FR, Clerici M, Cagliani R, Mascheretti S.
A common genetic variant in FOXP2 is associated with language-based learning (dis)abilities: Evidence from two Italian independent samples. *Am J Med Genet B Neuropsychiatr Genet*. 2017; 174(5):578-586 doi: 10.1002/ajmg.b.32546.
- 103 Al-Daghri NM, Pontremoli C, Cagliani R, Forni D, Alokail MS, Al-Attas OS, Sabico S, Riva S, Clerici M, **Sironi M**.
Susceptibility to type 2 diabetes may be modulated by haplotypes in G6PC2, a target of positive selection. *BMC Evol Biol*. 2017; 17(1):43. doi: 10.1186/s12862-017-0897-z.
- 104 Biasin M, **Sironi M**, Saulle I, Pontremoli C, Garziano M, Cagliani R, Trabattoni D, Lo Caputo S, Vichi F, Mazzotta F, Forni D, Riva S, Aguilar-Jimenez W, Cedeño S, Sanchez J, Brander C, Zapata W, Rugeles MT, Clerici M.
A 6-amino acid insertion/deletion polymorphism in the mucin domain of TIM-1 confers protections against HIV-1 infection. *Microbes Infect*. 2017; 19(1):69-74. doi: 10.1016/j.micinf.2016.09.005.
- 105 Forni D, Cagliani R, Clerici M, **Sironi M**.
Molecular Evolution of Human Coronavirus Genomes. *Trends Microbiol*. 2017; 25(1):35-48. doi: 10.1016/j.tim.2016.09.001. Review.
- 106 Pontremoli C, Forni D, Cagliani R, Pozzoli U, Riva S, Bravo IG, Clerici M, **Sironi M**.
Evolutionary analysis of Old World arenaviruses reveals a major adaptive contribution of the viral polymerase. *Mol Ecol*. 2017; 26(19):5173-5188. doi: 10.1111/mec.14282.
- 107 Mozzi A, Forni D, Cagliani R, Pozzoli U, Clerici M, **Sironi M**.
Distinct selective forces and Neanderthal introgression shaped genetic diversity at genes involved in

- neurodevelopmental disorders. *Sci Rep.* 2017; 7(1):6116. doi:10.1038/s41598-017-06440-4.
- 108 Mozzi A, Guerini FR, Forni D, Costa AS, Nemni R, Baglio F, Cabinio M, Riva S, Pontremoli C, Clerici M, **Sironi M**, Cagliani R.
REST, a master regulator of neurogenesis, evolved under strong positive selection in humans and in non human primates. *Sci Rep.* 2017; 7(1):9530. doi: 10.1038/s41598-017-10245-w.
- 109 Mozzi A, Pontremoli C, **Sironi M**.
Genetic susceptibility to infectious diseases: Current status and future perspectives from genome-wide approaches. *Infect Genet Evol.* 2018; 66:286-307. doi:10.1016/j.meegid.2017.09.028. Review.
- 110 Forni D, Pontremoli C, Pozzoli U, Clerici M, Cagliani R, **Sironi M**.
Ancient Evolution of Mammarenaviruses: Adaptation via Changes in the L Protein and No Evidence for Host-Virus Codivergence. *Genome Biol Evol.* 2018; 10(3):863-874. doi: 10.1093/gbe/evy050.
- 111 Forni D, Cagliani R, Clerici M, **Sironi M**.
Origin and dispersal of Hepatitis E virus. *Emerg Microbes Infect.* 2018; 7(1):11. doi: 10.1038/s41426-017-0009-6.
- 112 Forni D, Cagliani R, Pontremoli C, Pozzoli U, Vertemara J, De Gioia L, Clerici M, **Sironi M**.
Evolutionary Analysis Provides Insight Into the Origin and Adaptation of HCV. *Front Microbiol.* 2018; 9:854. doi: 10.3389/fmicb.2018.00854.
- 113 Forni D, Pontremoli C, Cagliani R, Pozzoli U, Clerici M, **Sironi M**.
Multiple Selected Changes May Modulate the Molecular Interaction between Laverania RH5 and Primate Basigin. *MBio.* 2018; 9(3):e00476-18. doi:10.1128/mBio.00476-18.
- 114 Riva V, Mozzi A, Forni D, Trezzi V, Giorda R, Riva S, Villa M, **Sironi M**, Cagliani R, Mascheretti S.
The influence of DCDC2 risk genetic variants on reading: Testing main and haplotypic effects. *Neuropsychologia.* 2018; 130:52-58. doi: 10.1016/j.neuropsychologia.2018.05.021.
- 115 Pontremoli C, Forni D, Cagliani R, **Sironi M**.
Analysis of Reptarenavirus genomes indicates different selective forces acting on the S and L segments and recent expansion of common genotypes. *Infect Genet Evol.* 2018; 64:212-218. doi: 10.1016/j.meegid.2018.06.031.
- 116 Pontremoli C, Forni D, Cagliani R, Pozzoli U, Clerici M, **Sironi M**.
Evolutionary rates of mammalian telomere-stability genes correlate with karyotype features and female germline expression. *Nucleic Acids Res.* 2018; 46(14):7153-7168. doi: 10.1093/nar/gky494.
- 117 Pautasso S, Galitska G, Dell'Oste V, Biolatti M, Cagliani R, Forni D, De Andrea M, Gariglio M, **Sironi M**, Landolfo S.
Strategy of Human Cytomegalovirus To Escape Interferon Beta-Induced APOBEC3G Editing Activity. *J Virol.* 2018; 92(19):e01224-18. doi: 10.1128/JVI.01224-18.
- 118 **Sironi M**, Forni D, Clerici M, Cagliani R.
Genetic conflicts with Plasmodium parasites and functional constraints shape the evolution of erythrocyte cytoskeletal proteins. *Sci Rep.* 2018; 8(1):14682. doi:10.1038/s41598-018-33049-y.
- 119 Mozzi A, Forni D, Clerici M, Cagliani R, **Sironi M**.
The Diversity of Mammalian Hemoproteins and Microbial Heme Scavengers Is Shaped by an Arms Race

for Iron Piracy. *Front Immunol.* 2018; 9:2086. doi: 10.3389/fimmu.2018.02086.

- 120 Pontremoli C, Forni D, **Sironi M**.
Arenavirus genomics: novel insights into viral diversity, origin, and evolution. *Curr Opin Virol.* 2018; 34:18-28. doi: 10.1016/j.coviro.2018.11.001. Review.
- 121 Maes P, Adkins S, Alkhovsky SV, Avšič-Županc T, Ballinger MJ, Bente DA, Beer M, Bergeron É, Blair CD, Briese T, Buchmeier MJ, Burt FJ, Calisher CH, Charrel RN, Choi IR, Clegg JCS, de la Torre JC, de Lamballerie X, DeRisi JL, Digiaro M, Drebot M, Ebihara H, Elbeaino T, Ergünay K, Fulhorst CF, Garrison AR, Gão GF, Gonzalez JJ, Groschup MH, Günther S, Haenni AL, Hall RA, Hewson R, Hughes HR, Jain RK, Jonson MG, Junglen S, Klempa B, Klingström J, Kormelink R, Lambert AJ, Langevin SA, Lukashevich IS, Marklewitz M, Martelli GP, Mielke-Ehret N, Mirazimi A, Mühlbach HP, Naidu R, Nunes MRT, Palacios G, Papa A, Pawęska JT, Peters CJ, Plyusnin A, Radoshitzky SR, Resende RO, Romanowski V, Sall AA, Salvato MS, Sasaya T, Schmaljohn C, Shí X, Shirako Y, Simmonds P, **Sironi M**, Song JW, Spengler JR, Stenglein MD, Tesh RB, Turina M, Wèi T, Whitfield AE, Yeh SD, Zerbini FM, Zhang YZ, Zhou X, Kuhn JH.
Taxonomy of the order Bunyavirales: second update 2018. *Arch Virol.* 2019; 164(3):927-941. doi: 10.1007/s00705-018-04127-3
- 122 Abudurexiti A, Adkins S, Alioto D, Alkhovsky SV, Avšič-Županc T, Ballinger MJ, Bente DA, Beer M, Bergeron É, Blair CD, Briese T, Buchmeier MJ, Burt FJ, Calisher CH, Cháng C, Charrel RN, Choi IR, Clegg JCS, de la Torre JC, de Lamballerie X, Dèng F, Di Serio F, Digiaro M, Drebot MA, Duàn X, Ebihara H, Elbeaino T, Ergünay K, Fulhorst CF, Garrison AR, Gão GF, Gonzalez JJ, Groschup MH, Günther S, Haenni AL, Hall RA, Hepojoki J, Hewson R, Hú Z, Hughes HR, Jonson MG, Junglen S, Klempa B, Klingström J, Kòu C, Laenen L, Lambert AJ, Langevin SA, Liu D, Lukashevich IS, Luò T, Lǚ C, Maes P, de Souza WM, Marklewitz M, Martelli GP, Matsuno K, Mielke-Ehret N, Minutolo M, Mirazimi A, Moming A, Mühlbach HP, Naidu R, Navarro B, Nunes MRT, Palacios G, Papa A, Pauvolid-Corrêa A, Pawęska JT, Qiáo J, Radoshitzky SR, Resende RO, Romanowski V, Sall AA, Salvato MS, Sasaya T, Shěn S, Shí X, Shirako Y, Simmonds P, **Sironi M**, Song JW, Spengler JR, Stenglein MD, Sū Z, Sūn S, Táng S, Turina M, Wáng B, Wáng C, Wáng H, Wáng J, Wèi T, Whitfield AE, Zerbini FM, Zhāng J, Zhāng L, Zhāng Y, Zhang YZ, Zhāng Y, Zhou X, Zhū L, Kuhn JH.
Taxonomy of the order Bunyavirales: update 2019. *Arch Virol.* 2019. ;164(7):1949-1965. doi: 10.1007/s00705-019-04253-6.
- 123 Pontremoli C, Forni D, Clerici M, Cagliani R, **Sironi M**.
Possible European origin of circulating Varicella-zoster virus strains. *J Infect Dis.* 2019; 221:1286-1294. doi: 10.1093/infdis/jiz227.
- 124 Bandera A, Gori A, Clerici M, **Sironi M**.
Phylogenies in ART: HIV reservoirs, HIV latency and drug resistance. *Curr Opin Pharmacol.* 2019; 48:24-32. doi: 10.1016/j.coph.2019.03.003. Review.
- 125 Radoshitzky SR, Buchmeier MJ, Charrel RN, Clegg JCS, Gonzalez JJ, Günther S, Hepojoki J, Kuhn JH, Lukashevich IS, Romanowski V, Salvato MS, **Sironi M**, Stenglein MD, de la Torre JC.
ICTV Report Consortium. ICTV Virus Taxonomy Profile: Arenaviridae. *J Gen Virol.* 2019; 100(8):1200-1201. doi: 10.1099/jgv.0.001280.
- 126 Forni D, Cagliani R, Clerici M, Pozzoli U, **Sironi M**.
You will never walk alone: co-dispersal of JC polyomavirus with human populations. *Mol Biol Evol.* 2019; 37(2):442-454. doi: 10.1093/molbev/msz227.
- 127 Cagliani R, Forni D, **Sironi M**.
Mode and tempo of human hepatitis virus evolution. *Comput Struct Biotechnol J.* 2019; 17:1384-1395.

doi: 10.1016/j.csbj.2019.09.007. Review.

- 128 **Sironi M**, de la Torre JC.
The chameleonic genetics of Lassa virus. *Lancet Infect Dis.* 2019, 19(12):1276-1277. doi:10.1016/S1473-3099(19)30528-6. Comment.
- 129 Forni D, Pontremoli C, Clerici M, Pozzoli U, Cagliani R, **Sironi M**.
Recent out-of-Africa migration of human herpes simplex viruses. *Mol Biol Evol.* 2020; 37(5):1259-1271. doi: 10.1093/molbev/msaa001.
- 130 Mozzi A, Biolatti M, Cagliani R, Forni D, Dell'Oste V, Pontremoli C, Vantaggiato C, Pozzoli U, Clerici M, Landolfo S, **Sironi M**.
Past and ongoing adaptation of human cytomegalovirus to its host. *PLoS Pathog.* 2020; 16(5):e1008476. doi: 10.1371/journal.ppat.1008476.
- 131 Forni D, Cagliani R, Clerici M, Pozzoli U, **Sironi M**.
Evolutionary analysis of exogenous and integrated HHV-6A/HHV-6B populations. *Virus Evol.* 2020; 6(1):veaa035. doi: 10.1093/ve/veaa035.
- 132 **Sironi M**, Hasnain SE, Rosenthal B, Phan T, Luciani F, Shaw MA, Sallum MA, Mirhashemi ME, Morand S, González-Candelas F.
SARS-CoV-2 and COVID-19: A genetic, epidemiological, and evolutionary perspective. *Infect Genet Evol.* 2020; 84:104384. doi: 10.1016/j.meegid.2020.104384. Review.
- 133 Mozzi A, Forni D, Cagliani R, Clerici M, Pozzoli U, **Sironi M**.
Intrinsically disordered regions are abundant in simplevirus proteomes and display signatures of positive selection. *Virus Evol.* 2020; 6(1):veaa028. Doi: 10.1093/ve/veaa028.
- 134 Cagliani R, Forni D, Clerici M, **Sironi M**.
Coding potential and sequence conservation of SARS-CoV-2 and related animal viruses. *Infect Genet Evol.* 2020; 83:104353. doi: 10.1016/j.meegid.2020.104353.
- 135 Cagliani R, Forni D, Mozzi A, **Sironi M**.
Evolution and Genetic Diversity of Primate Cytomegaloviruses. *Microorganisms.* 2020; 8(5):624. doi: 10.3390/microorganisms8050624.
- 136 Forni D, **Sironi M**.
Population structure of Lassa Mammarenavirus in West Africa. *Viruses.* 2020; 12(4):437. doi: 10.3390/v12040437.
- 137 Kuhn JH, Adkins S, Alioto D, Alkhovsky SV, Amarasinghe GK, Anthony SJ, Avšič-Županc T, Ayllón MA, Bahl J, Balkema-Buschmann A, Ballinger MJ, Bartonička T, Basler C, Bavari S, Beer M, Bente DA, Bergeron É, Bird BH, Blair C, Blasdel KR, Bradfute SB, Breyta R, Briese T, Brown PA, Buchholz UJ, Buchmeier MJ, Bukreyev A, Burt F, Buzkan N, Calisher CH, Cao M, Casas I, Chamberlain J, Chandran K, Charrel RN, Chen B, Chiumenti M, Choi IR, Clegg JCS, Crozier I, da Graça JV, Dal Bó E, Dávila AMR, de la Torre JC, de Lamballerie X, de Swart RL, Di Bello PL, Di Paola N, Di Serio F, Dietzgen RG, Digiaro M, Dolja VV, Dolnik O, Drebot MA, Drexler JF, Dürwald R, Dufkova L, Dundon WG, Duprex WP, Dye JM, Easton AJ, Ebihara H, Elbeaino T, Ergünay K, Fernandes J, Fooks AR, Formenty PBH, Forth LF, Fouchier RAM, Freitas-Astúa J, Gago-Zachert S, Gão GF, García ML, García-Sastre A, Garrison AR, Gbakima A, Goldstein T, Gonzalez JJ, Griffiths A, Groschup MH, Günther S, Guterres A, Hall RA, Hammond J, Hassan M,

Hepojoki J, Hepojoki S, Hetzel U, Hewson R, Hoffmann B, Hongo S, Höper D, Horie M, Hughes HR, Hyndman TH, Jambai A, Jardim R, Jiāng D, Jin Q, Jonson GB, Junglen S, Karadağ S, Keller KE, Klempa B, Klingström J, Kobinger G, Kondō H, Koonin EV, Krupovic M, Kurath G, Kuzmin IV, Laenen L, Lamb RA, Lambert AJ, Langevin SL, Lee B, Lemos ERS, Leroy EM, Li D, Lǐ J, Liang M, Liú W, Liú Y, Lukashevich IS, Maes P, Marciel de Souza W, Marklewitz M, Marshall SH, Martelli GP, Martin RR, Marzano SL, Massart S, McCauley JW, Mielke-Ehret N, Minafra A, Minutolo M, Mirazimi A, Mühlbach HP, Mühlberger E, Naidu R, Natsuaki T, Navarro B, Navarro JA, Netesov SV, Neumann G, Nowotny N, Nunes MRT, Nylund A, Økland AL, Oliveira RC, Palacios G, Pallas V, Pályi B, Papa A, Parrish CR, Pauvolid-Corrêa A, Pawęska JT, Payne S, Pérez DR, Pfaff F, Radoshitzky SR, Rahman AU, Ramos-González PL, Resende RO, Reyes CA, Rima BK, Romanowski V, Robles Luna G, Rota P, Rubbenstroth D, Runstadler JA, Ruzek D, Sabanadzovic S, Salát J, Sall AA, Salvato MS, Sarpkaya K, Sasaya T, Schwemmle M, Shabbir MZ, Shí X, Shí Z, Shirako Y, Simmonds P, Širmarová J, **Sironi M**, Smither S, Smura T, Song JW, Spann KM, Spengler JR, Stenglein MD, Stone DM, Straková P, Takada A, Tesh RB, Thornburg NJ, Tomonaga K, Tordo N, Towner JS, Turina M, Tzanetakis I, Ulrich RG, Vaira AM, van den Hoogen B, Varsani A, Vasilakis N, Verbeek M, Wahl V, Walker PJ, Wang H, Wang J, Wang X, Wang LF, Wèi T, Wells H, Whitfield AE, Williams JV, Wolf YI, Wú Z, Yang X, Yáng X, Yu X, Yutin N, Zerbini FM, Zhang T, Zhang YZ, Zhou G, Zhou X.

2020 taxonomic update for phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. Arch Virol. 2020; 165(12):3023-3072. doi: 10.1007/s00705-020-04731-2.

- 138 Cagliani R, Forni D, Clerici M, **Sironi M**.
Computational Inference of Selection Underlying the Evolution of the Novel Coronavirus, Severe Acute Respiratory Syndrome Coronavirus 2. J Virol. 2020; 94(12):e00411-20. doi: 10.1128/JVI.00411-20.
- 139 Forni D, Cagliani R, Pontremoli C, Mozzi A, Pozzoli U, Clerici M, **Sironi M**.
Antigenic variation of SARS-CoV-2 in response to immune pressure. Mol Ecol. 2020; 2:10.1111/mec.15730. doi: 10.1111/mec.15730.
- 140 Pontremoli C, Forni D, Pozzoli U, Clerici M, Cagliani R, **Sironi M**.
Kinetochore proteins and microtubule-destabilizing factors are fast evolving in eutherian mammals. Mol Ecol. 2021; 30(6):1505-1515. doi: 10.1111/mec.15812.
- 141 Forni D, Cagliani R, **Sironi M**.
Recombination and Positive Selection Differentially Shaped the Diversity of Betacoronavirus Subgenera. Viruses. 2020; 12(11):1313. doi: 10.3390/v12111313.
- 142 Galitska G, Coscia A, Forni D, Steinbrueck L, De Meo S, Biolatti M, De Andrea M, Cagliani R, Leone A, Bertino E, Schulz T, Santoni A, Landolfo S, **Sironi M**, Cerboni C, Dell'Oste V.
Genetic Variability of Human Cytomegalovirus Clinical Isolates Correlates With Altered Expression of Natural Killer Cell-Activating Ligands and IFN-γ. Front Immunol. 2021; 12:532484. doi: 10.3389/fimmu.2021.532484.
- 143 González-Candelas F, Shaw MA, Phan T, Kulkarni-Kale U, Paraskevis D, Luciani F, Kimura H, **Sironi M**.
One year into the pandemic: Short-term evolution of SARS-CoV-2 and emergence of new lineages. Infect Genet Evol. 2021; 92:104869. doi: 10.1016/j.meegid.2021.104869. Review.
- 144 Pontremoli C, Forni D, Clerici M, Cagliani R, **Sironi M**.
Alternation between taxonomically divergent hosts is not the major determinant of flavivirus evolution. Virus Evol. 2021; 7(1):veab040. doi: 10.1093/ve/veab040.

- 145 Kuhn JH, Adkins S, Agwanda BR, Al Kubrusli R, Alkhovsky SV, Amarasinghe GK, Avšič-Županc T, Ayllón MA, Bahl J, Balkema-Buschmann A, Ballinger MJ, Basler CF, Bavari S, Beer M, Bejerman N, Bennett AJ, Bente DA, Bergeron É, Bird BH, Blair CD, Blasdel KR, Blystad DR, Bojko J, Borth WB, Bradfute S, Breyta R, Briese T, Brown PA, Brown JK, Buchholz UJ, Buchmeier MJ, Bukreyev A, Burt F, Büttner C, Calisher CH, Cao M, Casas I, Chandran K, Charrel RN, Cheng Q, Chiaki Y, Chiapello M, Choi IR, Ciuffo M, Clegg JCS, Crozier I, Dal Bó E, de la Torre JC, de Lamballerie X, de Swart RL, Debat H, Dheilly NM, Di Cicco E, Di Paola N, Di Serio F, Dietzgen RG, Digiaro M, Dolnik O, Drebot MA, Drexler JF, Dundon WG, Duprex WP, Dürwald R, Dye JM, Easton AJ, Ebihara H, Elbeaino T, Ergünay K, Ferguson HW, Fooks AR, Forgia M, Formenty PBH, Fránová J, Freitas-Astúa J, Fu J, Fül S, Gago-Zachert S, Gão GF, García ML, García-Sastre A, Garrison AR, Gaskin T, Gonzalez JJ, Griffiths A, Goldberg TL, Groschup MH, Günther S, Hall RA, Hammond J, Han T, Hepojoki J, Hewson R, Hong J, Hong N, Hongo S, Horie M, Hu JS, Hu T, Hughes HR, Hüttner F, Hyndman TH, Ilyas M, Jalkanen R, Jiāng D, Jonson GB, Junglen S, Kadono F, Kaukinen KH, Kawate M, Klempa B, Klingström J, Kobinger G, Koloniuk I, Kondō H, Koonin EV, Krupovic M, Kubota K, Kurath G, Laenen L, Lambert AJ, Langevin SL, Lee B, Lefkowitz EJ, Leroy EM, Li S, Li L, Lǐ J, Liu H, Lukashevich IS, Maes P, de Souza WM, Marklewitz M, Marshall SH, Marzano SL, Massart S, McCauley JW, Melzer M, Mielke-Ehret N, Miller KM, Ming TJ, Mirazimi A, Mordecai GJ, Mühlbach HP, Mühlberger E, Naidu R, Natsuaki T, Navarro JA, Netesov SV, Neumann G, Nowotny N, Nunes MRT, Olmedo-Velarde A, Palacios G, Pallás V, Pályi B, Papa A, Paraskevopoulou S, Park AC, Parrish CR, Patterson DA, Pauvolid-Corrêa A, Pawęska JT, Payne S, Peracchio C, Pérez DR, Postler TS, Qi L, Radoshitzky SR, Resende RO, Reyes CA, Rima BK, Luna GR, Romanowski V, Rota P, Rubbenstroth D, Rubino L, Runstadler JA, Sabanadzovic S, Sall AA, Salvato MS, Sang R, Sasaya T, Schulze AD, Schwemmle M, Shi M, Shí X, Shí Z, Shimamoto Y, Shirako Y, Siddell SG, Simmonds P, **Sironi M**, Smagghe G, Smither S, Song JW, Spann K, Spengler JR, Stenglein MD, Stone DM, Sugano J, Suttle CA, Tabata A, Takada A, Takeuchi S, Tchouassi DP, Teffer A, Tesh RB, Thornburg NJ, Tomitaka Y, Tomonaga K, Tordo N, Torto B, Towner JS, Tsuda S, Tu C, Turina M, Tzanetakis IE, Uchida J, Usugi T, Vaira AM, Vallino M, van den Hoogen B, Varsani A, Vasilakis N, Verbeek M, von Bargen S, Wada J, Wahl V, Walker PJ, Wang LF, Wang G, Wang Y, Wang Y, Waqas M, Wèi T, Wen S, Whitfield AE, Williams JV, Wolf YI, Wu J, Xu L, Yanagisawa H, Yang C, Yang Z, Zerbini FM, Zhai L, Zhang YZ, Zhang S, Zhang J, Zhang Z, Zhou X.

2021 Taxonomic update of phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. Arch Virol. 2021; 166(12):3513-3566. doi: 10.1007/s00705-021-05143-6.

- 146 Forni D, Cagliani R, Pontremoli C, Clerici M, **Sironi M**.

The substitution spectra of coronavirus genomes. Brief Bioinform. 2021; 23(1):bbab382. doi: 10.1093/bib/bbab382.

- 147 Forni D, Cagliani R, Arrigoni F, Benvenuti M, Mozzi A, Pozzoli U, Clerici M, De Gioia L, **Sironi M**.

Adaptation of the endemic coronaviruses HCoV-OC43 and HCoV-229E to the human host. Virus Evol. 2021 ;7(2):veab061. doi: 10.1093/ve/veab061.

- 148 Barizzone N, Cagliani R, Basagni C, Clarelli F, Mendozzi L, Agliardi C, Forni D, Tosi M, Mascia E, Favero F, Corà D, Corrado L, Sorosina M, Esposito F, Zuccalà M, Vecchio D, Liguori M, Comi C, Comi G, Martinelli V, Filippi M, Leone M, Martinelli-Boneschi F, Caputo D, **Sironi M**, Guerini FR, D'Alfonso S.

An Investigation of the Role of Common and Rare Variants in a Large Italian Multiplex Family of Multiple Sclerosis Patients. Genes (Basel). 2021; 12(10):1607. doi: 10.3390/genes12101607.

- 149 Molteni C, Forni D, Cagliani R, Clerici M, **Sironi M**.

Genetic ancestry and population structure of vaccinia virus. NPJ Vaccines. 2022; 7(1):92. doi: 10.1038/s41541-022-00519-4.

- 150 Forni D, Cagliani R, Clerici M, **Sironi M**.
Disease-causing human viruses: novelty and legacy. *Trends Microbiol.* 2022; 30(12):1232-1242. doi: 10.1016/j.tim.2022.07.002. Review.
- 151 Forni D, Molteni C, Cagliani R, **Sironi M**.
Geographic structuring and divergence time frame of monkeypox virus in the endemic region. *J Infect Dis.* 2022; 227(6):742-751. doi: 10.1093/infdis/jiac298.
- 152 Mozzi A, Cagliani R, Pontremoli C, Forni D, Saulle I, Saresella M, Pozzoli U, Cappelletti G, Vantaggiato C, Clerici M, Biasin M, **Sironi M**.
Simplexviruses Successfully Adapt to Their Host by Fine-Tuning Immune Responses. *Mol Biol Evol.* 2022; 39(7):msac142. doi: 10.1093/molbev/msac142.
- 153 Forni D, Cagliani R, Pozzoli U, Mozzi A, Arrigoni F, De Gioia L, Clerici M, **Sironi M**.
Dating the Emergence of Human Endemic Coronaviruses. *Viruses.* 2022; 14(5):1095. doi: 10.3390/v14051095.
- 154 Forni D, Cagliani R, Molteni C, Arrigoni F, Mozzi A, Clerici M, De Gioia L, **Sironi M**.
Homology-based classification of accessory proteins in coronavirus genomes uncovers extremely dynamic evolution of gene content. *Mol Ecol.* 2022; 31(13):3672-3692. doi: 10.1111/mec.16531.
- 155 Forni D, **Sironi M**, Cagliani R.
Evolutionary history of type II transmembrane serine proteases involved in viral priming. *Hum Genet.* 2022; 5:1-18. doi: 10.1007/s00439-022-02435-y.
- 156 **Sironi M**, Cagliani R, Biasin M, Lo Caputo S, Saulle I, Forni D, Real LM, Pineda JA, Exposito A, Saez ME, Sinangil F, Forthal D, Caruz A, Clerici M.
No association of a risk variant for severe COVID-19 with HIV protection in three cohorts of highly exposed individuals. *PNAS Nexus*, 2022, pgac138. doi: 10.1093/pnasnexus/pgac138.
- 157 Molteni C, Forni D, Cagliani R, Mozzi A, Clerici M, **Sironi M**.
Evolution of the orthopoxvirus core genome. *Virus Res.* 2022 Oct 21;323:198975. doi: 10.1016/j.virusres.2022.198975.
- 158 Forni D, Cagliani R, Molteni C, Clerici M, **Sironi M**.
Monkeypox virus: The changing facets of a zoonotic pathogen. *Infect Genet Evol.* 2022 Oct 4;105:105372. doi: 10.1016/j.meegid.2022.105372. Review.
- 159 Forni D, Molteni C, Cagliani R, Clerici M, **Sironi M**.
Analysis of variola virus molecular evolution suggests an old origin of the virus consistent with historical records, *Microb Genom.* 2023 Jan;9(1):mgen000932. doi: 10.1099/mgen.0.000932
- 160 Kuhn JH, Adkins S, Alkhovsky SV, Avšič-Županc T, Ayllón MA, Bahl J, Balkema-Buschmann A, Ballinger MJ, Bandte M, Beer M, Bejerman N, Bergeron É, Biedenkopf N, Bigarré L, Blair CD, Blasdel KR, Bradfute SB, Briesse T, Brown PA, Bruggmann R, Buchholz UJ, Buchmeier MJ, Bukreyev A, Burt F, Büttner C, Calisher CH, Candresse T, Carson J, Casas I, Chandran K, Charrel RN, Chiaki Y, Crane A, Crane M, Dacheux L, Bó ED, de la Torre JC, de Lamballerie X, de Souza WM, de Swart RL, Dheilly NM, Di Paola N, Di Serio F, Dietzgen RG, Digiario M, Drexler JF, Duprex WP, Dürrwald R, Easton AJ, Elbeaino T, Ergünay K, Feng G, Feuvrier C, Firth AE, Fooks AR, Formenty PBH, Freitas-Astúa J, Gago-Zachert S, García ML, García-Sastre A, Garrison AR, Godwin SE, Gonzalez JJ, de Bellocq JG, Griffiths A, Groschup MH, Günther S, Hammond

J, Hepojoki J, Hierweger MM, Hongō S, Horie M, Horikawa H, Hughes HR, Hume AJ, Hyndman TH, Jiāng D, Jonson GB, Junglen S, Kadono F, Karlin DG, Klempa B, Klingström J, Koch MC, Kondō H, Koonin EV, Krásová J, Krupovic M, Kubota K, Kuzmin IV, Laenen L, Lambert AJ, Lǐ J, Li JM, Lieffrig F, Lukashevich IS, Luo D, Maes P, Marklewitz M, Marshall SH, Marzano SL, McCauley JW, Mirazimi A, Mohr PG, Moody NJG, Morita Y, Morrison RN, Mühlberger E, Naidu R, Natsuaki T, Navarro JA, Neriya Y, Netesov SV, Neumann G, Nowotny N, Ochoa-Corona FM, Palacios G, Pallandre L, Pallás V, Papa A, Paraskevopoulou S, Parrish CR, Pauvolid-Corrêa A, Pawęska JT, Pérez DR, Pfaff F, Plemper RK, Postler TS, Pozet F, Radoshitzky SR, Ramos-González PL, Rehanek M, Resende RO, Reyes CA, Romanowski V, Rubbenstroth D, Rubino L, Rumbou A, Runstadler JA, Rupp M, Sabanadzovic S, Sasaya T, Schmidt-Posthaus H, Schwemmle M, Seuberlich T, Sharpe SR, Shi M, **Sironi M**, Smither S, Song JW, Spann KM, Spengler JR, Stenglein MD, Takada A, Tesh RB, Těšíková J, Thornburg NJ, Tischler ND, Tomitaka Y, Tomonaga K, Tordo N, Tsunekawa K, Turina M, Tzanetakis IE, Vaira AM, van den Hoogen B, Vanmechelen B, Vasilakis N, Verbeek M, von Bargen S, Wada J, Wahl V, Walker PJ, Whitfield AE, Williams JV, Wolf YI, Yamasaki J, Yanagisawa H, Ye G, Zhang YZ, Økland AL.

2022 taxonomic update of phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. *Arch Virol.* 2022; 167(12):2857-2906. doi: 10.1007/s00705-022-05546-z.

- 161 Moltrasio C, Cagliani R, **Sironi M**, Clerici M, Pontremoli C, Maronese CA, Tricarico PM, Crovella S, Marzano AV.
Autoinflammation in Syndromic Hidradenitis Suppurativa: The Role of AIM2. *Vaccines (Basel).* 2023; 11(1):162. doi: 10.3390/vaccines11010162.
- 162 Forni D, Moltrasio C, **Sironi M**, Mozzi A, Quattri E, Venegoni L, Zamprogno M, Citterio A, Clerici M, Marzano AV, Cagliani R.
Whole-Genome Sequencing of hMPXV1 in five Italian cases confirms the occurrence of the predominant epidemic lineage. *J Med Virol.* 2023; 95(2):e28493. doi: 10.1002/jmv.28493.
- 163 Forni D, Cagliani R, Pozzoli U, **Sironi M**.
An APOBEC3 Mutational Signature in the Genomes of Human-Infecting Orthopoxviruses. *MSphere.* 2023; 8(2):e0006223. doi: 10.1128/msphere.00062-23.
- 164 Mozzi A, Oldani M, Forcella ME, Vantaggiato C, Cappelletti G, Pontremoli C, Valenti F, Forni D, Saresella M, Biasin M, **Sironi M**, Fusi P, Cagliani R.
SARS-CoV-2 ORF3c impairs mitochondrial respiratory metabolism, oxidative stress, and autophagic flux. *IScience.* 2023; 26(7):107118. doi: 0.1016/j.isci.2023.107118.
- 165 Molteni C, Forni D, Cagliani R, Arrigoni F, Pozzoli U, De Gioia L, **Sironi M**.
Selective events at individual sites underlie the evolution of monkeypox virus clades. *Virus Evol.* 2023; 9(1):vead031. doi: 10.1093/ve/vead031. eCollection 2023
- 166 Moltrasio C, Boggio FL, Romagnuolo M, Cagliani R, **Sironi M**, Di Benedetto A, Marzano AV, Biagio EL, Vergani B.
Monkeypox: A Histopathological and Transmission Electron Microscopy Study. *Microorganisms.* 2023; 11(7):1781. doi: 10.3390/microorganisms11071781
- 167 Radoshitzky SR, Buchmeier MJ, Charrel RN, Gonzalez JJ, Günther S, Hepojoki J, Kuhn JH, Lukashevich IS, Romanowski V, Salvato MS, **Sironi M**, Stenglein MD, Torre JC.
ICTV Virus Taxonomy Profile: Arenaviridae 2023. *J Gen Virol.* 2023; 104(9). doi: 10.1099/jgv.0.001891.

- 168 Kuhn JH, Abe J, Adkins S, Alkhovsky SV, Avšič-Županc T, Ayllón MA, Bahl J, Balkema-Buschmann A, Ballinger MJ, Kumar Baranwal V, Beer M, Bejerman N, Bergeron É, Biedenkopf N, Blair CD, Blasdel KR, Blouin AG, Bradfute SB, Briesse T, Brown PA, Buchholz UJ, Buchmeier MJ, Bukreyev A, Burt F, Büttner C, Calisher CH, Cao M, Casas I, Chandran K, Charrel RN, Kumar Chaturvedi K, Chooi KM, Crane A, Dal Bó E, Carlos de la Torre J, de Souza WM, de Swart RL, Debat H, Dheilly NM, Di Paola N, Di Serio F, Dietzgen RG, Digiaro M, Drexler JF, Duprex WP, Dürrwald R, Easton AJ, Elbeaino T, Ergünay K, Feng G, Firth AE, Fooks AR, Formenty PBH, Freitas-Astúa J, Gago-Zachert S, Laura García M, García-Sastre A, Garrison AR, Gaskin TR, Gong W, Gonzalez JJ, de Bellocq J, Griffiths A, Groschup MH, Günther I, Günther S, Hammond J, Hasegawa Y, Hayashi K, Hepojoki J, Higgins CM, Hongō S, Horie M, Hughes HR, Hume AJ, Hyndman TH, Ikeda K, Jiāng D, Jonson GB, Junglen S, Klempa B, Klingström J, Kondō H, Koonin EV, Krupovic M, Kubota K, Kurath G, Laenen L, Lambert AJ, Li J, Li JM, Liu R, Lukashevich IS, MacDiarmid RM, Maes P, Marklewitz M, Marshall SH, Marzano SL, McCauley JW, Mirazimi A, Mühlberger E, Nabeshima T, et al. Annual (2023) taxonomic update of RNA-directed RNA polymerase-encoding negative-sense RNA viruses (realm Riboviria: kingdom Orthornavirae: phylum Negarnaviricota). *J Gen Virol.* 2023; 104(8). doi: 10.1099/jgv.0.001864.
- 169 Molteni C, Forni D, Cagliani R, Bravo IG, **Sironi M**. Evolution and diversity of nucleotide and dinucleotide composition in poxviruses. *J Gen Virol.* 2023; 104(10). doi: 10.1099/jgv.0.001897
- 170 Forni D, Pozzoli U, Cagliani R, Clerici M, **Sironi M**. Dinucleotide biases in RNA viruses that infect vertebrates or invertebrates. *Microbiol Spectr.* 2023; 11(6):e0252923. doi: 10.1128/spectrum.02529-23
- 171 Bonaglia MC, Salvo E, **Sironi M**, Bertuzzo S, Errichiello E, Mattina T, Zuffardi O. Case Report: Decrypting an interchromosomal insertion associated with Marfan's syndrome: how optical genome mapping emphasizes the morbid burden of copy-neutral variants. *Front Genet.* 2023; 14:1244983. doi: 10.3389/fgene.2023.1244983
- 172 Forni D, Pozzoli U, Cagliani R, Clerici M, **Sironi M**. Dinucleotide biases in the genomes of prokaryotic and eukaryotic dsDNA viruses and their hosts. *Mol Ecol.* 2024 Jan 23:e17287. doi: 10.1111/mec.17287
- 173 Cagliani R, Forni D, Mozzi A, Fuchs R, Tussia-Cohen D, Arrigoni F, Pozzoli U, De Gioia L, Hagai T, **Sironi M**. Evolution of Virus-like Features and Intrinsically Disordered Regions in Retrotransposon-derived Mammalian Genes. *Mol Biol Evol.* 2024 Aug 2;41(8):msae154. doi: 10.1093/molbev/msae154.
- 174 Forni D, Pozzoli U, Mozzi A, Cagliani R, **Sironi M**. Depletion of CpG dinucleotides in bacterial genomes may represent an adaptation to high temperatures. *NAR Genom Bioinform.* 2024 Jul 27;6(3):lqae088. doi: 10.1093/nargab/lqae088.
- 175 Molteni C, Forni D, Cagliani R, **Sironi M**. Comparative genomics reveal a novel phylotaxonomic order in the genus *Fusobacterium*. *Commun Biol.* 2024 Sep 7;7(1):1102. doi: 10.1038/s42003-024-06825-y.
- 176 Cagliani R, Forni D, Mozzi A, Fuchs R, Hagai T, **Sironi M**. Evolutionary analysis of ZAP and its cofactors identifies intrinsically disordered regions as central elements in host-pathogen interactions. *Comput Struct Biotechnol J.* 2024 Aug 2;23:3143-3154. doi: 10.1016/j.csbj.2024.07.022.

- 177 Njoku RC, Martinelli M, Giubbi C, De Marco S, Torsello B, d'Avenia M, **Sironi M**, Bianchi C, Cocuzza CE. Evaluation of C-C Motif Chemokine Receptor 5 (CCR5) as a Sample Adequacy Control in HPV Molecular Diagnostics. *Diagnostics (Basel)*. 2024 Sep 30;14(19):2194. doi: 10.3390/diagnostics14192194.
- 178 Forni D, Mozzi A, **Sironi M**, Cagliani R. Positive Selection Drives the Evolution of the Structural Maintenance of Chromosomes (SMC) Complexes. *Genes (Basel)*. 2024 Sep 3;15(9):1159. doi: 10.3390/genes15091159.
- 179 Pozzoli U, Forni D, Arrigoni F, Mozzi A, Cagliani R, De Gioia L, **Sironi M**. Systematic analysis of structural disorder in the minimal proteome of *Mycoplasma pneumoniae*. *Microbiol Spectr*. 2025 Jun 18: e0096825. doi: 10.1128/spectrum.00968-25.
- 180 Kuhn JH, Adkins S, Alkhovsky Альховский Сергей Владимирович SV, An 安雯霞 W, Avšič-Županc T, Ayllón MA, Bačnik K, Bahl J, Balkema-Buschmann A, Ballinger MJ, Beer M, Bejerman N, Bergeron É, Biedenkopf N, Blair CD, Blasdel KR, Bradfute SB, Briesse T, Brown K, Brown PA, Buchholz UJ, Buchmeier MJ, Bukreyev A, Burt F, Calisher CH, Calvelage S, Cao 曹孟籍 M, Casas I, Chabi-Jesus C, Chandran K, Charrel RN, Crane A, Cuypers LN, Bó ED, de la Torre JC, de Souza WM, de Swart RL, Debat HJ, Dheilly NM, Di Paola N, Di Serio F, Dietzgen RG, Digiario M, Drexler JF, Duprex WP, Dürrwald R, Easton AJ, Elbeaino T, Ergünay K, Eshak MIY, Feng 冯国忠 G, Firth AE, Fooks AR, Formenty PBH, Freitas-Astúa J, Freuling CM, Gadd T, Gago-Zachert S, García ML, García-Sastre A, Garrison AR, Goldberg TL, Gonzalez JJ, Goüy de Bellocq J, Griffiths A, Groschup MH, Gryseels S, Gutiérrez-Aguirre I, Günther S, Hammond J, Hepojoki J, Horie 堀江真行 M, Hume AJ, Hyndman TH, Höper D, Jiāng 姜道宏 D, Junglen S, Klempa B, Klingström J, Kondō 近藤秀樹 H, Koonin EV, Krupovic M, Kubota 久保田健嗣 K, Kurath G, Kutnjak D, Laenen L, Lambert AJ, Lee B, Li 李呈宇 C, Li 李建荣 J, Li 李俊敏 JM, Lukashevich IS, Maes P, Marklewitz M, Marshall SH, Marzano SL, McCauley JW, et al. Annual (2024) taxonomic update of RNA-directed RNA polymerase-encoding negative-sense RNA viruses (realm Riboviria: kingdom Orthornavirae: phylum Negarnaviricota). *J Gen Virol*. 2025 Jun;106(6). doi: 10.1099/jgv.0.002077.
- 181 Mozzi A, Forni D, Cagliani R, Molteni C, Clerici M, **Sironi M**. Population Genetic Structure and Human Adaptation of Kaposi Sarcoma-Associated Herpesvirus. *Open Forum Infect Dis*. 2025 Feb 24;12(3):ofaf111. doi: 10.1093/ofid/ofaf111.

Book chapters

Cagliani R., Mozzi A., Pontremoli C., **Sironi M**.

Evolution and Origin of Human Viruses. In *Virology – Wiley Online Library*. 20 April 2021. doi:10.1002/9781119818526

Sironi M, Forni D. de la Torre JC.

Mammarenavirus Genetic Diversity and Its Biological Implications. In “Viral Fitness and Evolution - Population Dynamics and Adaptive Mechanisms”; part of the book series: *Current Topics in Microbiology and Immunology (CT MICROBIOLOGY, volume 439)* (Springer, 2023). doi: 10.1007/978-3-031-15640-3_8.

Sironi M and Gonzalez Candelas F.

The evolutionary landscape of SARS-CoV-2. In “Genetics and Evolution of Infectious Diseases, 3rd edition”. Elsevier, in press.

I grant permission for my personal information to be used, ref. law 196/2003