Professor Nicole Soranzo

BSc, PhD, FMedSci, EMBO, MEA

Curriculum Vitae

Current Positions

Jan 2023-	Associate Faculty, Wellcome Sanger Institute, Hinxton, UK
Jan 2021-	Head of Genomics Research Centre - Population & Medical Genomics, Human Technopole, Milan, Italy
Oct 2015-	Professor of Human Genetics, School of Clinical Medicine, University of Cambridge, Cambridge, UK

Previous Positions

1999-2002	Post-doctoral research fellow, University of Milan, Italy
2002-2005	Post-doctoral research fellow, University College London, UK
2005-2007	Senior Scientist, Pharmacogenomics Department, Johnson and Johnson Pharmaceutical Research and Development, Raritan, NJ, USA
2007-2009	Senior Staff Scientist, Wellcome Trust Sanger Institute, Hinxton, Cambridge, UK
2008-2009	Honorary Lecturer, King's College London School of Medicine, London, UK
2009-2011	Honorary Senior Lecturer, King's College London School of Medicine, London, UK
2009-2012	Career Development Group Leader, Wellcome Trust Sanger Institute, Hinxton, UK
2013-2015	Principal of Research, University of Cambridge, Cambridge, UK
2012-2017	Group Leader, Wellcome Trust Sanger Institute, Hinxton, UK
	2017-2022 Senior Group Leader, Wellcome Sanger Institute, Hinxton, UK

Education and training

1996-1999	PhD in Genetics and Biotechnology, University of Dundee, UK
1989-1994	Bachelor of Science in Biological Sciences (110/110 cum laude), University of Milan, Italy

Grants

2012-2017	NIHR Cambridge Biomedical Research Centre, NIHR, (total £110,073,288), Co-applicant
2012-2015	EpiGeneSys RISE 1 new investigator award, EU FP7, € 199,995, Principal Investigator
2013-2017	ESPOD fellowship to Valentina Iotchkova, WT/ EMBL, £81,000 (total £162,000), Co-applicant
2015-2018	Center for Therapeutic Target Validation, GSK/EMBL/WT, £131,336, Principal Investigator
2015-2018	ESPOD fellowship to Na Cai, WT/ EMBL, £81,000 (total £162,000), Co-applicant
2015-2020	NIHR Biomedical Research Unit in Donor Health and Genomics, NIHR, £217,022 (total £4,099,619), Co-applicant
2019-2022	Target Validation Using Metabolomics, BioMarin Pharmaceuticals, £1,000,042, Principal Investigator
2019-2023	Centre of Research Excellence, British Heart Foundation, £750,000 (total £5,996,000), Co-applicant
2021-2022	Chan Zuckerberg Foundation, £2,800,000, Principal Investigator
2022-2027	Horizon Europe – NeuroCOV, European Commission, € 144,000.00, Co-applicant
2024 - 2025	Personalised Rna- Oriented MedIciNE in Italy Novel Therapeutics PROMINENT Italian Ministry of University and Research (MUR), € 178,362.50, Coordinator
2024 - 2027	Genome of Europe, European Commission, € 1,120,718.67, Co-applicant

2024 - 2026 Phenotypic Prediction from Population – Scale Single-Cell RNA-Seq, Chan Zuckerberg Initiative, $110,059.00, Co-applicant

Awards and honours

2010 Paula und Richard von Hertwig-Preis for International Cooperation
2012 MRC Suffrage Science Award
2014 Movers and Shakers in Biobusiness, BioBeats
2016 Top Italian Women Scientist
2018 Fellow of the Academy of Medical Sciences (FMedSci)
2019 Fellow of the European Molecular Biology Organisation (EMBO)
2020 Forbes Italia - Top 100 Italian Women 2020
2022 Member of the Academia Europaea (MAE)
2022 Best Female Scientists in the World 2022 Ranking | Research.com

Positions of Trust and Institutional Roles (more recent)

2016- Mentoring Circle (several mentoring activities within and outside the institute)
2016- Member of the Steering Committee, BHF Cambridge Centre of Excellence (CRE)
2016 Member of the Selection Committee, Investigator Awards, Academy of Finland
2017- Member of the Scientific Advisory Board, MRC Integrative Epidemiology Unit (IEU)
2017- Member of the Steering Committee, Cambridge Biomedical Research Centre (BRC)
2017-2019 Member of the Expert Review Panel (Genetics and Genomics), Wellcome Trust
2018-2021 Chair of the Equality in Science Committee, Wellcome Sanger Institute
2018-2022 Chair of the Post-graduate Development Committee, Wellcome Sanger Institute
2018- Member of the Steering Committee, Cardiovascular Strategic Research Initiative (SRI)
2018 Member of the Management Committee, Human Technopole (HT)
2018 Member of the Board of Electors to the Professorship of Donor Health and Genomics (University of Cambridge)
2018 Member of the Review Panel, CIFAR Genetic Networks Program, Canada
2019-2022 Member of the Organising Committee, International Common Disease Alliance
2019-2022 Member of the Scientific Advisory Board, MRC WIMM Center of Computational Biology
2020 Member of the Recruitment panel, Director of Heart and Lung Institute, University of Cambridge
2020 Member of the Board of Electors to the Professorship of Molecular Endocrinology (University of Cambridge)
2022 Member of the Evaluation Panel, CRG Bioinformatics and Genomics, Barcelona
2022 Member of the Evaluation Panel, Consolidator Grant, European Research Council
2022 Member of the Selection Committee for Group Leader in Computational Biology, The Francis Crick Institute
2022- Member of the Scientific Advisory Board, Milieu Intérieur (MI) Consortium, Institut Pasteur, Paris
2022- Member of the Executive Committee, International Common Disease Alliance (Global)
2022- Member of the Scientific Advisory Board, Centre of Computational Biology, University of Lausanne
2023- Member of the Scientific Advisory Board, GENCODE project
2023- Member of the Scientific Advisory Board, EMBL Human Ecosystems
2024- Member of the International Evaluation Committee (IEC) for SciLifeLab
2025 Member of the Local Advisory Board for the conference CIBB2025 - Computational Intelligence Methods for Bioinformatics and Biostatistics

Publications

H-index = 137, 115,013 citations

87,584 citations
H index = 126

Full list of publications: soranzo, nicole [AU] - Search Results - PubMed (nih.gov)

Garrison E, Guarracino A, Heumos S, Villani F, Bao Z, Tattini L, Hagmann J, Vorbrugg S, Marco-Sola S, Kubica Ashbrook DG, Thorell K, Rusholme-Pilcher RL, Liti G, Rudbeck E, Golicz AA, Nahnsen S, Yang Z, Mwaniki M Nobrega FL, Wu Y, Chen H, de Ligt J, Sudmant PH, Huang S, Weigel D, **Soranzo N**, Colonna V, Williams RW, Prins P. (2024) Building pangenome graphs. Nat Methods. 2024 Oct 21.

Bolognini D*., Halgren A., Lou R.N., Raveane A*., Rocha J.L., Guarracino A., **Soranzo N.,** Chin J., Garrison E., Sudmant P.H. (2024) Global diversity, recurrent evolution, and recent selection on amylase structural haplotypes i humans. Nature 634, 617–625

Kundu K., Tardaguila M., Mann A.L., Watt S., Ponstingl H., Vasquez L., Von Schiller D., Morrell N.W., Stegle O., Pastinen T., Sawcer S.J., Anderson C.A., Walter K., **Soranzo N**. (2022) Genetic associations at regulatory phenotypes improve fine-mapping of causal variants for 12 immune-mediated diseases. Nat Genet. 54(3):251-262

Cai N., [26 authors], and **Soranzo N**. (2021) Mitochondrial DNA variants modulate N-formylmethionine, proteostasis and risk of late-onset human diseases. Nat Med. 27(9):1564-1575.

Watt S., [25 authors] and **Soranzo N.** (2021) Genetic perturbation of PU.1 binding and chromatin looping at neutrophil enhancers associates with autoimmune disease. Nat Commun. 16;12(1):2298.

Vuckovic D., [110 authors] and **Soranzo, N**. (2020) The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell. 3;182(5):1214-1231.e11.

Iotchkova, V., Ritchie, G.R.S, Geihs, M., Morganella, S., Min, J.L., Walter, K., Timpson, N.J.; UK10K Consortium, Dunham, I., Birney, E., **Soranzo, N**. (2019) GARFIELD classifies disease-relevant genomic features through integration of functional annotations with association signals. Nat Genet. Feb;51(2):343-353.

Tardaguila, M., **Soranzo, N.** (2019) Resolving variant-to-function relationships in hematopoiesis. Nat Genet. 51(4):581-583.

Ecker, S., [40 authors], **Soranzo, N*** and Paul, D*. (2017) Genome-wide analysis of differential transcriptional an epigenetic variability across human immune cell types. Gen Biol 26;18(1):18.

Iotchova, V., [66 authors], and **Soranzo, N.** (2016) Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nat Genet. 48:1303-1312.

Astle, W.J., [45 authors], and **Soranzo, N**. (2016) The allelic landscape of human blood cell trait variation and link to common complex disease. Cell 167;5;1415-1429.e19

Chen, L., [80 authors], and **Soranzo, N**. (2016) Genetic drivers of epigenetic and transcriptional variation in hum immune cells. Cell 167;5;1398-1414.e24

Vasquez, L. J., Mann, A. L., Chen, L. and **Soranzo, N**. (2016). From GWAS to function: lessons from blood cells ISBT Science Series, 11: 211–219.

UK10K Consortium, [29 authors], and **Soranzo, N**. (2015). The UK10K project identifies rare variants in health and disease. Nature 526, 82-90.

Huang, J., [17 authors], and **Soranzo, N.** (2015). Improved imputation of low-frequency and rare variants using t UK10K haplotype reference panel. Nat Commun 6, 8111.

Chen, L., [67 authors, **Soranzo, N.**: 63], and Rendon, A. (2014). Transcriptional diversity during lineage commitment of human blood progenitors. Science 345, 1251033.

Timpson, N.J., [35 authors], and **Soranzo, N**. (2014). A rare variant in APOC3 is associated with plasma triglyceri and VLDL levels in Europeans. Nat Commun 5, 4871.

Shin, S.Y., [36 authors], and **Soranzo, N**. (2014). An atlas of genetic influences on human blood metabolites. Nat Genet 46, 543-550.

Shin, S.Y., [21 authors], and **Soranzo, N.** (2014). Interrogating causal pathways linking genetic variants, small molecule metabolites, and circulating lipids. Genome Med 6, 25.

Menni, C., [22 authors, **Soranzo, N**.: 21], and Spector, T.D. (2013). Biomarkers for type 2 diabetes and impaired fasting glucose using a nontargeted metabolomics approach. Diabetes 62, 4270-4276.

Paul, D.S., [11 authors, **Soranzo, N**.: 9], and Deloukas, P. (2013). Maps of open chromatin highlight cell type-restricted patterns of regulatory sequence variation at hematological trait loci. Genome Res 23, 1130-1141.

van der Harst, P., [195 authors, **Soranzo, N**.: 194], and Chambers, J.C. (2012). Seventy-five genetic loci influencing the human red blood cell. Nature 492, 369-375.

Soranzo, N. (2011). Genetic determinants of variability in glycated hemoglobin (HbA(1c)) in humans: review of recent progress and prospects for use in diabetes care. Curr Diab Rep 11, 562-569.

Gieger, C., [163 authors], and **Soranzo, N**. (2011). New gene functions in megakaryopoiesis and platelet formatic Nature 480, 201-208.

Suhre, K., [33 authors, **Soranzo, N**.: 32], and Gieger, C. (2011). Human metabolic individuality in biomedical and pharmaceutical research. Nature 477, 54-60.

Paul, D.S., [18 authors, **Soranzo, N.:** 16], and Deloukas, P. (2011). Maps of open chromatin guide the functional follow-up of genome-wide association signals: application to hematological traits. PLoS Genet 7, e1002139.

Soranzo, N., [177 authors], and Meigs, J.B. (2010). Common variants at 10 genomic loci influence hemoglobin A(1)(C) levels via glycemic and nonglycemic pathways. Diabetes 59, 3229-3239.

International HapMap Consortium, [89 authors, **Soranzo, N**.: 47], and McEwen, J.E. (2010). Integrating commo and rare genetic variation in diverse human populations. Nature 467, 52-58.

Dupuis, J., [308 authors, **Soranzo, N**.: 5], and Barroso, I. (2010). New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nat Genet 42, 105-116.

Soranzo, N., [80 authors], and Gieger, C. (2009). A genome-wide meta-analysis identifies 22 loci associated with eight hematological parameters in the HaemGen consortium. Nat Genet 41, 1182-1190.

Ganesh, S.K., [62 authors, **Soranzo, N.:** 4], and Lin, J.P. (2009). Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium. Nat Genet 41, 1191-1198.

Soranzo, N., [29 authors], and Ouwehand, W.H. (2009). A novel variant on chromosome 7q22.3 associated with mean platelet volume, counts, and function. Blood 113, 3831-3837.

Prokopenko, I., [108 authors, **Soranzo, N.:** 5], and Abecasis, G.R. (2009). Variants in MTNR1B influence fasting glucose levels. Nat Genet 41, 77-81.