

BIOGRAPHICAL SKETCH

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NAME: Niccolò Bolli

eRA COMMONS USER NAME (credential, e.g., agency login): BOLLIN

POSITION TITLE: Associate Professor of Hematology, University of Milan and Consultant in Hematology, Fondazione IRCCS Ca' Granda Ospedale Maggiore Policlinico, Milan, Italy

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE (if applicable)	Completion Date MM/YYYY	FIELD OF STUDY
University of Perugia	M.D.	07/2001	Medicine and Surgery
University of Perugia	Residency	10/2005	Hematology
University of Perugia	Ph.D.	03/2010	Hematology
Dana-Farber Cancer Institute and Harvard Medical School	Postdoctoral fellow	03/2011	Hematology
University of Cambridge	Clinical Lecturer	04/2015	Hematology

A. Personal Statement

I am an Associate Professor of Hematology at the University of Milan and Consultant in Hematology / Director of the Haematology Research Lab at the Fondazione IRCCS Ca' Granda Ospedale Maggiore Policlinico. I am an onco-hematologist with a strong focus on translational research, and a clear commitment to a successful career in academic hematology. I have been simultaneously carrying out research, teaching and clinical activity for the past ten years, first as a clinical lecturer at the University of Cambridge, then as an Associate Professor at the University of Milan. I have been working on research for the past 15 years, with a solid track record of projects in cellular biology, animal models, and genomic analysis carried out in four different groups in three different countries over my career. In my country, I was among the youngest associate professors across academic disciplines: only 5% are below 40 years of age, and I have been extremely determined to continue on this successful pace of accomplishments. With both depth and breadth of expertise in the field of molecular pathogenesis of hematological cancers, I have obtained over €4M in grants and fellowships over the past ten years and have acquired leadership abilities working with students and post-docs both in medicine and biological sciences. Thanks to the appointment as Director of the Haematology Research Lab, I can rely on a seamless sample supply from the Hospital patients' cohort, therefore facilitating the development of explorative genomic large-scale studies.

B. Positions and Honors

2022 – Director, Haematology Research Lab, Fondazione IRCCS Ca' Granda Ospedale Maggiore Policlinico, Milan, Italy

- 2020 – Consultant in Hematology, Fondazione IRCCS Ca' Granda Ospedale Maggiore Policlinico, Milan, Italy
- 2015 – Associate Professor of Hematology, Department of Oncology and Onco-Hematology, University of Milan, Milan, Italy
- 2015 – 2020 Consultant in Hematology, Fondazione IRCCS Istituto Nazionale dei Tumori, Milan, Italy
- 2011 – 2015 Academic Clinical Lecturer in Haematology, Department of Haematology, University of Cambridge, Cambridge, UK and Cancer Genome Project, Wellcome Trust Sanger Institute, Cambridge, UK
- 2009 – 2011 Post-Doctoral research fellow, Department of Pediatric Oncology, Dana-Farber Cancer Institute, Harvard Medical School, Boston, USA.

Institutional Responsibilities

- 2024 – present Member of the Board of the Honeur Project
- 2023 – present Member of the steering committee of the yearly meeting “Under 40 in Hematology – Giovani ematologi a confronto”
- 2021 – 2023 Member of the Research Foundation, Flanders (FWO) Review College
- 2021 – present Board Member of the Grants and Fellowship Committee of the European Hematology Association (EHA)
- 2018 – 2023 Counsellor of the Italian Society of Experimental Hematology (SIES)
- 2018 – present Member of the European Myeloma Network (EMN) and the EHA scientific Working Group on myeloma
- 2016 – 2017 Member of the evaluating commission for post-doctoral applications of the University of Milan
- 2014 Faculty of the yearly meeting “Under 40 in Hematology – Giovani ematologi a confronto”

Fellowships

- 2011 – 2014 European Hematology Association (EHA) Research Fellow
- 2009 – 2011 Leukemia & Lymphoma Society Special Fellow
- 2008 – 2009 American-Italian Cancer Foundation fellowship
- 2006 – 2008 Federazione Italiana Ricerca sul Cancro (FIRC) fellowship

Honors and awards

2013

First prize “Under 40 in Hematology – Giovani ematologi a confronto” promosso dalla Società Italiana di Ematologia. EUR 6.000

2012

Winner of the Young Scientist Award at the 17th meeting of the European Haematology Association with an abstract titled: “Whole Exome Sequencing Defines Clonal Architecture and Genomic Evolution in Multiple Myeloma”. EUR 5.000

2011

Winner of a Lady Tata Award for a project titled: “Genetic modifiers of the phenotypic landscape in JAK2V617F myeloproliferative neoplasms”. EUR 12.000

2006

Winner of the “Grazia Caiani Bartocci” prize from the Accademia Anatomico-Chirurgica of the University of Perugia with a project titled “Aspetti funzionali delle mutazioni del gene NPM1”. EUR 4.000

C. Contributions to Science

My most important scientific contribution has been the work I carried out to dissect the subclonal architecture of multiple myeloma and its evolution over time and after treatment – a now widely accepted concept that I then expanded to the field of spontaneous evolution of smoldering multiple myeloma. My early achievements granted me a position as an associate professor of Hematology at the University of Milan. While establishing myself as an independent investigator at my Institution, I was able to maintain

international collaborations with the previous institutions where I worked, based on an analysis framework that I have developed and validated to perform clinically useful extended genotyping of multiple myeloma that is now widely used in the international community.

Over the last 10 years I have contributed extensively to the understanding of the molecular pathogenesis of MM through genomic studies, from asymptomatic conditions to diagnosis and on to chemo-resistant stages. I have been the first to describe genomic modes of spontaneous evolution of MGUS/SMM into symptomatic MM through innovative protocols aimed at clonal PC purification and whole-genome sequencing from low-input samples. I described how progressive and non-progressive MGUS/SMM cases show clear differences from a genomic point of view that are not apparent from a clinical and laboratory analysis. Furthermore, I have been able to time the first acquisition of genomic events that drives spontaneous disease evolution years before the actual sampling, opening the field for the search of clonal plasma cells in healthy individuals and their interrelationships with other clonal BM conditions.

In my career, I have authored and co-authored 139 publications, with 18.608 citations and an H-index of 46 (Scopus, May 27th 2025). My main scientific achievements relative to the research proposed are testified by the following selected papers:

1. Poletti A. et al. Unique molecular assay (UMA): a next-generation sequencing targeted panel for efficient and comprehensive genomic profiling and risk stratification of multiple myeloma. *Haematologica*. 2025 May 15. doi: 10.3324/haematol.2025.287559. Online ahead of print.
2. Lionetti M. et al. Clonal hematopoiesis is clonally unrelated to multiple myeloma and is associated with specific microenvironmental changes. *Blood*. 2025 Mar 20;blood.2024026236. doi: 10.1182/blood.2024026236. Online ahead of print.
3. Da Vià M. et al. Aberrant single-cell phenotype and clinical implications of genotypically defined polyclonal plasma cells in myeloma. *Blood*. 2025 Feb 26;blood.2024025643. doi: 10.1182/blood.2024025643. Online ahead of print.
4. Lazzaroni F. et al. Inference of genomic lesions from single-cell RNA-seq in myeloma improves functional intraclonal and interclonal analysis. *Blood Adv*. 2024 Aug 13;8(15):3972-3984.
5. Da Vià, M. et al. MGUS and clonal hematopoiesis show unrelated clinical and biological trajectories in an older population cohort. *Blood Advances* 6, 5702–5706 (2022)
6. Ziccheddu, B. et al. Functional Impact of Genomic Complexity on the Transcriptome of Multiple Myeloma. *Clin Cancer Res* 27, 6479–6490 (2021).
7. Oben, B. et al. Whole-genome sequencing reveals progressive versus stable myeloma precursor conditions as two distinct entities. *Nat Commun* 12, 1861 (2021).
8. Ziccheddu, B. et al. Integrative analysis of the genomic and transcriptomic landscape of double-refractory multiple myeloma. *Blood Advances* 4, 830–844 (2020).
9. Maura, F. et al. A practical guide for mutational signature analysis in hematological malignancies. *Nature Communications* 10, 2969 (2019).
10. Maura, F. et al. Biological and prognostic impact of APOBEC-induced mutations in the spectrum of plasma cell dyscrasias and multiple myeloma cell lines. *Leukemia* 32, 1044–1048 (2018).
11. Bolli, N. et al. Genomic patterns of progression in smoldering multiple myeloma. *Nature Communications* 9, 3363 (2018).
12. Bolli, N. et al. Analysis of the genomic landscape of multiple myeloma highlights novel prognostic markers and disease subgroups. *Leukemia* 32, 2604–2616 (2018).
13. Bolli, N. et al. A DNA target-enrichment approach to detect mutations, copy number changes and immunoglobulin translocations in multiple myeloma. *Blood Cancer J* 6, e467 (2016).
14. Bolli, N. et al. Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. *Nature Communications* 5, 2997 (2014).