Curriculum vitae

AL MAGNIFICO RETTORE
DELL'UNIVERSITA' DEGLI STUDI DI MILANO **COD. ID: 5519**

Il sottoscritto chiede di essere ammesso a partecipare alla selezione pubblica, per titoli ed esami, per il conferimento di un assegno di ricerca presso il Dipartimento di **Biotecnologie Mediche e Medicina Traslazionale**

Responsabile scientifico: **Prof. Massimiliano Pagani**

Michaela Fakiola

CURRICULUM VITAE

INFORMAZIONI PERSONALI

Cognome	FAKIOLA
Nome	MICHAELA

OCCUPAZIONE ATTUALE

Incarico	**Struttura**
Post-doctoral Researcher	IFOM ETS - The AIRC Institute of Molecular Oncology, Milan, Italy

ISTRUZIONE E FORMAZIONE

Titolo	**Corso di studi**	**Università**	**anno conseguimento titolo**
Laurea Magistrale o equivalente	BIOLOGY	ARISTOTLE UNIVERSITY, THESSALONIKI, GREECE	2001 (awarded 2002)
Specializzazione			
Dottorato Di Ricerca	Medicine (Human Genetics)	UNIVERSITY OF CAMBRIDGE, UK	2009
Master	Environmental Technology (Health and Environment Option)	IMPERIAL COLLEGE OF LONDON, UK	2002
Diploma Di Specializzazione Medica			
Diploma Di Specializzazione Europea			
Altro			

ISCRIZIONE AD ORDINI PROFESSIONALI

Data iscrizione	Ordine	Città

LINGUE STRANIERE CONOSCIUTE

lingue	livello di conoscenza
ENGLISH	Fluent
ITALIAN	Basic
GREEK	Fluent

PREMI, RICONOSCIMENTI E BORSE DI STUDIO

anno	Descrizione premio
2021	Post-doctoral Research Fellowship, Fondazione UMBERTO VERONESI, Italy
2020	Post-doctoral Research Fellowship, Fondazione UMBERTO VERONESI, Italy
2018	Post-doctoral Research Fellowship, Fondazione UMBERTO VERONESI, Italy
2016	Post-doctoral Research Fellowship, Fondazione UMBERTO VERONESI, Italy
2013	Raine International Visiting Award, Raine Medical Research Foundation, University of Western Australia

ATTIVITÀ DI FORMAZIONE O DI RICERCA

descrizione dell'attività

During my PhD and postdoctoral studies in UK, Australia and USA, I developed expertise in human genetic susceptibility and participated in international collaborative projects (funded by the Wellcome Trust, UK and the National Institutes of Health, USA) that identified clinically relevant genes, and common and rare genetic risk variants for infectious diseases, metabolic disorders and immune-related diseases. These studies were complemented by transcriptional, cellular, and computational approaches to provide further leads on disease pathogenesis. Moving from Cambridge to Milan, I obtained funding from Fondazione Umberto Veronesi to apply my knowhow in genetic studies towards investigating the role of long non-coding RNAs in genetic predisposition to cancer and immune-related diseases. I subsequently reoriented my interests towards cancer research seeking to understand how the transcriptional and epigenetic reprogramming of lymphocyte populations and cancer cells lead to the impairment of immune responses and tumor growth. These studies expanded my expertise in omics-based data, including analyses of RNA-seq, ChIP-seq, ATAC-seq, whole-exome sequencing, single-cell RNA-seq, and transcription factor footprinting. My current and past research has focused on the following main areas:

- Tracing the roots of T lymphocyte-mediated immune suppression and dysfunction in cancer through epigenomics (ChIP-seq, ATAC-seq) and single-cell multiomics.

- Dissecting the molecular complexity of colorectal cancer by analyzing the genetic (mutational burden), transcriptional and epigenetic landscape of genetically heterogeneous patient-derived tumor organoids and identifying the key regulators of a shared pan-cancer enhancerome.

- Molecular/Experimental studies to understand the host-parasite interactions and the associated immune responses under the influence of the risk/protective HLA proteins, including transcriptional profiling, epitope capture from dendritic cells, and imputation of classical HLA alleles and amino acids.

- A genome-wide association study of visceral leishmaniasis conducted as part of the Wellcome Trust Case Control Consortium (WTCCC2), providing novel insights into the role of the MHC class II HLA-DRB1 locus as the most important genetic risk factor for this infectious disease.

- Identification of genetic risk factors for a number of infectious diseases and complex traits by conducting genome-wide association studies in large genetic datasets of diverse populations.

ATTIVITÀ PROGETTUALE

Anno	Progetto
2022-2022	Histone mark profiling of brain metastases to decipher their distinct and shared epigenomic patterns compared to the primary tumors from which they originate. IFOM ETS - The AIRC Institute of Molecular Oncology, Milan, Italy - Pagani group
2021-2022	3D genome characterization of patient-derived colorectal cancer (CRC) organoids to decipher the genome-wide chromosomal interactions and target genes of a pan-cancer enhancerome. The project employs chromosome conformation capture techniques (e.g. capture HiC for enhancers and promoters). IFOM ETS - The AIRC Institute of Molecular Oncology, Milan, Italy - Pagani group
2020-2022	Molecular profiling of tumor-infiltrating T cell lymphocytes through the integration of epigenetic (ChIP-seq for histone marks and ATAC-seq), bulk and single-cell RNA-seq data, and transcription factor footprinting. IFOM ETS - The AIRC Institute of Molecular Oncology, Milan, Italy - Pagani group
2017-2020	Characterization of patient-derived CRC organoids through transcriptional (RNA-seq), genetic (WES), and epigenomic (ChIP-seq) analyses. IFOM ETS - The AIRC Institute of Molecular Oncology, Milan, Italy - Pagani group
2020-2020	Identification of genetic variants contributing to severe otitis media in an Aboriginal community using exome sequencing and FUnctional and Mapping and Annotation analyses. IFOM ETS - The AIRC Institute of Molecular Oncology, Milan, Italy
2019-2020	Genome-wide association study (GWAS) to identify risk loci contributing to cutaneous leishmaniasis. INGM – Instituto Nazionale di Genetica Molecolare, Milan, Italy
2016-2017	Identification of lymphocyte-specific long intergenic non-coding RNAs (lncRNAs) within known regions of genetic predisposition to cancer and immune-related diseases. INGM – Instituto Nazionale di Genetica Molecolare, Milan, Italy
2016-2021	The role of IL-10 as modulator of the transcriptional responses to leishmanial antigens in VL patients. Department of Pathology, University of Cambridge, UK and INGM – Instituto Nazionale di Genetica Molecolare, Milan, Italy
2012-2019	Deciphering the genome-wide transcriptional blood signatures of active and treated visceral leishmaniasis patients and endemic healthy controls. Department of Pathology, University of Cambridge, UK
2014-2014	Differential expression of major histocompatibility (MHC) class II molecules in intestinal tissues.

	Department of Pathology, University of Cambridge, UK – Kaufman group
2013-2017	Understanding the molecular mechanisms underpinning the association of HLA-DRB1 alleles with risk versus protection in visceral leishmaniasis using HLA imputation, epitope capture from dendritic cells, and in silico epitope binding predictions of leishmanial antigens to HLA-DRB1 alleles. Department of Pathology, University of Cambridge, UK – Blackwell group
2010-2015	Genome-wide association study of Type 2 Diabetes in an Australian Aboriginal population. Telethon Kids Institute, University of Western Australia, Australia - Blackwell group
2009-2012	Genome-wide association study of visceral leishmaniasis in two independent case-control and family cohorts from endemic population as part of the Wellcome Trust Case Control Consortium 2 (WTCCC2). Cambridge Institute for Medical Research (CIMR), Cambridge, UK - Blackwell group
2007-2012	Genetic and functional evaluation of the role of DLL1, SLC11A1, CXCR1 and CXCR2 in visceral leishmaniasis Cambridge Institute for Medical Research (CIMR), Cambridge, UK - Blackwell group
2005-2010	The genetic and functional role of the Notch ligand DLL1 in human susceptibility to visceral leishmaniasis using haplotype association, gene expression analyses and discovery of conserved non-coding regulatory elements Cambridge Institute for Medical Research (CIMR), Cambridge, UK - Blackwell group
2004-2007	Genome-wide linkage scan analysis with refined mapping for human susceptibility to visceral leishmaniasis in India. Cambridge Institute for Medical Research (CIMR), Cambridge, UK - Blackwell group
2003-2004	The genetics of infectious diseases in endemic populations using genome wide linkage scan analyses. Cambridge Institute for Medical Research (CIMR), Cambridge, UK - Blackwell group

TITOLARITÀ DI BREVETTI

Brevetto

CONGRESSI, CONVEGNI E SEMINARI

Data	**Titolo**	**Sede**
05/04/2022 09/04/2022	Keystone Symposium - Single Cell Biology: Pushing New Frontiers in the Life Sciences "Charting the epigenome of intratumoral CD4+ Type 1 regulatory T-cells through an integrative omics approach"	Florence, Italy

19-03-2014 20-03-2014	Visceral Leishmaniasis workshop organized by the National Institutes of Health (NIH) at the Bill & Melinda Gates Foundation Conference Center "Technical and ethical feasibility of genetic fingerprinting across a study population"	Seatle, WA, USA
13-11-2013	Cambridge Infectious Diseases 2013 Meeting of Minds "Major genetic risk factor for visceral leishmaniasis lies at the heart of eliciting CD4 T cell immunity"	University of Cambridge, UK
13-05-2013 17-05-2013	5th World Congress on Leishmaniasis "HLA class II association with visceral leishmaniasis: implications for vaccine development"	Porto de Galinhas, Pernambuco, Brazil
01-05-2013	Invited Speaker at the Telethon Institute for Child Health Research (currently known as Telethon Kids Institute) "HLA Class II association with visceral leishmaniasis: a potential role in vaccine development?"	Perth, Australia
15-08-2010 20-08-2010	XIIth International Congress of Parasitology (ICOPA) "Genome wide linkage study for visceral leishmaniasis in India"	Melbourne, Australia
03/02/2009 07/02/2009	4th World Congress on Leishmaniasis "The genetics of susceptibility to visceral leishmaniasis in India"	Lucknow, India

PUBBLICAZIONI

Libri

Book Chapter

Fakiola M, Lu W, Jamieson SE, Peacock CS. Genomics and infectious diseases: susceptibility, resistance, response and anti-microbial therapy. In *Genomic Medicine: Principles and Practice* (2nd edition), **2014**, **Oxford University Press**.

Edited by Dhavendra Kumar and Charis Eng.

Articoli su riviste

1. Della Chiara G*, Gervasoni F*, **Fakiola M***, Godano C*, […], Piccolo S, Pagani M. Epigenomic landscape of human colorectal cancer unveils an aberrant core of pan-cancer enhancers orchestrated by YAP/TAZ. ***Nature Communications***, **2021** Apr 20;12(1):2340. *Equal first authorship

2. Singh OP, Syn G, Nylén S, Engwerda C, Sacks D, Wilson ME, Kumar R, Chakravarty J, Sundar S, Blackwell JM*, **Fakiola M***. Anti-Interleukin-10 unleashes transcriptional response to leishmanial antigens in visceral leishmaniasis patients. ***Journal of Infectious Diseases***, **2021** Feb 13;223(3):517-521. *Joint senior authors

3. Jamieson SE*, **Fakiola M***, Tang D, Scaman E, Syn G, Francis RW, Coates HL, Anderson D, Lassmann T, Cordell HJ, Blackwell JM. Common and rare genetic variants that could contribute to severe otitis media

in an Australian Aboriginal population. ***Clinical Infectious Diseases*, 2021** Mar 9:ciab216 *Equal first authorship

4. Blackwell JM, **Fakiola M**, Singh OP. Genetics, Transcriptomics and Meta-Taxonomics in Visceral Leishmaniasis. ***Frontiers in Cellular and Infection Microbiology*, 2020** Nov 25;10:590888. eCollection 2020.

5. Castellucci LC*, Almeida L*, Cherlin S*, **Fakiola M***, Francis RW, Carvalho E, Santos da Hora A, Souza do Lago T, Figueiredo AB, Cavalcanti CM, Alves NS, Morais KLP, Teixeira-Carvalho A, Dutra WO, Gollob KJ, Cordell HJ, Blackwell JM. A Genome-Wide Association Study Identifies SERPINB10, CRLF3, STX7, LAMP3, IFNG-AS1 and KRT80 As Risk Loci Contributing to Cutaneous Leishmaniasis In Brazil. ***Clinical Infectious Diseases*, 2020** Aug 23:ciaa1230. Online ahead of print. *Equal first authorship

6. Blackwell JM, **Fakiola M**, Castellucci LC. Human genetics of leishmania infections. ***Human Genetics*, 2020** Jun;139(6-7):813-819. Review.

7. **Fakiola M**, Singh OP, Syn G, Singh T, Singh B, Chakravarty J, Sundar S, Blackwell JM. Transcriptional blood signatures for active and amphotericin B treated visceral leishmaniasis in India. ***PLoS Neglected Tropical Diseases*, 2019** Aug 16 ;13(8):e0007673.

8. Chakravarty J, Hasker E, Kansal S, Singh OP, Malaviya P, Singh AK, Chourasia A, Singh T, Sudarshan M, Singh AP, Singh B, Singh RP, Ostyn B, **Fakiola M**, Picado A, Menten J, Blackwell JM, Wilson ME, Sacks D, Boelaert M, Sundar S. Determinants for progression from asymptomatic infection to symptomatic visceral leishmaniasis: A cohort study. ***PLoS Neglected Tropical Diseases*, 2019** Mar 27;13(3):e0007216.

9. Singh B, **Fakiola M**, Sudarshan M, Oommen J, Singh SS, Sundar S, Blackwell JM. HLA-DR Class II expression on myeloid and lymphoid cells in relation to HLA-DRB1 as a genetic risk factor for visceral leishmaniasis. ***Immunology*, 2019** Feb;156(2):174-186.

10. Tang D, **Fakiola M**, Syn G, Anderson D, Cordell HJ, Scaman ESH, Davis E, Miles SJ, McLeay T, Jamieson SE, Lassmann T, Blackwell JM. Arylsulphatase A Pseudodeficiency (ARSA-PD), hypertension and chronic renal disease in Aboriginal Australians. ***Scientific Reports*, 2018** Jul 19;8(1):10912.

11. Chen L, **Fakiola M**, Staines K, Butter C and Kaufman J. Functional Alleles of Chicken BG Genes, Members of the Butyrophilin Gene Family, in Peripheral T Cells. ***Frontiers in Immunology*, 2018** May 1;9:930.

12. Singh T*, **Fakiola M***, Oommen J, Singh AP, Singh AK, Smith N, Chakravarty J, Sundar S, Blackwell JM. Epitope-Binding Characteristics for Risk versus Protective DRB1 Alleles for Visceral Leishmaniasis. ***Journal of Immunology*, 2018** Mar 5. Apr 15;200(8):2727-2737. *Equal first authorship

13. Salih MAM, **Fakiola M**, Lyons PA, Younis BM, Musa AM, Elhassan AM, Anderson D, Syn G, Ibrahim ME, Blackwell JM, Mohamed HS. Expression profiling of Sudanese visceral leishmaniasis patients pre- and post-treatment with sodium stibogluconate. ***Parasite Immunology*, 2017** Jun;39(6).

14. Weirather JL, Duggal P, Nascimento EL, Monteiro GR, Martins DR, Lacerda HG, **Fakiola M**, Blackwell JM, Jeronimo SM, Wilson ME. Comprehensive candidate gene analysis for symptomatic or asymptomatic outcomes of Leishmania infantum infection in Brazil. ***Annals of Human Genetics*, 2017** Jan;81(1):41-48.

15. Weirather JL, Duggal P, Nascimento EL, Monteiro GR, Martins DR, Lacerda HG, **Fakiola M**, Blackwell JM, Jeronimo SM, Wilson ME. Fine mapping under linkage peaks for symptomatic or asymptomatic outcomes of Leishmania infantum infection in Brazil. **Infection, Genetics and Evolution**, **2016** Sep;43:1-5.

16. Anderson D*, **Fakiola M***, Hales BJ, Pennell CE, Thomas WR, Blackwell JM. Genome-wide association study of IgG1 responses to the choline-binding protein PspC of *Streptococcus pneumonia*. ***Genes and Immunity***, **2015** Jul-Aug;16(5):289-96. *Equal first authorship

17. Anderson D*, Cordell HJ*, **Fakiola M***, Francis RW, Syn G, Scaman ESH, Davis E, Miles SJ, McLeay T, Jamieson SE, Blackwell JM. First genome-wide association study in an Australian Aboriginal population provides insights into genetic risk factors for body mass index and type 2 diabetes. ***PLoS ONE***, **2015** Mar 11;10(3):e0119333. *Equal first authorship

18. Salih MA, **Fakiola M**, Abdelraheem MH, Younis BM, Musa AM, El Hassan AM, Blackwell JM, Ibrahim ME, Mohamed HS. Insights into the possible role of IFNG and IFNGR1 in Kala-azar and Post Kala-azar Dermal Leishmaniasis in Sudanese patients. ***BMC Infectious Diseases***, **2014** Dec 3;14:662.

19. Eu-ahsunthornwattana J, Miller EN, **Fakiola M**, Wellcome Trust Case Control Consortium 2, Jeronimo SM, Blackwell JM, Cordell HJ. Comparison of methods to account for relatedness in genome-wide association studies with family-based data. ***PLoS Genetics***, **2014** Jul 17;10(7).

20. Castellucci LC, Almeida LF, Jamieson SE, **Fakiola M**, Carvalho EM, Blackwell JM. Host genetic factors in American cutaneous leishmaniasis: a critical appraisal of studies conducted in an endemic area of Brazil. ***Memorias do Instituto Oswaldo Cruz***, **2014** Jun;109(3):279-88.

21. Al Safar HS, Cordell HJ, Jafer O, Anderson D, Jamieson SE, **Fakiola M**, Khazanehdari K, Tay GK, Blackwell JM. A genome-wide search for type 2 diabetes susceptibility genes in an extended Arab family. ***Annals of Human Genetics***, **2013** Nov;77(6):488-503.

22. **Fakiola M***, Strange A*, Cordell HJ, et al., (The LeishGEN Consortium and the Wellcome Trust Case Control Consortium 2). Common variants in the HLA-DRB1-HLA-DQA1 HLA class II region are associated with susceptibility to visceral leishmaniasis. ***Nature Genetics***, **2013** Feb;45(2):208-13. Epub 2013 Jan 6. *Equal first authorship

23. Dutra MS, Béla SR, Peixoto-Rangel AL, Fakiola M, Cruz AG, Gazzinelli A, Quites HF, Bahia-Oliveira LM, Peixe RG, Campos WR, Higino-Rocha AC, Miller NE, Blackwell JM, Antonelli LR, Gazzinelli RT. Association of a NOD2 gene polymorphism and T-helper 17 cells with presumed ocular toxoplasmosis. ***Journal of Infectious Diseases***, **2013** Jan 1;207(1):152-63. Epub 2012 Oct 24.

24. Mehrotra S*, **Fakiola M***, Mishra A, Sudharshan M, Tiwary P, Rani DS, Thangaraj K, Rai M, Sundar S, Blackwell JM. Genetic and functional evaluation of the role of DLL1 in susceptibility to visceral leishmaniasis in India. ***Infection, Genetics and Evolution***, **2012** Aug;12(6):1195-201. Epub 2012 Apr 24. *Equal first authorship.

25. Castellucci L, Jamieson SE, Almeida L, Oliveira J, Guimarães LH, Lessa M, **Fakiola M**, Jesus AR, Miller EN, Carvalho EM, Blackwell JM. Wound healing genes and susceptibility to cutaneous leishmaniasis in Brazil. ***Infection, Genetics and Evolution***, **2012** Jul;12(5):1102-10.

26. Mehrotra S, **Fakiola M**, Oommen J, Jamieson SE, Mishra A, Sudarshan M, Tiwary P, Rani DS, Thangaraj K, Rai M, Sundar S, Blackwell JM. Genetic and functional evaluation of the role of CXCR1 and CXCR2 in susceptibility to visceral leishmaniasis in north-east India. ***BMC Medical Genetics***, **2011** Dec 15;12:162.

27. **Fakiola M**, Miller EN, Fadl M, Mohamed HS, Jamieson SE, Francis RW, Cordell HJ, Peacock CS, Raju M, Khalil EA, Elhassan A, Musa AM, Silveira F, Shaw JJ, Sundar S, Jeronimo SB, Ibrahim ME, Blackwell JM. Genetic and Functional Evidence Implicating DLL1 as the Gene that Influences Susceptibility to Visceral Leishmaniasis at Chromosome 6q27. ***Journal of Infectious Diseases***, **2011** Aug 1;204(3):467-77.

28. Mehrotra S, Oommen J, Mishra A, Sudharshan M, Tiwary P, Jamieson SE, **Fakiola M**, Rani DS, Thangaraj K, Rai M, Sundar S, Blackwell JM. No evidence for association between SLC11A1 and visceral leishmaniasis in India. ***BMC Medical Genetics***, **2011** May 20;12:71.

29. **Fakiola M***, Mishra A*, Rai M, Singh SP, O'Leary RA, Ball S, Francis RW, Firth MJ, Radford BT, Miller EN, Sundar S, Blackwell JM. Classification and regression tree and spatial analyses reveal geographic heterogeneity in genome wide linkage study of Indian visceral leishmaniasis. ***PLoS ONE***, **2010** Dec 31; 5(12):e15807. *Equal first authorship

30. Blackwell JM, **Fakiola M**, Ibrahim ME, Jamieson SE, Jeronimo SB, Miller EN, Mishra A, Mohamed HS, Peacock CS, Raju M, Sundar S, Wilson ME. Genetics and visceral leishmaniasis: of mice and man. ***Parasite Immunology***, **2009** May;31(5):254-66. (REVIEW)

31. Miller EN, Fadl M, Mohamed HS, Elzein A, Jamieson SE, Cordell HJ, Peacock CS, **Fakiola M**, Raju M, Khalil EA, Elhassan A, Musa AM, Ibrahim ME, Blackwell JM. Y chromosome lineage- and village-specific genes on chromosomes 1p22 and 6q27 control visceral leishmaniasis in Sudan. ***PLoS Genetics***, **2007** May 11;3(5):e71. Epub 2007 Mar 19.

32. Jamieson SE, Miller EN, Peacock CS, **Fakiola M**, Wilson ME, Bales-Holst A, Shaw MA, Silveira F, Shaw JJ, Jeronimo SM, Blackwell JM. Genome-wide scan for visceral leishmaniasis susceptibility genes in Brazil. ***Genes and Immunity***, **2007** Jan;8(1):84-90.

33. Dubaniewicz A, Jamieson SE, Dubaniewicz-Wybieralska M, **Fakiola M**, Miller EN, Blackwell JM. Association between SLC11A1 (formerly NRAMP1) and the risk of sarcoidosis in Poland. ***European Journal of Human Genetics***, **2005** Jul;13(7):829-34.

34. Miller EN, Jamieson SE, Joberty C, Fakiola M, Hudson D, Peacock CS, Cordell HJ, Shaw MA, Lins-Lainson Z, Shaw JJ, Ramos F, Silveira F, Blackwell JM. Genome-wide scans for leprosy and tuberculosis susceptibility genes in Brazilians. ***Genes and Immunity***, **2004** Jan;5(1):63-7.

ALTRE INFORMAZIONI

2022 Abilitazione Scientifica Nazionale di Seconda Fascia nel Settore Concorsuale:

05/E2 - BIOLOGIA MOLECOLARE

05/I1 - GENETICA

06/A1 - GENETICA MEDICA

2015-2017 Receiving Editor for the ELSEVIER Journal *Infection, Genetics, and Evolution*.

Research Grants:

- 2012-2017 NIH-Tropical Medicine Research Center multi-project grant. co-PI for Project 4: Molecular and cellular action of HLA class II molecules, the major genetic risk factors for visceral leishmaniasis in India.
- 2015 Isaac Newton / Wellcome Trust ISSF / University of Cambridge Joint Research Grants Scheme: An integrated strategy to understand the diversity and complexity of pathogen peptides presented to the immune system during Leishmania infection.
- 2012 Associate Investigator in a University of Western Australia (UWA) Research Collaborative Award to

study the role of the HLA-DRB1 gene in human leishmaniasis using HLA-DRB1-humanised mouse models at Prof Mary Wilson research group, Iowa University, Carver College of Medicine, IA, USA.

Teaching activities:

- 2019-present Co-supervision of Master and PhD students in the Pagani group, IFOM ETS, The AIRC Institute of Molecular Oncology, Milan, Italy
- 2022 PhD Program, University of Milan: Course on "Next generation sequencing: from the bench to the data analysis"
- 2017-2018 International Medical School, University of Milan: Lecture on Human Genetic Variation
- 2014-2015 Department of Pathology, University of Cambridge: Lecturing, and supervising research projects for final year undergraduates, marking annual exam papers, and demonstrating on immunology practicals.
- 2005-2016 Co-supervision and hands-on training of PhD students, visiting postdoctoral fellows and research assistants in the Blackwell group, Cambridge Institute for Medical Research, Cambridge, UK

Reviewer for scientific journals, including Human Genetics, PLoS ONE, Human Immunology, PLoS Neglected Tropical Diseases, Journal of Infectious Diseases.

Memberships: British Society for Immunology, British Society for Parasitology, and Cambridge Infectious Diseases society.

Le dichiarazioni rese nel presente curriculum sono da ritenersi rilasciate ai sensi degli artt. 46 e 47 del DPR n. 445/2000.

Il presente curriculum, non contiene dati sensibili e dati giudiziari di cui all'art. 4, comma 1, lettere d) ed e) del D.Lgs. 30.6.2003 n. 196.

RICORDIAMO che **i curricula SARANNO RESI PUBBLICI sul sito di Ateneo** e pertanto si prega di non inserire dati sensibili e personali. Il presente modello è già precostruito per soddisfare la necessità di pubblicazione senza dati sensibili.

Si prega pertanto di **NON FIRMARE** il presente modello.

Luogo e data: _MILANO, ITALY, ____28/11/22_____