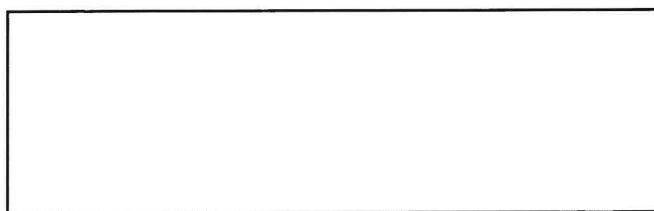
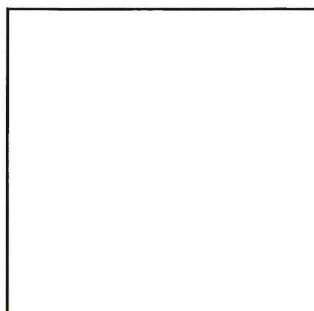


PERSONAL INFORMATION

EMILIANO BIASINIBirth Date Nationality ITALIAN

PROFESSIONAL EXPERIENCE

- Current Associate Professor (Assistant Professor from 10/2015 to 09/2018)
Dulbecco Telethon Laboratory of Prions & Amyloids, Center for Integrative Biology (CIBIO), University of Trento, ITALY
- 2017 - to date Co-Founder & Scientific Advisor
Sibylla Biotech SRL (www.sibyllabiotech.it)
- 2013 - 2015 Principal Investigator
Italian National Institute of Health, Rome, ITALY c/o Department of Neuroscience, Mario Negri Institute for Pharmacological Research, Milan, ITALY
- 2010 - 2014 Adjunct Instructor
Department of Biochemistry, Boston University School of Medicine, USA
- 2008 - 2009 Research Associate
Mario Negri Institute for Pharmacological Research, Milan, ITALY
- 2005 - 2007 Postdoctoral Fellow
Department of Cell Biology and Physiology, Washington University in St Louis, USA

DEGREES

- 2018 Professorship Habilitation (05/E1 - Biochemistry, Full Professor)
Italian Ministry of University and Research (MIUR)
- 2015 Specialization in Applied Genetics (70/70 cum laude)
University of La Sapienza, Rome, ITALY
- 2014 Specialization in Pharmacological Research
Mario Negri Institute for Pharmacological Research, Milan, ITALY
- 2018 Master Degree in Biological Sciences (110/110 cum laude)
University of RomaTre, Rome, ITALY

TEACHING ACTIVITY

- 2016 - 2019 Biochemistry (Master in Quantitative & Computational Biology 0521H, 145551)
Applied Biochemistry (Bachelor in Biomolecular Sciences 0516G, 145608)
University of Trento, ITALY
- 2011 - 2013 Techniques in Biochemistry and Molecular Biology (BI777 A1-2012)
Boston University School of Medicine, Boston, MA, USA

GRANTS & AWARDS

- 2015-2020 Career Award (TCP14009)
Telethon Foundation (ITALY)
- 2016 MS Society Pilot Grant
Multiple Sclerosis Society (USA)
- 2015 CJD Research Grants
CJD Foundation (USA)
- 2013 - 2016 Young Investigator Grant (GR-2010-2312769)
Italian Ministry of Health, Rome (ITALY)
- 2013 Life Science Award
Boston University Technology Office (USA)
- 2013 BioEconomy Award
CNCCS (ITALY)
- 2012 The Carlton Maddrey Wilson Research Grant
CJD Foundation (USA)
- 2005 - 2007 Telethon Research Grant (GFP0400)
Telethon Foundation (ITALY)

SELECTED ORAL
PRESENTATIONS

- 2019 ERASMUS+ Lecturer
KAIST, Daejeon, SOUTH KOREA
- 2019 Late Breaking News Speaker, Prion 2019
Edmonton Conference Center, Alberta, CANADA
- 2018 ERASMUS+ Lecturer
University of Nagasaki, JAPAN
- 2017 Invited Speaker, Summer School on Prion Disorders
Desenzano del Garda, ITALY
- 2017 ERASMUS+ Lecturer
University of Melbourne, AUSTRALIA
- 2017 Invited Speaker, Telethon Convention
Riva del Garda, ITALY
- 2016 Invited Keynote Speaker, XXIV Meeting of Medicinal Chemistry
Perugia, ITALY
- 2016 Invited Speaker, Diffrazioni Festival
Florence, ITALY
- 2015 Invited Speaker, 13th CJD Foundation Family Conference
Washington DC, USA

PEER-REVIEWED
PUBLICATIONS

As first () or corresponding (#) author*

- 2019 Spagnolli G, Rigoli M, Orioli S, Sevilano AM, Faccioli P, Wille H, **Biasini E*** & Requena JR#. Full atomistic model of prion structure and conversion. PLoS Pathog. 2019 Jul 11;15(7):e1007864. doi: 10.1371/journal.ppat.1007864.
- 2019 Biggi S, Pancher M, Stincardini C, Luotti S, Massignan T, Dalle Vedove A, Astolfi A, Gatto P, Lolli G, Barreca ML, Bonetto V, Adami V and **Biasini E***. Identification of compounds inhibiting prion replication and toxicity by removing PrPC from the cell surface. J Neurochem. J Neurochem. 2019 Jul 2. doi: 10.1111/jnc.14805.
- 2019 Rigoli M, Spagnolli G, Faccioli P, Requena JR & **Biasini E*** Ok Google, how could I design therapeutics against prion diseases? Curr Opin Pharmacol. 2019 May 3;44:39-45. doi: 10.1016/j.coph.2019.03.015 (Featured Cover Article)
- 2019 **Biasini E.*** A designer chaperone against prion diseases. Nature Biomed. Eng. 2019 Mar;3(3):167-168. doi: 10.1038/s41551-019-0367-6.
- 2018 Barreca ML, Iraci N, Biggi S, Cecchetti V and **Biasini E***. Pharmacological agents targeting the cellular prion protein. Pathogens. 2018 Mar 7;7(1).
- 2018 T Islam AM, Adlard PA, Finkelstein DI, Lewis V, Biggi S, **Biasini E***, Collins SJ#. Acute Neurotoxicity Models of Prion Disease. ACS Chem Neurosci. 2018 Feb 14.
- 2017 Stincardini C, Massignan T, Biggi S, Elezgarai SR, Sangiovanni V, Vanni I, Pancher M, Adami V, Moreno J, Stravalaci M, Maietta G, Gobbi M, Negro A, Requena JR, Castilla J, Nonno R, **Biasini E***. An antipsychotic drug exerts anti-prion effects by altering the localization of the cellular prion protein. PLOS One. 2017 Aug 7;12(8):e0182589.
- 2017 Massignan T, Sangiovanni V, Biggi S, Stincardini C, Elezgarai SR, Maietta G, Andreev IA, Ratmanova NK, Belov DS, Lukyanenko ER, Belov GM, Barreca ML, Altieri A, Kurkin AV, **Biasini E***. A Small-Molecule Inhibitor of Prion Replication and Mutant Prion Protein Toxicity. ChemMedChem. 2017 Aug 22;12(16):1286-1292.
- 2016 Nyeste A, Stincardini C, Bencsura P, Cerovic M, **Biasini E***, Welker E#. The prion protein family member Shadoo induces spontaneous ionic currents in cultured cells. Sci Rep. 2016 Nov 7;6:36441.
- 2016 Elezgarai SR, **Biasini E***. Common therapeutic strategies for prion and Alzheimer's diseases. Biol Chem. 2016 Nov 1;397(11):1115-1124.
- 2016 Massignan T, Cimini S, Stincardini C, Cerovic M, Vanni I, Elezgarai SR, Moreno J, Stravalaci M, Negro A, Sangiovanni V, Restelli E, Riccardi G, Gobbi M, Castilla J, Borsello T, Nonno R, **Biasini E.*** A cationic tetrapyrrole inhibits toxic activities of the cellular prion protein. Sci Rep. 2016 Mar 15;6:23180.
- 2015 Iraci N, Stincardini C, Barreca ML, **Biasini E.*** Decoding the function of the N-terminal tail of the cellular prion protein to inspire novel therapeutic avenues for neurodegenerative diseases. Virus Res. 2015 Sep 2;207:62-8.
- 2013 **Biasini E.*** Unterberger U, Solomon IH, Massignan T, Senatore A, Bian H, Voigtlaender T, Bowman FP, Bonetto V, Chiesa R, Luebke J, Toselli P and Harris DA#. A mutant prion protein sensitizes neurons to glutamate-induced excitotoxicity. J Neurosci. 2013 Feb 6;33(6):2408-18.
- 2013 Fluharty BR*, **Biasini E,*#** Stravalaci M, Scip A, Diomede L, Balducci C, La Vitola P, Messa M, Colombo L, Forloni G, Borsello T, Gobbi M, Harris DA.* An N-terminal fragment of the prion protein binds to amyloid- β oligomers and inhibits their neurotoxicity in vivo. J Biol Chem. 2013 Mar 15;288(11):7857-66
- 2012 **Biasini E*** and Harris DA#. Targeting the cellular prion protein to treat neurodegeneration. Future Med Chem. 2012 Sep;4(13):1655-8.
- 2012 **Biasini E***, Turnbaugh JA*, Massignan T, Veglianesi P, Forloni G, Bonetto V, Chiesa R and Harris DA#. The toxicity of a mutant prion protein is cell-autonomous, and can be suppressed by wild-type prion protein on adjacent cells. PLOS One 2012. 2012;7(3):e33472.
- 2012 **Biasini E.*** Turnbaugh JA*, Unterberger U, Harris DA. Prion protein at the crossroads of physiology and disease. Trends Neurosci. 2012 Feb;35(2):92-103.
- 2010 **Biasini E.*** Tapella L, Restelli L, Pozzoli M, Massignan T, and Chiesa R#. The hydrophobic core region governs mutant prion protein aggregation and intracellular retention. Biochem J. 2010 Aug 27;430(3):477-86.
- 2009 **Biasini E.*** Tapella L, Mantovani S, Stravalaci M, Gobbi M, Harris DA and Chiesa R#. Immunopurification of pathological prion protein aggregates. PLOS One 2009 Nov 12;4(11):e7816.

- 2008 **Biasini E**,* Seegulam MS, Patti BN, Solforosi L, Medrano AZ, Christensen HM, Senatore S, Chiesa R., Williamson AR., and Harris DA[‡]. Non-infectious aggregates of the prion protein react with several PrP^{Sc}-directed antibodies. *J Neurochem*. 2008 Jun; 105(6): 2190-2204
 - Biasini E**,* Medrano A, Thellung S, Chiesa R, Harris DA[‡]. Multiple biochemical similarities between infectious and non-infectious aggregates of a prion protein carrying an octapeptide insertion. *J Neurochem*. 2008 Mar;104(5):1293-308.
 - 2006 **Biasini E**,* Massignan T, Fioriti L, Rossi V, Dossena S, Salmona M, Forloni G, Bonetto V, Chiesa R[‡]. Analysis of the cerebellar proteome in a transgenic mouse model of inherited prion disease reveals preclinical alteration of calcineurin activity. *Proteomics*. 2006 May;6(9):2823-34.
 - 2004 **Biasini E**,* Fioriti L, Ceglia I, Invernizzi R, Bertoli A, Chiesa R, Forloni G. Proteasome inhibition and aggregation in Parkinson's disease: a comparative study in untransfected and transfected cells. *J Neurochem*. 2004 Feb;88(3):545-53.
- As co-author**
- 2018 Manzoni L, Zucal C, Maio DD, D'Agostino VG, Thongon N, Bonomo I, Lal P, Miceli M, Baj V, Brambilla M, Cerofolini L, Elezgarai S, **Biasini E**, Luchinat C, Novellino E, Fragai M, Marinelli L, Provenzano A, Seneci P. Interfering with HuR-RNA Interaction: Design, Synthesis and Biological Characterization of Tanshinone Mimics as Novel, Effective HuR Inhibitors. *J Med Chem*. 2018 Feb 22;61(4):1483-1498.
 - 2017 Lal P, Cerofolini L, D'Agostino VG, Zucal C, Fuccio C, Bonomo I, Dassi E, Giuntini S, Di Maio D, Vishwakarma V, Preet R, Williams SN, Fairlamb MS, Munk R, Lehmann E, Abdelmohsen K, Elezgarai SR, Luchinat C, Novellino E, Quattrone A, **Biasini E**, Manzoni L, Gorospe M, Dixon DA, Seneci P, Marinelli L, Fragai M, Provenzano A. Regulation of HuR structure and function by dihydrotanshinone-I. *Nucleic Acids Res*. 2017 Sep 19;45(16):9514-9527.
 - 2016 Stravalaci M, Tapella L, Beeg M, Rossi A, Joshi P, Pizzi E, Mazzanti M, Balducci C, Forloni G, **Biasini E**, Salmona M, Diomedea L, Chiesa R, Gobbi M. The Anti-Prion Antibody 15B3 Detects Toxic Amyloid- β Oligomers. *J Alzheimers Dis*. 2016 Jul 6;53(4):1485-97.
 - 2016 Sempou E, **Biasini E**, Pinzón-Olejua A, Harris DA, Málaga-Trillo E. Activation of zebrafish Src family kinases by the prion protein is an amyloid- β -sensitive signal that prevents the endocytosis and degradation of E-cadherin/ β -catenin complexes in vivo. *Mol Neurodegener*. 2016 Feb 9;11:18.
 - 2015 Vercelli A, Biggi S, Scip A, Repetto IE, Cimini S, Falleroni F, Tomasi S, Monti R, Tonna N, Morelli F, Grande V, Stravalaci M, **Biasini E**, Marin O, Bianco F, di Marino D, Borsello T. Exploring the role of MKK7 in excitotoxicity and cerebral ischemia: a novel pharmacological strategy against brain injury. *Cell Death Dis*. 2015 Aug 13;6:e1854.
 - 2014 Botto L, Cunati D, Coco S, Sesana S, Bulbarelli A, **Biasini E**, Colombo L, Negro A, Chiesa R, Masserini M and Palestini P. Role of lipid rafts and GM1 in the segregation and processing of Prion Protein . *PLOS One*. 2014 May 23;9(5):e98344.
 - 2013 Tapella L, Stravalaci M, Bastone A, **Biasini E**, Gobbi M and Chiesa R. Epitope scanning indicates structural differences in brain-derived, monomeric and aggregated mutant prion proteins related to genetic prion diseases. *Biochem J*. 2013 Sep 15;454(3):417-25.
 - 2012 Turnbaugh JA, Unterberger U, Saa P, Massignan T, Fluharty B, Bowman R, Miller M, Supattapone S, **Biasini E** and David Harris. The N-terminal, polybasic region of PrPC dictates the efficiency of prion propagation by binding to PrP^{Sc}. *J Neurosci*. 2012 Jun 27;32(26):8817-30.
 - 2012 Solomon IH, **Biasini E**, and Harris DA. Ion channels induced by the prion protein: mediators of neurotoxicity. *Prion*. 2012 Jan-Mar;6(1):40-5.
 - 2011 Turnbaugh JA, Westergard L, Unterberger U, **Biasini E**, Harris DA. The N-terminal, polybasic region is critical for prion protein neuroprotective activity. *PLOS One*. 2011;6(9):e25675.
 - 2011 Solomon IH, Khatri N, **Biasini E**, Massignan T, Huettner JE, Harris DA. An N-terminal polybasic domain and cell surface localization are required for mutant prion protein toxicity. *J Biol Chem*. 2011 Apr 22;286(16):14724-36.
 - 2011 Massignan T, **Biasini E**, Harris DA. A Drug-Based Cellular Assay (DBCA) for studying cytotoxic and cytoprotective activities of the prion protein: A practical guide. *Methods*. 2011 Mar; 53(3):214

- 2010 Balducci C, Beeg M, Stravalaci M, Bastone M, Scip A, **Biasini E**, Tapella L, Colombo L, Manzoni C, Borsello T, Chiesa R, Gobbi M, Salmona M and Forloni G. A β oligomers impair memory independently of cellular prion protein. *Proc Natl Acad Sci U S A*. 2010 Feb 2; 107(5):2295-300.
- 2010 Massignan T, **Biasini E**, Veglianesi P, Harris DA, Salmona M, Chiesa R, and Bonetto V. Mutant prion protein expression is associated with an alteration of the Rab GDP dissociation inhibitor alpha (GDI)/Rab11 pathway. *Mol Cell Proteomics*. 2010 Apr;9(4):611-22.
- 2010 Massignan T, Stewart RS, **Biasini E**, Solomon IH, Bonetto V, Chiesa R, Harris DA. A novel, drug-based, cellular assay for the activity of neurotoxic mutants of the prion protein. *J Biol Chem*. 2010 Mar 5;285(10):7752.
- 2008 Chiesa R, Piccardo P., **Biasini E**, Ghetti B, and Harris DA. Aggregated, wild-type prion protein causes neurological dysfunction and synaptic abnormalities. *J Neurosci*. 2008 Dec 3(49):13258-67.
- 2008 Medrano AZ, Barmada SJ, **Biasini E**, and Harris DA. GFP-tagged mutant prion protein forms intra-axonal aggregates in transgenic mice. *Neurobiol Dis*. 2008 Jul;31(1):20-32.
- 2007 Yin S, Pham N, Yu S, Li C, Wong P, Chang B, Kang S, **Biasini E**, Harris DA, Sy MS. Human prion proteins with pathogenic mutations share common conformational changes resulting in enhanced binding to glycosaminoglycans. *Proc Natl Acad Sci U S A*. 2007 May 1;104(18):46-51.
- 2007 Massignan T, Casoni F, Basso M, Stefanazzi P, **Biasini E**, Tortarolo M, Salmona M, Gianazza E, Bendotti C, Bonetto V. Proteomic analysis of spinal cord of symptomatic amyotrophic lateral sclerosis G93A SOD1 mouse. *Biochem Biophys Res Commun*. 2007 Feb 16;353(3):719-25.
- 2006 Ghezzi P, Casagrande S, Massignan T, Bellacchio E, Eberini I, Gianazza E, **Biasini E**, Mollica L, Fratelli M, Salmona M, Sherry B, Bonetto V. Glutathionylation of cyclophilin A in T lymphocytes: Influence on structure and function. *Proteomics*. 2006 Feb;6(3):817-25.
- 2003 Drisaldi B, Stewart R, Adles A, Stewart L, Quaglio E, **Biasini E**, Fioriti L, Chiesa R, and Harris DA. Mutant PrP is delayed in its exit from the endoplasmic reticulum, but neither wild-type nor mutant PrP undergoes retrotranslocation prior to proteasomal degradation. *J Biol Chem*. 2003 Jun 13;278(24):21732-43.

BOOK CHAPTERS

- 2012 **Biasini E** and Harris DA. Infectious and pathogenic forms of PrP. Chapter in *Prions and Prion Diseases*, Springer Science 2012 (ISBN 978-1-4614-5305-5)

PATENTS

- 2020 **Biasini E**, Barreca ML, Faccioli P. Small Molecules Inducing the Degradation of the Cellular Prion Protein by Exploiting the Method "Pharmacological Protein Inactivation by Folded Intermediate Targeting" (PPI-FIT). *Pending*
- 2018 Faccioli P and **Biasini E**. Pharmacological Protein Inactivation by Folding Intermediate Targeting (PPI-FIT). Pub. No.: WPO/2020021493A1
- 2014 **Biasini E**, Harris DA, Beeler A, Fluharty B, Barreca ML, Iraci N, Ingham O. Prion protein ligands as therapeutic agents for neurodegenerative disorders. International Application No. PCT/US2013/053796; Pub. No.: WO/2014/025785; Publication Date: 13/02/2014

Nicola Segata

Ph.D.

Department CIBIO
University of Trento,
via Sommarive n. 9
38123 Povo (Trento), Italy

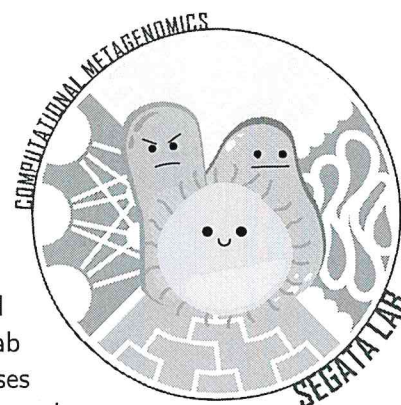
Curriculum Vitae - May 14, 2020

Personal Information

birth date
nationality

research
statement

I am working in the fields of human microbiome research and computational biology. The Computational Metagenomics Lab <http://segatalab.cibio.unitn.it> I lead at the Dep. CIBIO comprises 8 postdocs, two research assistants, 9 Ph.D. students, and several pre-doctoral students. In the lab, we use experimental metagenomic tools and novel computational approaches to study the diversity of the human microbiome and its cross-talk with the human body in health and disease.



Current position

Jan 2018 -
now

Associate Professor and Principal Investigator,
Laboratory of Computational Metagenomics,
Department CIBIO, University of Trento, Italy.



UNIVERSITY
OF TRENTO



Past research positions

Jan 2013-
Dec 2017

Assistant Professor and Principal Investigator, *Laboratory of Computational Metagenomics, Centre for Integrative Biology (CIBIO), University of Trento, Italy.*

Jul 2010-
Oct 2012

Postdoctoral fellow, *Harvard School of Public Health (HSPH), Biostatistics department, Harvard University, Boston, MA, USA. Mentor: prof. Curtis Huttenhower.*

Jan 2010-
Jun 2010

Postdoctoral fellow, *Laboratory of Microbial Genomics, Centre for Integrative Biology (CIBIO), University of Trento, Italy. Mentor: prof. Olivier Jousson.*

Education

2009

PhD Dissertation, *Dept. of Information Engineering & Computer Science, University of Trento.* Discussion of the thesis "Local approaches for fast, scalable and accurate learning with kernels" under the supervision of prof. Enrico Blanzieri.

2006

Master Degree in Computer Science, *University of Trento, Grade 110/110 cum laude.* Discussion of the thesis "Beta-binders and π -calculus approaches for quantitative modelling of biological pathways", under the supervision of prof. C. Priami and prof. E. Blanzieri.

2004

Bachelor Degree in Computer Science, *University of Trento, Grade 110/110 cum laude.* Discussion of the thesis "Sistemi di monitoraggio video: il problema dello sfondo in presenza di variazioni globali di illuminazione", under the supervision of prof. C. Priami and dott. S. Messelodi.

Awards

- 2020 **Knight of the Order of Merit of the Italian Republic** appointed by the President of the Italian Republic.
- 2019 **Pharmabiotics 2019 Young Investigators Award (10,000 EUR)** by Institut Merieux and the Pharmabiotic Research Institute.
- 2019 **Listed as one of the 88 “Highly Cited Researcher” in Italy in 2019** by Clarivate Analytics and Web of Science.
- 2019 **X Prêmio 2019 “Octavio Frias de Oliveira” (Co-recipient)** awarded by the São Paulo State câncer center and the São Paulo faculty of medicine for the paper [Thomas, Manghi, ... , Segata, Nature Medicine 2019].
- 2019 **Invited member of the “Gruppo 2003” association** of the “most influential Italian scientists by citation indexes”.
- 2018 **Listed as one of the 91 “Highly Cited Researcher” in Italy in 2018** by Clarivate Analytics and Web of Science.
- 2018 **H.G. Goldman Award (Co-recipient)** by the SIdP for the work by [Ghensi, Manghi, ..., Segata, 2019] on the oral microbiome in peri-implantitis.
- 2017 **Dr. Darwin award (Co-recipient)** by the Italian Society for Evolutionary Biology for the paper [Asnicar, Manara, ... , Segata, mSystems 2016].
- 2015 **LEO Pharma Research Foundation Gold Award 2015 (1M DKK, 134k EUR)** awarded by LEO Pharma in association with the European Society for Dermatology. The award is “given to talented and committed young researchers in recognition of their exceptional contribution to science”.
- 2012 **Travel fellowship** awarded by ISCB with grant funds obtained from the NSF-National Science Foundation Bio-Directorate.
- 2012 **IHMC-2012 travel award** from the National Institutes of Health (NIH).
- 2011 **PQG travel fellowship award** from the Program in Quantitative Genomics at the Harvard School of Public Health.
- 2011 **Travel fellowship award** from the International Society for Computational Biology (ISCB) funded by DOE-Department of Energy Office of Science, NSF-National Science Foundation Bio-Directorate, and NIH NIMGS-National Institute of General Medical Sciences.
- 2009 **Best Paper Award** at the 6th International Conference on Machine Learning and Data Mining, for the paper: Nicola Segata, Enrico Blanzieri: “Fast local support vector machines for large datasets”.

Research visits

- 2008 **University College Dublin, Dublin (Ireland)**, three months research visit.
Case-Based Reasoning and Bioinformatics research under the supervision of prof. P. Cunningham.
- 2004 **ITC-irst, TeV (Tecnologie della Visione) division, Trento (Italy)**, stage period.
Research in computer vision for video-surveillance under the supervision of dott. S. Messelodi.
- 2003 **Technical University of Denmark, Lyngby, Copenhagen (Denmark)**, Erasmus student.

Teaching

- 2016-now "Computational Microbial Genomics", Master Course, Master in Quantitative and Computational Biology, University of Trento, Trento, Italy
- 2014-now "Introduction to Metagenomics", PhD Course, International PhD Program in Biomolecular Sciences, University of Trento, Trento, Italy
- 2013-2015 "High-throughput methodologies 2: data analysis", Master Degree in Cellular and Molecular Biotechnology, University of Trento, Trento, Italy
- Spring 2010 Assistant teacher for the course "Informatica e Principi di Programmazione", Bachelor Degree in Cognitive Science, University of Trento, Rovereto, Italy.
- Fall 2009 Assistant teacher for the course "Data Mining for Biological Data" (teaching language English), Master Degree in Computer Science - Bioinformatics specialization, University of Trento, Trento, Italy
- Fall 2009 Teacher for the additional course "Informatica e Principi di Programmazione", Bachelor Degree in Cognitive Science, University of Trento, Rovereto, Italy.

Grants

- Total funding Overall, I secured over 6 million € for research in my laboratory since 2013. Funding from commercial contracts ("conto terzi") are not considered here.
- 2019-2024 **ONCOBIOME**. H2020 Better Health and care, economic growth and sustainable health systems H2020-SC1-BHC-2018-2020 Grant (Work Package Leader) (1,502,618 € to N.S.)
- 2019-2021 Simons Foundation Autism Research Initiative - Pilot Award (Co-Investigator) (125,400 \$ to N.S.)
- 2019-2024 U01 award by the National Institutes of Health (NIH) and National Cancer Institute (NCI) (Senior/Key Person) (329,056 \$ to N.S.)
- 2019-2023 **MASTER**. H2020 Sustainable Food Security H2020-SFS-2018-2020 Grant (Work Package Leader) (509,950 € to N.S.)
- 2019-2023 PRIN MIUR (LS6 Sector, Local PI) (148,000 € to N.S.)
- 2019-2024 **VACCIBIOME**. Collaborator/Investigator for the H2020 ERC Advanced Investigator Grant to prof. Guido Grandi (Investigator) (150,000 € to N.S.)
- 2019-2023 Award from the Institut Merieux and the Pharmabiotic Research Institute (10,000 € to N.S.)
- 2018-2022 Italian Ministry of Health 2018, "Ricerca Finalizzata" (Local PI) (90,000 € to N.S.)
- 2018-2020 NIH Sub-award from the Forsyth Institute (105,000 € to N.S.)
- 2017-2021 Italian Ministry of Health 2016, "Ricerca Finalizzata" (Local PI) (90,000 € to N.S.)
- 2017-2022 **MetaPG**. H2020 ERC Starting Investigator grant (PI) (1,500,000 € to N.S.)
- 2017-2022 **MODULATE**. H2020 ERC Starting Investigator Grant to prof. Harry Sokol (Third linked party - Local PI) (150,000 € to N.S.)
- 2016-2018 Eklund Foundation (40,000 € to N.S.)
- 2017-2019 ITI International Team for Implantology Foundation (40,600 € to N.S.)
- 2013-2016 Futuro in Ricerca 2013 (MIUR) (PI) (348,000 € to N.S.)
- 2015-2017 LEO Pharma Research Foundation Gold Prize 2015 (PI) (134,000 € to N.S.)
- 2016-2018 Marie Skłodowska-Curie Individual Fellowships (Scientific Coordinator for the Fellowship to Edoardo Pasolli) (180,277 €)

- 2016-2018 Marie Skłodowska-Curie Individual Fellowships (Scientific Coordinator for the Fellowship to Federica Pinto) (180,277 €)
- 2016-2018 SIdP (PI) (30,000 € to N.S.)
- 2016-2018 Lega Italiana per la Lotta contro i Tumori (PI) (72,000 € to N.S.)
- 2015-2016 Italian Cystic Fibrosis foundation (External Collaboration) (24,000 € to N.S.)
- 2013-2017 FP7 Marie Curie Career Integration Grant (PI) (100,000 € to N.S.)
- 2013-2017 CARITRO - Giovani Ricercatori 2013 (PI) (213,000 € to N.S.)
- 2013-2015 Terme di Comano - Skin Microbiome (PI) (78,000 € to N.S.)
- 2014 UNITN award for reaching the final stage of the ERC Starting Grant (PI)(10,000 € to N.S.)
- 2010-2012 Postdoctoral fellowship at the Harvard School of Public Health, Biostatistics Department, Huttenhower lab, Harvard University, Boston.
- 2010 Postdoctoral research grant at the Laboratory of Microbial Genomics, Centre for Integrative Biology (CIBIO), University of Trento, Italy.
- 2006–2009 PhD research grant at the Department of Information Engineering and Computer Science (XXII cycle), University of Trento, Italy.

(Co)organization of Conferences, Schools, and Workshops

- Jun 27-30, 2021 **EMBO|EMBL Symposium on "The Human Microbiome"** (third edition), Heidelberg, Germany. Coorganizer with Peer Bork and Manimozhiyan Arumugam
- Jul 23, 2019 **MICROBIOME C.O.S.I. day at ISMB 2019**, Basel, Switzerland. Coorganizer and Co-chair
- Oct 10, 2018 **Microbiota: tra ricerca di base e applicazioni cliniche**, Comano, Italy. Coorganizer
- Sep 16-19, 2018 **EMBO|EMBL Symposium on "The Human Microbiome"** (second edition), Heidelberg, Germany. Coorganizer with Peer Bork and Manimozhiyan Arumugam
- Oct 21, 2017 **Microbiota: le nuove frontiere della medicina**, Comano, Italy. Coorganizer
- Sep 24, 2016 **Microbiota nella medicina del futuro**, Comano, Italy. Coorganizer
- Oct 03, 2015 **Microbiota: salute, terme e alimentazione**, Comano, Italy. Coorganizer
- Sep 08-11, 2014 **Biology Summer School: Systems, Synthetic and Semantic Biology**, Trento, Italy. Coorganizer
- Feb 15, 2014 **Il microbiota: interazione tra microrganismi e corpo umano**, Comano, Italy. Coorganizer

Other collaborations and activities

- 2018 - now Co-founder and scientific advisor of PreBiomics s.r.l. on the use of the plaque microbiome for oral health, <http://www.prebiomics.com/>
- 2017 - now Scientific consultant for ZOE on the use of gut metagenomics for personalized nutrition, <https://joinzoe.com/>

Editorial, Reviewer, and Scientific Committee Activity

- 2019-now Editorial Board Member for Genome Biology
- 2018-now Member of the "Comitato Tecnico Sanitario" for the Italian Ministry of Health
- 2017-now Associate Editor for PLOS Computational Biology
- 2016-now Member of the International Scientific Committee of the Biocodex Microbiota Foundation
- 2015-now Editor for mSystems by ASM
- 2014-now Associate Editor for BMC Nutrition

2018-2019 Associate Editor for Frontiers in Microbiology
 2014 Invited Editor for mBio
 2011-now Reviewer for: Nature, Cell, Nature Microbiology, Cell Host and Microbe, Nature Biotechnology, Nature Methods, Scientific Data, Gut, Genome Medicine, FEMS Microbiology Reviews, Briefings in Bioinformatics, Scientific Reports, ELife, Current Biology, Alimentary Pharmacology & Therapeutics, Proteomics, Nature Communications, Nucleic Acid Research, PLoS Computational Biology, BMC Bioinformatics, BMC Microbiology, International Journal of Food Microbiology, BMC Evolutionary Biology, ISME journal, PLoS One, Genome Research, Bioinformatics, Genome Biology

Talks, Invited Talks, Tutorials, and Seminars

Feb 08, 2020 **Lo studio del microbioma umano e risvolti clinici.** Invited Talk at the Workshop "The gut microbiome: state of the art and innovative approaches", Trento, Italy

Feb 07, 2020 **The hidden human microbiome diversity and personalized host-microbiome interaction.** Invited Plenary Talk at the "MicrobiotaMi 2020", Milan, Italy

Feb 05, 2020 **Metagenomics for the study of the human microbiome.** Invited Seminar at the "Genomics PhD SEMM Coursei at IEO", Milan, Italy

Jan 31, 2020 **Gut microbiome, diet, and host health.** Invited Talk at the "EMERGENCE mini-symposium: Metabolism and Nutrition in cancer prevention and treatment: from basic science to interventions", Paris, France

Jan 23, 2020 **Exploring the hidden diversity and transmission patterns of the human gut microbiome.** Invited Keynote Talk at the conference "13th Finnish Gut Day", Helsinki, Finland

Jan 13, 2020 **From system biology to network medicine in Infectious Diseases: the metagenomics approach.** Invited Talk (in remote) at the conference "From system biology to network medicine in Infectious Diseases: a brainstorming meeting", Rome, Italy

Nov 21, 2019 **Metagenomics of the human microbiome.** Invited Talk at the conference "MIBIOC – The way of the microbiota in cancer", Milan, Italy

Nov 01, 2019 **Vertical microbiome transmission from mother to infants.** Invited Talk at the conference "World of Microbiome: Pregnancy, Birth and Infancy", Milan, Italy

Oct 18, 2019 **Strain-resolved large-scale metagenomics.** Invited Keynote Talk at the 5th International Conference on Clinical Metagenomics, Geneva, Switzerland

Oct 09, 2019 **Shotgun metagenomics for high-resolution investigations of the human microbiome.** Invited Talk at the Ceppellini School "Microbes, Immunity and Cancer", Anacapri, Italy

Sep 28, 2019 **The human microbiome and metagenomics: what's next.** Invited Talk at the Join Meeting AGI-SIMAG, Cortona, Italy

Sep 26, 2019 **High-resolution large-scale profiling of pathogens and commensals from metagenomics.** Invited Keynote Talk at the "5th International Symposium on systems Biology and Microbial Infections", Jena, Germany

Sep 19, 2019 **Uncovering the unexplored human microbiome diversity.** Invited Talk at the "Microbiome in Lupus Meeting", New York, USA

Sep 18, 2019 **Uncovering the hidden diversity of the human microbiome for biomedical applications.** Invited Keynote Talk at the workshop "NextStep: la giovane ricerca avanza", Milan, Italy

Sep 11, 2019 **Large-scale discovery of novel strains and species in the global human microbiome.** Invited Talk at the 14th International Symposium on the Genetics of Industrial Microorganisms, Pisa, Italy

- Jul 24, 2019 **Phylogenetic analysis of genomes from metagenomes: novel species and strain-level population genetics.** Invited Keynote Talk at the SMBE 2019 Meeting, Manchester, United Kingdom
- Jul 22, 2019 **Strain-level population genomics of unexplored members of the human microbiome.** Invited Seminar at the Department of Biomedicine of University of Basel, Basel, Switzerland
- Jul 03, 2019 **Uncovering the hidden diversity of the human microbiome.** Invited Talk at the SEB 2019 annual Meeting, Seville, Spain
- Jun 29, 2019 **Toward Uncovering the Hidden Diversity of the Human Microbiome.** Invited Talk at the "12th Seeon Conference - Microbiota, Probiotics and Host", Seeon, Germany
- Jun 25, 2019 **Shotgun metagenomics.** Seminar and tutorials at the "EMBO Practical Course on Bioinformatics and genome analyses", San Michele, Italy
- May 28, 2019 **The gut microbiome.** Invited Seminar at the Academy of Sciences of the Institute of Bologna, Bologna, Italy
- May 06, 2019 **Unexplored diversity and strain-level variability in the human microbiome.** Invited Talk at the "10th International Course in Microbial Ecology", Milan, Italy
- Apr 13, 2019 **The oral microbiome and metagenomics.** Invited Talk at the "AIO Periodontology and Peri-implantology workshop", Nogaredo, Italy
- Apr 01, 2019 **Multi-Resolution Phylogenetic Analysis Of Known And Unexplored Members Of The Human Microbiome With PhyloPhlAn2.** Invited Talk at the "3rd Workshop on Statistical and Algorithmic Challenges in Microbiome Data Analysis", New York, USA
- Mar 25, 2019 **Uncovering extensive species and strain-level diversity in the human microbiome.** Invited Talk at the "Revolutionizing Next-Generation Sequencing (3rd edition)", Antwerpen, Belgium
- Mar 13, 2019 **Uncovering species and strains in the human microbiome for personalized interventions.** Invited Talk at the "Pharmabiotics 2019", Paris, France
- Feb 21, 2019 **The human microbiome and metagenomes.** Invited Talk at the "Accademia Nazionale dei Lincei", Rome, Italy
- Jan 10, 2019 **Shotgun metagenomics for high-resolution microbiome studies.** Invited Talk at the "Host-microbial interactions: at the mucosal surfaces and in systemic organs", Bern, Switzerland
- Oct 24, 2018 **Uncovering the hidden and strain-level diversity of the human microbiome with large scale shotgun metagenomics.** Invited Talk at the "Symposium: insights into the complexity of host microbiome interactions", Copenhagen, Denmark
- Oct 23, 2018 **Large-scale strain-level comparative metagenomics.** Keynote Talk at the "Capacity-Building Workshop: Metagenomics in the Diagnostic Laboratory", Groningen, Netherlands
- Oct 19, 2018 **Toward strain-resolved metagenomics for microbial epidemiology and pathogen monitoring.** Invited Talk at the "13th Annual Workshop of the National Reference Laboratories for E. coli in the EU", Roma, Italy
- Oct 11, 2018 **The skin microbiota: from health to disease.** Invited Talk at the "2nd European Workshop on Skin immune mediated inflammatory diseases (SIMID)", Verona, Italy
- Oct 06, 2018 **Vertical mother-to-infant microbiome transmission.** Invited Talk at "Microbiota 5", Como, Italy
- Jul 07, 2018 **Are we ready for cultivation-free microbial GWAS?** Invited Talk at the 7th Sardinian International Summer School, Pula, Italy
- Jun 28, 2018 **Computational metagenomics for large-scale strain-resolved human microbiome studies.** Invited Keynote Talk at the 15th Annual Meeting of the Bioinformatics Italian Society, Turin, Italy
- Jun 27, 2018 **Career paths in computational biology.** Invited Talk at BITS2018-CAREER MORNING, Turin, Italy

- Jun 21, 2018 **Transmission and population biology of members of the human microbiome.** Invited Talk at "The Barcelona Debates on the Human Microbiome: From Microbes to Medicines", Barcelona, Spain
- Jun 19, 2018 **The human microbiome at the resolution of single microbial strains.** Invited Talk at the Workshop "Metaorganisms, microbial biorefineries and human health", Bologna, Italy
- Jun 11, 2018 **Shotgun metagenomics for large-scale strain-resolved profiling of the human microbiome.** Invited Seminar at the European Institute of Oncology (IEO), Milan, Italy
- Jun 08, 2018 **Large-scale strain-resolved comparative metagenomics for the human microbiome.** Invited Seminar at the Science for Life Laboratory (SciLifeLab), Stockholm, Sweden
- Apr 26, 2018 **Shotgun metagenomics for high-resolution microbiome studies.** Invited Talk at the International Workshop "The Gut-Brain-Microbiome connection in neuropsychiatric diseases of children and adults", Genova, Italy
- Feb 26, 2018 **Host-microbiome symbiosis at the resolution of single microbial strains.** Invited Talk at DGMIM 2018, Hamburg, Germany
- Feb 22, 2018 **Strain and gene-level metagenomic profiling to unravel microbial risk factors for colorectal cancer.** Invited Talk at the Gustave Roussy Cancer Center, Paris, France
- Feb 15, 2018 **Biotechnological challenges in the study of the human microbiome.** Invited Talk at BioFacility Day 2018, Trento, Italy
- Dec 06, 2017 **Computational metagenomics for large-scale strain-resolved microbiome profiling.** Invited Seminar EMBL, Heidelberg, Germany
- Dec 01, 2017 **Studying the human microbiome and its connections with human health.** Invited Seminar at the University of Naples, Naples, Italy
- Nov 29, 2017 **Large-Scale Microbiome Meta-Analysis with Strain-Level Resolution.** Invited Talk at the "3rd Annual European Microbiome Conference", London, United Kingdom
- Nov 14, 2017 **Shotgun metagenomics with strain-level resolution: tools and clinical applications.** Invited Talk at "AMCLI 2017", Rimini, Italy
- Oct 21, 2017 **Le nuove frontiere nello studio del microbioma cutaneo, orale, e intestinale.** Invited Talk at the "Fourth Microbiota workshop", Comano, Italy
- Oct 09, 2017 **Computational metagenomics for large-scale strain-resolved microbiome profiling.** Invited Keynote Talk at the "Workshop on Recent Computational Advances in Metagenomics (RCAM'17)", Institut Pasteur, Paris, France
- Sep 13, 2017 **Shotgun metagenomics with strain-level resolution: tools and clinical applications.** Invited Talk at the "EMBL-EBI Industry Programme Workshop on The Human Microbiome: challenges and opportunities for novel therapeutics", EMBL-EBI, London, United Kingdom
- Aug 29, 2017 **Microbial population structure and biogeography from metagenomic data.** Invited Keynote Talk at the "Evoluzione 2017" conference, Rome, Italy
- Jul 04, 2017 **Meta'omics for studying the human microbiome.** Invited Talk at the Course "A Field Trip into Metagenomics", University of Milan-Bicocca, Milan, Italy
- Jun 28, 2017 **Shotgun metagenomics with strain-level resolution.** Invited Talk at the IRSAE Course "Integrating Omics Technologies into Aquatic Ecology: New perspectives in Metagenomic, Metabolomic and Bioinformatic applications in the study of aquatic ecosystems", San Michele all'Adige, Italy
- Jun 20, 2017 **Large-scale strain-level population genomics from metagenomics.** Invited Talk at the "Workshop on Computational Metagenomics: Methods, Standards and Experimental Procedures", Bari, Italy

- Jun 05, 2017 **Microbiome meta-analysis and microbial strain profiling using thousands of metagenomic samples.** Invited Plenary Talk at the ASM Microbe 2017, New Orleans, Louisiana, USA
- Jun 02, 2017 **Microbial strain-level population genomics from metagenomes.** Invited Talk at the "Population Genomics" session at ASM Microbe 2017, New Orleans, Louisiana, USA
- May 23, 2017 **High resolution metagenomic analysis to compare the human microbiome across geography and diseases.** Invited Seminar at the Istituto di Tecnologie Biomediche CNR, Segrate Milan, Italy
- May 13, 2017 **The skin microbiome in healthy and disease.** Invited Talk at SIME2017, Rome, Italy
- May 04, 2017 **Large-scale strain-level population genomics of the human microbiome.** Invited Seminar at Institute of Food Research (IFR), Norwich Research Park, Norwich, United Kingdom
- Dec 03, 2016 **The skin microbiome.** Invited Seminar at "The second school of Psoriasis", Naples, Italy
- Dec 02, 2016 **Strain-level metagenomics for pathogen detection and profiling.** Invited Keynote Speaker at "One Health Symposium: Focus on Genomics of Pathogenic *Escherichia coli*", Utrecht, The Netherlands
- Nov 17, 2016 **The skin microbiome in psoriasis.** Invited Speaker at SIDAPA, Verona, Italy
- Oct 20, 2016 **Studying MRSA in cystic fibrosis patients with an integrated metagenomic approach.** Invited Seminar at the Meyer Hospital, Florence, Italy
- Oct 18, 2016 **Strain-level population structure and genetic diversity of the human microbiome.** Invited Plenary Seminar at the San Raffaele Scientific Institute, Milan, Italy
- Oct 05, 2016 **Computational challenges in large-scale metagenomics.** Invited Keynote talk at the WIVACE 2016 Conference, Salerno, Italy
- Sep 30, 2016 **Perspectives for studying the oral microbiome with strain-level resolution.** Invited Seminar at the Institute of Odontology of the University of Gothenburg, Gothenburg, Sweden
- Sep 24, 2016 **Our research on the human microbiome.** Invited Talk at the "Third Microbiota workshop", Comano, Italy
- Sep 09, 2016 **The skin microbiome: a potential target for cosmeceutical approaches?.** Invited Talk at the "Prime Giornate di Medicina Estetica in Trentino Alto Adige", Trento, Italy
- Sep 07, 2016 **Strain-level population metagenomics: personalization, transmission and biogeography of the human microbiome.** Invited Talk at the "Second European Summer school on Nutrigenomics", Camerino, Italy
- Jul 06, 2016 **Uncovering the diversity of NTM: the computational (meta)genomic approach.** Invited Keynote Talk at "The 37th Annual Congress of the European Society of Mycobacteriology", Catania, Italy
- Jul 01, 2016 **Strain-level microbial epidemiology and population genomics from shotgun metagenomics.** Invited Talk at "The Barcelona Debates on the Human Microbiome: From Microbes to Medicines", Barcelona, Spain
- Jun 23, 2016 **Metagenomic analysis of the human microbiome with strain-level resolution.** Invited Keynote talk at the Joint UniMIB-UniSR PhD Course on "The Gut Microbiota Impact on the Immune System: Implications for Autoimmunity and Cancer", Milan, Italy
- Jun 17, 2016 **Strain-level microbiome profiling and "personalized" intestinal microbes.** Invited Keynote talk at the Third Paris Metagenomic Analysis Group, Paris, France
- Mar 24, 2016 **Shotgun metagenomics for studying oral and intestinal microbiomes at the strain-level.** Invited Seminar at the Center for Biomedicine, EURAC, Bolzano, Italy
- Feb 23, 2016 **The skin microbiome.** Invited Seminar at "LEO Pharma Italy", Rome, Italy

- Nov 20, 2015 **The human microbiome seen through shotgun metagenomics.** Invited Keynote Seminar at "Science Day 2015", University of Sassari, Sassari, Italy
- Nov 06, 2015 **Dieta, salute e microorganismi intestinali.** Invited talk at "Pensa Trasversale", Rovereto, Italy
- Oct 19, 2015 **Strain-level microbiome profiling for comparative (meta)genomics.** Invited Keynote talk at the "2nd Theodor Escherich Symposium on Medical Microbiome Research", Graz, Austria
- Oct 08, 2015 **Strain-level microbial comparative genomics using shotgun metagenomics.** Invited Keynote talk at "RECOMB Comparative Genomics 2015", Frankfurt, Germany
- Oct 03, 2015 **Trasmissione, personalizzazione, e modulazione del microbiota umano.** Invited talk at the "Second Microbiota workshop", Comano Terme, Italy
- Sep 10, 2015 **Metagenomics of the Skin: Results and Perspectives on our Microbial Interface.** Gold Prize Winner talk at the "45th Annual Meeting of the European Society for Dermatological Research", Rotterdam, The Netherlands
- Jun 06, 2015 **Strain-level population genomics of microbial organisms from shotgun metagenomics.** Invited talk at the "Symbiomes: Systems Biology of Host-Microbiome Interactions" conference, Pulstuk, Poland
- May 12, 2015 **Gut microbiota: The new world inside the human body.** Invited talk at the "Neurogenetics and genetics of the enteric nervous system" conference, Bologna, Italy
- Apr 16, 2015 **Metagenomic approaches for microbial epidemiology with strain-level resolution.** Invited talk at the "Parassitome workshop", Rome, Italy
- Apr 01, 2015 **Pangenome-based, meta'omic analysis highlights association of E. coli accessory gene content with risk of necrotizing enterocolitis in a cohort of pre-term infants.** Talk at the 5th International Human Microbiome Congress - IHMC Congress, Luxembourg City, Luxembourg
- Mar 19, 2015 **Next generation human microbiome research with computational shotgun metagenomics.** Invited seminar at the Institute of Biomembranes and Bioenergetics of the National Research Council, Bari, Italy
- Mar 05, 2015 **Computational shotgun metagenomics for high precision microbiome research.** Invited seminar at "New frontiers in Systems Biology" day for the PhD School in "Complex Systems for Life Sciences", Turin, Italy
- Sep 06, 2014 **Machine learning challenges in computational meta'omics.** Invited keynote talk at "Eighth International Workshop on Machine Learning in Systems Biology", Strasbourg, France
- Jun 27, 2014 **Theory and practical tutorial on shotgun metagenomic sequencing.** Invited session at "WebValley 2014", San Lorenzo in Banale, Italy
- Jun 26, 2014 **Theory and practical tutorial on 16S sequencing.** Invited session at "WebValley 2014", San Lorenzo in Banale, Italy
- Jun 24, 2014 **Approcci metagenomici per lo studio del microbiota umano.** Invited Talk at "Microbiota come genotipo esteso", Cortona, Italy
- Jun 11, 2014 **Strain-level microbiome characterization with shotgun metagenomics.** Invited Talk at "SocBiN Bioinformatics 2014", Oslo, Norway
- Mar 17, 2014 **Metagenomic Sequencing and Data Analysis in Class: The experience in the Master of Biotechnology at the University of Trento.** Invited Talk at "Assessment of training methods in NGS data analysis" COST Action BM1006 (SeqAhead), Instituto Gulbenkian de Ciência, Oeiras, Portugal
- Feb 15, 2014 **The human microbiome in health and disease.** Invited Talk at the "Microbiota", Trento, IT
- Oct 28, 2013 **Computational shotgun metagenomics for microbiome studies.** Invited Talk at the "8th CeBiTec Symposium: The Genomics Revolution and its Impact on Future Biotechnology", Bielefeld University, Bielefeld, DE

- Jul 04, 2013 **Computational shotgun metagenomics for human microbiome studies.** Seminar at University of Parma, Parma, Italy
- Jun 17, 2013 **Computational Marker-based Shotgun Metagenomics for Accurate Microbiome Studies.** "Next Generation Sequencing Data Congress", CBI Conference Centre, London, UK
- May 12, 2013 **Automating and improving taxonomic assignment with a high-resolution microbial phylogeny for microbiome studies.** Cell Symposia: Microbiome and Host Health, Lisbon, Portugal
- Mar 13, 2013 **Biogeography and diversity of the human microbiome characterized by shotgun metagenomics.** "Symbiomes: systems metagenomics of host microbe interactions", Fondazione Edmund Mach, San Michele, IT
- Nov 23, 2012 **Integrative computational methods for shotgun metagenomics.** "With a little help from your friends: tools and strategies for analysing microbiome sequence data", Glasgow Polyomics and University of Glasgow, Glasgow, UK
- Oct 26, 2012 **Computational shotgun metagenomics and the healthy human microbiome.** CIBIO seminar, Trento, Italy
- Oct 08, 2012 **Computational methods for shotgun metagenomics.** Bertinoro Computational Biology 2012, Bertinoro, Italy
- Jul 16, 2012 **Fast and accurate metagenomic profiling of microbial community composition using unique clade-specific marker genes.** 20th Annual International Conference on Intelligent Systems for Molecular Biology, Long Beach, CA, USA
- Sep 22, 2011 **Microbial community function and biomarker discovery in the human microbiome.** Beyond the Genome 2011, Washington DC, USA
- Jul 17, 2011 **Metagenomic biomarker discovery and the human microbiome.** 19th Annual International Conference on Intelligent Systems for Molecular Biology, Vienna, Austria
- Apr 15, 2011 **Metagenomic biomarker discovery and the human microbiome.** First Annual PQG/Interdisciplinary Training Grant Retreat. Harvard School of Public Health, Boston, MA, USA
- Mar 11, 2011 **Tutorial on LEfSe and HUMAnN.** DPWG Bioinformatics Tutorials Sessions, International Human Microbiome Congress, Vancouver, BC, Canada
- Mar 01, 2011 **Metagenomic biomarker discovery and the human microbiome.** Program in Quantitative Genomics (PQG): Working Group Series. Harvard School of Public Health, Boston, MA, USA
- Feb 23, 2011 **Metagenomic biomarker discovery and the human microbiome.** Seminar Series: The Microbial Systems (and Beyond) Seminar. Department of Civil & Environmental Engineering, Massachusetts Institute of Technology (MIT), Boston, MA, USA
- Dec 15, 2010 **Metagenomic biomarker discovery.** Department of Information Engineering and Computer Science, University of Trento, Italy.
- Feb 19, 2010 **Local machine learning approaches and process algebras for computational systems biology.** Department of Biostatistics, Harvard School of Public Health, Boston, MA, USA.
- Jul 23, 2009 **A scalable noise reduction technique for large case-based systems.** 8th International Conference on Case-Based Reasoning, Seattle, USA.
- Jun 11, 2009 **Local kernel machines.** Invited Seminar at the "Instance-Based Learning" doctoral course at DISI, Trento, Italy.
- May 19, 2009 **Empirical assessment of classification accuracy of Local SVM.** 19th Annual Belgian-Dutch Conference on Machine Learning, Tilburg, Belgium.
- Sep 06, 2005 **A Kalman filter based background updating algorithm robust to sharp illumination changes.** 13th International Conference on Image Analysis and Processing, Cagliari, Italy

Thesis supervisor

- 2020 **Germana Baldi (Master)** Large-scale metagenomic analysis of a previously unknown family of prevalent intestinal bacteria across populations
- 2020 **Davide Golzato (Master)** Evaluation of metagenomic protocols for gut microbiome analysis: from sampling to microbial genome reconstruction
- 2020 **Jasmine Chini (Bachelor)** Impact of different agricultural management practices and seasons on the structure and composition of soil bacterial communities
- 2020 **Giulia Calia (Master)** BRAN: a novel tool to explore subclonal genetic variants
- 2019 **Serena Manara (Ph.D.)** Strain-level (meta)genomic profiling of bacteria from hospital pathogens to non-human primate commensals
- 2019 **Chiara Mazzoni (Master)** Metagenomic and phylogenetic characterization of unexplored members of the human gut microbiome: the Christensenellaceae family
- 2019 **Paolo Ghensi (Ph.D.)** Characterization of biological and microbiological properties of dental implant surfaces and their relation with peri-implant diseases
- 2019 **Giacomo D'Amato. (Bachelor)** Expanding the curation and meta-analysis of human-associated metagenomic data
- 2019 **Francesco Asnicar (Ph.D.)** A phylogenetic framework for large-scale analysis of microbial communities
- 2019 **Eleonora Nigro. (Master)** Expanding the genetic diversity of the Elusimicrobia bacterial phylum by multi-environment metagenomic analysis
- 2019 **Gianmarco Piccinno. (Master)** Inference of microbial interaction network from metagenomics for two intestinal microbes: *Eubacterium rectale* and *Prevotella copri*
- 2019 **Claudia Mengoni. (Bachelor)** Extension of a phylogenetic framework for integrated analysis of microbial genomes from cultivation and metagenomics
- 2018 **Davide Bazzani. (Bachelor)** Meta-analysis of non-human primate gut microbiomes and their overlap with the human microbiome
- 2017 **Stefano Marangoni. (Bachelor)**
- 2017 **Giulia Corsi. (Master)** Comparative genomics of multiple strains of the pathogenic human parasite *Cryptosporidium parvum*
- 2017 **Francesco Beghini. (Master)** Association between tobacco exposure and the oral microbiome in the New York City HANES study
- 2016 **Moreno Zolfo. (Master)** Identification, Discovery and Characterisation of Viruses in the Human Microbiome
- 2016 **Pamela Ferretti. (Master)** Improving the reconstruction of bacterial genomes and metagenomes by combining short- and long-read sequencing technologies
- 2016 **Federico Taverna. (Master)** Overcoming the curse of compositionality with a novel approach for biomarker discovery in Metagenomics
- 2015 **Serena Manara. (Master)** Design and validation of a metatranscriptomic protocol for in-vivo gene expression profiling of lower airways and intestinal bacterial strains
- 2015 **Calogero Zarbo. (Master)** A Deep Learning predictive framework for Metagenomics based on microbiome functional potential profiles
- 2015 **Francesco Beghini. (Bachelor)** A computational meta-analysis of Blastocystis parasites in the human gut microbiome from shotgun metagenomic data

- 2015 **Thomas Tolio. (Master)** PanPhlAn: Strain-level Characterization of Microbes from Complex Metagenomic Samples
- 2014 **Francesco Asnicar. (Master)** PhyloPhlAn2 and GraPhlAn: novel reconstruction and visualization tools for large-scale whole-genome phylogenomics
- 2014 **Moreno Zolfo. (Bachelor)** A computational metagenomic pipeline for cultivation-free microbial strain typing
- 2014 **Pamela Ferretti. (Bachelor)** Empirical evaluation of DNA sequence assemblers and genome reconstruction of novel clinically relevant pathogen strains
- 2014 **Tiziana Gasperetti. (Bachelor)** Bioinformatic approaches to study the evolution of visual opsin genes on the Drosophila phylogeny
- 2013 **Temesgen Dadi. (Bachelor)** An integrative kernel-based machine learning framework for accurate microbiome studies

Publications

H-index	48 (Google Scholar), 42 (Scopus)
i10-index	80 (Google Scholar), 72 (Scopus)
# citations	>21,000 (Google Scholar), >15,000 (Scopus)

15 most representative papers as last and corresponding author in the last three years

- [1] Francesco Asnicar, Andrew Maltez Thomas, Francesco Beghini, Claudia Mengoni, Serena Manara, Paolo Manghi, Qiyun Zhu, Mattia Bolzan, Fabio Cumbo, Uyen May, Jon G Sanders, Moreno Zolfo, Evguenia Kopylova, Edoardo Pasolli, Rob Knight, Siavash Mirarab, Curtis Huttenhower, and Nicola Segata. Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. **Nature Communications**, (accepted), 2020.
- [2] Maria Carmen Collado and Nicola Segata. Initial exploration of in utero microbial colonization. **Nature Medicine (News&Views commentary)**, 26(4):469–470, 2020.
- [3] Nicolai Karcher, Edoardo Pasolli, Francesco Asnicar, Kun Huang, Adrian Tett, Serena Manara, Federica Armanini, Debbie Bain, Sylvia H Duncan, Petra Louis, Moreno Zolfo, Paolo Manghi, Mireia Vallescolomer, Roberta Raffaetà, Omar Rota-Stabelli, Maria Carmen Collado, Georg Zeller, Daniel Falush, Frank Maixner, Alan W Walker, Curtis Huttenhower, and Nicola Segata. Analysis of 1,321 Eubacterium rectale genomes from metagenomes uncovers complex phylogeographic population structures and subspecies functional adaptations. **Genome Biology**, (in press), 2020.
- [4] Moreno Zolfo, Federica Pinto, Francesco Asnicar, Adrian Tett, Frederic D Bushman, and Nicola Segata. Detecting contamination in viromes using ViromeQC. **Nature Biotechnology**, [I.F. 35.7], 37:1408–1412, 2019.
- [5] Adrian Tett, Kun Huang, Francesco Asnicar, Hannah Fehlner-Peach, Edoardo Pasolli, Nicolai Karcher, Federica Armanini, Paolo Manghi, Kevin Bonham, Moreno Zolfo, Francesca De Filippis, Cara Magnabosco, Richard Bonneau, John Lusingu, John Amuasi, Karl Reinhard, Thomas Rattei, Fredrik Boulund, Lars Engstrand, Albert Zink, Maria Carmen Collado, Dan Littman, Daniel Eibach, Danilo Ercolini, Omar Rota-Stabelli, Curtis Huttenhower, Frank Maixner, and Nicola Segata. The Prevotella copri complex comprises four distinct clades underrepresented in Westernized populations. **Cell Host & Microbe**, [I.F. 17.87], 26(5):666–679, 2019.
- [6] Nicola Segata. No bacteria found in healthy placentas. **Nature (News&Views commentary)**, [I.F. 41.6], 572(7769):317–318, 2019.
- [7] Edoardo Pasolli, Francesco Asnicar, Serena Manara, Moreno Zolfo, Nicolai Karcher, Federica Armanini, Francesco Beghini, Paolo Manghi, Adrian Tett, Paolo Ghensi, Maria Carmen Collado, Benjamin L Rice, Casey DuLong, Xochitl C Morgan, Christopher D Golden, Christopher Quince, Curtis Huttenhower, and Nicola Segata. Extensive unexplored human microbiome diversity revealed by over 150,000 genomes from metagenomes spanning age, geography, and lifestyle. **Cell**, [I.F. 31.40], 176(3):649–662, 2019.

- [8] Andrew Maltez Thomas, Paolo Manghi, Francesco Asnicar, Edoardo Pasolli, Federica Armanini, Moreno Zolfo, Francesco Beghini, Serena Manara, Nicolai Karcher, Chiara Pozzi, Sara Gandini, Davide Serrano, Sonia Tarallo, Antonio Francavilla, Gaetano Gallo, Mario Trompetto, Giulio Ferrero, Sayaka Mizutani, Hirotugu Shiroma, Satoshi Shiba, Tatsuhiro Shibata, Shinichi Yachida, Takuji Yamada, Jacob Wirbel, Petra Schrotz-King, Cornelia M Ulrich, Hermann Brenner, Manimozhiyan Arumugam, Peer Bork, Georg Zeller, Francesca Cordero, Emmanuel Dias-Neto, Joao Carlos Setubal, Adrian Tett, Barbara Pardini, Maria Rescigno, Levi Waldron, Alessio Naccarati, and Nicola Segata. Metagenomic analysis of colorectal cancer datasets identifies cross-cohort microbial diagnostic signatures and a link with choline degradation. **Nature Medicine**, [I.F. 32.62], 25:667–678, 2019.
- [9] Pamela Ferretti, Edoardo Pasolli, Adrian Tett, Francesco Asnicar, Valentina Gorfer, Sabina Fedi, Federica Armanini, Duy Tin Truong, Serena Manara, Moreno Zolfo, Francesco Beghini, Roberto Bertorelli, Veronica De Sanctis, Ilaria Bariletti, Rosarita Canto, Rosanna Clementi, Marina Cologna, Tiziana Crifò, Giuseppina Cusumano, Stefania Gottardi, Claudia Innamorati, Caterina Masè, Daniela Postai, Daniela Savoi, Sabrina Duranti, Gabriele A Andrea, Leonardo Mancabelli, Francesca Turroni, Chiara Ferrario, Christian Milani, Marta Mangifesta, Rosaria Anzalone, Alice Viappiani, Moran Yassour, Hera Vlamakis, Ramnik Xavier, Maria Carmen Collado, Omry Koren, Saverio Tateo, Massimo Soffiati, Anna Pedrotti, Marco Ventura, Curtis Huttenhower, Peer Bork, and Nicola Segata. Mother-to-infant microbial transmission from different body sites shapes the developing infant gut microbiome. **Cell Host & Microbe**, [I.F. 17.87], 24:133–145, 2018.
- [10] Serena Manara, Edoardo Pasolli, Daniela Dolce, Novella Ravenni, Silvia Campana, Federica Armanini, Francesco Asnicar, Alessio Mengoni, Luisa Galli, Carlotta Montagnani, Elisabetta Venturini, Omar Rota-Stabelli, Guido Grandi, Giovanni Taccetti, and Nicola Segata. Whole-genome epidemiology, characterization, and phylogenetic reconstruction of *Staphylococcus aureus* in a paediatric hospital. **Genome Medicine**, [I.F. 8.90], 10(82), 2018.
- [11] Edoardo Pasolli, Lucas Schiffer, Paolo Manghi, Audrey Renson, Valerie Obenchain, Duy Tin Truong, Francesco Beghini, Faizan Malik, Marcel Ramos, Jennifer B Dowd, Curtis Huttenhower, Martin Morgan, Nicola Segata*, and Levi Waldron*. Accessible, curated metagenomic data through ExperimentHub. **Nature Methods**, [I.F. 25.06], 14:1023–1024, 2017.
- [12] Christopher Quince, Jared T Simpson, Alan W Walker, Nicholas J Loman, and Nicola Segata. Shotgun metagenomics, from sampling to analysis. **Nature Biotechnology**, [I.F. 41.67], 35(9):833–844, 2017.
- [13] Francesco Beghini, Edoardo Pasolli, Duy Tin Truong, Lorenza Putignani, Simone Caccio, and Nicola Segata. Large-scale comparative metagenomics of *Blastocystis*, a common member of the human gut microbiome. **ISME Journal**, [I.F. 9.30], 11:2848–2863, 2017.
- [14] Duy Tin Truong, Adrian Tett, Edoardo Pasolli, Curtis Huttenhower, and Nicola Segata. Microbial strain-level population structure and genetic diversity from metagenomes. **Genome Research**, [I.F. 11.28], 27(4):626–638, 2017.
- [15] Adrian Tett, Edoardo Pasolli, Stefania Farina, Duy Tin Truong, Francesco Asnicar, Moreno Zolfo, Francesco Beghini, Federica Armanini, Olivier Jousson, Veronica De Sanctis, Roberto Bertorelli, Giampiero Girolomoni, Mario Cristofolini, and Nicola Segata. Unexplored diversity and strain-level structure of the skin microbiome associated with psoriasis. **npj Biofilms and Microbiomes**, 3(14):1–23, 2017.

All Papers (titles are web links)

- [1] Elena Zagato, Chiara Pozzi, Alice Bertocchi, Tiziana Schioppa, Fabiana Saccheri, Silvia Guglietta, Bruno Fosso, Laura Melocchi, Giulia Nizzoli, Jacopo Troisi, Marinella Marzano, Bianca Oresta, Ilaria Spadoni, Koji Atarashi, Sara Carloni, Stefania Arioli, Giulia Fornasa, Francesco Asnicar, Nicola Segata, Simone Guglielmetti, Kenya Honda, Graziano Pesole, William Vermi, Giuseppe Penna, and Maria Rescigno. Endogenous murine microbiota member *Faecalibaculum rodentium* and its human homologue protect from intestinal tumor growth. **Nature Microbiology**, [I.F. 14.3], 5:511–524, 2020.
- [2] Alexandre Almeida, Stephen Nayfach, Miguel Boland, Francesco Strozzi, Martin Beracochea, Zhou Jason Shi, Katherine S. Pollard, Ekaterina Sakharova, Donovan H. Parks, Philip Hugenholtz, Nicola Segata, Nikos C. Kyrpides, and Robert D. Finn. A unified sequence catalogue of over 200,000 genomes obtained from the human gut microbiome. **Nature Biotechnology**, (in press), 2020.
- [3] Francesco Asnicar, Andrew Maltez Thomas, Francesco Beghini, Claudia Mengoni, Serena Manara, Paolo Manghi, Qiyun Zhu, Mattia Bolzan, Fabio Cumbo, Uyen May, Jon G Sanders, Moreno Zolfo, Evguenia

Kopylova, Edoardo Pasolli, Rob Knight, Siavash Mirarab, Curtis Huttenhower, and Nicola Segata. Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. **Nature Communications**, (accepted), 2020.

- [4] Sarah E Berry, Ana M Valdes, David A Drew, Francesco Asnicar, Mohsen Mazidi, Jonathan Wolf, Joan Capdevila, George Hadjigeorgiou, Richard Davies, Haya Al Khatib, Christopher Bonnet, Sajaysura Ganesh, Elco Bakker, Deborah Hart, Massimo Mangino, Jordi Merino, Inbar Linenberg, Patrick Wyatt, Jose M Ordovas, Christopher D Gardner, Linda M Delahanty, Andrew T Chan*, Nicola Segata*, Paul W Franks*, and Tim D Spector*. Decoding Human Postprandial Responses to Food and their Potential for Precision Nutrition : the PREDICT 1 Study. **Nature Medicine**, in press, 2020.
- [5] Maria Carmen Collado and Nicola Segata. Initial exploration of in utero microbial colonization. **Nature Medicine (News&Views commentary)**, 26(4):469–470, 2020.
- [6] Lisa Derosa, Bertrand Routy, Marine Fidelle, Valerio Iebba, Laurie Alla, Edoardo Pasolli, Nicola Segata, Aude Desnoyer, Filippo Pietrantonio, Gladys Ferrere, Jean Eudes Fahrner, Emmanuelle Le Chatellier, Nicolas Pons, Nathalie Galleron, Hugo Roume, Connie P.M. Duong, Laura Mondragón, Kristina Iribarren, Mélodie Bonvalet, Safae Terrisse, Conrad Rauber, Anne Gaëlle Goubet, Romain Daillère, Fabien Lemaître, Anna Reni, Beatrice Casu, Maryam Tidjani Alou, Carolina Alves Costa Silva, Didier Raoult, Karim Fizazi, Bernard Escudier, Guido Kroemer, Laurence Albiges, and Laurence Zitvogel. Gut Bacteria Composition Drives Primary Resistance to Cancer Immunotherapy in Renal Cell Carcinoma Patients. **European Urology**, pages 1–12, 2020.
- [7] Aurélie Fluckiger, Romain Daillère, Mohamed Sassi, Barbara S Sixt, Peng Liu, Loos Friedemann, Richard Corentin, Catherine Rabu, Maryam T Alou, Anne-Gaëlle Goubet, Fabien Lemaître, Gladys Ferrere, Lisa Derosa, Connie PM Duong, Meriem Messaoudene, Andréanne Gagné, Philippe Joubert, Luisa De Sordi, Laurent Debarbieux, Sylvain Simon, Clara-Maria Scarlata, Maha Ayyoub, Belinda Parlermo, Francesco Facciolo, Romain Boidot, Richard Wheeler, Ivo G Boneca, Zsofia Sztupinszki, Krisztian Papp, Istvan Csabai, Edoardo Pasolli, Nicola Segata, Carlos Lopez-Otin, Zoltan Szallasi, Fabrice Andre, Valerio Iebba, Valentin Quiniou, David Klatzmann, Jacques Boukhalil, Saber Khelaifia, Didier Raoult, Laurence Albiges, Bernard Escudier, Alexander Eggermont, Fathia Mami-Chouaib, Paola Nistico, François Ghiringhelli, Bertrand Routy, Nathalie Labarrière, Vincent Cattoir, Guido Kroemer, and Laurence Zitvogel. Cross-reactivity between MHC class I-restricted antigens from cancer cells and an enterococcal bacteriophage. **Science**, (in press), 2020.
- [8] Nicolai Karcher, Edoardo Pasolli, Francesco Asnicar, Kun Huang, Adrian Tett, Serena Manara, Federica Armanini, Debbie Bain, Sylvia H Duncan, Petra Louis, Moreno Zolfo, Paolo Manghi, Mireia Valles-colomer, Roberta Raffaetà, Omar Rota-Stabelli, Maria Carmen Collado, Georg Zeller, Daniel Falush, Frank Maixner, Alan W Walker, Curtis Huttenhower, and Nicola Segata. Analysis of 1,321 *Eubacterium rectale* genomes from metagenomes uncovers complex phylogeographic population structures and subspecies functional adaptations. **Genome Biology**, (in press), 2020.
- [9] Thomas Yssing Michaelsen, Jakob Brandt, Caitlin Singleton, Rasmus Hansen Kirkegaard, Nicola Segata, and Mads Albertsen. The signal and the noise - characteristics of antisense RNA in complex microbial communities. **mSystems**, 5(1):e00587–19, 2020.
- [10] Edoardo Pasolli, Francesca De Filippis, Italia E Mauriello, Fabio Cumbo, Aaron M Walsh, John Leech, Paul D Cotter, Nicola Segata, and Danilo Ercolini. Large-scale genome-wide analysis links lactic acid bacteria from food with the gut microbiome. **Nature Communications**, accepted, 2020.
- [11] Serena Petrini, Paola Foladori, Francesco Beghini, Federica Armanini, Nicola Segata, and Gianni Andreotola. How inoculation affects the development and the performances of microalgal-bacterial consortia treating real municipal wastewater. **Journal of Environmental Management**, 263(March):110427, 2020.
- [12] Nan Qin, Peng Liang, Chunyan Wu, Guanqun Wang, Qian Xu, Xiao Xiong, Tingting Wang, Moreno Zolfo, Nicola Segata, Huanlong Qin, Rob Knight, Jack A. Gilbert, and Ting F. Zhu. Longitudinal survey of microbiome associated with particulate matter in a megacity. **Genome biology**, 21(1):55, 2020.
- [13] J. R. Swann, M. Rajilic-Stojanovic, A. Salonen, O. Sakwinska, C. Gill, A. Meynier, P. Faça-Berthon, B. Schelkle, N. Segata, C. Shortt, K. Tuohy, and O. Hasselwander. Considerations for the design and conduct of human gut microbiota intervention studies relating to foods. **European Journal of Nutrition**, (0123456789), 2020.

- [14] Moreno Zolfo, Federica Pinto, Francesco Asnicar, Adrian Tett, Frederic D Bushman, and Nicola Segata. Detecting contamination in viromes using ViromeQC. **Nature Biotechnology**, [I.F. 35.7], 37:1408–1412, 2019.
- [15] Adrian Tett, Kun Huang, Francesco Asnicar, Hannah Fehlner-Peach, Edoardo Pasolli, Nicolai Karcher, Federica Armanini, Paolo Manghi, Kevin Bonham, Moreno Zolfo, Francesca De Filippis, Cara Magnabosco, Richard Bonneau, John Lusingu, John Amuasi, Karl Reinhard, Thomas Rattei, Fredrik Boulund, Lars Engstrand, Albert Zink, Maria Carmen Collado, Dan Littman, Daniel Eibach, Danilo Ercolini, Omar Rota-Stabelli, Curtis Huttenhower, Frank Maixner, and Nicola Segata. The *Prevotella copri* complex comprises four distinct clades underrepresented in Westernized populations. **Cell Host & Microbe**, [I.F. 17.87], 26(5):666–679, 2019.
- [16] Sonia Tarallo, Giulio Ferrero, Gaetano Gallo, Antonio Francavilla, Giuseppe Clerico, Alberto Realis Luc, Paolo Manghi, Andrew Maltez Thomas, Paolo Vineis, Nicola Segata, Barbara Pardini, Alessio Naccarati, and Francesca Cordero. Altered fecal small RNA profiles in colorectal cancer reflect gut microbiome composition in stool samples. **mSystems**, [I.F. 5.8], 4(5):e00289–19, 2019.
- [17] Nicola Segata. No bacteria found in healthy placentas. **Nature (News&Views commentary)**, [I.F. 41.6], 572(7769):317–318, 2019.
- [18] Evan Bolyen, Jai Ram Rideout, Matthew R Dillon, Nicholas A Bokulich, Christian Abnet, Gabriel A Al-Ghalith, Harriet Alexander, Eric J Alm, Manimozhiyan Arumugam, Francesco Asnicar, Yang Bai, Jordan E Bisanz, Kyle Bittinger, Asker Brejnrod, Colin J Brislawn, C Titus Brown, Benjamin J Callahan, Andrés Mauricio Caraballo-Rodríguez, John Chase, Emily Cope, Ricardo Da Silva, Pieter C Dorrestein, Gavin M Douglas, Daniel M Durall, Claire Duvallet, Christian F Edwardson, Madeleine Ernst, Mehrbod Estaki, Jennifer Fouquier, Julia M Gauglitz, Deanna L Gibson, Antonio Gonzalez, Kestrel Gorlick, Jiarong Guo, Benjamin Hillmann, Susan Holmes, Hannes Holste, Curtis Huttenhower, Gavin Huttley, Stefan Janssen, Alan K Jarmusch, Lingjing Jiang, Benjamin Kaehler, Kyo Bin Kang, Christopher R Keefe, Paul Keim, Scott T Kelley, Dan Knights, Irina Koester, Tomasz Kosciolk, Jorden Kreps, Morgan G Langille, Joslynn Lee, Ruth Ley, Yong-Xin Liu, Erika Loftfield, Catherine Lozupone, Massoud Maher, Clarisse Marotz, Bryan Martin, Daniel McDonald, Lauren J McIver, Alexey V Melnik, Jessica L Metcalf, Sydney C Morgan, Jamie Morton, Ahmad Turan Naimey, Jose A Navas-Molina, Louis Felix Nothias, Stephanie B Orchanian, Talima Pearson, Samuel L Peoples, Daniel Petras, Mary Lai Preuss, Elmar Priesse, Lasse Buur Rasmussen, Adam Rivers, Il Michael S Robeson, Patrick Rosenthal, Nicola Segata, Michael Shaffer, Arron Shiffer, Rashmi Sinha, Se Jin Song, John R Spear, Austin D Swafford, Luke R Thompson, Pedro J Torres, Pauline Trinh, Anupriya Tripathi, Peter J Turnbaugh, Sabah Ul-Hasan, Justin JJ van der Hooft, Fernando Vargas, Yoshiaki Vázquez-Baeza, Emily Vogtmann, Max von Hippel, William Walters, Yunhu Wan, Mingxun Wang, Jonathan Warren, Kyle C Weber, Chase HD Williamson, Amy D Willis, Zhenjiang Zech Xu, Jesse R Zaneveld, Yilong Zhang, Rob Knight, and J Gregory Caporaso. Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. **Nature Biotechnology**, [I.F. 35.7], 37:848–857, 2019.
- [19] Francesco Beghini, Audrey Renson, Christine P. Zolnik, Ludwig Geistlinger, Mykhaylo Usyk, Thomas U. Moody, Lorna Thorpe, Jennifer B. Dowd, Robert Burk, Nicola Segata, Heidi E. Jones, and Levi Waldron. Tobacco exposure associated with oral microbiota oxygen utilization in the New York City Health and Nutrition Examination Study. **Annals of Epidemiology**, [I.F. 2.8], 34:18–25.e3, 2019.
- [20] Francesca De Filippis, Edoardo Pasolli, Adrian Tett, Sonia Tarallo, Alessio Naccarati, Maria De Angelis, Erasmo Neviani, Luca Cocolin, Marco Gobetti, Nicola Segata, and Danilo Ercolini. Distinct genetic and functional strains of human intestinal *Prevotella copri* are associated with different habitual diets. **Cell Host & Microbe**, [I.F. 17.87], 25(3):444–453, 2019.
- [21] Daniela Dolce, Stella Neri, Laura Grisotto, Silvia Campana, Novella Ravenni, Francesca Miselli, Erica Camera, Lucia Zavataro, Cesare Braggion, Ersilia Fiscarelli, Vincenzina Lucidi, Lisa Cariani, Daniela Girelli, Nadia Faelli, Carla Colombo, Cristina Lucanto, Mariangela Lombardo, Giuseppe Magazzu, Antonella Tosco, Valeria Raia, Serena Manara, Edoardo Pasolli, Federica Armanini, Nicola Segata, Annibale Biggeri, and Giovanni Taccetti. Methicillin-resistant *Staphylococcus aureus* eradication in cystic fibrosis patients: a randomized multicenter study. **PLOS ONE**, 14(3), 2019.
- [22] Hannah Fehlner-Peach, Cara Magnabosco, Varsha Raghavan, Jose U Scher, Adrian Tett, Laura M Cox, Claire Gottsegen, Aaron Watters, John D Wiltshire-Gordon, Nicola Segata, Richard Bonneau, and Dan R Littman. Distinct polysaccharide growth profiles of human intestinal *Prevotella copri* isolates. **Cell host & microbe**, 26(5):680–690, 2019.

- [23] Paolo Ghensi, Elia Bettio, Devid Maniglio, Emiliana Bonomi, Federico Piccoli, Silvia Gross, Patrizio Caciagli, Nicola Segata, Giandomenico Nollo, and Francesco Tassarolo. Dental Implants with Anti-Biofilm Properties: A Pilot Study for Developing a New Sericin-Based Coating. **Materials**, 12(2429):1–15, 2019.
- [24] Luigi Francesco Iannone, Alberto Preda, Hervé M Blottière, Gerard Clarke, Diego Albani, Vincenzo Belcastro, Marco Carotenuto, Annamaria Cattaneo, Rita Citraro, Cinzia Ferraris, Francesca Ronchi, Gaia Lungo, Elisa Santocchi, Letizia Guiducci, Pietro Baldelli, Paola Iannetti, Sigrid Pedersen, Andrea Petretto, Stefania Provasi, Kaja Selmer, Alberto Spalice, Anna Tagliabue, Alberto Verrotti, Nicola Segata, Jakob Zimmermann, Carlo Minetti, Paolo Mainardi, Carmen Giordano, Sanjay Sisodiya, Federico Zara, Emilio Russo, and Pasquale Striano. Microbiota-gut brain axis involvement in neuropsychiatric disorders. **Expert review of neurotherapeutics**, (1473-7175):1–14, 2019.
- [25] Serena Manara, Francesco Asnicar, Francesco Beghini, Davide Bazzani, Fabio Cumbo, Moreno Zolfo, Eleonora Nigto, Nicolai Karcher, Paolo Manghi, Marisa Isabell Metzger, Edoardo Pasolli, and Nicola Segata. Microbial genomes from gut metagenomes of non-human primates expand the tree-of-life with over 1,000 novel species. **Genome Biology**, 20(299), 2019.
- [26] Andrew McBain, Catherine O'Neill, Alejandro Amézquita, Laura Price, Karoline Faust, Adrian Tett, Nicola Segata, Jonathan Swann, Adrian Smith, Barry Murphy, Mike Hoptroff, Gordon James, Yugandhar Reddy, Anindya Dasgupta, Thomas Ross, Iain Chapple, William Wade, and Judith Fernandez-Piquer. Consumer Safety Considerations of Skin and Oral Microbiome Perturbation. **Clinical Microbiology Reviews**, [I.F. 17.4], 32(4):e00051–19, 2019.
- [27] Edoardo Pasolli, Francesco Asnicar, Serena Manara, Moreno Zolfo, Nicolai Karcher, Federica Armanini, Francesco Beghini, Paolo Manghi, Adrian Tett, Paolo Ghensi, Maria Carmen Collado, Benjamin L Rice, Casey DuLong, Xochitl C Morgan, Christopher D Golden, Christopher Quince, Curtis Huttenhower, and Nicola Segata. Extensive unexplored human microbiome diversity revealed by over 150,000 genomes from metagenomes spanning age, geography, and lifestyle. **Cell**, [I.F. 31.40], 176(3):649–662, 2019.
- [28] Renato Pedron, Alfonso Esposito, Irene Bianconi, Edoardo Pasolli, Adrian Tett, Francesco Asnicar, Mario Cristofolini, Nicola Segata, and Olivier Jousson. Genomic and metagenomic insights into the microbial community of a thermal spring. **Microbiome**, [I.F. 10.5], 7(8), 2019.
- [29] Audrey Renson, Heidi E. Jones, Francesco Beghini, Nicola Segata, Christine P. Zolnik, Mykhaylo Usyk, Thomas U. Moody, Lorna Thorpe, Robert Burk, Levi Waldron, and Jennifer B. Dowd. Sociodemographic variation in the oral microbiome. **Annals of Epidemiology**, [I.F. 2.8], 35:73–80.e2, 2019.
- [30] Lucas Schiffer, Rimsha Azhar, Lori Shepherd, Marcel Ramos, Ludwig Geistlinger, Curtis Huttenhower, Jennifer B. Dowd, Nicola Segata, and Levi Waldron. HMP16SData: Efficient Access to the Human Microbiome Project Through Bioconductor. **American journal of epidemiology**, [I.F. 4.5], 188(6):1023–1026, 2019.
- [31] Andrew Maltez Thomas, Paolo Manghi, Francesco Asnicar, Edoardo Pasolli, Federica Armanini, Moreno Zolfo, Francesco Beghini, Serena Manara, Nicolai Karcher, Chiara Pozzi, Sara Gandini, Davide Serrano, Sonia Tarallo, Antonio Francavilla, Gaetano Gallo, Mario Trompetto, Giulio Ferrero, Sayaka Mizutani, Hirotugu Shiroma, Satoshi Shiba, Tatsuhiro Shibata, Shinichi Yachida, Takuji Yamada, Jacob Wirbel, Petra Schrotz-King, Cornelia M Ulrich, Hermann Brenner, Manimozhiyan Arumugam, Peer Bork, Georg Zeller, Francesca Cordero, Emmanuel Dias-Neto, Joao Carlos Setubal, Adrian Tett, Barbara Pardini, Maria Rescigno, Levi Waldron, Alessio Naccarati, and Nicola Segata. Metagenomic analysis of colorectal cancer datasets identifies cross-cohort microbial diagnostic signatures and a link with choline degradation. **Nature Medicine**, [I.F. 32.62], 25:667–678, 2019.
- [32] Andrew Maltez Thomas and Nicola Segata. Multiple levels of the unknown in microbiome research. **BMC Biology**, [I.F. 6.7], 17(48), 2019.
- [33] Levi Waldron, Lucas Schiffer, Rimsha Azhar, Marcel Ramos, Ludwig Geistlinger, and Nicola Segata. Waldron et al. Reply to "Commentary on the HMP16SData Bioconductor Package". **American journal of epidemiology**, [I.F. 4.5], 188(6):1031–1032, 2019.
- [34] Jacob Wirbel, Pyl Paul Theodor, Ece Kartal, Konrad Zych, Alireza Kashani, Alessio Milanese, Fleck Jonas S, Voigt Anita Y, Albert Palleja, Ruby Ponnudurai, Shinichi Sunagawa, Coelho Luis Pedro, Petra Schrotz-King, Emily Vogtmann, Nina Habermann, Emma Niméus, Andrew Thomas, Paolo Manghi, Sara Gandini, Davide Serrano, Sayaka Mizutani, Hirotugu Shiroma, Satoshi Shiba, Tatsuhiro Shibata, Shinichi Yachida, Takuji Yamada, Levi Waldron, Alessio Naccarati, Nicola Segata, Rashmi Sinha, Cornelia M Ulrich, Hermann Brenner, Manimozhiyan Arumugam, Peer Bork, and Georg Zeller. Meta-analysis of

fecal metagenomes reveals global microbial signatures that are specific for colorectal cancer. **Nature Medicine**, [I.F. 32.62], 25:679–689, 2019.

- [35] Sander Wuyts and Nicola Segata. At the forefront of the sequencing revolution - notes from the RINGS19 conference. **Genome Biology**, [I.F. 13.2], 20(93):19–21, 2019.
- [36] Qiyum Zhu, Uyen Mai, Wayne Pfeiffer, Stefan Janssen, Francesco Asnicar, Jon G Sanders, Pedro Belda-Ferre, Gabriel A Al-Ghalith, Evguenia Kopylova, Daniel McDonald, Tomasz Kosciolk, John B Yin, Shi Huang, Nimaichand Salam, Jian-Yu Jiao, Zijun Wu, Zhenjiang Z Xu, Kalem Cantrell, Yimeng Yang, Erfan Sayyari, Maryam Rabiee, James T Morton, Sheila Podell, Dan Knights, Wen-Jun Li, Curtis Huttenhower, Nicola Segata, Larry Smarr, Siavash Mirarab, and Rob Knight. Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. **Nature Communications**, 10(5477), 2019.
- [37] Erik Dassi, Pamela Ferretti, Giuseppina Covello, HTM-CMB-2015, Roberto Bertorelli, Michela A Denti, Veronica De Sanctis, Adrian Tett, and Nicola Segata. The short-term impact of probiotic consumption on the oral cavity microbiome. **Scientific Reports**, [I.F. 4.12], 8(10476), 2018.
- [38] Pamela Ferretti, Edoardo Pasolli, Adrian Tett, Francesco Asnicar, Valentina Gorfer, Sabina Fedi, Federica Armanini, Duy Tin Truong, Serena Manara, Moreno Zolfo, Francesco Beghini, Roberto Bertorelli, Veronica De Sanctis, Iliaria Bariletti, Rosarita Canto, Rosanna Clementi, Marina Cologna, Tiziana Crifò, Giuseppina Cusumano, Stefania Gottardi, Claudia Innamorati, Caterina Masè, Daniela Postai, Daniela Savoi, Sabrina Duranti, Gabriele A Andrea, Leonardo Mancabelli, Francesca Turroni, Chiara Ferrario, Christian Milani, Marta Mangifesta, Rosaria Anzalone, Alice Viappiani, Moran Yassour, Hera Vlamakis, Ramnik Xavier, Maria Carmen Collado, Omry Koren, Saverio Tateo, Massimo Soffiati, Anna Pedrotti, Marco Ventura, Curtis Huttenhower, Peer Bork, and Nicola Segata. Mother-to-infant microbial transmission from different body sites shapes the developing infant gut microbiome. **Cell Host & Microbe**, [I.F. 17.87], 24:133–145, 2018.
- [39] Eric A Franzosa, Lauren J Mciver, Gholamali Rahnavard, Luke R Thompson, Melanie Schirmer, George Weingart, Karen Schwarzberg Lipson, Rob Knight, Gregory Caporaso, Nicola Segata, and Curtis Huttenhower. Species-level functional profiling of metagenomes and metatranscriptomes. **Nature Methods**, [I.F. 26.92], 15:962–968, 2018.
- [40] Daniel Kissling, Jorge Ahumada, Anne Bowser, Miguel Fernandez, Nestor Fernandez, Enrique Alonso Garcia, Robert Guralnick, Nick Isaac, Steve Kelling, Wouter Los, Louise McRae, Jean-Baptiste Mihoub, Matthias Obst, Monica Santamaria, Andrew Skidmore, Kristen Williams, Donat Agosti, Daniel Amariles, Christos Arvanitidis, Lucy Bastin, Francesca De Leo, Willi Egloff, Jane Elith, Donald Hobern, David Martin, Henrique Pereira, Graziano Pesole, Johannes Peterseil, Hannu Saarenmaa, Dmitry Schigel, Dirk Schmeller, Nicola Segata, Eren Turak, Paul Uhler, Brian Wee, and Alex Hardisty. Building essential biodiversity variables (EBVs) of species distribution and abundance at a global scale. **Biological Reviews**, [I.F. 11.61], 93(1):600–625, 2018.
- [41] Katri Korpela, Paul Costea, Luis Pedro Coelho, Stefanie Kandels-Lewis, Gonneke Willemsen, Dorret I Boomsma, Nicola Segata, and Peer Bork. Selective maternal seeding and environment shape the human gut microbiome. **Genome Research**, [I.F. 11.28], 28:561–568, 2018.
- [42] Serena Manara, Edoardo Pasolli, Daniela Dolce, Novella Ravenni, Silvia Campana, Federica Armanini, Francesco Asnicar, Alessio Mengoni, Luisa Galli, Carlotta Montagnani, Elisabetta Venturini, Omar Rota-Stabelli, Guido Grandi, Giovanni Taccetti, and Nicola Segata. Whole-genome epidemiology, characterization, and phylogenetic reconstruction of *Staphylococcus aureus* in a paediatric hospital. **Genome Medicine**, [I.F. 8.90], 10(82), 2018.
- [43] Federica Pinto, Adrian Tett, Federica Armanini, Francesco Asnicar, Adriano Boscaini, Edoardo Pasolli, Moreno Zolfo, Claudio Donati, Nico Salmasso, and Nicola Segata. Draft genome sequences of novel *Pseudomonas*, *Flavobacterium*, and *Sediminibacterium* strains from a freshwater ecosystem. **Genome Announcements**, pages 2–4, 2018.
- [44] Nicola Segata. On the road to strain-resolved comparative metagenomics. **mSystems**, [I.F. 5.75], 3(2), 2018.
- [45] Heba Shaaban, David A. Westfall, Rawhi Mohammad, David Danko, Daniela Bezdán, Ebrahim Afshinnekoo, Nicola Segata, and Christopher E. Mason. The Microbe Directory: An annotated, searchable inventory of microbes' characteristics. **Gates Open Research**, 2018.

- [46] Angelo Joshua Victoria, Ernelea Cao, Nico Salmaso, Nicola Segata, and Claudio Donati. Draft Genome Sequence of the Cadmium-Resistant Strain JJU2, Belonging to the Family *Hapalosiphonaceae* of the *Cyanobacteria*. **Microbiology Resource Announcements**, 7(8):4–5, 2018.
- [47] Moran Yassour, Larson Hogstrom, Eeva Jason, Heli Siljander, Jenni Selvenius, Sami Oikarinen, Heikki Hyöty, Jorma Ilonen, Suvi Virtanen, Pamela Ferretti, Edoardo Pasolli, Adrian Tett, Francesco Asnicar, Nicola Segata, Hera Vlamakis, Eric Lander, Curtis Huttenhower, Mikael Knip, and Ramnik Xavier. Strain-level analysis of mother-to-child bacterial transmission during the first few months of life. **Cell Host & Microbe**, [I.F. 17.87], 24:146–154, 2018.
- [48] Moreno Zolfo, Francesco Asnicar, Paolo Manghi, Edoardo Pasolli, Adrian Tett, and Nicola Segata. Profiling microbial strains in urban environments using metagenomic sequencing data. **Biology Direct**, 13(9), 2018.
- [49] Edoardo Pasolli, Lucas Schiffer, Paolo Manghi, Audrey Renson, Valerie Obenchain, Duy Tin Truong, Francesco Beghini, Faizan Malik, Marcel Ramos, Jennifer B Dowd, Curtis Huttenhower, Martin Morgan, Nicola Segata*, and Levi Waldron*. Accessible, curated metagenomic data through ExperimentHub. **Nature Methods**, [I.F. 25.06], 14:1023–1024, 2017.
- [50] Christopher Quince, Jared T Simpson, Alan W Walker, Nicholas J Loman, and Nicola Segata. Shotgun metagenomics, from sampling to analysis. **Nature Biotechnology**, [I.F. 41.67], 35(9):833–844, 2017.
- [51] Francesco Beghini, Edoardo Pasolli, Duy Tin Truong, Lorenza Putignani, Simone Caccio, and Nicola Segata. Large-scale comparative metagenomics of *Blastocystis*, a common member of the human gut microbiome. **ISME Journal**, [I.F. 9.30], 11:2848–2863, 2017.
- [52] Duy Tin Truong, Adrian Tett, Edoardo Pasolli, Curtis Huttenhower, and Nicola Segata. Microbial strain-level population structure and genetic diversity from metagenomes. **Genome Research**, [I.F. 11.28], 27(4):626–638, 2017.
- [53] Francesco Asnicar, Serena Manara, Moreno Zolfo, Duy Tin Truong, Matthias Scholz, Federica Armanini, Pamela Ferretti, Valentina Gorfer, Anna Pedrotti, Adrian Tett, and Nicola Segata. Studying vertical microbiome transmission from mothers to infants by strain-level metagenomic profiling. **mSystems**, 2(1), 2017.
- [54] Giovanni Bacci, Alessio Mengoni, Ersilia Fiscarelli, Nicola Segata, Giovanni Taccetti, Daniela Dolce, Patrizia Paganin, Patrizia Morelli, Vanessa Tuccio, Alessandra De Alessandri, Vincenzina Lucidi, and Annamaria Bevivino. A Different Microbiome Gene Repertoire in the Airways of Cystic Fibrosis Patients with Severe Lung Disease. **International Journal of Molecular Sciences**, 18(8):1654, 2017.
- [55] Sabrina Duranti, Gabriele Andrea Lugli, Leonardo Mancabelli, Federica Armanini, Francesca Turrone, Kieran James, Pamela Ferretti, Valentina Gorfer, Chiara Ferrario, Christian Milani, Marta Mangifesta, Rosaria Anzalone, Moreno Zolfo, Alice Viappiani, Edoardo Pasolli, Ilaria Bariletti, Rosarita Canto, Rosanna Clementi, Marina Cologna, Tiziana Crifò, Giuseppina Cusumano, Sabina Fedi, Stefania Gottardi, Claudia Innamorati, Caterina Masè, Daniela Postai, Daniela Savoi, Massimo Soffiati, Saverio Tateo, Anna Pedrotti, Nicola Segata, Douwe van Sinderen, and Marco Ventura. Maternal inheritance of bifidobacterial communities and bifidophages in infants through vertical transmission. **Microbiome**, [I.F. 8.50], 5(1):66, 2017.
- [56] Tarcisio Fedrizzi, Conor J Meehan, Antonella Grottola, Elisabetta Giacobazzi, Fregni Serpini, Sara Tagli-azucchi, Anna Fabio, Clotilde Bettua, Roberto Bertorelli, Veronica De Sanctis, Fabio Rumpianesi, Monica Pecorari, Olivier Jousson, Enrico Tortoli, and Nicola Segata. Genomic characterization of Nontuberculous Mycobacteria. **Scientific Reports**, [I.F. 5.23], 7(45254):1–19, 2017.
- [57] Pamela Ferretti, Stefania Farina, Mario Cristofoloni, Giampiero Girolomoni, Adrian Tett, and Nicola Segata. Experimental metagenomics and ribosomal profiling of the human skin microbiome. **Experimental Dermatology**, [I.F. 2.67], 26(3):211–219, 2017.
- [58] Lauren J Mciver, Galeb Abu-ali, Eric A Franzosa, Randall Schwager, Xochitl C. Morgan, Levi Waldron, Nicola Segata, and Curtis Huttenhower. bioBakery: A meta’omic analysis environment. **Bioinformatics**, [I.F. 7.30], btx754, 2017.
- [59] Federica Pinto, Adrian Tett, Federica Armanini, Francesco Asnicar, Adriano Boscaini, Edoardo Pasolli, Moreno Zolfo, Claudio Donati, Nico Salmaso, and Nicola Segata. Draft Genome Sequence of the Planktic Cyanobacterium *Tychonema bourrellyi*, Isolated from Alpine Lentic Freshwater. **Genome Announcements**, 5(47):49–50, 2017.

- [60] Adrian Tett, Edoardo Pasolli, Stefania Farina, Duy Tin Truong, Francesco Asnicar, Moreno Zolfo, Francesco Beghini, Federica Armanini, Olivier Jousson, Veronica De Sanctis, Roberto Bertorelli, Giampiero Girolomoni, Mario Cristofolini, and Nicola Segata. Unexplored diversity and strain-level structure of the skin microbiome associated with psoriasis. **npj Biofilms and Microbiomes**, 3(14):1–23, 2017.
- [61] Enrico Tortoli, Tarcisio Fedrizzi, Conor J Meehan, Antonella Grottola, Elisabetta Giacobazzi, Giulia Fregni, Sara Tagliazucchi, Anna Fabio, Clotilde Bettua, Francesca Frascaro, Veronica De Sanctis, Olivier Jousson, Nicola Segata, Daniela M Cirillo, Anna Fabio, Clotilde Bettua, Roberto Bertorelli, Francesca Frascaro, Veronica De Sanctis, Monica Pecorari, Olivier Jousson, Nicola Segata*, and Daniela M Cirillo*. The new phylogeny of the genus *Mycobacterium*: The old and the news Enrico. **Infection, Genetics and Evolution**, 56(October):19–25, 2017.
- [62] Lorenzo Tosi, Viswanadham Sridhara, Yunlong Yang, Dongli Gua, Polina Shpilker, Nicola Segata, Harry Larman, and Biju Parekkadan. Long-adapter single-stranded oligonucleotide probes for the massively multiplexed cloning of kilobase genome regions. **Nature Biomedical Engineering**, 1(0092), 2017.
- [63] Sander Wuyts, Stijn Wittouck, Ilke De Boeck, Camille Allonsius, Pasolli Edoardo, Nicola Segata, and Sarah Lebeer. Large-scale phylogenomics of the *Lactobacillus casei* group highlights taxonomic inconsistencies and reveals novel clade-associated features. **mSystems**, 2(4), 2017.
- [64] Moreno Zolfo, Adrian Tett, Olivier Jousson, Claudio Donati, and Nicola Segata. MetaMLST: multi-locus strain-level bacterial typing from metagenomic samples. **Nucleic Acid Research**, [I.F. 10.16], 45(2):e7, 2017.
- [65] Claudio Donati, Moreno Zolfo, Davide Albanese, Duy Tin Truong, Francesco Asnicar, Valerio Iebba, Duccio Cavalieri, Olivier Jousson, Carlotta De Filippo, Curtis Huttenhower, and Nicola Segata. Uncovering oral *Neisseria* tropism and persistence using metagenomic sequencing. **Nature Microbiology**, [I.F. 14.17], (16070), 2016.
- [66] Edoardo Pasolli, Tin Truong, Faizan Malik, Levi Waldron, and Nicola Segata. Machine learning meta-analysis of large metagenomic datasets : tools and biological insights. **PLoS Computational Biology**, [I.F. 4.62], 12(7):e1004977, 2016.
- [67] Matthias Scholz*, Doyle Ward*, Thomas Tolio, Moreno Zolfo, Francesco Asnicar, Duy Tin Truong, Edoardo Pasolli, Adrian Tett, Ardythe Morrow, and Nicola Segata. Strain-level microbial epidemiology and population genomics from shotgun metagenomics. **Nature Methods**, [I.F. 32.1], 13(5):435–438, 2016.
- [68] Nicola Segata, Francesco Baldini, Julien Pompon, Wendy S Garrett, Duy Tin Truong, Rock K Dabiré, Abdoulaye Diabaté, Elena A Levashina, and Flaminia Catteruccia. The reproductive tracts of two malaria vectors are populated by a core microbiome and by gender- and swarm-enriched microbial biomarkers. **Scientific Reports**, [I.F. 5.6], 6(24207):1–10, 2016.
- [69] The MetaSUB International Consortium (including Nicola Segata). The Metagenomics and Metadesign of the Subways and Urban Biomes (MetaSUB) International Consortium inaugural meeting report. **Microbiome**, 4(24), 2016.
- [70] Doyle Ward, Matthias Scholz, Moreno Zolfo, Diana H Taft, Kurt R Schibler, Adrian Tett, Nicola Segata*, and Ardythe L Morrow*. Metagenomic sequencing with strain-level resolution implicates uropathogenic *E. coli* in necrotizing enterocolitis and death in preterm infants. **Cell Reports**, [I.F. 8.4], 14:1–13, 2016.
- [71] Duy Tin Truong, Eric Franzosa, Timothy Tickle, Matthias Scholz, George Weingart, Edoardo Pasolli, Adrian Tett, Curtis Huttenhower, and Nicola Segata. MetaPhlAn2 for enhanced metagenomic taxonomic profiling. **Nature Methods**, [I.F. 32.07], 12(10):902–903, 2015.
- [72] Christian Milani, Gabriele Andrea Lugli, Sabrina Duranti, Francesca Turrone, Leonardo Mancabelli, Chiara Ferrario, Marta Mangifesta, Arancha González, Alice Viappiani, Matthias Scholz, Stefania Arioli, Borja Sanchez, Jonathan Lane, Doyle V Ward, Rita Hickey, Diego Mora, Nicola Segata, Abelardo Margolles, Douwe Van Sinderen, and Marco Ventura. Bifidobacteria exhibit social behavior through carbohydrate resource sharing in the gut. **Scientific Reports**, 5(15782), 2015.
- [73] Nicola Segata. Gut Microbiome: Westernization and the Disappearance of Intestinal Diversity. **Current Biology**, [I.F. 9.57], 25(14):R611–R613, 2015.
- [74] James Kaminski, Molly K Gibson, Eric A Franzosa, Nicola Segata, Gautam Dantas, and Curtis Huttenhower. High-specificity targeted functional profiling in microbial communities with ShortBRED. **PLoS computational biology**, [I.F. 4.62], 11(12):e1004557, 2015.

- [75] Francesco Asnicar, George Weingart, Timothy L. Tickle, Curtis Huttenhower, and Nicola Segata. Compact graphical representation of phylogenetic data and metadata with GraPhlAn. **PeerJ**, 3:e1029, 2015.
- [76] Ana R. Fusco da Costa, Tarcisio Fedrizzi, Maria L Lopes, Monica Pecorari, Wana L Oliveira da Costa, Elisabetta Giacobazzi, Jeann R da Costa Bahia, Veronica De Sanctis, Karla V Batista Lima, Roberto Bertorelli, Antonella Grottola, Anna Fabio, Pamela Ferretti, Francesca Di Leva, Giulia Fregni Serpini, Sara Tagliazucchi, Fabio Rumpianesi, Olivier Jousson, Nicola Segata, and Enrico Tortoli. Characterization of 17 strains belonging to the *Mycobacterium simiae* complex and description of *Mycobacterium paraense* sp. nov. **International Journal of Systematic and Evolutionary Microbiology**, 2015.
- [77] Christian Milani, Leonardo Mancabelli, Gabriele Andrea Lugli, Sabrina Duranti, Francesca Turrone, Chiara Ferrario, Marta Mangifesta, Alice Viappiani, Pamela Ferretti, Valentina Gorfer, Adrian Tett, Nicola Segata, Sinderen van Douwe, and Marco Ventura. Exploring vertical transmission of bifidobacteria from mother to child. **Applied and environmental microbiology**, [I.F. 3.67], 81(20):02037–15, 2015.
- [78] Kieran Tuohy, Francesca Fava, and Nicola Segata. Studying the microbiota and microbial ecology of the GI tract in the Omics Era: Tools for stools. In *Probiotics and Prebiotics: Current Research and Future Trends*, page 560. 2015.
- [79] Francesco Baldini*, Nicola Segata*, Julien Pompon*, Roch Dabiré, Abdoulaye Diabaté, Elena Levashina[^], and Flaminia Catteruccia[^]. Evidence of natural Wolbachia infections in field populations of *Anopheles gambiae*. **Nature Communications**, [I.F 10.74], 5, 2014.
- [80] Eric A Franzosa, Xochitl C Morgan, Nicola Segata, Levi Waldron, Joshua Reyes, Ashlee M Earl, Georgia Giannoukos, Matthew Boylan, Dawn M Ciulla, Dirk Gevers, Jacques Izard, Wendy S Garrett, Andrew T Chan, and Curtis Huttenhower. Relating the metatranscriptome and metagenome of the human gut. **Proceedings of the National Academy of Sciences of the United States of America**, [I.F. 9.81], 111(22), 2014.
- [81] Michelle G Rooks, Patrick Veiga, LH Wardwell-Scott, Timothy L Tickle, Nicola Segata, Carey A Gallini, Chloé Beal, Monia Michaud, Johan ET Van Hylckama-Vlieg, Sonia A Ballal, Xochitl C Morgan, Jonathan N Glickman, Dirk Gevers, Curtis Huttenhower, and Wendy S Garrett. Gut microbiome composition and function in experimental colitis during active disease and treatment-induced remission. **The ISME journal**, [I.F. 8.95], pages 1–15, 2014.
- [82] Katherine Huang, Arthur Brady, Anup Mahurkar, Owen White, Dirk Gevers, Curtis Huttenhower, and Nicola Segata. MetaRef: a pan-genomic database for comparative and community microbial genomics. **Nucleic Acid Research**, [I.F. 8.80], 42(D1):D617–D624, 2014.
- [83] Erik Dassi, Annalisa Ballarini, Giuseppina Covello, HTM CMB2013, Alessandro Quattrone, Olivier Jousson, Veronica De Sanctis, Roberto Bertorelli, Michela A Denti, and Nicola Segata. Enhanced microbial diversity in the saliva microbiome induced by short-term probiotic intake revealed by 16S rRNA sequencing on the IonTorrent PGM platform. **Journal of Biotechnology**, [I.F. 3.18], 190:30 – 39, 2014.
- [84] Christian Milani, Gabriele Lugli, Francesca Turrone, Leonardo Mancabelli, Sabrina Duranti, Alice Viappiani, Marta Mangifesta, Nicola Segata, Douwe van Sinderen, and Marco Ventura. Evaluation of bifidobacterial community composition in the human gut by means of an ITS-metagenomics protocol. **FEMS Microbiology Ecology**, [I.F. 3.88], 90(2), 2014.
- [85] Matthias Scholz, Adrian Tett, and Nicola Segata. Computational tools for taxonomic microbiome profiling of shotgun metagenomes. In *Metagenomics for Microbiology*, page 188. 2014.
- [86] Jose U Scher, Andrew Szczesnak, Randy S Longman, Nicola Segata, Carles Ubeda, Craig Bielski, Eric G Pamer, Steven Abramson, Curtis Huttenhower, and Dan Littman. Expansion of intestinal *Prevotella copri* correlates with enhanced susceptibility to arthritis. **eLIFE**, [I.F. 8,52], 2:e01202, 2013.
- [87] Nicola Segata, Daniela Börnigen, Xochitl Morgan, and Curtis Huttenhower. PhyloPhlAn is a new method for improved phylogenetic and taxonomic placement of microbes. **Nature Communications**, [I.F. 10.01], 4:2304, 2013.
- [88] Timothy L. Tickle, Nicola Segata, Levi Waldron, and Curtis Huttenhower. Two-stage microbial community experimental design. **The ISME Journal**, [I.F. 8.95], pages 1–10, 2013.
- [89] Nicola Segata, Daniela Boernigen, Timothy L Tickle, Xochitl Morgan, Wendy S Garrett, and Curtis Huttenhower. Computational meta'omics for microbial community studies. **Molecular Systems Biology**,

[Recommended as being of special significance in its field by Jack Gilbert from the F1000 Faculty I.F. 11.34], 9(666):1–15, 2013.

- [90] Nicola Segata, Annalisa Ballarini, and Olivier Jousson. Genome sequence of *Pseudomonas aeruginosa* PA45, a highly virulent strain isolated from a patient with bloodstream infection. **Genome Announcements**, 1(3), 2013.
- [91] Omry Koren, Dan Knights, Antonio Gonzales, Levi Waldron, Nicola Segata, Rob Knight, Curtis Huttenhower, and Ruth E. Ley. A Guide to Enterotypes across the Human Body: Meta- Analysis of Microbial Community Structures in Human Microbiome Datasets. **PLoS computational biology**, [I.F. 5.22], 9(1):e1002863, 2013.
- [92] Xothitl Morgan, Nicola Segata, and Curtis Huttenhower. Biodiversity and Functional Genomics in the Human Microbiome. **Trends in Genetics**, [I.F. 9.77], 20(1):51–58, 2013.
- [93] Annalisa Ballarini*, Nicola Segata*, Curtis Huttenhower^, and Olivier Jousson^. Simultaneous quantification of multiple bacteria by the BactoChip microarray designed to target species-specific marker genes. **Plos One**, [I.F. 4.09], 8(2):e55763, 2013.
- [94] Nicola Segata, Levi Waldron, Annalisa Ballarini, Vagheesh Narasimhan, Olivier Jousson, and Curtis Huttenhower. Metagenomic microbial community profiling using unique clade-specific marker genes. **Nature Methods**, [I.F. 19.27], 9:811–814, 2012.
- [95] Nicola Segata, Susan Kinder Haake, Peter Mannon, Katherine P Lemon, Levi Waldron, Dirk Gevers, Curtis Huttenhower, and Jacques Izard. Composition of the Adult Digestive Tract Microbiome Based on Seven Mouth Surfaces, Tonsils, Throat and Stool Samples. **Genome Biology**, [article flagged as "Highly accessed", I.F. 6.89], 13(6):R42, 2012.
- [96] The Human Microbiome Consortium (including Nicola Segata). A Framework for Human Microbiome Research. **Nature**, [I.F. 36.28], 486(7402):215–221, 2012.
- [97] The Human Microbiome Consortium (including Nicola Segata). Structure, function and diversity of the healthy human microbiome. **Nature**, [I.F. 36.28], 486(7402):207–214, 2012.
- [98] Kjersti Aagaard, Kevin Riehle, Jun Ma, Nicola Segata, Toni-Ann Mistretta, Cristian Coarfa, Sabeen Raza, Sean Rosenbaum, Ignatia Van Den Veyver, Aleksandar Milosavljevic, Dirk Gevers, Curtis Huttenhower, Joseph Petrosino, and James Versalovic. A Metagenomic Approach To Characterization Of The Vaginal Microbiome Signature In Pregnancy. **PloS ONE**, [I.F. 4.09], 7(6):e36466, 2012.
- [99] Sahar Abubucker, Nicola Segata, Johannes Goll, Alyxandria Schubert, Jacques Izard, Brandi L. Cantarel, Beltran Rodriguez-Mueller, Jeremy Zucker, Mathangi Thiagarajan, Bernard Henrissat, Owen White, Scott T Kelley, Barbara Methe, Patrick D Schloss, Dirk Gevers, Makedonka Mitreva, and Curtis Huttenhower. Metabolic Reconstruction for Metagenomic Data and Its Application to the Human Microbiome. **PLoS Computational Biology**, [I.F. 5.22], 8(6):e1002358, 2012.
- [100] Karoline Faust*, Fah J Sathirapongsasuti*, Jacques Izard, Nicola Segata, Dirk Gevers, Jeroen Raes*, and Curtis Huttenhower*. Microbial co-occurrence relationships in the human microbiome. **PLoS Computational Biology**, [I.F. 5.22], 8(7):e1002606, 2012.
- [101] Janjua Hussnain, Nicola Segata, Paola Bernabò, Sabrina Tamburini, Albert Ellen, and Olivier Jousson. Clinical populations of *Pseudomonas aeruginosa* isolated from acute infections show a high virulence range partially correlated with population structure and virulence gene expression. **Microbiology**, [I.F. 3.06], 158(Pt 8):2089–2098, 2012.
- [102] Sarah Jane Delany, Nicola Segata, and Brian Mac Namee. Profiling Instances in Noise Reduction. **Knowledge-Based Systems**, [I.F. 2.42], 31:28–40, 2012.
- [103] Nicola Segata*, Edoardo Pasolli*, Farid Melgani, and Enrico Blanzieri. Local SVM Approaches for Fast and Accurate Classification of Remote Sensing Images. **International Journal of Remote Sensing**, [I.F. 1.12], 33(19):6186–6201, 2012.
- [104] Levi Waldron, Shuji Ogino, Yujin Hoshida, Kaori Shima, Amy McCart Reed, Peter Simpson, Yoshifumi Baba, Katsuhiko Noshio, Nicola Segata, Gregory J. Kirkner, Edward Giovannucci, John Quackenbus, Georgia Chenevix-Trench, Todd R. Golub, Charles S. Fuchs, Giovanni Parmigiani, and Curtis Huttenhower. Expression profiling of archival tissues for long-term health studies. **Clinical Cancer Research**, [I.F. 7.74], 18(22):6136–46, 2012.

- [105] Andrew Szczesnak, Nicola Segata, Xiang Qin, Dirk Gevers, Joseph F Petrosino, Curtis Huttenhower, Dan Littman, and Ivaylo Ivanov. The genome of Th17 cell-inducing segmented filamentous bacteria reveals extensive auxotrophy and adaptations to the intestinal environment. **Cell Host & Microbe**, [I.F. 13.73], 10:260–272, 2011.
- [106] Nicola Segata and Curtis Huttenhower. Toward an efficient method of identifying core genes for evolutionary and functional microbial phylogenies. **PLoS ONE**, [I.F. 4.41], 6(9):e24704, 2011.
- [107] Nicola Segata, Jacques Izard, Levi Waldron, Dirk Gevers, Larisa Miropolsky, Wendy S Garrett, and Curtis Huttenhower. Metagenomic Biomarker Discovery and Explanation. **Genome Biology**, [article flagged as "Highly accessed" and selected for journal cover, I.F. 6.89], 12:R60, 2011.
- [108] Sonia A Ballal, Carey Ann Gallini, Nicola Segata, Curtis Huttenhower, and Wendy S Garrett. Host and gut microbiota symbiotic factors: lessons from inflammatory bowel disease and successful symbionts. **Cellular microbiology**, [I.F. 5.63], 13(4):508–517, 2011.
- [109] Nicola Segata and Enrico Blanzieri. Operators for transforming kernels into quasi-local kernels that improve SVM accuracy. **Journal of Intelligent Information Systems**, [I.F. 1.08], 37(2):155–186, 2011.
- [110] Mikalai Krapivin, Aliaksandr Autayeu, Maurizio Marchese, Enrico Blanzieri, and Nicola Segata. Keyphrases Extraction from Scientific Documents: Improving Machine Learning Approaches with Natural Language Processing. In G Chowdhury, C Khoo, and J Hunter, editors, *The Role of Digital Libraries in a Time of Global Change*, Lecture Notes in Computer Science, pages 102–111. Springer, 2010.
- [111] Nicola Segata and Enrico Blanzieri. Fast and Scalable Local Kernel Machines. **Journal of Machine Learning Research**, [I.F. 3.12], 11:1883–1926, 2010.
- [112] Nicola Segata, Enrico Blanzieri, Sarah Jane Delany, and Pádraig Cunningham. Noise Reduction for Instance-Based Learning with a Local Maximal Margin Approach. **Journal of Intelligent Information Systems**, [I.F. 1.08], 35:301–331, 2010.
- [113] Nicola Segata and Enrico Blanzieri. Stochastic TT-Calculus Modelling of Multisite Phosphorylation Based Signaling: The PHO Pathway in *Saccharomyces Cerevisiae*. **Transactions on Computational Systems Biology**, X:163–196, 2008.
- [114] Nicola Segata, Enrico Blanzieri, and Corrado Priami. Towards the integration of computational systems biology and high-throughput data: supporting differential analysis of microarray gene expression data. **Journal of Integrative Bioinformatics**, 5(1), 2008.

INFORMAZIONI PERSONALI

Pamela Gatto

POSIZIONE RICOPERTA

Facility Manager

ESPERIENZA
PROFESSIONALE

Da 12/06 2013 - ora

Facility Manager (personale tecnico dipendente di Unitn da 02/02/2015)

Università degli Studi di Trento, Dipartimento CIBIO, HTS and Validation Facility

Via Sommarive, 9 38123, Trento, Italia

- Gestione della Facility "High Throughput Screening (HTS) and Validation"

Attività o settore:

- Supporto ai ricercatori nella:
- Pianificazione, assistenza ed esecuzione di screening di piccole molecole in modelli cellulari e biochimici mediante saggi biochimici, metabolici o fenotipici (high content screening).
- Analisi di immagini (HCA, "high content analysis") di cellule fissate o vive, in cinetica o a tempo finale mediante microscopio automatizzato e software di analisi di dati multiparametrici.
- Pianificazione, training ed esecuzione di protocolli sperimentali di quantificazione e controllo qualità degli acidi nucleici, di analisi genomiche e trascrittomiche (microarray, real-time PCR, digital PCR).
- Manutenimento e gestione della strumentazione e dei consumabili della facility; manipolazione ed organizzazione delle librerie di molecole.

Da 20/05/2013 – 21/05/2012

Post-doc

Università degli Studi di Trento, Centro di Ricerca CIBIO, Laboratory of Translational Genomics, Prof. Alessandro Quattrone

Via delle Regole, 101, 38123, Trento, Italia

- Attività di ricerca sperimentale

Attività o settore Messa a punto di un approccio di screening per l'identificazione di piccole molecole che modulano il controllo traduzionale in modelli cellulari animali.

Da 20/02/2012 – 01/06/2012

Docente – Attività di supporto alla didattica

Università degli Studi di Trento, Centro di Ricerca CIBIO

Via Sommarive, 38123, Trento, Italia

- Svolgimento in qualità di docente di attività di supporto alla didattica nell'ambito dell'insegnamento "Biologia Cellulare" del Corso di Laurea in Scienze e Tecnologie Biomolecolari, tenuto dal Prof. Alessandro Quattrone.

Attività o settore: Organizzazione e svolgimento di esercitazioni di laboratorio previste per gli studenti del Corso.

Da 14/09/2009 – 22/12/2009

Docente – Attività di supporto alla didattica

Università degli Studi di Trento, Centro di Ricerca CIBIO

Via Sommarive, 38123, Trento, Italia

- Svolgimento in qualità di docente di attività di supporto alla didattica nell'ambito dell'insegnamento "Biologia Cellulare" del Corso di Laurea in Scienze e Tecnologie Biomolecolari, tenuto dal Prof. Alessandro Quattrone.

Attività o settore: Organizzazione e svolgimento di esercitazioni di laboratorio previste per gli studenti del corso.

Da 01/05/2008 – 30/04/2012

Post-doc

Università degli Studi di Trento, Centro di Ricerca CIBIO, Laboratory of Translational Genomics, Prof. Alessandro Quattrone.

Via delle Regole, 101, 38123, Trento, Italia

- Attività di ricerca nell'area genomica nutrizionale per il progetto dal titolo "Genomica funzionale del potenziale di NEUroriparazione dei FLAvonoidi" (acronimo NEUFLA) finanziato dalla Provincia Autonoma di Trento.

Attività di ricerca sperimentale

Attività o settore: Studio dell'attività cellulare e molecolare di composti naturali su linee cellulari neuronali e tumorali con approccio high-throughput screening.

Da 16/05/2005 – 30/04/2008

Post-doc

Istituto Agrario di San Michele all'Adige (IASMA), Centro Sperimentale IASMA, Dipartimento Biologia e Genetica Molecolare, dott. Riccardo Velasco

Via E. Mach n.1, 38010 S. Michele all'Adige (TN), Italia

- Attività di ricerca sperimentale

Attività o settore: Genomica della vite e del melo, in particolare trascrittomica del metabolismo secondario della vite (progetto PARALLELOMICS e GENOMA DELLA VITE) e della risposta di difesa del melo alla fitoplasmosi AP (progetto "SMAPII") svolta anche presso il centro di ricerca AIPlanta di RLP Agroscience GmbH di Neustadt/Weinstrasse (D). Collaborazione al progetto "CARPOL" per lo sviluppo di un approccio diagnostico-molecolare per l'identificazione e la quantificazione di pollini allergenici

Da 01/12/2001 – 30/04/2005

Dottorato

Istituto Agrario di San Michele all'Adige (IASMA), Centro Sperimentale IASMA, Area di Ricerca Biologia Avanzata (BA), dott. Riccardo Velasco.

Via E. Mach n.1, 38010 S. Michele all'Adige (TN), Italia

- Attività di ricerca sperimentale in qualità di dottorando dell'Università di Verona

Attività o settore: Progetto "Resveratrol" finanziato dal Fondo Unico della Provincia Autonoma di Trento, in collaborazione con l'Istitut Fraunhofer IME di Aachen e finalizzato all'analisi molecolare della via metabolica dei composti fenolici in vite mediante l'approccio dei DNA array. 18 mesi di permanenza presso Institut Fraunhofer IME di Aachen (D).

Da 01/10/2000 – 31/10/2001

Ricercatore

Policlinico dell'Università di Regensburg, Dipartimento di Dermatologia, Prof. Dr. med. M. Landthaler

Franz-Josef-Strauß-Allee 11, 93053 Regensburg (D)

- Attività di ricerca sperimentale

Attività o settore: Terapia fotodinamica (PDT) applicata alla dermatologia.

STRUZIONE E FORMAZIONE

Da 25/03/2002 – 13/04/2005

Dottorato di Ricerca in Biotecnologie AgroIndustriali

Sostituire con il livello
OEQ o altro, se
conosciuto

XVII Ciclo del Corso di Dottorato di Ricerca in "Biotecnologie AgroIndustriali" della Facoltà di Scienze MM., FF., NN., Università degli Studi di Verona. Strada le Grazie, 15 I – 37134 VERONA

- L'ambito in cui è stato sviluppato il progetto di ricerca riguarda l'esplorazione della struttura e della regolazione del genoma vegetale in particolare l'analisi funzionale del genoma della vite e lo studio dei parametri genetici e fisiologici che regolano il metabolismo secondario della vite. L'attività di ricerca è stata condotta presso l'Area Biologia Avanzata del Centro Sperimentale dell'Istituto Agrario di San Michele all'Adige (TN). Titolo della tesi di dottorato: "Gene expression profiling of the polyphenols pathway of the species Vitis vinifera L. using cDNA array". Relatore: Prof. Mario Pezzotti.

Da 03/10/1993 – 01/07/1999

Laurea in Scienze Biologiche ad Indirizzo Biomolecolare

Sostituire con il livello
OEQ o altro, se
conosciuto

Corso di laurea in Scienze Biologiche ad Indirizzo Biomolecolare, Facoltà di Scienze MM. FF. NN. dell'Università degli Studi di Padova. Via Ugo Bassi, 58/B, 35121, Padova

- Attività di ricerca svolta durante l'internato di laurea: applicazione di alcune tecniche di microbiologia, biologia cellulare e spettroscopia per lo studio di una ftalocianina tetracationica come fotosensibilizzatore ad azione antibatterica. Titolo della tesi sperimentale: „Attività fotosensibilizzatrice di una Zn (II)-Ftalocianina cationica su cellule batteriche“. Relatore: Prof. Giulio Jori (Dipartimento di Biologia).

Da 15/09/1999 – 15/09/2000

Tirocinio

Sostituire con il livello
OEQ o altro, se
conosciuto

Istituto Agrario di San Michele all'Adige (IASMA), Centro Sperimentale IASMA, Unità Operativa di Biotecnologie, Laboratorio di Genetica Molecolare, dott.ssa Maria Stella Grando.

Via E. Mach n.1, 38010 S. Michele all'Adige (TN)

- Utilizzo dei marcatori molecolari per il riconoscimento varietale e clonale delle cultivar di vite

COMPETENZE PERSONALI

Lingua madre Italiano

Altre lingue

	COMPRESIONE		PARLATO		PRODUZIONE SCRITTA
	Ascolto	Lettura	Interazione	Produzione orale	
Inglese	B2	B2	B2	B2	B2
Tedesco	A2	A2	A2	A2	A2

Livelli: A1/A2: Utente base - B1/B2: Utente intermedio - C1/C2: Utente avanzato
Quadro Comune Europeo di Riferimento delle Lingue

Competenze organizzative e gestionali

- Co-Responsabile della HTS and Validation Facility

Competenze professionali

- Mantenimento e differenziamento di colture cellulari primarie e linee cellulari animali
- Utilizzo di vettori lentivirali per RNA silencing (siRNA e shRNA)

- Estrazione di DNA, e RNA totale e polisomiale
- Estrazione di proteine totali e polisomiali
- Utilizzo dello strumento Teledyne Isco - Density Gradient Fractionation System
- Saggi cellulari per la vitalità, tossicità, apoptosi, ciclo cellulare Label free, real-time cell analyzer (xCELLigence System, Roche)
- Principi teorici e tecnici di High-Throughput Drug screening su modelli cellulari e biochimici
- Microscopio a fluorescenza automatizzato per High-Content Screening (Operetta, PE)
- Immunofluorescenza, Western blotting, PCR, trascrizione in vitro, traduzione in vitro, RT-PCR, Real-time PCR
- Microarray (Agilent Microarray technology)
- Uso di stazioni di lavoro robotizzate per High-Throughput Drug screening, dispensazione di reagenti e replicazione piastre

Competenze digitali

AUTOVALUTAZIONE				
Elaborazione delle informazioni	Comunicazione	Creazione di Contenuti	Sicurezza	Risoluzione di problemi
Utente intermedio	Utente intermedio	Utente base	Utente base	Utente base

Livelli: Utente base - Utente intermedio - Utente avanzato
 Competenze digitali - Scheda per l'autovalutazione

- Sistemi operativi: Windows 10 e precedenti
- Applicazioni pacchetto Microsoft Office
- Software specifici per:
- Analisi di immagine: software Harmony e Columbus (Perkin Elmer)
- analisi statistiche: R language, KNIME
- analisi drug combination: Compusyn, Mixlow
- analisi dati microarray: Bioconductor, DAVID, Ingenuity Pathway Analysis
- analisi primer e dati Real-time PCR: REST, DART, LinRegPCR
- analisi dati di lettore di micropiastre: Magellan Data Analysis Software Tecan

Patente di guida B

ULTERIORI INFORMAZIONI

Pubblicazioni

- Tripathy D, Migazzi A, Costa F, et al. Increased transcription of transglutaminase 1 mediates neuronal death in in vitro models of neuronal stress and A β 1-42-mediated toxicity. *Neurobiol Dis.* 2020;140:104849. doi:10.1016/j.nbd.2020.104849
- Precazzini F, Pancher M, Gatto P, et al. Automated in vivo screen in zebrafish identifies Clotrimazole as targeting a metabolic vulnerability in a melanoma model. *Dev Biol.* 2020;457(2):215-225. doi:10.1016/j.ydbio.2019.04.005
- Biggi S, Pancher M, Stincardini C, et al. Identification of compounds inhibiting prion replication and toxicity by removing PrPC from the cell surface. *J Neurochem.* 2020;152(1):136-150. doi:10.1111/jnc.14805
- Rocchi A, Milioto C, Parodi S, et al. Glycolytic-to-oxidative fiber-type switch and mTOR signaling activation are early-onset features of SBMA muscle modified by high-fat diet. *Acta Neuropathol.* 2016;132(1):127-144. doi:10.1007/s00401-016-1550-4
- Quattrone A, Aveic S, Parodi F, et al. A High-Content Screening of Anticancer Compounds Suggests the Multiple Tyrosine Kinase Inhibitor Ponatinib for Repurposing in Neuroblastoma Therapy. *Mol Cancer Ther.* 2018;17(7):1405-1415. doi:10.1158/1535-7163.mct-17-0841.
- Sella S, Adami V, Amati E, et al. In-vitro analysis of quantum molecular resonance effects on human

- mesenchymal stromal cells. *PLoS One*. 2018;13(1). doi:10.1371/journal.pone.0190082.
- Lauria F, Tebaldi T, Lunelli L, et al. RiboAbacus: A model trained on polyribosome images predicts ribosome density and translational efficiency from mammalian transcriptomes. *Nucleic Acids Res*. 2015;43(22). doi:10.1093/nar/gkv781.
- Sidarovich V, Adami V, Gatto P, et al. Translational downregulation of HSP90 expression by iron chelators in neuroblastoma cells. *Mol Pharmacol*. 2015;87(3). doi:10.1124/mol.114.095729.
- Latorre E, Castiglioni I, Gatto P, Carelli S, Quattrone A, Provenzano A. Loss of protein kinase C δ /HuR interaction is necessary to doxorubicin resistance in breast cancer cell lines. *J Pharmacol Exp Ther*. 2014;349(4). doi:10.1124/jpet.113.211839
- Longhi S, Cristofori A, Gatto P, Cristofolini F, Grando MS, Gottardini E. Biomolecular identification of allergenic pollen: A new perspective for aerobiological monitoring? *Ann Allergy, Asthma Immunol*. 2009;103(6). doi:10.1016/S1081-1206(10)60268-2.
- Zamboni A, Gatto P, Cestaro A, et al. Grapevine cell early activation of specific responses to DIMEB, a resveratrol elicitor. *BMC Genomics*. 2009;10. doi:10.1186/1471-2164-10-363.
- Gatto P, Vrhovsek U, Muth J, et al. Ripening and genotype control stilbene accumulation in healthy grapes. *J Agric Food Chem*. 2008;56(24). doi:10.1021/jf8017707.
- Velasco R, Zharkikh A, Troggio M, et al. A high quality draft consensus sequence of the genome of a heterozygous grapevine variety. *PLoS One*. 2007;2(12). doi:10.1371/journal.pone.0001326.
- Moser C, Segala C, Fontana P, et al. Comparative analysis of expressed sequence tags from different organs of *Vitis vinifera* L. *Funct Integr Genomics*. 2005;5(4). doi:10.1007/s10142-005-0143-4.
- Moser C, Gatto P, Moser M, Pindo M, Velasco R. Isolation of functional RNA from small amounts of different grape and apple tissues. *Appl Biochem Biotechnol - Part B Mol Biotechnol*. 2004;26(2). doi:10.1385/MB:26:2:95.

Conferenze Corsi

- Droplet Digital PCR Scientific Conference Series, Milano 2019
- European High Content Screening User Group Meeting (PerkinElmer), Barcellona 2019
- Swiss Image-Based Screening Conference SIBS, Basilea (CH), 2015
- MipTec e SLAS Short Course "Label-Free / Biophysics Methods for Screening", Basilea (CH), 2014
- EMBL Advanced Course: Computational Aspects of High-Throughput Screening planning and analysis, Heidelberg (D) 2013
- ELRIG, European laboratory robotics interest group, Drug Discovery, Manchester, UK, 2012

Dati personali

- Autorizzo il trattamento dei miei dati personali ai sensi del Decreto Legislativo 30 giugno 2003, n. 196 "Codice in materia di protezione dei dati personali".