EUROPEAN CURRICULUM VITAE FORMAT

PERSONAL INFORMATION

Name	**BABBI GIULIA**
Address	**Via Aldini 16, Cesena (FC), 47521 ITALY**
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E-mail	**giulia.babbi@unibo.it** **giubabbi@gmail.com**
Website	https://www.unibo.it/sitoweb/giulia.babbi http://www.biocomp.unibo.it/
Nationality	Italian
Date of birth	03/01/1991
Sex	Female, she/her

EDUCATION AND TRAINING

• Dates	2015 – 2019
• Title of qualification awarded	**PhD in Earth, Life and Environmental Science – Curriculum Biology** **SSD BIO/10 Subject: Computational Biology** Supervisor: Prof. Pier Luigi Martelli
• Organization providing education and training	School of Science (Dept. of Biological, Geological and Environmental sciences) Alma Mater Studiorum – University of Bologna
• Thesis Title	The biological complexity of the genotype-phenotype relation: from genes and proteins to phenotypes and diseases (in humans)

• Dates	2013 – 2015
• Title of qualification awarded	**Master's Degree in Bioinformatics** – LM-06
• Final Evaluation	110/110 cum laude
• Organization providing education and training	Alma Mater Studiorum – University of Bologna
• Thesis Title	Analysing the association between protein variants and human diseases (SSD BIO/10)

• Dates	2010 – 2013
• Title of qualification awarded	**Bachelor's Degree in Biotechnology** – L-2
• Final Evaluation	110/110 cum laude
• Organization providing education and training	Alma Mater Studiorum – University of Bologna
• Thesis Title	Annotation of the human membrane proteome with BAR+ (SSD BIO/10)

WORK EXPERIENCE

• Dates	From February 2023
• Occupation or position held	**Junior assistant professor (RTD-A)** (SSD: BIO/10)
• Name and address of employer	Department of Pharmacy and Biotechnology (FaBiT) – University of Bologna, Via Belmeloro, 6, 40126 Bologna (BO), ITALY
• Project	“National Center for HPC, Big Data and Quantum Computing", code: CN00000013, CUP: J33C22001170001. Funded by the European Union - NextGenerationEU, PNRR - Mission 4 - Component 2 - Investment 1.4 "Strengthening research structures and creation of "national R&D champions" on some Key Enabling Technologies" D.D. 3138 of 12/16/2021 corrected with D.D. 3175 of 12/18/2021.
• Main activities and responsibilities	Development of computational tools for integrated analysis of omics data and the structural and functional characterization of biological macromolecules

• Dates	From December 2020 to January 2023
• Occupation or position held	**Junior assistant professor (RTD-A)** (SSD: BIO/10)
• Name and address of employer	Department of Pharmacy and Biotechnology (FaBiT) – University of Bologna, Via Belmeloro, 6, 40126 Bologna (BO), ITALY
• Project	European project H2020-CIRCLES: “Controlling mIcRobiomes CircuLations for bEtter food Systems”.
• Main activities and responsibilities	Implementation of a computational infrastructure for the management of omics data produced with "high throughput" tools, development of bioinformatics tools for data analysis, integration and interpretation.

• Dates	January 2020-November 2020
• Occupation or position held	**Research Fellow**
• Name and address of employer	Department of Pharmacy and Biotechnology (FaBiT) – University of Bologna, Via Belmeloro, 6, 40126 Bologna (BO), ITALY
• Project	PRIN 2017, project: “Protein Bioinformatics for Human Health”
• Main activities and responsibilities	Curation of databases and tools devoted to the elucidation of the relations between protein variations, diseases and phenotypes. Implementation of novel computational tools for large-scale prediction/annotation of protein function and features.

• Dates	April 2018 – July 2018
• Occupation or position held	**Bioinformatic Researcher - Internship as PhD student**
• Name and address of employer	GRIB – IMIM, PRBB, C/Dr. Aiguader, 88, 08003 – Barcelona, SPAIN
• Supervisor	Prof. Laura I. Furlong, - Pompeu Fabra University (UPF)
• Main activities and responsibilities	Updating online webservers, integration of platforms for the analysis of high volume of data, development of new tools and feature for existing resources in the field of gene-disease associations studies, with a specific interest in DisGeNet database.

• Dates	January 2015 – July 2015
• Occupation or position held	**Bioinformatic Researcher – Thesis Internship**

• Name and address of employer	Bologna Biocomputing Group – University of Bologna Via S.Giacomo 9/2 – 40126 Bologna (BO), ITALY
• Supervisor	Prof. Rita Casadio, University of Bologna
• Main activities and responsibilities	Bioinformatics for the annotation of genomic variations data; implementation of a platform for genome analysis and SNPs annotation. Integration of different bioinformatics tools to annotate genomic variations in terms of molecular consequence, with proteomic and transcriptomic data. Mapping of diseases-related variations on the human genome, and statistical validation of the outcomes.

• Dates	January 2013 – July 2013
• Occupation or position held	**Biotechnology Researcher – Thesis Internship**
• Name and address of employer	Bologna Biocomputing Group – University of Bologna Via S.Giacomo 9/2 – 40126 Bologna (BO), ITALY
• Supervisor	Prof. Rita Casadio, University of Bologna
• Main activities and responsibilities	Analysis of the outcomes of BAR+, the Bologna Annotation Resource tool developed by the Bologna Biocomputing Group. Comparison among the curated BAR+ annotation with other databases to demonstrate the increasing quality of the data obtained with the implemented annotation in comparison with not curated experimental data. Modelling of protein complexes of particular interest.

RESEARCH ACTIVITY

BIBLIOMETRICS

• Identifiers	ORCID 0000-0002-9816-4737 SCOPUS 57190161567
• Dates	Research activity from 2016 Leave of absence: 16th March – 16th August 2019 (maternity) 22nd May – 22nd October 2022 (maternity)
• Indicators relating to scientific production in relation to the ASN thresholds	**H-index: 10**, as to Scopus 12th June 2024 **Citations: 284** by 231 documents, as to Scopus 12th June 2024 **Publications: 31**, as to Scopus 12th June 2024 ASN threshold of the SC 05/E1: H-index 10, citations 278, publications 10 **In the SC 05/E1 - BIOCHIMICA GENERALE E BIOCHIMICA CLINICA, complying with thresholds qualifying as an associate professor** The list of publications and contribution in scientific conferences is present at the bottom of this document.
• Other indexes	Cumulative Impact Factor 202: 160.7 as to Web of Science 12th June 2024 Cumulative Impact Factor Five Year: 179.4 as to Web of Science 12th June 2024
• Publications during the PNRR-RTDa contract	10 publications, 5 papers under revision.

PARTICIPATION IN PROJECTS

• Dates	February 2023- ongoing
• International project	**National Center for HPC, Big Data and Quantum Computing",** code: CN00000013, CUP: J33C22001170001. Funded by the European Union - **NextGenerationEU, PNRR** - Mission 4 - Component 2 - Investment 1.4 "Strengthening research structures and creation of "national R&D champions" on some Key Enabling Technologies" D.D. 3138 of 12/16/2021 corrected with D.D. 3175 of 12/18/2021
• Occupation or position held	Junior Researcher responsible of the development of computational methods for i) the annotation of structural and functional characteristics of genes, proteins and their variants; ii) the characterization of complex biological processes through the integration of heterogeneous data, including genomic, transcriptomic, proteomic, metabolomics and metagenomics; iii) the characterization of the association between variants genes and diseases.
• Dates	November 2019 – ongoing
• International project	**CIRCLES "Controlling mIcRobiomes CircuLations for bEtter food Systems"** funded by the **European Union's Horizon 2020** research and innovation programme
• Occupation or position held	Junior Researcher responsible of the development of bioinformatics tools for data analysis, integration and interpretation and of the management of a computational infrastructure for omics data produced with "high throughput" tools
• Dates	July 2020 – October 2020
• International project	**Collaboration with NASA** Ames Research Center, Space Biosciences Branch for the Human Research Program
• Occupation or position held	Collaboration for the analysis and annotation of human and mouse genetic variations for the investigation of markers of sensitivity to radiation
• Dates	July 2020 - ongoing
• International experiment	**CAFA**, The Critical Assessment of protein Function Annotation algorithms https://biofunctionprediction.org/cafa/
• Occupation or position held	Participant making computational predictions contributing to CAFA, an experiment designed to provide a large-scale assessment of computational methods dedicated to predicting protein function
• Dates	February 2019 - ongoing
• International project	**ELIXIR**, an intergovernmental organisation that brings together life science resources from across Europe https://elixir-europe.org/
• Occupation or position held	Part of the Bioschemas and Rare Diseases communities supported by ELIXIR, that is a European life sciences infrastructure, bringing together scientists from 24 countries and over 250 research institutes.
• Dates	November 2016 - ongoing
• International experiment	**CAGI**, Critical Assessment of Genome Interpretation

	https://genomeinterpretation.org/
• Occupation or position held	Participant making computational predictions, with the overarching goal of establishing the state of the art in the field of interpreting genomic variation recognizing best prediction strategies, highlighting innovation and identifying bottlenecks that prevent the field from advancing. This is the aim of the CAGI experiment, pursued through periodic editions and extensive dissemination of its outcomes.
• Dates	2019-2023
• National project	National project: **PRIN 2017: “Protein Bioinformatics for Human Health”**
• Occupation or position held	Research fellow involved in the analysis of the relations between protein variations, diseases and phenotypes, contributing in the implementation of novel computational tools for large-scale prediction/annotation of protein function and features.

EDITORIAL ACTIVITIES

• Occupation or position held	Guest Associate Editor
• Dates	2022-2023
• Journal	Frontiers in Genetics
• Topic	Omics Integration and Network Medicine to Decipher Human Complex Diseases
• Number of aritcles	9 articles
• Occupation or position held	Review Editor
• Dates	From 2022
• Journal	Frontiers in in Molecular Diagnostics and Therapeutics Frontiers in in Translational Medicine

PRIZES AND AWARDS

• Dates	2019
• International award	The image of the article “Benchmarking predictions of allostery in liver pyruvate kinase in CAGI4” has been selected as Cover Image for the Human Mutation Special Issue: the Critical Assessment of Genome Interpretation (CAGI)
• Dates	2024
• National award	Winner of the SIB scholarship “Borsa di partecipazione al 48 FEBS Congress”
• Dates	2021
• National award	Winner of the SIB scholarship “Borsa di partecipazione al 45 Virtual FEBS Congress”
• Dates	2017
• National award	Second classified at the 3MT competition, University of Bologna

MEMBERSHIPS

• Occupation or position held	Member of the Italian Society of Biochemistry and Molecular Biology (SIB) – from 2015
• Occupation or position held	Member of the International Society for Computational Biology in 2016

TEACHING EXPERIENCE

• Dates	AA 2023-2024
• Occupation or position held	**Professor of the course PROTEOMES, INTERACTOMES AND BIOLOGICAL NETWORKS** (module 1 and module 2, 62 hours, SSD: BIO/10) at the first cycle degree programme in Genomics (L-2)
• Name and address of employer	Department of Pharmacy and Biotechnology (FaBiT) – University of Bologna, Via Belmeloro, 6, 40126 Bologna (BO), ITALY
• Main activities and responsibilities	By the end of the course, the student has the basic knowledge of the experimental techniques for analyzing at large proteins expressed in a biological systems and their interactions. The student is familiar with the publicly available databases collecting proteomics and interactomics data and knows how to represent and analyze the structural complexity of interactions with the Network theory.
• Dates	AA 2022-2023
• Occupation or position held	**Professor of the course PROTEOMES, INTERACTOMES AND BIOLOGICAL NETWORKS** (module 2, 22 hours, SSD: BIO/10) at the first cycle degree programme in Genomics (L-2)
• Name and address of employer	Department of Pharmacy and Biotechnology (FaBiT) – University of Bologna, Via Belmeloro, 6, 40126 Bologna (BO), ITALY
• Main activities and responsibilities	By the end of the course, students have the basic knowledge of the experimental techniques for analysing proteins expressed in a biological system and their interactions. Among the others, activities include Bash scripting and Python programming; information retrieval in web available databases; analysis of protein structure and protein-protein complexes; analysis and visualization of biological networks.
• Dates	AA 2020-2021
• Occupation or position held	**Teaching tutor of Laboratory of Bioinformatics 2** (SSD: BIO/10) at the Second cycle degree programme in Bioinformatics (LM-06)
• Name and address of employer	Department of Pharmacy and Biotechnology (FaBiT) – University of Bologna, Via Belmeloro, 6, 40126 Bologna (BO), ITALY
• Main activities and responsibilities	The main topics of the course include simple linear classifiers and machine learning approach, and their interpretation/evaluation. It requires knowledge of the libsvm package for SVM development, of cross-validation procedure, of scoring indices like confusion matrix, sensitivity, specificity, accuracy, Matthews correlation coefficient.
• Dates	AA 2015 - 2016 AA 2016 - 2017 AA 2017 - 2018 AA 2018 - 2019
• Occupation or position held	**Teaching tutor of Laboratory of Bioinformatics 1** (SSD: BIO/10) at the Second cycle degree programme in Bioinformatics (LM-06)
• Name and address of employer	Alma Mater Studiorum – University of Bologna School of Science (BiGeA), Via Selmi 3 – 40126 Bologna (BO), ITALY

• Main activities and responsibilities

The main topics are the problems of protein 3D-strucuture modelling following the building by homology approach, tools for the analysis of protein sequences, sequence alignments, Hidden Markov Models for the recognition and modelling of protein domains. The lectures required the knowledge of programming language (Python) and many software packages (RasMol, Procheck, jCe, Modeller, HMMER).

• Supervisor

Tatiana Nassar, 2024, first cycle degree programme in Genomics (L-2) (ongoing)

• CoSupervisor

Maria Aurora Murgia, 2024, first cycle degree programme in Genomics (L-2) (ongoing)

• CoSupervisor

“Toolkit for differential analysis of microbiome data” (SSD: BIO/10), presented by Óscar San José Rodríguez, 2022, at the Second cycle degree programme in Bioinformatics (LM-06)

INSTITUTIONAL ACTIVITIES

• Occupation or position held

- From 2024: Member of Com4Fabit, the FABIT Department Communications Croup, as elected representative of Young Researchers.
- From 2024: Responsible for FABIT Departmental Seminars
- From 2022: Representative of the Young Section Committee for the Group Computation and System Biology in the Italian Society of Biochemistry and Molecular Biology (SIB)
- From 2015 to 2017: Ambassador of the Italian Regional Student Group of the International Society For Computational Biology (ISCB-RSG)

CONFERENCE ORGANIZATION

• Occupation or position held
• Events

Member of the local organizing committee of:

National Conference on: BioProSys - Biotechnology Proteins System Biology Groups of SIB - Naples 18-19 May 2023

National Conference on: WebPro - Proteins on the Web 2021- on line conference, Protein Group of SIB (Italian Society of Biochemistry and Molecular Biology, 20-21 May 2021

• Occupation or position held
• Events

Member of the local committee of:

- Advanced school: Bologna Winter School 2024 “Artificial Intelligence, Deep Learning and protein functional annotation: the state-of-the-art” – Online event, February 8-22, 2024
- Advanced school: Bologna Winter School 2023 “Bioinformatics and Deep learning for biodata analysis” – Online event, February 14-27, 2023
- Advanced school: Bologna Winter School 2022: “Structural Bioinformatics in the era of AlphaFold2” - on line event, February 9-25, 2022
- Advanced school: Bologna Winter School 2021: “Bioinformatics for Discovery in Structural and Functional Biology” - on line event, February 9-19, 2021
- Advanced one week-school: Bologna Winter School 2020: “What can we learn from protein structure?” – Bologna, February 17-21, 2020

- Advanced one week-school: Bologna Winter School 2019 "Data Science for Bioinformatics" - Bologna, February 18-22, 2019
- Advanced one week-school: Bologna Winter School 2018: "Big Data and Bioinformatics" – Bologna, February 12-16, 2018
- Advanced one week-school: Bologna Winter School 2017: "Revisiting Bioinformatics Foundations" - Bologna, February 13-17, 2017
- National Conference on: Proteine 2016: "Dissecting the Biological Complexity at the Molecular level" – Bologna, March 30- April 1, 2016
- Advanced one week-school: Bologna Winter School 2016: "In Silico Markers for Precision Medicine" – Bologna, February 22-26, 2016

ADVANCED COURSES

International Course: "Training on strategies to foster solutions of undiagnosed rare disease cases", organized by the European Joint Programme on rare Diseases, 13-15 March 2024, ISS, Rome.

Advanced school: Bologna Winter School 2024
"Artificial Intelligence, Deep Learning and protein functional annotation: the state-of-the-art" – Online event, February 8-22, 2024

Advanced school: Bologna Winter School 2023
"Bioinformatics and Deep learning for biodata analysis" – Online event, February 14-27, 2023

Advanced school: Bologna Winter School 2022
"Structural Bioinformatics in the era of AlphaFold2" – Online event, February 9-25, 2022

Advanced school: Bologna Winter School 2021
"Bioinformatics for Discovery in Structural and Functional Biology" – Online event, February 9-19, 2021

Advanced one week-school: Bologna Winter School 2020
"What can we learn from protein structure?" – Bologna, February 17-21, 2020

Advanced one week-school: Bologna Winter School 2018
"Big Data and Bioinformatics" – Bologna, February 12-16, 2018

Advanced one week course: "Protein modelling and docking" – Bologna, February 5-9, 2018
Prof. Allegra Via – University of Bologna

Advanced course: "Cracking the disease code: mapping genomes to pathogenesis pathways"– Bologna, May 29 - June 1, 2017
Prof. Yana Bromberg -Department of Biochemistry and Microbiology - Rutgers University, New Brunswick, NJ (USA)

Advanced one week-school: Bologna Winter School 2017:
"Revisiting Bioinformatics Foundations" – Bologna, February 13-17, 2017

Advanced one week course: “Protein protein interaction and docking” – Bologna, February 2-10, 2017
Prof. Allegra Via – University of Bologna

Prof. Ugur Sezerman – Acibadem University – Advanced Course: Network based analysis of omics data to study the affected pathways in disease aetiology – Bologna, February 29 - March 4, 2016

Advanced one week-school: Bologna Winter School 2016:
“In Silico Markers for Precision Medicine” – Bologna, February 22-26, 2016

Advanced one week training course: “Protein Network and System Biology” – Bologna, December 14-18, 2015, ELIXIR-ITA

Advanced course: "Cracking the disease code: mapping genomes to pathogenesis pathways" – Bologna, May 28 - June 5, 2015
Prof. Yana Bromberg -Department of Genetics - Rutgers University, New Brunswick (NJ, USA)

Advanced course: "Omics & multi-omics" – Bologna, March 2-5, 2015
Dr. Christine Nardini - Department of Molecular Systems Biology - CAS-MPG Partner Institute for Computational Biology, Shanghai

Advanced one week-school: Bologna Winter School 2015:
“NGS data, Bioinformatics and New Molecular Scenarios” – Bologna, February 2-6, 2015

Advanced Course in NGS data analysis: "Nucleotide Sequences Homology Modelling in the Next Gen Sequencing Era", September 22-26, 2014
Prof. Cédric Notredame - Centro de Regulacio Genomica - Barcelona.

Advanced course: "Pattern Recognition in Bioinformatics", May 5-9, 2014
Prof. Hong-Bin Shen - Computational and Systems Biology Group - Shanghai Jiao Tong University.

Advanced one week-school: Bologna Winter School 2014:
“Bioinformatics for Biological Complexity” – Bologna, February 10-14, 2014

Advanced course: "Introduction to Bioinformatics" – Bologna, February 3-7, 2014
Prof. Arthur Lesk - Biochemistry and Molecular Biology - PennState University

SEMINARS

Webinar: EMA’s Orphan Medicines Office on Rare Disease Day, online event, 29 February 2024 – Organized by EMA

Seminar: Towards the application of quantum computing in computational biology, online event, May 13, 2021
Prof. Pier Luigi Martelli – Organized by University of Pisa

Webinar: Introducing the new UniProt Disease Portal, 19 October, 2020

Galaxy-ELIXIR webinar series: FAIR data and Open Infrastructures to tackle the COVID-19 pandemic

“Introduction to Galaxy and the Galaxy workflows for SARS-CoV-2 data analysis” April 30, 2020

“Galaxy-ELIXIR webinar series: Genomics/Variant Calling” May 7, 2020

Seminars: Biomedical Informatics Research Programme - Retreat IMIM
“RNA sequencing of archived neonatal dried blood spots from extremely preterm newborns” – Prof. Robert Castelo
“The human endogenous metabolome as a pharmacology baseline for drug Discovery” – Prof. Jordi Mestres
“Text mining of clinical notes from PSMAR electronic health records” – Prof Laura Furlong
“The role of RNA processing alterations in disease” – Prof. Eduardo Eyras
“Signaling bias in GPCR drug discovery” – Prof. Jana Selent
IMIM, PRBB Barcelona, July 4, 2018

Seminar: “Dementia” Prof. Miguel Angel Mayer
IMIM, PRBB Barcelona, May 15, 2018

Seminar: “DisGeNET: A discovery platform to support translational research on human diseases” – Prof Laura Furlong
ECTB 2018, PRBB Barcelona, April 17, 2018

Seminar: “Towards a structure/function simulation of a cancer cell”
Bologna, September 26, 2017
Prof. Trey Ideker – Institute for Genomic Medicine, UCSD USA

Workshop: Workshop of the SIB group “Computational and Systems Biology”, Bologna, June 28, 2017

Advanced seminar: “Evolution of the metabolic biodiversity in plant organisms”, Bologna, May 11, 2017
Prof. Annalisa Tassoni – Organized by the Department of BiGeA, University of Bologna

Advanced seminar: “The self-consistency test for measuring bias in prediction protein destabilization upon mutation. Finding multi-dimensional epistasis in high-throughput data”, Bologna, April 21, 2017
Prof. Dmitry Ivankov – Center for Genomic Regulation, Barcelona (ES)

Seminar: “La diffusione della disinformazione scientifica: l'eco della rete”,
Bologna, April 11, 2017
Prof Pierluigi Contucci, Dott. Giuseppe Profiti, Prof. Marco Ciardi _Organized by “Accademia delle Scienze”, University of Bologna

Advanced seminar: “Towards the understanding of the genetic bases of complex adaptations in the human genome", Bologna, 19 October 2016
Prof. Jaume Bertranpetit – Organized by the Departement of BiGeA, University of Bologna

Advanced Lecture: "Biclustering Algorithms for Biomedical Data Analysis",
Bologna, June 14, 2016
Prof. Sara Madeira, Eurias Fellow

Advanced seminar: “Models of growth and population dynamics”,
Bologna, June 14, 2016,
Prof. Stefano Goffredo – Departement of BiGeA, University of Bologna

Advanced seminar: “The animal mitochondrial genome: adaptation and evolution”, Bologna, June 13, 2016,
Prof. Marco Passamonti – Departement of BiGeA, University of Bologna

Advanced seminar: “Genomic approaches to the study of adaptation of populations in response to selective pressures”, Bologna, April 29, 2016,
Prof. Marco Sazzini – Departement of BiGeA, University of Bologna

PERSONAL SKILLS AND COMPETENCES

RESEARCH FIELDS AND TECHNICAL SKILLS

I'm able to apply Bioinformatics/Computational-Biology techniques for the development of tools for data mining. In particular I have skills in the analysis of different kinds of biological data and in the integration/interpretation of results from a Systems Biology point of view. I implemented databases and computational infrastructures to store and analyse high volume of data; I collaborated in implementing predictors for the effect of protein variants, and I used these tools in international experiments. I have experience in building pipelines for the characterization of genes, proteins and biological processes, curating their annotation and integrating resources from other primary databases.

General informatics skills

Knowledge of:

- Windows and Ubuntu as Operative Systems;
- Office and OpenOffice suites.

Computational Biology

- Protein 3D modelling
- Protein sequence comparison and analysis
- Functional annotation of bio sequences and variants
- Modeller and PyMol for protein structure homology modelling and protein structure inspection
- Databases, standards and ontologies for bioinformatics (HGNC, dbSNP, OMIM, HPO, GO terms, ClinVar, Humsavar, DisGeNet, PDB)
- Database implementation with PostgreSQL, SQLite and MySQL for database management
- HMMER for biosequence analysis using profile HMM
- Cytoscape for graph analysis
- Chimera and Rasmol for protein model visualization
- Python and its libraries (such as Biopython and Web2Py)
- Java and its libraries for XML parsing

- Handling XML, OBO and OWL file
- JSON format and graph visualization with D3js
- DataTables plug-in for jQuery
- CSS and Javascript for HTML documents
- R for the analysis of biological data

Experimental skills

- Biochemical techniques such as protein extraction and purification, enzymatic activity measurement, electrophoresis and blotting
- Molecular Biology techniques such as DNA extraction and purification, PCR, electrophoresis, blotting, analysis of polymorphism (RFLP)
- Recombinant DNA technology for Plant/Industrial/Animal biotechnologies

Safety training

- General worker training on safety and health (module 1)
- Specific worker training on safety and health, low risk (module 2)
- The protection of personal data - training course

TEACHING SKILLS

Certified courses followed at the University of Bologna:

Training course for teachers - 24 credits

- Anthropology, 6 credits, mark:30L
- General Teaching Methodologies and Technologies 6credits, mark: 30
- Pedagogy, Special Pedagogy and Inclusion Teaching, 6 credits, mark: 30L
- Psychology, 6 credits, mark: 30

MOTHER TONGUE	**Italian**	
OTHER LANGUAGES	**English**	**French**
• Reading skills	C1	B1
• Writing skills	C1	B1
• Verbal skills	C1	A2
• Certification	B2– Exam during bachelor's degree 11/01/2013	B1 – Exam during bachelor's degree 10/01/2013

•Social skills and competences

Activities carried out while researching, and participation to national and international projects gave me the opportunity to work in heterogeneous teams several times. These experiences gave me the possibility to establish relations with people with different backgrounds, acquiring knowledge and skills necessary for interdisciplinary communication, team working, and project planning.

PUBLICATIONS

2024

Bertolini E*, **Babbi G*,** Savojardo C, Martelli PL, Casadio R. MultifacetedProtDB: a database of human proteins with multiple functions. Nucleic Acids Res. 2024 Jan 5;52(D1):D494-D501.
DOI: 10.1093/nar/gkad783.
Citations [Scopus]: 2
Subject Area [Scopus]: Biochemistry, Genetics and Molecular Biology
Journal Impact Factor 2022 [web of science]: 14.9
Journal Impact Factor Five Year [web of science]: 16.4
Quartile and subject [web of science]: Q1 in BIOCHEMISTRY & MOLECULAR BIOLOGY

Babbi G, Manfredi M, Bertolini E, Savojardo C, Martelli PL, Casadio R, Bioinformatic Sweeties: a unified portal for characterizing human proteins and their variants, Top Italian Scientists Journal, 2024;1(2)
DOI: 10.62684/HDYO1899
Citations: 0
Journal with no Impact factor.

Scicchitano D., Leuzzi D., **Babbi G**. et al. Dispersion of antimicrobial resistant bacteria in pig farms and in the surrounding environment, Animal microbiome, 6, 17 (2024).
DOI: 10.1186/s42523-024-00305-8
Citations [Scopus]: 0
Subject Area [Scopus]: Agricultural and Biological Sciences: Animal Science and Zoology, Veterinary: Veterinary (miscellaneous), Agricultural and Biological Sciences: Agricultural and Biological Sciences (miscellaneous), Medicine: Microbiology (medical)
Journal Impact Factor 2022 [web of science]: 4.7
Journal Impact Factor Five Year [web of science]: 5.1
Quartile and subject [web of science]: Q1 in MICROBIOLOGY and VETERINARY SCIENCES

Scicchitano D, **Babbi G**, Palladino G, Turroni S, Mekonnen YT, Laczny C, Wilmes P, Leekitcharoenphon P, Castagnetti A, D'Amico F, Brigidi P, Savojardo C, Manfreda G, Martelli PL, De Cesare A, Aarestrup FM, Candela M, Rampelli S, “Routes of dispersion of antibiotic resistance genes from the poultry farm system”, Science of The Total Environment, Volume 912, 2024
DOI: 10.1016/j.scitotenv.2023.169086
Citations [Scopus]: 0
Subject Area [Scopus]: Environmental Science: Environmental Chemistry
Journal Impact Factor 2022 [web of science]: 9.8
Journal Impact Factor Five Year [web of science]: 9.6
Quartile and subject [web of science]: Q1 in ENVIRONMENTAL SCIENCES

The Critical Assessment of Genome Interpretation Consortium. (2024) CAGI, the Critical Assessment of Genome Interpretation, establishes progress and prospects for computational genetic variant interpretation methods. Genome Biol 25, 53 (2024).
DOI: 10.1186/s13059-023-03113-6
Citations [Scopus]: 2
Subject Area [Scopus]: Biochemistry, Genetics and Molecular Biology
Journal Impact Factor 2022 [web of science]: 12.3
Journal Impact Factor Five Year [web of science]: 17.4
Quartile and subject [web of science]: Q1 in BIOTECHNOLOGY & APPLIED MICROBIOLOGY and GENETICS & HEREDITY

Stenton SL, O'Leary M, Lemire G, VanNoy GE, DiTroia S, Ganesh VS, Groopman E, O'Heir E, Mangilog B, Osei-Owusu I, Pais LS, Serrano J, Singer-Berk M, Weisburd B, Wilson M, Austin-Tse C, Abdelhakim M, Althagafi A, **Babbi G**, et al. Critical assessment of variant prioritization methods for rare disease diagnosis within the rare genomes project. Hum Genomics 18, 44 (2024).

DOI: 10.1186/s40246-024-00604-w
Citations [Scopus]: 1
Subject Area [Scopus]: Biochemistry, Genetics and Molecular Biology: Genetics; Pharmacology, Toxicology and Pharmaceutics: Drug Discovery; Biochemistry, Genetics and Molecular Biology: Molecular Medicine; Biochemistry, Genetics and Molecular Biology: Molecular Biology
Journal Impact Factor 2022 [web of science]: 4.5
Journal Impact Factor Five Year [web of science]: 4.9
Quartile and subject [web of science]: Q1 GENETICS & HEREDITY

Zhang J, Kinch L, Katsonis P, Lichtarge O, Jagota M,Song YS, Sun Y, Shen Y, Kuru N, Dereli O, Adebali O, Alladin MA, Pal D, Capriotti E, Turina MP, Savojardo C, Martelli PL, **Babbi G**, Casadio R, et al. Assessing predictions on fitness effects of missense variants in HMBS in CAGI6, **accepted** for publication in Human Genetics.

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ORAL PRESENTATIONS

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National meeting of Italian ELIXIR -Rare Disease Community, “Reactome pathways and Rare Diseases”, Rome 28-29 November, 2023

International Conference: CAGI:** “Disease associations of proteins with multiple functions”, Boston, Massachusetts, USA, September 29-October 1, 2023

National Conference: SIB 2023: “”The DAR database: mapping disease related enzymes to Reactome pathways” Firenze, September 7-9,2023

National Conference: BBCC2022 Bioinformatics and Computational Biology Conference: “Protein structural and functional features relate human variations to diseases” – virtual event, remote attendance, Naples, Italy, December 13-15, 2022

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International Conference: ISMB/ECCB 2021: “Physico-chemical and structural features of pathogenic and benign human protein missense variations collected from HUMSAVAR and ClinVar”, virtual event, remote attendance, July 25 - 30, 2021

National Conference: BITS 2021, Annual Meeting of the Bioinformatics Italian Society: “A large-scale analysis of human protein missense variations collected from HUMSAVAR and ClinVar”, virtual event, remote attendance, July 01-02, 2021

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International Conference: R2B OnAir – Research to Business is the International Exhibition on Industrial Research and Skills for Innovation: “Bioinformatic tools and services for the analysis of biological big data”, virtual event, remote attendance, 10-12 June, 2020

National Conference: BBCC2017 Bioinformatics and Computational Biology Conference: “From phenotypes to molecular mechanisms and pathways” – Naples, Italy, December 18-20, 2017

International Conference: NGS 2017: structural variation and population genomics: “eDGAR: a webserver for analysing the relationship among genes and polygenic diseases” – Barcellona (Spain), April 3-5, 2017

Local session of the International Competition: 3MT competition - University of Bologna: “Organizing the knowledge for genome editing”– Bologna (Italy), March 28, 2017

National Conference: Proteine 2016: “Dissecting the Biological Complexity at the Molecular level” – Bologna (Italy), March 30- April 1, 2016

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ABSTRACTS

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Palladino G, Scicchitano D, Brigidi P, Laczny C, Halder R, Trevisi P, Luise D, De Cesare A, Manfreda G, Martelli PL, **Babbi G**, Turroni S, Candela M, Rampelli S. (2022) *Resistome and xenobiome temporal dynamics in poultry and swine production chains: the CIRCLES project* - Federation of European Microbiological Societies (FEMS) Conference in Balgrade, Serbia, 30 June – 2 July, 2022

Savojardo C, Martelli PL, **Babbi G**, Anteghini M, Manfredi M, Madeo G, Capriotti E, et al. (2021) *SB4ER: An ELIXIR Service Bundle for Epidemic Response*. BioHackrXiv. March 25.

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Savojardo C, Martelli PL, **Babbi G**, Tartari G, Baldazzi D and Casadio R. (2020) *A Bologna Biocomputing pipeline combining multiple tools for protein functional annotation in CAFA4*, International conference “Intelligent Systems for Molecular Biology” (ISMB), 13-16 July, 2020

Savojardo C, Martelli PL, Fariselli P, **Babbi G** and Casadio R. (2018) *INPS and INPS-3D: sequence- and structure-based prediction of protein stability change upon single-point variations,* Conference on the Criticall Assessment of Genome Interpretation (CAGI5), Chicago, July 5-7, 2018

Babbi G, Profiti G, Martelli PL and Casadio R. (2018) *From phenotypes to molecular mechanisms and pathway. Informal proceeding of the Human Genetic Variation and Disease*, Gordon Research Conference, University of New England, June 10 - 15, 2018

Martelli PL, **Babbi G**, Profiti G and Casadio R. (2018) *Predicting protein-protein interaction sites with computational approaches.* Proteine 2018, University of Verona, May 20 -30, 2018

Babbi G, Martelli PL, Bovo S, Casadio R. (2018), *EDGAR and PhenPath, from diseases and phenotypes to* *processes and pathways. Poster at the Human Genetic Variation and Disease,* Gordon Research Conference, University of New England, June 10 - 15, 2018

Andreoletti G, Hoskins RA, Moult J, Brenner SE, **The Cagi Participants.** (2017) *Findings from the Fourth Critical Assessment of Genome Interpretation, a community experiment to evaluate phenotype prediction*. International Conference “NGS 2017: structural variation and population genomics”, pp. 55 – 56 - Barcellona, Spain, April 3-5, 2017

Babbi G, Martelli PL, Profiti G, Bovo S, Savojardo C and Casadio R. (2017), *Analysing the relations among genes and polygenic diseases with eDGAR.* Proceedings of the 59th Congress of the Italian Society of Biochemistry of Molecular Biology (SIB 2017), Caserta, September 20 – 22, 2017

Babbi G, Martelli PL, Profiti G, Bovo S, Savojardo C, Casadio R. (2017) *Analysing the relations among genes and polygenic diseases with eDGAR. BITS,* Proceedings of the 14th Annual Meeting of the Bioinformatics Italian Society, p. 134-135. Cagliari, July 5-7, 2017

Bovo S, **Babbi G**, Martelli PL, Casadio R. (2016) *Liver pyruvate kinase (L-PYK): predict the effects of missense mutations on kinase activity and allosteric regulation.* Conference on the Critical Assessment of Genome Interpretation (CAGI4), 25-27 March 2016, San Francisco, California, USA.

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Bovo S, Martelli PL, **Babbi G,** Casadio R. (2016) *Discriminating sick from healthy individuals by annotating exome variations.* Conference on the Critical Assessment of Genome Interpretation (CAGI4), 25-27 March 2016, San Francisco, California, USA.

Babbi G, Martelli PL, Bovo S, Casadio R. (2016) *Predicting the effect of variations on NPM-ALK functional activity and binding affinity with Hsp90.* Conference on the Critical Assessment of Genome Interpretation (CAGI4), 25-27 March 2016, San Francisco, California, USA.

Martelli PL, **Babbi G**, Bovo S, Casadio R. (2016) *Mapping of OMIM diseases and their associated genes in the chromosome space: addressing the complexity of polygenic disorders.* – Conference book, Gordon Research Conference - Human Single Nucleotide Polymorphisms & Disease - Mount Holyoke College, South Hadley, MA - June 12-17, 2016

Diquigiovanni C, Bergamini C, Evangelisti C, Costanzini A, Isidori F, Anbunathan H, Bowcock A, Casadio R, **Babbi G**, Rhoden KJ, Lenaz G, Fato R, Seri M, Romeo G, Bonora E. *Mutation in MYO1F cause familial non-medullary thyroid cancer* (FNMTC). European Human Genetics Conference. Barcelona, Spain. May 21-24, 2016.

OTHER ATTENDED CONFERENCES

National symposium on: Space biomedicine for future missions of Human Exploration of Space: a Call to Action, ASI, Rome – remote attendance, 15-17 March 2023

Elixir All-Hands meeting 2021, virtual conference, 1-11 June 2021

BIOHACKATHON-EUROPE - ELIXIR, virtual hackathon, 9-13 November 2020

Interoperability F2F meeting – ELIXIR, virtual hackathon, 11-12 May, 2020

National Conference: From molecules to complex biological functions: The computational method – Bologna (Italy), July 12, 2016

International Symposium on: The impact of Genomic Deep Sequencing from Pediatric Research and Clinical Practice – Bologna (Italy), 19-20 November 2015

58th National Meeting of the Italian Society of Biochemistry and Molecular Biology – Urbino (Italy), September 14-16, 2015