

Ai fini della pubblicazione.

ALLEGRA VIA Curriculum Vitae

Place: Rome, Italy
 Date: 25/01/2022

Part I – General Information

Current position

Since 30/12/2016	Institute of Molecular Biology and Pathology (IBPM), Consiglio Nazionale delle Ricerche (CNR)	Research Scientist (Ricercatore III livello)
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National Scientific Qualification (Abilitazione Scientifica Nazionale)

Year	Sector	
2012	05/E1 - SSD BIO/10 – Biochimica Generale e Biochimica Clinica	II Fascia
2012	05/E2 - SSD BIO/11 – Biologia Molecolare	II Fascia
2012	02/B3 - SSD FIS/07 – Fisica Applicata	II Fascia

Part II – Education

Type	Year	Institution	Notes (Degree, Experience,...)
Master Degree in Physics	1997	Sapienza University of Rome, Italy	<ul style="list-style-type: none"> <u>Thesis Title</u>: Analytical study of the Sherrington and Kirkpatrick spin-glass model <u>Supervisor</u>: Prof. Giorgio Parisi <u>Sector</u>: Theoretical Physics, Physics of Complex Systems, Condensed matter, Statistical Mechanics, Spin-glasses
Post-graduate fellowship	1998-1999	Department of Biology, University of Rome "Tor Vergata", Italy	<ul style="list-style-type: none"> <u>Activities</u>: Research in protein sequence, structure and function. Modular domains. Modelling of biological systems <u>Sector</u>: Bioinformatics and Computational Biology
PhD in Cellular and Molecular Biology	1999-2003	Department of Biology, University of Rome "Tor Vergata", Italy	<ul style="list-style-type: none"> <u>Thesis title</u>: Protein structural study for the optimization and analysis of sequence functional motifs <u>Supervisor</u>: Prof. Manuela Helmer-Citterich <u>Activities</u>: research in protein sequence, structure and function. Protein phosphorylation. Linear motifs. Modular domains. Modelling of biological systems. Teacher assistant. Undergraduate student tutoring. <u>Sector</u>: Bioinformatics and Computational Biology

Part III – Positions and Appointments

III A – Previous positions

Start	End	Institution	Position
10/2016	12/2016	IBIOM-CNR <ul style="list-style-type: none"> • ELIXIR-IT training platform coordination activities • Research on the structure, function of proteins • Research on cognitive and educational psychology and learning processes • Bioinformatics teaching and training; tutoring of university students, graduates and doctoral students; supervision of bachelor's and master's degree theses 	Researcher (RTD)
01/2016	09/2016	IBIOM-CNR (previously IBBE-CNR) <ul style="list-style-type: none"> • ELIXIR-IT training platform coordination activities • Research on the structure, function of proteins • Research on cognitive and educational psychology and learning processes • Bioinformatics teaching and training; tutoring of undergraduate, master, and PhD students; supervision of bachelor's and master's degree theses 	Research fellowship (Assegno di Ricerca)
01/2013	12/2015	Sapienza University of Rome, Department of Physics, Italy <ul style="list-style-type: none"> • Research in the field of structure and function of proteins; study of proteins and mechanisms of host-pathogen interactions; study of therapeutic targets • Bioinformatics teaching and training; tutoring of master and PhD students; supervision of master's degree theses • Coordination of scientific collaborations 	Researcher (RTDA)
01/2009	12/2012	Sapienza University of Rome, Department of Biochemical Sciences "A. Rossi Fanelli", Italy <ul style="list-style-type: none"> • Research in the field of diseases and the structure and function of proteins; study of proteins involved in host-pathogen interactions; study of therapeutic targets • Bioinformatics teaching and training; tutoring of LM and PhD students; supervision of master's degree theses • Coordination of scientific collaborations 	Researcher (RTDA)
12/2007	11/2009	Sapienza University of Rome, Department of Biochemical Sciences "A. Rossi Fanelli", Italy <ul style="list-style-type: none"> • Research in the field of structure and function of proteins; protein phosphorylation; structural and sequence functional motifs; post-translational modifications • Modelling of biological systems, development of bioinformatics methods and algorithms • Teaching; tutoring of LM and PhD students 	Postdoc (FIRB fellowship)
12/2006	11/2007	Alma Mater Studiorum Università di Bologna <ul style="list-style-type: none"> • Research in the field of the structure and function of proteins, protein phosphorylation, structural and linear functional motifs • Modelling of biological systems, application of neural networks to the inference of protein-peptide interaction specificity, development of bioinformatics methods and algorithms • Bioinformatics teaching and teaching assistance. Tutoring of LM and PhD students. 	Research fellowship (assegno di ricerca)
09/2006	11/2006	University of Rome "Tor Vergata", Department of Biology, Italy <ul style="list-style-type: none"> • Research in the field of the structure and function of proteins, protein phosphorylation, linear functional motifs • Modelling of biological systems, application of neural networks to the inference of SH3 domain interaction specificity; development of bioinformatics methods and algorithms • Bioinformatics teaching and teaching assistance. Tutoring of LM and PhD students 	Postdoc (Co.Co.Co)
09/2003	08/2006	University of Rome "Tor Vergata", Department of Biology, Italy	

		<ul style="list-style-type: none"> • Research in the field of the structure and function of proteins, protein phosphorylation, linear functional motifs 	Postdoc (FIRB fellowship)
		<ul style="list-style-type: none"> • Modelling of biological systems; application of neural networks to the inference of SH3 domain interaction specificity; development of bioinformatics methods and algorithms 	
		<ul style="list-style-type: none"> • Bioinformatics teaching and teaching assistance. Tutoring of undergraduate, master and PhD students 	
05/2003	08/2003	University of Rome “Tor Vergata”, Department of Biology, Italy	Postdoc (Telethon fellowship)
		<ul style="list-style-type: none"> • Research in the field of the structure and function of proteins, protein phosphorylation, linear functional motifs, protein domain interaction specificity 	
		<ul style="list-style-type: none"> • Modelling of biological systems, development of bioinformatics methods and algorithms 	
		<ul style="list-style-type: none"> • Teaching assistance. Tutoring of undergraduate students 	

III B – Academic Appointments

AA 2020	2022	University of Campania Luigi Vanvitelli	Teaching appointment
		<ul style="list-style-type: none"> • Design and provision of the course: “Effective practices for teaching and learning” addressed to Research Associates (RTDB) of the University. Two course editions each year, each of 16h 	
AA 2017	2022	Sapienza University, GdL QuID (Quality and Innovation of Teaching working group)	Expert adviser
		The GdL QuID provides the Dean of Sapienza University with advice and proposals for possible strategies and guidelines for the progress, improvement and innovation of teaching, with particular reference to the following aspects: training of teachers and teaching strategies centred on student learning; innovative teaching methodologies, technologies and materials, useful for improving teaching quality and effectiveness; dissemination of a culture of Quality and Innovation of Teaching; enhancing the commitment of teachers in innovative and quality teaching; collaboration with national and international bodies aimed at developing activities useful for their own purposes; indicators of the quality of teaching; collaboration between teaching, research, third mission.	
		<ul style="list-style-type: none"> • Design, planning and provision of training activities for Sapienza Researchers (RTDB) and Professors 	
		<ul style="list-style-type: none"> • Development of teaching material 	
AA 2017	2022	Sapienza University, bachelor’s degree in Biological Sciences , Course of Laboratory of Bioinformatics	Adjunct Professor
		<ul style="list-style-type: none"> • Teaching protein interactions and protein-protein interaction networks in the Laboratory of Bioinformatics semester course 	
AA 2020	2021	University of Bologna, School of Science, MD in Bioinformatics, Course Computational Methods for Bioinformatics	Adjunct Professor
		<ul style="list-style-type: none"> • Teaching sequence alignment algorithms and algorithm implementation in the Python programming language 	
		<ul style="list-style-type: none"> • Master’s degree thesis supervising 	
AA 2018	2020	University of Bologna, School of Science, MD in Bioinformatics, Course of Programming for Bioinformatics	Adjunct Professor
		<ul style="list-style-type: none"> • Teaching sequence alignment algorithms and algorithm implementation in the Python programming language 	
AA 2016	2020	University of Bologna, School of Science, MD in Bioinformatics, Course of Laboratory for Bioinformatics 1	Adjunct Professor
		<ul style="list-style-type: none"> • Teaching Bioinformatics methods for PPI and PPI network analysis 	
		<ul style="list-style-type: none"> • Master’s degree thesis supervising 	

III C – Other appointments

Start	End	Institution / Organisation	Position
2015	present	ELIXIR-IT <ul style="list-style-type: none"> Coordination of training activities for the Italian node of ELIXIR (www.elixir-europe.org). ELIXIR is the European Infrastructure for Bioinformatics envisaged in the ESFRI Roadmap to support research in the field of Life Sciences, and translational activities for medicine, the environment, biotechnology, industries and society. ELIXIR-IT (www.elixir-italy.org), the Italian node of ELIXIR, is a Joint Research Unit coordinated by the CNR, whose members are the main Italian academic, technological and research institutions, including, among other universities, Sapienza University. Establishment of the ELIXIR-IT training programme in Bioinformatics (https://elixir-iib-training.github.io/website/). Coordination of the ELIXIR-IT Training Team. 	Training Coordinator
2015	present	ELIXIR Training Platform <ul style="list-style-type: none"> Founder and Co-lead of the ELIXIR Train-the-Trainer (TtT) programme (https://elixir-europe.org/platforms/training/train-the-trainer). Research in cognitive and learning processes and curriculum development Produced publications and lessons 	Co-lead of the Training Capacity Building Task
2018	present	ELIXIR Tools Platform <ul style="list-style-type: none"> Establishment of best practices and standards in research software development within the ELIXIR scientific community (https://elixir-europe.org/platforms/tools/software-best-practices). Developed and consolidated the ELIXIR Software Management Plan Enabling adoption of research software development best practices Liaising with industry to promote software development best practices Produced publications and a lesson on 4 simple recommendations for Open Source Software (https://softdev4research.github.io/4OSS-lesson/) 	Co-lead of the ELIXIR Best Practices for Software Development for Life Sciences Task

Part IV – Personal skills

Mother tongue	Italian
Other languages	English: Proficient in spoken and written language (C1/C2) French: Proficient in spoken and written language (C1/C2) German: Basic communication skills (A1)
Programming & Software	<ul style="list-style-type: none"> UNIX/Linux, MacOSX Programming and scripting (Python, R) Web programming (HTML, CGI, MD) MySQL, PostgreSQL PyMOL, Chimera, SwissPDBviewer Docking packages and tools (e.g. Autodock, ClusPro) Network analysis software (Cytoscape) Several Bioinformatics and Computational Biology software (e.g. local Blast+, ClustalW, Modeller, etc.) Videoconferencing platforms (Zoom, Google Meet, Microsoft Teams, Adobe Connect, WebEx)
Communication skills	<ul style="list-style-type: none"> good communication and public speaking skills gained through the experience as teacher, trainer and public speaker; experienced in scientific manuscript and grant writing; good communication over distance skills acquired in conference calls; comfortable in speaking to interdisciplinary audiences about technical and scientific topics.

Organisational/managerial skills	<ul style="list-style-type: none"> ▪ leadership (lead of the ELIXIR-IT Training Platform; co-lead of the ELIXIR Train the Trainer programme; co-chair of the ELIXIR-Carpentries Working Group) ▪ project coordination ability (coordination of ELIXIR WG; coordination of the ELIXIR-IT Training Platform, WP/task PI in European and national projects) ▪ management of Research Infrastructures (participant in the Open Programme of the Executive master in management of Research Infrastructures - EMMRI, University of Milano Bicocca) ▪ manuscript review management capability (as Editorial Board member and reviewer of scientific journals) ▪ network management (as Chair of BTN, ELIXIR-IIB Training Platform coordinator, co-lead of ELIXIR programmes and working groups) ▪ workshop and course organisation skills (obtained co-organising workshops, conferences, training courses)
Other skills	Passionate about working and engaging with others to achieve goals; adaptable; independent; team player; interested in community building; proactive; perfectionist; curious. Passionate about drawing, painting and writing

Part V – Teaching experience

Part V A – Academic courses

Year(s)	Institution	Lecture/Course
2020/2022	University of Bologna, Italy	Computational Methods for Bioinformatics - Modulo 2 (3 CFU/year) – International Master Degree in Bioinformatics (English)
2018/2020	University of Bologna, Italy	Programming for Bioinformatics - Modulo 2 (3 CFU/year) – International Master Degree in Bioinformatics (English)
2017/2022	Sapienza University of Rome, Italy	Laboratory of Bioinformatics - Module 2 (3 CFU). Degree in Biological Sciences, Sapienza University of Rome, Rome, IT (Italian)
2016/2020	University of Bologna, Italy	Laboratory of Bioinformatics 1 - Modulo 3 (2.5 CFU/year) – International Master Degree in Bioinformatics (English)
2010/2015	Sapienza University of Rome, Italy	Macromolecular structures (6 CFU/year), MD in Engineering of Nanotechnology (in English AA 2014-2015)
2011/2012	Sapienza University of Rome, Italy	Biochemistry (6 CFU), MD in Physics of Biosystems (Italian)
2005/2010	University of Rome "Tor Vergata", Italy	Metodi informatici della Biologia (Computational methods for Biology, 6 CFU/year), MD in Bioinformatics (Italian)

Part V B – International Training Courses

Year	Institution	Lecture/Course
2021	Online	5 ELIXIR Train the trainer (16h each)
2020	Online	5 ELIXIR Train the trainer (16h each)
2020	Online	Software Carpentry workshop: The Unix Shell, Version control with git, Programming with Python (16h)
2019	National Bioinformatics Infrastructure Sweden (NBIS), SciLifeLab, Stoccolma, Sweden	ELIXIR-Carpentries Instructor Training (16h)
2019	PhD School in Biology and Molecular Medicine (BEMM), Sapienza Università di Roma, Italy	Bioinformatics: Theory and applications from genomes to drugs (2h)
2018	PhD School in Biology and Molecular Medicine (BEMM), Sapienza Università di Roma, Italy	Bioinformatics: Theory and applications from genomes to drugs (2h)
2018	IBPM-CNR, Rome, Italy	EMBO Practical Course on Computational analysis of protein-protein interactions: Sequences, networks and diseases (4h)
2018	National Bioinformatics Infrastructure Sweden (NBIS), SciLifeLab, Stoccolma, SE	ELIXIR Train-the-Trainer (16h)
2018	IBPM- CNR c/o Sapienza Università	ELIXIR Train-the-Trainer (16h)
2018	Institut Pasteur, Parigi, France	ELIXIR Train-the-Trainer (16h)
2018	University of Losanna, Switzerland	ELIXIR Train-the-Trainer (16h)

2018	CINECA, Rome, Italy	Linux shell scripting for high-throughput biological data processing on supercomputers (16h)
2018	Institut Pasteur, Paris, France	Software Carpentry workshop: The Unix Shell, Version control with git, Programming with Python (16h)
2018	University of Milano Bicocca, Italy	Software Carpentry workshop: The Unix Shell, Version control with git, Programming with Python (16h)
2017	Università di Salerno, Italy	ELIXIR Train-the-Trainer (16h)
2017	University of Losanne, Switzerland	ELIXIR Train-the-Trainer (16h)
2017	IBPM-CNR c/o Sapienza Università di Roma, Italy	Python for Life Scientists (40h)
2017	Online	3 Carpentries Instructor Training workshop (16h x3)
2017	eScience, Utrecht, The Netherlands	Carpentries Instructor Training workshop (16h)
2016	University of Budapest, Hungary	EMBO practical course on "Computational analysis of protein-protein interactions: Sequences, networks and diseases (4h30)
2016	University of Ljubljana, Faculty of Medicine, Slovenia	ELIXIR Train-the-Trainer (16h)
2016	Instituto Gulbenkian de Ciência, Oeiras, Portugal	ELIXIR Train-the-Trainer (16h)
2016	University of Bari, Italy	Python for Life Scientists (40h)
2016	CNR, Napoli, Italy	NGS for evolutionary biologists: from basic scripting to variant calling (32h)
2016	University of Naples Federico II, Italy	RNA-seq data analysis workshop (6h)
2016	ICTP – International Centre for Theoretical Physics, Trieste, Italy	RDA-CODATA Research Data Science Summer School (4h)
2016	Sardinian Scientific and Technological Park, Pula (CA), Italy	Scientific School on “Computational modeling for Life Sciences” (4h30)
2015	University of Bologna	Protein networks and systems biology (40h)
2015	CINECA, Rome, Italy	NGS for evolutionary biologists: from basic scripting to variant calling (40h)
2015	CINECA, Rome, Italy	Gene expression profiling with HTS: RNA-Seq data analysis (32h)
2015	PhD School in Biology and Molecular Medicine, Sapienza Università di Roma, Italy	High Throughput Sequencing (HTS) data analysis (3h30)
2015	TGAC (today Earlham Institute), Norwich, United Kingdom	EMBO practical course on Computational Analysis of Protein-Protein Interactions: From Sequences to Networks (3h30)
2010-2018	Instituto Gulbenkian de Ciência, Oeiras, Portugal	GTPB practical course on Bioinformatics using Python for Biologists (40h each year)
2013-2014	TGAC (today Earlham Institute), Norwich, United Kingdom	Practical course on "Python for Life Scientists" (40h each year)
2012	Institut Pasteur, Tunis, Tunisia	Predicting globular domains and IUP, Predicting linear motifs, in particular phosphorylation sites (14h)

Part V C – Undergraduate, Master Degree, and PhD Student Supervising

Year	Role	Candidate/Thesis title
2021-2022	Thesis supervisor International Master Degree in Bioinformatics. University of Bologna, Italy	Candidate: Sahar Heidaribakavoli Thesis title: mapping SLiMs and point mutations on SARS-CoV-2 proteins interacting with human host proteins
2020-2021	Thesis supervisor Master Degree in Medical Biotechnologies. University of Rome “Tor Vergata”, Italy	Candidate: Alessia Pucilli Thesis title: Structural and functional analysis of missense variants of the SARS-CoV-2 Spike protein
2020-2021	Thesis supervisor International Master Degree in Bioinformatics. University of Bologna, Italy	Candidate: Ilaria Pirona Thesis title: Analysis of a cohort of patients carrying loss-of-function (LoF) mutations in APOB, MITP and ANGPTL3 genes to study the effects of low cholesterol syndromes on chronic liver and cardiovascular diseases
2017-2020	PhD supervisor PhD School in Biochemistry, Sapienza University of Rome, Italy	Candidate: David Sasah Staid Thesis title: Development of new algorithms for the identification of point mutations leading to drug resistance in pathogens
2018	Internship Tutor	Candidate: Gerda Užubalyté

	Programme Erasmus+	Internship programme: A bioinformatics study of antibiotic resistance genes
2015-2016	Thesis supervisor Master Degree in Engineering of Nanotechnology, Sapienza University of Rome, Italy	Candidate: Elisa Micarelli Thesis title: Development of a bioinformatics procedure for the identification of cellular targets of nanoparticles of biomedical interest
2014-2015	Thesis supervisor Master Degree in Engineering of Nanotechnology, Sapienza University of Rome, Italy	Candidate: Irene Bonafede Thesis title: Statistical and Biological Analysis of DNA methylation profiles in normal and cancer cells
2011-2012	Thesis supervisor Master Degree in Engineering of Nanotechnology, Master Degree in Engineering of Nanotechnology, Sapienza University of Rome, Italy	Candidate: Lucia Lenci Thesis title: A computational method for the inference of competing endogenous RNAs
2011-2012	Thesis supervisor Master Degree in Engineering of Nanotechnology, Sapienza University of Rome, Italy	Candidate: Francesca Ruggeri Thesis title: Protein mediated interactions between nanocarriers and giant unilamellar vesicles
2009-2010	Thesis supervisor Master Degree in Bioinformatics, University of Rome "Tor Vergata", Italy	Candidate: Giulia Gonnelli Thesis title: Computational analysis of drug-receptor interactions in <i>Schistosoma mansoni</i> : study of SmTGR and its inhibitors by docking techniques
2009-2010	Thesis supervisor Master Degree in Bioinformatics, University of Rome "Tor Vergata", Italy	Candidate: Rosalbe Lepore Thesis title: Analysis of drug / target inhibition in <i>S. mansoni</i> and <i>P. falciparum</i> using computational modeling methodologies for homology and docking studies

Part VI – Invited seminars / talks

Year	Conference/Workshop /Institution	Title
2021	61° SIB MEETING Virtual Edition	Next generation learning (and teaching): are we ready for the challenge?
2021	ISMB / ECCB 2021 virtual, Education COSI	Teaching the Instagram generation: a lesson learned in the pandemic era
2019	Curriculum Development: considerations for education and training	Pan African Bioinformatics Network for H3Africa (H3ABioNet), Education summit, Cape Town, South Africa
2018	The ELIXIR Italy Training Platform: supporting researchers and professionals in acquiring specialized computational and data management skills	GARR Conference on Data Revolution, Cagliari, IT
2018	ELIXIR: Safeguarding the results of life science research in Europe	EaPConnect e-Health workshop on Biomedical collaborations over National Research and Education networks: success stories and best practices, Istituto Superiore di Sanità, Rome, IT
2018	Cognitive psychology in the bioinformatics learning enterprise	ISMB COSI on Computational Biology Education, Chicago, US
2018	A critical look at competencies	ELIXIR workshop on ELIXIR Implementation Study on Learning Paths, Amsterdam, NL
2017	From knowledge, skills and abilities to learning paths: Using Mastery Rubrics for training	GOBLET AGM Workshop, Oeiras, PT
2017	Integrating protein-protein interaction and expression data for the identification of cellular targets in drug delivery	Workshop of the SIB group on "Computational and Systems Biology", Bologna, IT
2016	Ten simple rules to make your teaching more effective	BITS 2016 Conference, University of Salerno, Fisciano (SA), IT
2016	Role of structure-based homology modeling in biomolecular sciences	Scientific School on "Computational modeling for Life Sciences", Sardinian Scientific and Technological Park, Pula (CA), IT
2014	Computational approaches to the study of functional sites in biomolecules	Dept. of Experimental Medicine and Surgery, University of Rome "Tor Vergata", IT
2014	A computational approach for the study of therapeutic targets and their inhibitors in human pathogens	TAGC Inserm, Aix-Marseille Université, France
2013	Best practices in programming for biological data management	The Genome Analysis Centre, Norwich, UK
2013	GOBLET	NextGenBug 31st meeting, ARK Genomics, Roslin, Edinburgh, UK

2012	A structural approach to the study of therapeutical targets and their inhibitors in human pathogens	Bi-national Israel-Italy meeting, Tel Aviv University, IL
2009	Cross-talking between human genome variations and their protein environment: a computational study	IRB Barcelona, SP
2008	Structural bioinformatics: a meeting-place for Biology and Physics	Alma Mater Università di Bologna, IT
2007	High-throughput protein functional annotation based upon local structure similarity	Genome Annotation: a BioSapiens Network of Excellence Initiative. 5 th European Conference on Computational Biology (ECCB), IL
2001	Proteins: Structure, Function, Evolution	IUSS (Istituto Universitario di Studi Superiori), University of Pavia, IT
2001	The structure of Proteins	in the Course of "Problems in Biological Evolution"; Scuola di Genetica di Cortona, Associazione Genetica Italiana (AGI), Cortona, IT

Part VII – Activities as Editor and Reviewer

Scientific Journal Editorial Boards	▪ BMC Research Notes (http://www.biomedcentral.com/bmcrenotes)
	▪ Structural Biology (http://www.hindawi.com/journals/sb/)
	▪ The Scientific World Journal (http://www.hindawi.com/journals/tswj/)
	▪ Advances in Bioinformatics (Special Issue) (http://www.hindawi.com/journals/abi/)
	▪ Frontiers in Genetics (Research Topic) (http://www.frontiersin.org/systems_biology)
Scientific Journals Reviewer	▪ Bioinformatics
	▪ Bioorganic Chemistry
	▪ BMC Bioinformatics
	▪ BMC Research Notes
	▪ Briefings in Bioinformatics
	▪ Computational and Mathematical Methods in Medicine
	▪ Database
	▪ FEBS letters
	▪ GENE: Infection, Genetics, and Evolution
	▪ Journal of Computational Biology and Bioinformatics Research
	▪ Journal of Molecular Cell Biology
	▪ Molecular BioSystem
	▪ Nucleic Acids Research
	▪ PLoS Computational Biology
	▪ PLoS ONE
▪ Proteins	
▪ Proteomics	
▪ PeerJ	
Research Projects Reviewer	▪ Excellence project 2006, Fondazione Cariparo
	▪ Innovative health research 2012. EU grants

Part VIII – Conference, workshop, and course (co)organiser

Part VIII A - Conference and Workshop (co)Organiser

Year	Conference/Workshop	Location (n. of participants)
2017	ELIXIR All Hands meeting	Rome, Italy, (~400 participants)

2016	NETTAB 2016 workshop on Reproducibility, standards and SOP in bioinformatics	CNR, Rome, IT, ~100 participants
2016	BITS 2016 satellite workshop on Effective academic teaching	University of Salerno, Fisciano (SA), Italy, ~ 20 partecipanti
2012	Workshop n. 4 - ECCB '12 (European Conference on Computational Biology) on Bioinformatics Training for Life Scientists: Showcases and Challenges from Tutors' Persp	Basel, CH, 40 partecipanti
2008	ECCB'08 (European Conference on Computational Biology)	Cagliari, IT, > 400 partecipanti

Part VIII B –Training Course (co)Organiser

Year	Course Title	Institution	Goal
2021	Collaborare per contrastare la pandemia - Disponibilità e uso dei dati epidemiologici in pandemia: difficoltà e opportunità	Webinar within the EOSC-Life Training project	The webinar & tutorial series is aimed at raising awareness in researchers, clinicians and technicians who produce data and develop or use software related to COVID-19 about the outstanding importance of sharing data and software rapidly and openly.
2021	Collaborare per contrastare la pandemia - Il COVID-19 Data Portal italiano: un punto di riferimento nazionale per i dati della pandemia	Webinar within the EOSC-Life Training project	The webinar & tutorial series is aimed at raising awareness in researchers, clinicians and technicians who produce data and develop or use software related to COVID-19 about the outstanding importance of sharing data and software rapidly and openly.
2021	International Summer School on Rare Disease Registries and FAIRification of Data	Online (ISS, Rome, Italy)	As part of the training activities proposed by the EJP RD, the Summer School is a 5-day online training programme organised by ISS in close collaboration with EJP-RD task partners, aimed at the international research community, clinicians, medical specialists, registry curators, database managers, healthcare professionals and patients' representatives
2021	ELIXIR Train the Trainer	5 online courses	Build bioinformatics training capacity in Europe. Provide new instructors with tools, guidelines and suggestions for effective and innovative teaching
2020	ELIXIR Train the Trainer	5 online courses	Build bioinformatics training capacity in Europe. Provide new instructors with tools, guidelines and suggestions for effective and innovative teaching
2020	Collaborare per contrastare la pandemia - Covid-19 e condivisione dei dati: perché in Italia si fa troppo poco?	Webinar within the EOSC-Life Training project	The webinar & tutorial series is aimed at raising awareness in researchers, clinicians and technicians who produce data and develop or use software related to COVID-19 about the outstanding importance of sharing data and software rapidly and openly.
2020	International Summer School on Rare Disease Registries and FAIRification of Data	Online (ISS, Rome, Italy)	As part of the training activities proposed by the EJP RD, the Summer School is a 5-day online training programme organised by ISS in close collaboration with EJP-RD task partners, aimed at the international research community, clinicians, medical specialists, registry curators, database managers, healthcare professionals and patients' representatives
2019	Genome Assembly and Annotation	University of Milano-Bicocca, Italy	Guide participants through all stages of a genome assembly and annotation project, starting with quality control, moving on to genome assembly and assembly validation, and ending with structural and functional annotation.
2019	Docker and Reproducibility	University of Turin, Italy	Teaching the basic concepts of Docker; to evaluate the benefits of containerized software development and distribution; to use the Docker features needed to run containerized applications; how to use the Docker file and Docker hub to create a Docker image; the various network mechanisms available in Docker.
2019	ELIXIR - Software Carpentry workshop	IGB-CNR Naples, Italy	Help researchers get their jobs done in less time and effort by teaching them basic computer skills. Introduce basic concepts and tools, including program design, version controlling, data management, and task automation.
2018	Docker Advanced Course	University of Milano-Bicocca, Italy	Provide the basics and tools to allow a developer to "dockerize" their programs and manage a variety of

2018	ELIXIR-EXCELERATE Train the Trainer	4 courses: Padua (Italy), Stockholm (Sweden), Rome (Italy), Paris (France)	containers, thereby greatly improving the installation process. Build bioinformatics training capacity in Europe. Provide new instructors with tools, guidelines and suggestions for effective and innovative teaching.
2018	Population Genomics: background and tools	IGB-CNR, Naples, Italy	Provide an overview of cutting-edge methods in population genomics by combining lectures from highly experienced population geneticists and software developers.
2018	Software Carpentry Workshop	Institut Pasteur, Paris, France	Help researchers get their jobs done in less time and effort by teaching them basic computer skills. Introduce basic concepts and tools, including program design, version controlling, data management, and task automation.
2018	Linux shell scripting for high-throughput biological data processing on supercomputers	CINECA, Roma, Italy	Introduce the Linux shell and show how to navigate and work with files and directories, how to combine commands to do new things, how to perform the same actions on many different files, how to selectively filter and extract data from tables. To show how to connect to a remote supercomputer and how to use a supercomputing environment to analyse large amounts of biological data.
2018	EMBO Practical Course on Computational Analysis of PPI: Sequences, networks and diseases (https://meetings.embo.org/event/18-protein-protein)	IBPM-CNR, Rome, Italy	Train participants in bioinformatics techniques for gaining a network perspective on PPIs, predicting and analysing them, highlighting differences between globular (protein "domains") and non-globular (intrinsically disordered peptide) modules, and working with large datasets. Ideal participants for this course are bench scientists who are working to obtain data related to protein-protein interactions, or already have such data they want to analyse. Teach the importance of PPIs in biological systems, and how bioinformatics tools can be harnessed for understanding and controlling physiological states and when these states are perturbed by disease.
2017	Curation workshop on molecular and causal interactions	CNR, Roma, Italy	Discuss the state of the art of curating molecular interactions; define guidelines for the curation of causal interactions. Develop rules for curation, controlled vocabularies and standards, bearing in mind the FAIR (Findable, Accessible, Interoperable and Reusable) principles.
2017	Elixir-IIB/NETTAB Tutorial on Biological Networks: data analysis, visualization and medical application	ICAR-CNR, Palermo, Italy	Introduce participants to protein-protein interactions, biochemical reactions, and causal interactions. Expose the principles and methods of curating literature and the standards and ontologies adopted to describe the data retrieved from the literature in a standardized way.
2017	Best practices for RNA-Seq data analysis	University of Salerno, Italy	To make participants acquire a deeper understanding of RNA-Seq experiments, providing a theoretical introduction to the data processing steps, together with practical sessions that illustrate the use of the most popular data analysis tools
2017	Python for Life Scientists	Sapienza University, Rome, Italy	Introduce participants to all basic Python concepts such as computing, organizing data, reading and writing files, logic, and writing programs.
2017	RNA-Seq data analysis	University of Milan, Italy	Provide students with theoretical and practical knowledge on how to perform bioinformatic analyzes of RNA-Seq data, mainly aimed at identifying genes differentially expressed under different conditions
2017	Galaxy for Bioinformatics tool developers	Cagliari, Italy	Familiarize attendees with the Galaxy platform and prepare them to work independently, using best practice guidelines for creating, maintaining, and installing Galaxy tools
2017	Workshop & Summer School on Advanced Computational Metagenomics	University of Bari "Aldo Moro", Italy	Learning the computational aspects of metagenomic analysis, including reference databases, software and data analysis in the ecological, clinical and nutritional fields
2017	EMBO Practical Course on Population Genomics: background and tools	IGB-CNR, Naples, IT	Provide an overview of cutting-edge methods in population genomics by combining lectures from highly experienced population geneticists and software developer
2017	Computational approaches to the study of protein interactions and rational drug design	University of Padua, Italy	Familiarize participants with docking approaches for studying protein-protein and protein-small molecule interactions
2017	ELIXIR-EXCELERATE Train the Trainer	University of Salerno, Italy	Build bioinformatics training capacity in Europe. Provide new instructors with tools, guidelines and suggestions for effective and innovative teaching.

2016	ELIXIR-EXCELERATE Train the Trainer	IGC (Portugal), University of Cambridge (UK)	Build bioinformatics training capacity in Europe. Provide new instructors with tools, guidelines and suggestions for effective and innovative teaching.
2016	NETTAB 2016 satellite Goblet/ELIXIR-IIB joint tutorial on Train the Trainer	CNR, Rome, Italy	Provide participants with teaching principles that come directly from the cognitive research and experience of the speakers and their implications for teaching practice
2016	Python for Life Scientists	University of Bari "Aldo Moro", Italy	Introduce participants to all basic Python concepts such as computing, organizing data, reading and writing files, logic and writing programs.
2016	Exome analysis using Galaxy	University of Milano-Bicocca, Italy	Familiarize participants with the Galaxy platform and prepare them to work independently, using state-of-the-art tools for analysing exome sequencing data
2016	NGS for evolutionary biologists: from basic scripting to variant calling	IGB-CNR, Naples, Italy	Provide an introduction to next-generation sequencing platforms, data analysis and tools for data quality control, including alignment to a reference sequence, data management and visualization, and calling and variant filtering (single nucleotide polymorphisms and structural variants)
2015	Protein networks and systems biology	University of Bologna, Italy	Familiarize participants with different approaches to the study of protein-protein interactions (PPIs), protein interaction networks and systems biology.
2015	NGS for evolutionary biologists: from basic scripting to variant calling	CINECA, Rome, Italy	Teaching the analysis of variants from NGS data to laboratory scientists with no previous knowledge of statistical computing and programming package.
2015	Gene expression profiling with HTS: RNA-Seq data analysis.	CINECA, Rome, IT	Familiarize participants with the analysis of datasets generated through RNA-Seq assay
2015	High Throughput Sequencing (HTS) data analysis	PhD School in Biology and Molecular Medicine (BeMM), Sapienza University, Rome, Italy	The course is a formal didactic activity of the BeMM Doctoral School and is mainly aimed at students of the 2nd year of the doctorate. The purpose of this course is to familiarize participants with the analysis of data generated through two popular Next Generation Sequencing (NGS) assays: ChIP-seq and RNA-seq
2015	Python for Life Scientists	The Genome Analysis Centre, Norwich, UK	Introduce participants to all basic Python concepts such as computing, organizing data, reading and writing files, logic and writing programs
2013	Python for Life Scientists	The Genome Analysis Centre, Norwich, UK	Introduce participants to all basic Python concepts such as computing, organizing data, reading and writing files, logic and writing programs

Part VIII C – Dissemination activities (“Terza Missione”)

Year	Institution	Activity
2019	Liceo “Dante Alighieri”, Roma	Big data nell’Informazione Scientifica (e non) (4h)
2018	CNR, Aula Convegni, Piazzale Aldo Moro 7, Roma	Corso di formazione alla ricerca per circa 300 studenti del liceo di Roma “Augusto Righi”: Big data nella Scienza (8h)
2018	IBPM-CNR c/o Dipartimento di Scienze Biochimiche, Università di Roma “Sapienza”	Alternanza Scuola-Lavoro (ASL): corso di formazione alla ricerca per studenti di scuola superiore. Titolo: “Ricerca & salute: l’importanza della ricerca per affrontare nuove emergenze sanitarie (8h)
2017	IBPM-CNR c/o Dipartimento di Scienze Biochimiche, Università di Roma “Sapienza”	Alternanza Scuola-Lavoro (ASL): corso di formazione alla ricerca per studenti dei licei di Roma: “Giulio Cesare”, “Tasso”, “Righi” e “Plinio Seniore”: Relazione tra struttura e funzione delle proteine. Applicazioni biotecnologiche e biomediche (8h)
2018	Liceo Torquato Tasso, Roma	Percorso formativo per il personale scolastico pubblicato sulla piattaforma Miur S.O.F.I.A: Pratiche efficaci di didattica centrata sull’apprendimento (17h)
2017	Liceo Scientifico Augusto Righi, Roma	<i>Train the Trainer</i> rivolto a docenti di materie scientifiche della scuola superiore: Teniche efficaci di insegnamento (16h)

Part IX - Society memberships

Role	Society
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Member, former secretary	GOBLET (Global Organisation for Bioinformatics Learning Education and Training - http://www.mygoblet.org)
Member	ISCB (International Society for Computational Biology - http://www.iscb.org)
Member	SIB (Italian Society for Biochemistry)
Member	BITS (Bioinformatics Italian Society - http://www.bioinformatics.it)
Chair	BTN (Bioinformatics Training Network - https://www.nbic.nl/en/education/bioinformatics-training-network/index.html)

Part X - Funding Information

Part X A - Grants as PI-principal investigator or I-investigator

Year	AV's Role	Programme	Grant value (EUR)
2019 - 2023	Scientific coordinator of OR4 (Obiettivo Realizzativo 4) - Implementation of a platform for the training and development of multimedia courses	<p>Title: PIR01_00017 - Centro Nazionale di Ricerca in Bioinformatica per le Scienze "Omiche" – CNRBIOIMICS</p> <p>Grant type: PON Research and Innovation</p> <p>Goal: Implementation of the National Bioinformatics Research Centre for "Omics" sciences (CNRBioOmics) capable of responding to the modern needs of large-scale genomic data production and analysis</p>	<p>Tot: 14,5M</p> <p>OR4: 101 020</p>
2021 - 2023	Scientific coordinator of OR4 (Obiettivo Realizzativo 4) - Implementation of a platform for the training and development of multimedia courses	<p>Title: CIR01_00017 - Centro Nazionale di Ricerca in Bioinformatica per le scienze "Omiche" – Rafforzamento del capitale umano</p> <p>Grant type: PNIR - Programma Nazionale Infrastrutture di Ricerca (National Programme for Research Infrastructures)</p> <p>Goal: Strengthening of the human capital of the Research Infrastructure. Funds are targeted at three fellowships (assegni di ricerca) of 24 months each.</p>	<p>Tot: 1,95M</p> <p>OR4: 189 120</p>
2019 - 2023	WP16 Task 3 Manager - Online Academic education course	<p>Title: European Joint Programme on Rare Diseases – EJP RD</p> <p>Grant type: H2020-EU.3.1.3. – Call H2020-SC1-2018-Single-Stage-RTD; COFUND-EJP</p> <p>Goal: Enhance the integration, effectiveness, production and social impact of rare disease research through the development, demonstration and promotion of European / global sharing of clinical research and data, materials, processes, knowledge and know-how ; (ii) Implement and further develop an efficient financial support model for all types of rare disease research together with accelerated exploitation of research results for the benefit of patients.</p>	<p>Tot: 94,5M</p> <p>WP16 Task 3: 72 577</p>
2019 - 2021	co-PI of WP3 - ELIXIR RD Community training infrastructure	<p>Title: ELIXIR Infrastructure for the Rare Disease-Community 2019-2021</p> <p>Grant type: ELIXIR Hub - EMBL</p> <p>Goal: Survey the RD community to identify digital environment that can best support FAIRified training events and Materials. Identify the most suitable type of digital environments for the collection, sharing and reuse of training materials for the FAIRification of RD registries and develop a prototype of such digital environment.</p>	Granted to AV: 9682
2019 - 2021	co-PI	<p>Title: 2019-EIP3 Training Capacity Building</p> <p>Grant type: ELIXIR Hub - EMBL</p> <p>Goal: Empower the ELIXIR training community and support ELIXIR nodes in training new bioinformatics instructors</p>	<p>Tot: 12 746</p> <p>Granted to AV: 10539</p>
2019 - 2021	co-PI	<p>Title: 2019-EIP4 Software Best Practices</p> <p>Grant type: ELIXIR Hub - EMBL</p> <p>Goal: Promote good practices in the development of research software in a way that increases its quality</p>	<p>Tot: 17000</p> <p>Granted to AV: 5719</p>

		and sustainability. Create a Software Management Plan for ELIXIR.	
2019-2021	co-PI	Title: 2019-TP2 Gap analysis, training materials development and training delivery Grant type: ELIXIR Hub - EMBL	Granted to AV: 15000
		Goal: Develop (FAIR) training materials for a lesson on how to develop (FAIR) training materials	
2019-2021	ELIXIR Italy Training Coordinator	Title: 2019-travel Travel funds to ELIXIR Nodes Grant type: ELIXIR Hub - EMBL	Granted to AV: 10000
		Goal: Funds received to allow ELIXIR Italy training coordinator (AV) and her deputies to travel to other ELIXIR nodes for collaborations and meetings.	
2020-2021	PI	Title: Teaching researchers and clinicians how to share COVID-19-related data and software: a series of dedicated webinars and tutorials Grant type: EOSC-Life Training Open Call	Tot: 5000
		Goal: The webinar & tutorial series is aimed at raising awareness in researchers, clinicians and technicians who produce data and develop or use software related to COVID-19 about the outstanding importance of sharing data and software rapidly and openly.	
2015 - 2019	ELIXIR Italy Training Coordinator	Title: ELIXIR-EXCELERATE: Fast-track ELIXIR implementation and drive early user exploitation across the life-sciences Grant type: HORIZON 2020; Call H2020-INFRADEV-1-2015-1	Tot: 29M Granted to ELIXIR-IT: 329000
		Goal: Coordination and extension of national and international data resources to ensure the provision of life science data services worldwide. Development of a pan-European training program, anchored in national infrastructures, to increase bioinformatics capacity and competences	
2013	Principal Investigator	Title: Characterisation of Plasmodium falciparum antigens triggering autoimmune response Grant type: Progetto di Ateneo 2013, Sapienza University	Tot: 5000
		Goal: Development of a bioinformatics procedure for the identification and characterization of potential antigens of P. falciparum that stimulate autoimmune response in humans	
2011	Principal Investigator	Title: Identificazione di target molecolari in plasmodio e schistosoma e caratterizzazione delle loro interazioni con potenziali inibitori Grant type: Progetto di Ateneo 2011, Sapienza University	Tot: 3000
		Goal: Utilizzo di un approccio bioinformatico per la caratterizzazione, a livello molecolare, dei meccanismi di inibizione di <i>Plasmodium falciparum</i> e <i>Schistosoma mansoni</i> da parte di Artemether e Furoxan	

Part X B – Funds granted for AV participation

Year	AV's Role	Programme	Grant value (EUR)
2019 - 2023	Participant in WP14 (Training on data management & quality) Project Coordinator: Daria Julkowska	Title: European Joint Programme on Rare Diseases – EJP RD Grant type: H2020-EU.3.1.3. – Call H2020-SC1-2018-Single-Stage-RTD; COFUND-EJP Goal: Enhance the integration, effectiveness, production and social impact of rare disease research through the development, demonstration and promotion of European / global sharing of clinical research and data, materials,	Tot: 94,5M Funded for AV participation: 11620

		processes, knowledge and know-how; (ii) Implement and further develop an efficient financial support model for all types of rare disease research together with accelerated exploitation of research results for the benefit of patients.	
		AV's Activity:	
2020-2023	Participant in WP2 Task 3 - Capacity Building in Data Management and Stewardship	Title: ELIXIR-CONVERGE - Connect and align ELIXIR Nodes to deliver sustainable FAIR life-science data management services Grant type: HORIZON 2020, H2020-INFRADEV-2019-2 Goal: provisioning, across Europe, of distributed local support for data management and develop the national operations of the research infrastructure to drive good data management, reproducibility and reuse. AV's Activity: Collaboration in the "International Summer School on Rare Disease Registries and FAIRification of Data" (Istituto Superiore di Sanità, Rome)	Tot: 9,8M Funded for AV participation: 15492
2018-2019	PI: Prof. Graziano Pesole, University of Bari, Italy	Title: ELIXIR Implementation Studies IT-2018-WIDENING Grant type: ELIXIR Hub Goal: Develop a system that supports researchers in identifying the skills they need and the appropriate courses to acquire those skills AV Activity: Identification of skills for Bioinformatics and definition of a Learning Path model	Tot: 127500 Funded for AV participation: 7746

Part X C – Participation in scientific projects

Year	PI/Project Coordinator	Programme	Grant value (EUR)
2010-2012	PI: Anna Tramontano, Sapienza University of Rome, Italy	Title: Rational approach to the specific inhibition of Plasmodium falciparum and Schistosoma mansoni Grant type: Fondazione Banca di Roma	Tot: 1,1M
2008-2016	PI: Anna Tramontano, Sapienza University of Rome, Italy	Title: Computational Analysis of the Human Genome Grant type: King Abdullah University for Science and Technology (KAUST) Award Goal: Support high-level scholars who develop research in the fields of information technology, renewable energy, medicine and biotechnology AV's Activity: Analysis of the structure and function of the human genome and its pathogens.	Tot: 5,5M
2008-2012	PI of the University of Tor Vergata Research Unit: Manuela Helmer-Citterich Project Coordinator: Institut Pasteur	Title: LEISHDRUG: Targeting the Leishmania kinome for the development of novel anti-parasitic strategies Grant type: EU FP7 2008 FP7-HEALTH Goal: To reveal Leishmania signaling molecules associated with amastigote virulence, with the main goal of exploiting specific pathways of the parasite for the development of anti-leishmaniasis drugs. AV's Activity: Development of bioinformatics resources for the identification and analysis of phosphorylation sites	Tot: 2,85M Funded to the Research Unit:182077
2005-2008	PI: Manuela Helmer-Citterich, University of Rome "Tor Vergata"	Title: A structural approach for the analysis of recognition specificity in phospho-proteins Grant type: AIRC 2005 Goal: Study of specificity of recognition in phospho-proteins AV's Activity: Development of bioinformatics resources for the identification and analysis of phosphorylation sites	NA

2004-2006	PI: Manuela Helmer-Citterich, University of Rome "Tor Vergata", Italy	Title: A bioinformatic approach for the identification of interactors of proteins involved in genetic diseases (id GGP04273) Grant type: TELETHON 2004	NA
2003-2005	PI: Prof. Rita Casadio, University of Bologna, Italy	Title: LIBI- International Laboratory of Bioinformatics Grant type: FIRB 2003 Goal: Implementation of gene prediction methods in genomes of different organisms and identification of new genes. Development and implementation of new algorithms and resources for the prediction of structural and functional characteristics of proteins starting from their sequence. Development of automatic tools for the prediction of the three-dimensional structure of membrane and globular proteins. AV's Activity: Development of the Eukaryotic Linear Motifs (ELM) resource. Development of a protein structure-function link database. Development of a server for the prediction of the interaction specificity of SH3 domains. Development of a computational method for the comparison between protein structures.	NA
2002-2004	PI: Manuela Helmer-Citterich, University of Rome "Tor Vergata", Italy	GENEFUN: Geni e loro funzioni: un approccio integrato Grant type: MIUR FSSRIS 2002 (Fondo Speciale per lo Sviluppo della Ricerca di Interesse Strategico)	NA
2001-2003	PI: Manuela Helmer-Citterich, University of Rome "Tor Vergata", Italy	Title: Bioinformatics for genomics and proteomics Grant type: FIRB Progetti Negoziati 2001 AV's Activity: Construction of a database of patches of protein surfaces associated with function and its subsequent application to the prediction of function for proteins from structural genomics projects	NA
2001-2003	PI: Manuela Helmer-Citterich, University of Rome "Tor Vergata", Italy	Title: Specificity of recognition and/or interaction in phospho-proteins Grant type: AIRC 2001 Goal: Study of the specificity of interaction of phosphatase and kinase with methods for the comparison of protein surfaces AV's Activity: Development of methods for the comparison of protein surfaces	NA
2001-2004	Project coordinator: EUROPEAN MOLECULAR BIOLOGY LABORATORY, Germany	Title: ELM: The Eukaryotic Linear Motif Resource ELM: A new European Bioinformatics facility for revealing functional sites in modular proteins Grant type: FP5-LIFE QUALITY - Specific Programme for research, technological development and demonstration on "Quality of life and management of living resources", 1998-2002 AV's Activity: Development of a set of tools to identify and evaluate linear eukaryotic functional motifs in proteins using context-based rules for the reduction or elimination of false positives.	Tot: 1.29M

Part XI – Research Activities

Part XI A – Summary of Research Interests and Activities

My scientific research is in the field of bioinformatics. It focuses on the prediction and analysis of protein structure, functional sites, linear motifs (SLiMs), phosphorylation sites and protein-ligand interactions, aimed at understanding the molecular mechanisms characterizing the function and mis-functioning of proteins in various contexts, including host-pathogen interactions, protein-drug interactions, drug resistance, therapeutic targets and disease-related point mutations. Four main lines of research can be identified in my career. They are briefly described in the following.

Keywords

Brief Description

SLiM	Research in the field of the structure and function of proteins, protein phosphorylation, linear functional motifs, protein domain interaction specificity I did a post-graduate internship (1998-1999) and my PhD (1999-2003) in the group of Manuela Helmer-Citterich at the University of Rome "Tor Vergata". My research interests included the study of protein-domain interaction specificity and sequence and structural motifs (SLiMs). We studied the structural features of protein-domain (SH2, SH3) interactions and developed computational methods using such features to predict the specificity of interaction of protein domains (publications 51-54). In this period, the group also started a fruitful and long-lasting collaboration with the group of Toby Gibson at the EMBL (Germany) on the study of SLiMs, including post-translational modifications and phosphorylation sites in particular. Within this collaboration, the ELM (Eukaryotic Linear Motif) database was developed and deployed (publications 50, 34, 25). Based on the concept that what is structurally conserved is likely to be functionally relevant, for my PhD thesis, I carried out a protein structural study for the optimization and analysis of sequence functional motifs (publication 49). I kept working on this research line (publications 41, 40, 31, 27) and collaborating on ELM and Phospho.ELM until 2012 (publications 48, 42, 37, 35, 34, 30).
ELM, Eukaryotic Linear Motif	
Phospho.ELM	
Phosphorylation	
Domain interaction specificity	
SH2	
SH3	
Functional sites	
Modelling of biological systems	Modelling of biological systems, application of neural networks to the inference of protein domain interaction specificity; development of bioinformatics resources, methods and algorithms In 2003-2008, as a postdoc in the group of M. Helmer-Citterich, my activity of research software development became more intense. Modelling of biological systems and development of computational methods to analyse them and make inferences became my main activity (publications 36, 38, 39, 43, 44, 45, 46), as well as the construction of biological databases and their deployment on the web (publications 29, 42, 47). Within the collaboration with the Gibson's group, I developed the ELM structural filter, a piece of software for the identification of structural characteristics of SLiM matches in protein sequences (publication 35). The structural filter was aimed at discarding potential false positive ELM matches, by filtering out SLiMs occurring on secondary structure elements (as opposed to loops) and/or buried in the core of proteins, as they are unlikely to be functional. In the following years, my strong interest in programming and software development was mostly expressed by organising and teaching programming courses (see related Parts of this CV), in publishing a book on Python programming (publication 62) and by becoming one of the leads of the ELIXIR Tool Platform Software Best Practices working group, where I can contribute with my experience as research software developer. In 2019-2020, I had the chance to be involved in a collaboration with the cattaneoLab (University of Milan) and Vincenza Colonna (IGB-CNR) on the development of software for the analysis of sequences of the Huntingtin gene (HTT), sequenced with Nanopore techniques.
Neural networks	
Research software development	
Software best practices	
Computational methods	
Algorithms implementation	
Functional sites	Research in the field of structure and function of proteins; study of proteins and mechanisms of host-pathogen interactions; study of therapeutic targets In 2008 I joined the group of Anna Tramontano at the department of Biochemical Sciences A. Rossi Fanelli of Sapienza University of Rome, until 2012, and at the department of Physics until 2016, when I started working at the CNR, as a research fellow (assegnista) in 2016, research associate (end 2016) and as a permanent research scientist since 2017 (this is my current position). In the group of Anna, I started working on human pathogens and on specific classes of functional sites, in particular on binding sites involved in host-pathogen protein interactions and on functional sites characterizing drug-target interactions in pathogens. In this period, my work was characterized by the use of software and tools to analyse and understand molecular mechanisms of protein-ligand interactions. Docking studies and molecular dynamic experiments were carried out to study mechanisms of drug target inhibition and drug resistance (publications 13, 24, 26). Other studies on pathogens were carried out on mutations associated with resistance to Artemeter (publication 23) and on mechanism of chloroquine resistance in <i>P. falciparum</i> (publication 32) and a database on therapeutic targets in pathogens was developed and deployed (publication 20). My work of this period culminated with the publication of an invited review on TiBS (publication 15) on <i>How pathogens use linear motifs to perturb host cell networks</i> , which fruitfully put together my experience on SLiMs with the knowledge of host-pathogen interactions.
Pathogens	
Host-pathogen interactions	
Drug-target interactions	
Therapeutic target	
Drug resistance	
Point mutations associated with drug resistance	
<i>P. falciparum</i>	
<i>S. mansoni</i>	

Bioinformatics training	Research on cognitive and educational psychology and learning processes In 2010, I was involved in the Bioinformatics Training Network (BTN, https://www.nbic.nl/en/education/bioinformatics-training-network/index.html) (publication 22) and, since then, I developed new research interests, which currently also include educational psychology, learning processes, teaching practices, and curriculum and training material development (publications 26, 21, 17, 12, 10, 7, 6, 5, 4, 2, 57). In 2012, the BTN evolved into the Global Organisation for Bioinformatics Learning, Education and Training (GOBLET, https://www.mygoblet.org/). In 2014, I was appointed as the ELIXIR Training coordinator of the Italian Node (ELIXIR-IT). ELIXIR is a European intergovernmental organisation made up of life scientists, computer scientists and support staff helping researchers to collect, integrate, share, and analyse the huge amounts of data produced in the Life Sciences. ELIXIR is a distributed infrastructure for bioinformatics with 23 member countries (ELIXIR nodes). ELIXIR-IT is a network of 26 research institutions, including, among the others, the CNR and Sapienza University of Rome. Thanks to my work for and within ELIXIR, I also developed strong competencies in the areas of data and software management, sharing, integration, interoperability, and FAIRification (publications 19, 11, 8, 3, 56, 61). The competencies developed within this research line, made me able to support the design of the Master Degree in Biochemistry of Sapienza University of Rome, and become an expert adviser for the GdL QUID (Quality and Innovation of Teaching working group) of Sapienza University.
Teaching best practices	
Cognitive sciences	
Educational psychology	
Curriculum development	

Part XI B –Current Research Activities

Keywords

Antibiotic resistance
Point mutations associated with drug resistance
Bacteria
<i>Streptococcus pneumoniae</i>
Quinolones

SARS-CoV-2
Variant of Concern (VOC)
Spike
Point mutations
Missense variants

APOB
MTTP
ANGPL3
UK Biobank
Low cholesterol
Loss-of-function mutations

Brief Description

Identification and analysis of point mutations associated with drug resistance in bacteria: a lesson learnt from the resistance of <i>Streptococcus pneumoniae</i> to quinolones (stage: manuscript in preparation)
In 2018, I started working on the identification and analysis of variants involved in antibiotic resistance using structural bioinformatics approaches. An extensive structural analysis was carried out of the mutations involved in the resistance to quinolones affecting the gyrase and topoisomerase genes in <i>Streptococcus pneumoniae</i> . Results, extended to other bacterial species, have been collected in a database and can now be used – through a webserver - to analyse both known and yet unknown mutations occurring in bacterial topoisomerases and gyrases. Quinolones are a new class of antibiotics that bind bacterial topoisomerases and inhibit cell replication. Quinolones have been important in limiting the spread of penicillin- and macrolides-resistant <i>S. pneumoniae</i> .
Manuscript in preparation #58
Structural and functional analysis of SARS-CoV-2 Spike protein missense variants (stage: manuscript in preparation)
In 2020, I started a second project focusing on disease-related mutations. It is aimed at characterising, from a structural perspective, point mutations of the Sars-CoV-2 Spike protein present both in the Variants of Concern (VOC) and showing a frequency compatible with a high likelihood of fixation. We analysed the structural differences between wild-type and mutated residues of the SARS-CoV-2 Spike protein. In some cases, the mutation introduced important local structural and physico-chemical changes in the Spike protein, thus interfering with the Spike interactions with ACE2, Furin and the antibody neutralizer S2M1. Furthermore, the analysis of point mutations in the context of SARS-CoV-2 Variants of Concern allowed hypothesizing which molecular characteristics might confer functional advantage to the virus.
Manuscript in preparation #59
Analysis of a cohort of patients carrying loss-of-function (LOF) mutations in APOB, MTTP and ANGPTL3 genes to study the effects of low cholesterol syndromes on chronic liver and cardiovascular diseases
In Dec 2020, I started a collaboration with Prof. Marcello Arca and Dr Alessia di Costanzo (Sapienza University of Rome), aimed at analysing cohort of patients from UK Biobank carrying loss-of-function (LOF) mutations in APOB, MTTP and ANGPTL3 genes to study the effects of low cholesterol syndromes on chronic liver and cardiovascular diseases. Obtaining data from UK Biobank was a very time-consuming task and only at the very end of 2021 it was possible to access the resource and collect the data needed for the research. The research is aimed at elucidating the consequences of life-long exposure to low cholesterol on liver as well as on cardiovascular diseases by analysing the demographic, clinical and genotypic data of a cohort of patients selected by UK Biobank. The analyses will allow a safer assessment of the long-term risks of drugs capable of inhibiting the secretion of very low-density lipoproteins (VLDL). UK Biobank data will be used to perform a Mendelian randomization analysis by selecting individuals carrying loss-of-function (LOF) mutations in APOB, MTTP and ANGPTL3 genes, which mimic the inhibitory action of the above-mentioned drugs

Machine learning	Machine Learning and Deep Learning approaches to the study of chromatin organisation within the cell nucleus (stage: data collection)
Deep learning	
Chromatin	
Contact matrix	
	In 2019, I was involved as a member in the Working Group on “AI Applications in functional genomics”, which was born in 2019 within the CNR Observatory on AI, and constituted of the CNR research scientists Claudia Caudai, Antonella Galizia, Filippo Geraci, Loredana Le Pera (today ISS), Veronica Morea, Emanuele Salerno, Teresa Colombo, and myself. The WG published a paper on “AI applications in Functional Genomics” (publication #1) and recently started a new project on Machine Learning and Deep Learning approaches to the study of chromatin organisation within the cell nucleus. This new project is currently in its preliminary phase (data collection). It aims to use Machine Learning and Deep Learning methods to analyse contact frequency arrays derived from Chromosome Conformation Capture experiments.
	Publication #1
SARS-CoV-2	Analysis of point mutations to all Sars-CoV-2 proteins with the additional perspective of looking at point mutations occurring in functional motifs (stage: data collection)
Variants	
Protein-protein interactions	I'm currently extending the analysis of point mutations to all Sars-CoV-2 proteins with the additional perspective of looking at point mutations occurring in functional motifs. Starting from genomic data on Sars-CoV-2 variants, occurrence of evolutionary conserved point mutations will be detected in all the virus coding genes. Short Linear Motifs (SLiMs) from databases like ELM (elm.eu.org) will be searched as well in virus proteins. SLiMs provide a wide range of functionality to proteins and finding conserved point mutations that occur in functional motifs, may reveal how mutations affect the function of virus genes, possibly conferring advantage to the virus.
Protein functional motifs	
	Data collection and analysis

Part XII – Summary of Scientific Achievements

Product type	Number	Data Base	Start	End
Papers [international]	52	Scopus	2000	2021
Conference paper	2	Scopus	2017	2018
Preprint	2	BioHackrXiv, SocArXi	2020	2021
Books [teaching]	1	Scopus	2014	2014
Book chapters	3	ISBN	2002	2011

Total Impact factor	299,045
Average Impact factor per Publication (indexed on Scopus)	5,75
Impact Factor of the last 10 years	125,015
Average Impact factor per Publication in the last 10 year	5,2
Total Citations	2957
Average Citations per Product (indexed on Scopus)	53,76
Hirsch (H) index	26
Normalized H index**	1,24

**H index divided by the academic seniority.

Part XIII – Publications

Part XIII A – International Journals

n.	Title	Authors	Year	Ref data	DOI	IF	Scopus
1	AI applications in functional genomics	Caudai [†] C., Galizia [†] A., Geraci [†] F., Le Pera [†] L., Morea [†] V., Salerno [†] E., Via A[†] , Colombo T.	2021	Computational and Structural Biotechnology Journal, 19, pp. 5762-5790	10.1016/j.csbj.2021.10.009	7,271	0
2	A framework to assess the quality and impact of bioinformatics training across ELIXIR	Gurwitz K.T., Gaur P.S., Bellis L.J., Larcombe L., Alloza E., Balint B.L., Botzki A., Dimec J., del Angel V.D., Fernandes P.L., Korpelainen E., Krause R., Kuzak M., Le Pera L., Leskošek B., Lindvall J.M., Marek D., Martinez P.A., Muyltermans T., Nygård S., Palagi P.M., Peterson H., Psomopoulos F., Spiwok V., van Gelder C.W.G., Via A. , Vidak M., Wibberg D., Morgan S.L., Rustici G.	2020	PLoS Computational Biology, 16(7),e1007976	10.1371/journal.pcbi.1007976	4,712	3
3	Ten simple rules for making training materials FAIR	García L., Batut B., Burke M.L., Kuzak M., Psomopoulos F., Arcila R., Attwood T.K., Beard N., Carvalho-Silva D., Dimopoulos A.C., Del Angel V.D., Dumontier M., Gurwitz K.T., Krause R., McQuilton P., Le Pera L., Morgan S.L., Rauste P., Via A. , Kahlem P., Rustici G., Van Gelder C.W.G., Palagi P.M.	2020	PLoS Computational Biology, 16(5),e1007854	10.1371/journal.pcbi.1007854	4,712	6
4	Course design: Considerations for trainers – a Professional Guide]	Via A. , Palagi PM, Lindvall JM, Tractenberg RE, Attwood TK	2020	F1000Research, 9,1377	10.7490/f1000research.1118395.1		<u>NA</u>
5	The mastery rubric for bioinformatics: A tool to support design and evaluation of career-spanning education and training	Tractenberg R.E., Lindvall J.M., Attwood T.K., Via A.	2019	PLoS ONE, 14(11),e0225256	10.1371/journal.pone.0225256	2,74	3
6	A new pan-European Train-the-Trainer programme for bioinformatics: Pilot results on feasibility, utility and sustainability of learning	Via A. , Attwood T.K., Fernandes P.L., Morgan S.L., Schneider M.V., Palagi P.M., Rustici G., Tractenberg R.E.	2019	Briefings in Bioinformatics, 20(2), pp. 405-415	10.1093/bib/bbx112	5,818	6
7	The ELIXIR-EXCELERATE Train-the-Trainer pilot programme: Empower researchers to deliver high-quality training	Morgan S.L., Palagi P.M., Fernandes P.L., Koperlainen E., Dimec J., Marek D., Larcombe L., Rustici G., Attwood T.K., Via A.	2017	F1000Research, 6,1557	10.12688/f1000research.12332.1	2,13	5
8	Four simple recommendations to encourage best practices in research software	Jiménez R.C., Kuzak M., Alhamdoosh M., Barker M., Batut B., Borg M., Capella-Gutierrez S., Chue Hong N., Cook M., Corpas M., Flannery M., Garcia L., Gelpi J.L., Gladman S., Goble C., González Ferreiro M., Gonzalez-Beltran A., Griffin P.C., Grüning B., Hagberg J., Holub P., Hoof R., Ison J., Katz D.S., Leskošek B., López Gómez F., Oliveira L.J., Mellor D., Mosbergen R., Mulder N., Perez-Riverol Y., Pergl R., Pichler H., Pope B., Sanz F., Schneider M.V., Stodden V., Sucheckí R., Svobodová Vařeková R., Talvik H.-A., Todorov I., Treloar A., Tyagi S., van Gompel M., Vaughan D., Via A. , Wang X., Watson-Haigh N.S., Crouch S.	2017	F1000Research, 6,876	10.12688/f1000research.11407.1	2,13	47

9	Tools and data services registry: A community effort to document bioinformatics resources	Ison J., Rapacki K., Ménager H., Kalaš M., Rydzka E., Chmura P., Anthon C., Beard N., Berka K., Bolser D., Booth T., Bretaudeau A., Brezovsky J., Casadio R., Cesareni G., Coppens F., Cornell M., Cuccuru G., Davidsen K., Della Vedova G., Dogan T., Doppelt-Azeroual O., Emery L., Gasteiger E., Gatter T., Goldberg T., Grosjean M., Grüning B., Helmer-Citterich M., Ienasescu H., Ioannidis V., Jespersen M.C., Jimenez R., Juty N., Juven P., Koch M., Laibe C., Li J.-W., Licata L., Mareuil F., Mičetić I., Friberg R.M., Moretti S., Morris C., Möller S., Nenadic A., Peterson H., Profiti G., Rice P., Romano P., Roncaglia P., Saidi R., Schafferhans A., Schwämmle V., Smith C., Sperotto M.M., Stockinger H., Varčková R.S., Tosatto S.C.E., De La Torre V., Uva P., Via A. , Yachdav G., Zambelli F., Vriend G., Rost B., Parkinson H., Longreen P., Brunak S.	2016	Nucleic Acids Research, 44(D1), pp. D38-D47	10.1093/nar/gkv1116	10,599	76
10	Training in High-Throughput Sequencing: Common Guidelines to Enable Material Sharing, Dissemination and Re-Usability	Schiffthaler B, Kostadima M, the NGS Trainer Consortium , Delhomme N and Rustici G	2016	PLoS Computational Biology, 12(6): e1004937	10.1371/journal.pcbi.1004937	4,085	4
11	Data integration in biological research: an overview.	Lapatas V, Stefanidakis M, Jimenez RC, Via A , Schneider MV	2015	J Biol Res (Thessalon)	10.1186/s40709-015-0032-5	0,754	NA
12	GOBLET: The Global Organisation for Bioinformatics Learning, Education and Training	Atwood T.K., Bongcam-Rudloff E., Brazas M.E., Corpas M., Gaudet P., Lewitter F., Mulder N., Palagi P.M., Schneider M.V., van Gelder C.W.G., Attwood T.K., Banag C., Blackford S., Blatter M.C., Bongcam-Rudloff E., Brazas M.D., Brooksbank C., Budd A., Charleston M., Christoffels A., Conesa A., Crowe M., Davies A., de Crecy-Lagard V., De Las Rivas J., Doyle M., Edwards R., Facchiano A., Fernandes P., Gaeta B., Gaudet P., Heger A., Herringa J., Hughes D., Jimenez R.C., Kille P., Korpeläinen E., Kumuthini J., Lewitter F., MacLean D., Martinez S.A.R., McGrath A., Michalopoulos I., Mulder N., Ouellette B.F., Palagi P.M., Pearson W.R., Qi W., Romano P., Rother K., Sansone S-A., Schneider M.V., Schönbach C., Tastan-Bishop O., Trelles O., Twells R., van Gelder C.W.G., Via A , Vriend G., Warnow T., Watson M., Westervelt N., Zanzoni A., GOBLET Consortium	2015	PLoS Computational Biology, 11(4), e1004143	10.1371/journal.pcbi.1004143	5,101	39
13	Characterization of the differences in the cyclopirolic acid binding mode to mammalian and <i>P. falciparum</i> Ca ²⁺ pumps: A computational study	Di Marino D., D'Annese I., Coletta A., Via* A. , Tramontano A.	2015	Proteins: Structure, Function and Bioinformatics, 83(3), pp. 564-574	10.1002/prot.24734	2,717	12
14	Digestive peptidase evolution in holometabolous insects led to a divergent group of enzymes in Lepidoptera	Dias R.O., Via A. , Brandão M.M., Tramontano A., Silva-Filho M.C.	2015	Insect Biochemistry and Molecular Biology, 58, pp. 1-11	10.1016/j.ibmb.2014.12.009	4,944	14
15	How pathogens use linear motifs to perturb host cell networks	Via A. , Uyar B., Brun C., Zanzoni A.	2015	Trends in Biochemical Sciences, 40(1), pp. 36-48	10.1016/j.tibs.2014.11.001	13,265	49
16	A prismatic view of protein phosphorylation in health and disease	Via A. , Zanzoni A.	2015	Frontiers in Genetics, 6(APR), 131	10.3389/fgene.2015.00131	3,779	1

17	The GOBLET training portal: A global repository of bioinformatics training materials, courses and trainers	Corpas M., Jimenez R.C., Bongcam-Rudloff E., Budd A., Brazas M.D., Fernandes P.L., Gaeta B., Van Gelder C., Korpelainen E., Lewitter F., McGrath A., MacLean D., Palagi P.M., Rother K., Taylor J., Via A. , Watson M., Schneider M.V., Attwood T.K.	2015	Bioinformatics, 31(1), pp. 140-142	10.1093/bioinformatics/btu601	6,509	26
18	The crystal structure of Giardia duodenalis 14-3-3 in the apo form: When protein post-translational modifications make the difference	Fiorillo A., Di Marino D., Bertuccini L., Via A. , Pozio E., Camerini S., Ilari A., Lalle M.	2014	PLoS ONE, 9(3), e92902	10.1371/journal.pone.0092902	3,234	9
19	IAnn: An event sharing platform for the life sciences	Jimenez R.C., Albar J.P., Bhak J., Blatter M.-C., Blicher T., Brazas M.D., Brooksbank C., Budd A., De Las Rivas J., Dreyer J., Van Driel M.A., Dunn M.J., Fernandes P.L., Van Gelder C.W.G., Hermjakob H., Ioannidis V., Judge D.P., Kahlem P., Korpelainen E., Kraus H.-J., Loveland J., Mayer C., McDowall J., Moran F., Mulder N., Nyronen T., Rother K., Salazar G.A., Schneider R., Via A. , Villaveces J.M., Yu P., Schneider M.V., Attwood T.K., Corpas M.	2013	Bioinformatics, 29(15), pp. 1919-1921	10.1093/bioinformatics/btt306	5,307	4
20	TiPs: A database of therapeutic targets in pathogens and associated tools	Lepore R., Tramontano A., Via A.	2013	Bioinformatics, 29(14), pp. 1821-1822	10.1093/bioinformatics/btt289	5,307	1
21	Best practices in bioinformatics training for life scientists	Via A. , Blicher T., Bongcam-Rudloff E., Brazas M.D., Brooksbank C., Budd A., De Las Rivas J., Dreyer J., Fernandes P.L., Van Gelder C., Jacob J., Jimenez R.C., Loveland J., Moran F., Mulder N., Nyronen T., Rother K., Schneider M.V., Attwood T.K.	2013	Briefings in Bioinformatics, 14(5), bbt043, pp. 528-537	10.1093/bib/bbt043	5,917	37
22	Bioinformatics training network (BTN): A community resource for bioinformatics trainers	Schneider M.V., Walter P., Blatter M.-C., Watson J., Brazas M.D., Rother K., Budd A., Via A. , van Gelder C.W.G., Jacob J., Fernandes P., Nyronen T.H., De Las Rivas J., Blicher T., Jimenez R.C., Loveland J., McDowall J., Jones P., Vaughan B.W., Lopez R., Attwood T.K., Brooksbank C.	2012	Briefings in Bioinformatics, 13(3), bbr064, pp. 383-389	10.1093/bib/bbr064	5,863	19
23	Artemether resistance in vitro is linked to mutations in PfATP6 that also interact with mutations in PfMDR1 in travellers returning with Plasmodium falciparum infections	Pillai D.R., Lau R., Khairnar K., Lepore R., Via A. , Staines H.M., Krishna S.	2012	Malaria Journal, 11, 131	10.1186/1475-2875-11-131	3,874	28
24	Investigation of a potential mechanism for the inhibition of SmTGR by Auranofin and its implications for Plasmodium falciparum inhibition	Caroli A., Simeoni S., Lepore R., Tramontano A., Via A.	2012	Biochemical and Biophysical Research Communications, 417(1), pp. 576-581	10.1016/j.bbrc.2011.12.009	2,769	24
25	ELM - The database of eukaryotic linear motifs	Dinkel H., Michael S., Weatheritt R.J., Davey N.E., Van Roey K., Altenberg B., Toedt G., Uyar B., Seiler M., Budd A., Jödicke L., Dammert M.A., Schroeter C., Hammer M., Schmidt T., Jehl P., McGuigan C., Dymecka M., Chica C., Luck K., Via A. , Chatr-Aryamontri A., Haslam N., Grebnev G., Edwards R.J., Steinmetz M.O., Meiselbach H., Diella F., Gibson T.J.	2012	Nucleic Acids Research, 40(D1), pp. D242-D251	10.1093/nar/gkr1064	8,458	240
	Identification of the Schistosoma mansoni molecular target for the antimalarial drug artemether	Lepore R., Simeoni S., Raimondo D., Caroli A., Tramontano A., Via A.	2011	Journal of Chemical Information and Modeling, 51(11), pp. 3005-3016	10.1021/ci2001764	4,841	15

26	Ten simple rules for developing a short bioinformatics training course	Via A. , de Las Rivas J., Attwood T.K., Landsman D., Brazas M.D., Leunissen J.A.M., Tramontano A., Schneider M.V.	2011	PLoS Computational Biology, 7(10),e1002245	10.1371/journal.pcbi.1002245	6	26
27	Exploiting publicly available biological and biochemical information for the discovery of novel short linear motifs	Sayadi A., Briganti L., Tramontano A., Via A.	2011	PLoS ONE, 6(7),e22270	10.1371/journal.pone.0022270	4,092	2
28	Molecular evolution of a gene cluster of serine proteases expressed in the <i>Anopheles gambiae</i> female reproductive tract	Mancini E., Tammaro F., Baldini F., Via A. , Raimondo D., George P., Audisio P., Sharakhov I.V., Tramontano A., Catteruccia F., Torre A.D.	2011	BMC Evolutionary Biology, 11(1),72	10.1186/1471-2148-11-72	3,777	17
29	Phospho3D 2.0: An enhanced database of three-dimensional structures of phosphorylation sites	Zanzoni A., Carbajo D., Diella F., Gherardini P.F., Tramontano A., Helmer-Citterich M., Via A.	2011	Nucleic Acids Research, 39(SUPPL. 1), pp. D268-D271	10.1093/nar/gkq936	8,828	35
30	Phospho.ELM: A database of phosphorylation sites-update 2011	Dinkel H., Chica C., Via A. , Gould C.M., Jensen L.J., Gibson T.J., Diella F.	2011	Nucleic Acids Research, 39(SUPPL. 1), pp. D261-D267	10.1093/nar/gkq1104	8,828	418
31	From sequence to structural analysis in protein phosphorylation motifs	Via A. , Diella F., Gibson T.J., Helmer-Citterich M.	2011	Frontiers in Bioscience, 16(4), pp. 1261-1275	10.2741/3787	4,252	17
32	On the mechanism of chloroquine resistance in <i>Plasmodium falciparum</i>	Chinappi [†] M., Via[†] A. , Marcotili P., Tramontano A.	2010	PLoS ONE, 5(11),e14064	10.1371/journal.pone.0014064	4,411	46
33	Bioinformatics training: A review of challenges, actions and support requirements	Schneider M.V., Watson J., Attwood T., Rother K., Budd A., McDowall J., Via A. , Fernandes P., Nyronen T., Blicher T., Jones P., Blatter M.-C., de Las Rivas J., Judge D.P., van der Gool W., Brooksbank C.	2010	Briefings in Bioinformatics, 11(6),bbq021, pp. 544-551	10.1093/bib/bbq021	10,087	34
34	ELM: The status of the 2010 eukaryotic linear motif resource	Gould C.M., Diella F., Via A. , Puntervoll P., Gemünd C., Chabanis-Davidson S., Michael S., Sayadi A., Bryne J.C., Chica C., Seiler M., Davey N.E., Haslam N., Weatheritt R.J., Budd A., Hughes T., Paś J., Rychlewski L., Travé G., Aasland R., Helmer-Citterich M., Linding R., Gibson T.J.	2010	Nucleic Acids Research, 38(SUPPL.1),gkp1016, pp. D167-D180	10.1093/nar/gkp1016	7,693	205
35	A structure filter for the Eukaryotic Linear Motif Resource	Via A. , Gould C.M., Gemünd C., Gibson T.J., Helmer-Citterich M.	2009	BMC Bioinformatics,, 10,351	10.1186/1471-2105-10-351	3,791	36
36	FunClust: A web server for the identification of structural motifs in a set of non-homologous protein structures	Ausiello G., Gherardini P.F., Marcotili P., Tramontano A., Via A. , Helmer-Citterich M.	2008	BMC Bioinformatics, 9(SUPPL. 2), S2	10.1186/1471-2105-9-S2-S2	4,109	29
37	Phospho.ELM: A database of phosphorylation sites - Update 2008	Diella F., Gould C.M., Chica C., Via A. , Gibson T.J.	2008	Nucleic Acids Research, 36(SUPPL. 1), pp. D240-D244	10.1093/nar/gkm772	7,247	206
38	SH3-Hunter: Discovery of SH3 domain interaction sites in proteins	Ferraro E., Peluso D., Via A. , Ausiello G., Helmer-Citterich M.	2007	Nucleic Acids Research, 35(SUPPL.2), pp. W451-W454	10.1093/nar/gkm296	7,573	27
39	3dLOGO: A web server for the identification, analysis and use of conserved protein substructures	Via A. , Peluso D., Gherardini P.F., De Rinaldis E., Colombo T., Ausiello G., Helmer-Citterich M.	2007	Nucleic Acids Research, 35(SUPPL.2), pp. W416-W419	10.1093/nar/gkm228	7,573	6
40	Local comparison of protein structures highlights cases of convergent evolution in analogous functional sites	Ausiello G., Peluso D., Via A. , Helmer-Citterich M.	2007	BMC Bioinformatics, 8(SUPPL. 1),S24	10.1186/1471-2105-8-S1-S24	4,072	14
41	False occurrences of functional motifs in protein sequences highlight evolutionary constraints	Via A. , Gherardini P.F., Ferraro E., Ausiello G., Tomba G.S., Helmer-Citterich M.	2007	BMC Bioinformatics, 8,68	10.1186/1471-2105-8-68	4,072	7

42	Phospho3D: A database of three-dimensional structures of protein phosphorylation sites	Zanzoni A., Ausiello G., Via A. , Gherardini P.F., Helmer-Citterich M.	2007	Nucleic Acids Research, 35(SUPPL. 1), pp. D229-D231	10.1093/nar/gkl922	7,573	38
43	A novel structure-based encoding for machine-learning applied to the inference of SH3 domain specificity	Ferraro E., Via A. , Ausiello G., Helmer-Citterich M.	2006	Bioinformatics, 22(19), pp. 2333-2339	10.1093/bioinformatics/btl403	5,857	20
44	A neural strategy for the inference of SH3 domain-peptide interaction specificity	Ferraro E., Via A. , Ausiello G., Helmer-Citterich M.	2005	BMC Bioinformatics, 6(SUPPL.4),S13	10.1186/1471-2105-6-S4-S13	5,382	10
45	Query3d: A new method for high-throughput analysis of functional residues in protein structures	Ausiello G., Via A. , Helmer-Citterich M.	2005	BMC Bioinformatics, 6(SUPPL.4),S5	10.1186/1471-2105-6-S4-S5	5,382	48
46	pdbFun: Mass selection and fast comparison of annotated PDB residues	Ausiello G., Zanzoni A., Peluso D., Via A. , Helmer-Citterich M.	2005	Nucleic Acids Research 33(SUPPL. 2), pp. W133-W137	10.1093/nar/gki499	8,118	31
47	Seq2Struct: A resource for establishing sequence-structure links	Via A. , Zanzoni A., Helmer-Citterich M.	2005	Bioinformatics 21(4), pp. 551-553	10.1093/bioinformatics/bti049	6,34	8
48	Phospho.ELM: A database of experimentally verified phosphorylation sites in eukaryotic proteins	Diella F., Cameron S., Gemünd C., Linding R., Via A. , Kuster B., Sicheritz-Pontén T., Blom N., Gibson T.J.	2004	BMC Bioinformatics 5,79	10.1186/1471-2105-5-79	6,057	298
49	A structural study for the optimisation of functional motifs encoded in protein sequences	Via A. , Helmer-Citterich M.	2004	BMC Bioinformatics 5,50	10.1186/1471-2105-5-50	6,057	7
50	ELM server: A new resource for investigating short functional sites in modular eukaryotic proteins	Puntervoll P., Linding R., Gemünd C., Chabanis-Davidson S., Mattingdal M., Cameron S., Martin D.M.A., Ausiello G., Brannetti B., Costantini A., Ferrè F., Maselli V., Via A. , Cesareni G., Diella F., Superti-Furga G., Wyrwicz L., Ramu C., McGuigan C., Gudavalli R., Letunic I., Bork P., Rychlewski L., Küster B., Helmer-Citterich M., Hunter W.N., Aasland R., Gibson T.J.	2003	Nucleic Acids Research 31(13), pp. 3625-3630	10.1093/nar/gkg545	6,539	512
51	Development of computational tools for the inference of protein interaction specificity rules and functional annotation using structural information	Ferrè F., Via A. , Ausiello G., Brannetti B., Zanzoni A., Helmer-Citterich M.	2003	Comparative and Functional Genomics 4(4), pp. 416-419	10.1002/cfg.304	0,878	1
52	Three-dimensional view of the surface motif associated with the P-loop structure: Cis and trans of cases convergent evolution	Via A. , Ferrè F., Brannetti B., Valencia A., Helmer-Citterich M.	2000	Journal of Molecular Biology 303(4), pp. 455-465	10.1006/jmbi.2000.4151	5,42	69
53	SH3-SPOT: An algorithm to predict preferred ligands to different members of the SH3 gene family	Brannetti B., Via A. , Cestra G., Cesareni G., Citterich M.H.	2000	Journal of Molecular Biology 298(2), pp. 313-328	10.1006/jmbi.2000.3670	5,42	70
54	Protein surface similarities: A survey of methods to describe and compare protein surfaces	Via A. , Ferrè F., Brannetti B., Helmer-Citterich M.	2000	Cellular and Molecular Life Sciences 57(13-14), pp. 1970-1977	10.1007/PL00000677	3,803	54

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Part XIII B – Preprints and Articles in preparation

Title	Authors	Year	Archive/Status.	doi	
56	ELIXIR Software Management Plan for Life Sciences	Alves R, Bampalakis D, Jael Castro L, Fernández JM, Harrow J, Kuzak M, Martín del Pico E, Psomopoulos F, Via A	2021	BioHackrXiv, OCT 2021	10.37044/osf.io/k8znb
57	Guidelines for curriculum development in higher education: How learning outcomes drive all decision-making.	Tractenberg ET, Lindvall JM, Attwood KA, Via A	2020	SocArXiv, APR 2020	10.31235/osf.io/7qeh7
58	Identification and analysis of point mutations associated to drug resistance in bacteria: a lesson learnt from the resistance of <i>Streptococcus pneumoniae</i> to quinolones	Staid DS, Le Pera L, Nicotri S, Via A	2022	Manuscript in preparation	
59	Structural and functional analysis of SARS-CoV-2 Spike protein missense variants	Pucilli A, Staid DS, Via A	2022	Manuscript in preparation	

Part XIII C – Conference Proceedings indexed on Scopus

n.	Title	Authors	Year	Ref data	doi
60	Lesson development for open source software best practices adoption	Kuzak M, Harrow J, Jimenez R.C, Martinez P.A, Psomopoulos F.E., Svobodova Varekova R., Via A.	2018	Proceedings - IEEE 14th International Conference on eScience, e-Science 2018, 8588630, pp. 19-20	10.1109/eScience.2018.00011
61	The FAIRification of data and the potential of FAIR resources demonstrated in practice at the Rome Bring Your Own Data workshop	Carta C., Roos M., Jacobsen A., Kaliyaperumal R., Thompson M., Wilkinson M.D., Cornet R., Waagmeester A., Van Enckevort D., Jansen M., Licata L., Via A., Taruscio D.	2017	CEUR Workshop Proceedings, 2042	

Part XIII D – Books and Book Chapters

n.	Title	Author(s)	Year	Source	DOI/ISBN	Cit
62	Managing your biological data with python	Via A., Rother K., Tramontano A.	2014	Managing Your Biological Data with Python, pp. 1-526	10.1201/b16673	2
63	Protein structural motifs: identification, annotation and use in function prediction.	Via A., Tramontano A.	2011	In Sequence and Genome Analysis II – Methods and Applications. iConcept Press http://www.iconceptpress.com/books/sequence-and-genome-analysis-ii-methods-and-applications/	ISBN: 978-1463789138.	
64	Theoretical aspects of Protein Sequence Alignments.	Brannetti B.†, Via A.†	2002	In <i>The Internet for Cell and Molecular Biologists</i> - ed. A. Cabibbo, R.P. Grant, M. Helmer-Citterich, Horizon Scientific Press, pg. 73-87. https://www.caister.com/backlist/horizonscientificpress/icmb.html	ISBN-10: 1-898486-32-8	
65	Practical aspects of Protein Sequence Analysis.	Via A.	2002	In <i>The Internet for Cell and Molecular Biologists</i> - ed. A. Cabibbo, R.P. Grant, M. Helmer-Citterich, Horizon Scientific Press, pg. 163-232. https://www.caister.com/backlist/horizonscientificpress/icmb.html	ISBN-10: 1-898486-32-8	

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Part XIII E – Publications selected for the evaluation

n.	Title	Authors	Year	Ref data	DOI	IF	Scopus
1	AI applications in functional genomics	Caudai [†] C., Galizia [†] A., Geraci [†] F., Le Pera [†] L., Morea [†] V., Salerno [†] E., Via A[†] , Colombo T.	2021	Computational and Structural Biotechnology Journal, 19, pp. 5762-5790	10.1016/j.csbj.2021.10.009	7,271	0
2	Ten simple rules for making training materials FAIR	García L., Batut B., Burke M.L., Kuzak M., Psomopoulos F., Arcila R., Attwood T.K., Beard N., Carvalho-Silva D., Dimopoulos A.C., Del Angel V.D., Dumontier M., Gurwitz K.T., Krause R., McQuilton P., Le Pera L., Morgan S.L., Rauste P., Via A. , Kahlem P., Rustici G., Van Gelder C.W.G., Palagi P.M.	2020	PLoS Computational Biology, 16(5), e1007854	10.1371/journal.pcbi.1007854	4,712	6
3	A new pan-European Train-the-Trainer programme for bioinformatics: Pilot results on feasibility, utility and sustainability of learning	Via A. , Attwood T.K., Fernandes P.L., Morgan S.L., Schneider M.V., Palagi P.M., Rustici G., Tractenberg R.E.	2019	Briefings in Bioinformatics, 20(2), pp. 405-415	10.1093/bib/bbx112	5,818	6
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5	Characterization of the differences in the cyclopiiazonic acid binding mode to mammalian and <i>P. falciparum</i> Ca2+ pumps: A computational study	Di Marino D., D'Annessa I., Coletta A., Via A. , Tramontano A.	2015	Proteins: Structure, Function and Bioinformatics, 83(3), pp. 564-574	10.1002/prot.24734	2,717	12
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9	The crystal structure of <i>Giardia duodenalis</i> 14-3-3 in the apo form: When protein post-translational modifications make the difference	Fiorillo A., Di Marino D., Bertuccini L., Via A. , Pozio E., Camerini S., Ilari A., Lalle M.	2014	PLoS ONE, 9(3),e92902	10.1371/journal.pone.0092902	3,234	9
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13	Artemether resistance in vitro is linked to mutations in PfATP6 that also interact with mutations in PfMDR1 in travellers returning with <i>Plasmodium falciparum</i> infections	Pillai D.R., Lau R., Khairnar K., Lepore R., Via A. , Staines H.M., Krishna S.	2012	Malaria Journal, 11,131	10.1186/1475-2875-11-131	3,874	28
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Roma, 25 gennaio 2022

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