

Curriculum Vitae

Damiano Piovesan

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Professional Summary

I am an accomplished professional with a strong academic background in both biology and computer science. I hold a bachelor's degree in biotechnology and a master's degree in bioinformatics from the University of Bologna. In 2013, I completed my Ph.D. in bioinformatics at the same university. Following that, I joined the BioComputing laboratory at the Department of Biomedical Sciences at the University of Padua as a PostDoc. In 2019, I secured a position as a research assistant (Italian RTDB) and in 2022, I was appointed as an Associate Professor of Biochemistry (BIOS-07/A) at the University of Padua.

My expertise lies in the field of bioinformatics and computational biology, with a specific focus on the structural and mechanistic aspects of complex systems and modern machine learning techniques. Over the past decade, I have dedicated my research to the structural and functional characterization of non-globular proteins, recognizing their significance in cellular processes. I have developed software tools for the automated prediction of protein features and have contributed to the integration and standardization of experimental data for the functional characterization of intrinsically disordered proteins (IDPs). Recently, I have directed my studies towards exploring the intersection of cancer research and the functions of IDPs.

In terms of teaching, I have been actively involved in educating students about the historical perspective, algorithms, and methods developed in the last 30 years for the computational characterization of structural and functional properties of proteins. I have been a professor of Structural Bioinformatics and Biological Data courses in the Computer Science and Data Science degree programs, respectively, since 2019. These courses provide students with a foundational understanding of the fundamental aspects of life, the origins and limitations of current experimental data, and advanced machine learning techniques for protein feature prediction. The courses involve hands-on learning, including the implementation of scientific software and the reporting of scientific results. A number of students have successfully published their course project results in peer-reviewed journals. Additionally, I played a key role in the establishment of the new Data Science degree (LM-Data) in 2022, serving as a member of the evaluation committee (GAV) and reference professor for the Biological Data Analytics (BDA) curriculum in the Data Science program at the University of Padua.

Throughout my career, I have made notable contributions and taken on leadership roles in various projects aimed at establishing standards for experimental metadata ([HUPO-PSI](#), [MIADe](#), [DOME](#)) and promoting the adoption of FAIR principles in the European life-science infrastructure for IDP data ([ELIXIR](#), [InterPro Consortium](#)). I have also been actively involved in international initiatives focused on best practices for developing unbiased machine learning models in structural and functional bioinformatics ([CAID](#), [CASP](#), [CAFA](#)). Currently, I lead a team of researchers, including PostDocs, Ph.D. students, and Master's students, in the maintenance and development of the computational service infrastructure at the University of Padua ([MobiDB](#), [DisProt](#), [PED](#), [FuzDB](#), [INGA](#), [RING](#), ...).

Awards and Honors

Participant, as method developer, at the **Critical Assessment of protein Function Annotation (CAFA)** experiment. CAFA provides an independent evaluation of state-of-the-art methods for automatic Gene Ontology term annotation of protein sequences (<http://biofunctionprediction.org/cafa>).

- Ranked 2nd out of 80+ participants in CAFA 2019 with the INGA 3.0 method (*preliminary results*).
- Ranked 2nd out of 50+ participants in CAFA 2017 with the INGA 2.0 method (Zhou et al, *Genome Biol*, 2019, 20:244).
- Ranked 8th out of 50+ participants in CAFA 2014 with the INGA method (Jiang et al, *Genome Biol*, 2016, 17(1):184).
- Ranked 5th out of 50+ participants in CAFA 2011 with the BAR+ method (Radivojac et al, *Nat Methods*, 2013, 10(3):221-7).

Highlights

- Qualified for Full Professor (italian “prima fascia”) in Biochemistry from June 2021 to June 2032 (05/E1-BIOS-07/A, National Scientific Qualification examination, ASN).
- Co-lead of the Intrinsically Disordered Proteins Community of the ELIXIR Bioinformatic European Infrastructure (2019-2023).
- Chair of the Intrinsically Disordered Proteins (IDP) working group at the Human Proteome Organization - Proteomics Standards Initiative (HUPO-PSI) (since 2022).
- Organizer of the Critical Assessment of protein Intrinsic Disorder (CAID), since its first edition in 2018.
- Organizer of the Critical Assessment of protein Function Annotation algorithms (CAFA), since its fourth edition in 2019.
- Member of the Italian Society of Biochemistry and Molecular Biology (SIB)
- Member of the Bioinformatics Italian Society (BITS)
- Member of the International Society of Biocuration (ISB)
- Member of the International Society of Molecular Biology (ISMB)

Institutional Activities and Professional Service

- Commissioner for the National Research Council of Italy (CNR) - Call for the career advancement (italian “Primo Ricercatore”) for the CNR area “Genetics, computational biology, bioinformatics and system biology”, 2023-2024.
- Member of scientific committee for the Biological Sciences area at the University of Padova (2024-2028)
- Commissioner for the French National Research Agency (ANR) - Generic call for proposal (AAPG 2024), 2023-2024.
- Commissioner for the selection of a researcher (italian RTDa), Department of Biomedical Sciences, University of Padua, Biochemistry (05/E1-BIOS-07/A), 2022-2023.
- Member and president of several thesis committees for the Data Science degree at the University of Padua since 2019.
- Member of the evaluation committee (GAV) for the Master degree in Data Science at the University of Padua since 2022.
- Member of the commission for the creation of the new Data Science degree program (LM-Data) 2022/23 at the University of Padua.
- Commissioner for “Progetti di Rilevante Interesse Nazionale” (PRIN) 2020, Italian Ministry of University and Research, Italy
- Commissioner for FONDECYT Regular 2016 grant competition, Chilean National Science and Technology Commission (CONICYT - Chile)

Third mission

- Organization of the activity of the Dept. of Biomedical Science (University of Padua) at the EU researcher' night ("Notte dei ricercatori", VeneToNight, Science4All) from 2018. I co-organize a stand that provides a questionnaire for kids covering topics of structural biology. It is called. The Big Quiz: How much do you know about biology? ("Il Quizzone: Quanto ne sai di biologia?").
- Incontri di orientamento con studenti del liceo classico: "Dal classico allo STEM: cosa vuol dire fare ricerca", from 2022, high school (I.I.S.) Bruno-Franchetti, Venice.

Grants and Funding

Principal investigator or unit leader of competitive grants

AIRC - MFAG 2023 <ul style="list-style-type: none">• Title: Targeting undruggable intrinsically disordered regions in childhood malignant neoplasms• International grant• Principal Investigator• 500 000 €	<i>UniPD, IT</i> 2024 - 2029
PRIN 2022 <ul style="list-style-type: none">• PLANS: Proximity Ligation And Nanopore Sequencing for the characterization of native RNA-protein interactions• National grant• Unit leader• 80 000 €	<i>UniPD, IT</i> 2023 - 2026
AIRC - IF <ul style="list-style-type: none">• Title: Oxygen, HIF and friends: from oxygen sensing pathways to cancer development• International grant• Principal Investigator (Recipient of a 3 year individual fellowship)• 75 000 €	<i>UniPD, IT</i> 2015 - 2018

Internal grants (competitive inside the ELIXIR infrastructure or inside the University of Padua)

ELIXIR implementation study <ul style="list-style-type: none">• Title: Data Platform service plan• Leader WP3 and WP5• 13 PMs	<i>EMBL (EBI), IT</i> 2024 - 2026
ELIXIR implementation study <ul style="list-style-type: none">• Title: APICURON integration with curation databases• Co-leader• 6 PMs	<i>UniPD, IT</i> 2022 - 2023
ELIXIR implementation study <ul style="list-style-type: none">• Title: Improving IDP tools interoperability and integration into ELIXIR• Leader• 8 PMs	<i>UniPD, IT</i> 2021 - 2022
ELIXIR implementation study <ul style="list-style-type: none">• Title: Standardizing Intrinsically Disordered Proteins (IDPs) data	<i>UniPD, IT</i> 2021 - 2022

<ul style="list-style-type: none"> • Co-leader • 5 PMs 	
ELIXIR implementation study <ul style="list-style-type: none"> • Title: Integration of ELIXIR-IIB in ELIXIR Data Curation activities • Participant, project writing, task leader 	<i>UniPD, IT 2017 - 2018</i>
ELIXIR implementation study <ul style="list-style-type: none"> • Title: Integration and standardization of intrinsically disordered protein data • Project writing, collaborator, task leader 	<i>UniPD, IT 2018 - 2019</i>
University of Padua, bilateral exchange of researchers and professors <ul style="list-style-type: none"> • Visiting researcher at the National University of Quilmes, Argentina • Travel fellowship • 2 000 € 	<i>UniPD, IT 2015</i>

Project participation

MSCA Staff Exchanges <ul style="list-style-type: none"> • Title: Integrating novel data, artificial intelligence and molecular behaviour to expand functional characterization of intrinsically disordered proteins (IDPfun2) • Project writing, collaborator 	<i>UniPD, IT 2024 - 2028</i>
Twining <ul style="list-style-type: none"> • Title: Bringing Intrinsically Disordered Proteins to Biomedical Applications (IDP2Biomed) • Project writing, collaborator 	<i>ELTE, HU 2024 - 2027</i>
HORIZON-INFRA-EOSC <ul style="list-style-type: none"> • Title: European Virtual Institute for Research Software Excellence (EVERSE) • Project writing, task leader 	<i>CERTH, GR 2024 - 2027</i>
HORIZON-INFRA-DEV <ul style="list-style-type: none"> • Developing, consolidating and optimising the European research infrastructures landscape, maintaining global leadership (ELIXIR STEERS) • Project writing, task leader 	<i>EMBL, DE 2024 - 2027</i>
COST Action <ul style="list-style-type: none"> • Title: Non-globular proteins in the era of Machine Learning (ML4NGP) • Collaborator 	<i>UniPD, IT 2022 - 2026</i>
Twining <ul style="list-style-type: none"> • Title: Excellence Hub on Phase Transitions in Aging and Age-Related Disorders (PhasAGE) • Collaborator 	<i>Padua, IT 2021 - 2024</i>
MSCA Staff Exchanges <ul style="list-style-type: none"> • Title: Repeat protein Function Refinement, Annotation and Classification of Topologies (REFRACT) • Project writing, technical committee, collaborator 	<i>UniPD, IT 2019 - 2024</i>
MSCA Staff Exchanges <ul style="list-style-type: none"> • Title: Driving functional characterization of intrinsically disordered proteins (IDPfun) • Project writing, technical committee, collaborator 	<i>UniPD, IT 2018 - 2023</i>

Patents and Licenses

Commercial software licenses

RING software <ul style="list-style-type: none"> Title: Residue Interaction Network Generator - RING. Command line software written in C++ for the analysis of non-covalent interactions in structural experimental data or molecular dynamic simulations. Sold to different pharmaceutical companies for ca. 20 000 € per year. 	<i>UniPD, IT</i> <i>2015 - now</i>
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Teaching

Professor

Appointed professor (responsible of the course) <ul style="list-style-type: none"> MSc course of Structural Bioinformatics, Computer Science, University of Padova (course delivered in English). BIOS-07/A - 6 CFU - 48 hours (4 years since March 2021) 	<i>Padua, IT</i> <i>2021 - now</i>
Appointed professor (responsible of the course) <ul style="list-style-type: none"> MSc course of Biological Data (BIOS-07/A), Data Science, University of Padova (course delivered in English). BIOS-07/A - 5 CFU - 40 hours (3 years since October 2021) 	<i>Padua, IT</i> <i>2021 - now</i>
Professor <ul style="list-style-type: none"> BSc course of Basic chemistry, Dietistic, University of Padova (course delivered in Italian). BIOS-07/A - 2 CFU - 20 hours (3 years since October 2021) 	<i>Padua, IT</i> <i>2021 - now</i>
Appointed professor (responsible of the course) <ul style="list-style-type: none"> MSc course of Structural Bioinformatics, Computer Science, University of Padova (course delivered in English). BIOS-07/A - 4 CFU - 32 hours (2 years since March 2019) 	<i>Padua, IT</i> <i>2019 - 2020</i>
Appointed professor (responsible of the course) <ul style="list-style-type: none"> MSc course of Biological Data (BIOS-07/A), Data Science, University of Padova (course delivered in English). BIOS-07/A - 3 CFU - 24 hours (3 years, October 2018 - October 2020) 	<i>Padua, IT</i> <i>2018 - 2020</i>

Teaching assistant

<ul style="list-style-type: none"> MSc course of Structural Bioinformatics, Computer Science, University of Padova (3 years since 2015) Teaching assistant, MSc course of Bioinformatics & Computational Biology, Pharmacy Degree, University of Padova (3 years since 2015) 	<i>Padua, IT</i> <i>2015-2018</i>
<ul style="list-style-type: none"> “Tutor d’aula”, 3 contracts (2010, 2011, 2012), BSc Biotechnology, University of Bologna Lecturer and practicum developer at the International Bioinformatics MSc Degree 	<i>Bologna, IT</i> <i>2010 - 2012</i>

Lecturer at international schools

<ul style="list-style-type: none"> Lecturer at the Bioinformatics Workshop, Sultan Qaboos University 	<i>Muscat, OM</i> <i>Jan 2012</i>
<ul style="list-style-type: none"> Researchers bilateral exchange (Italian “Accordi bilaterali”) between the University of Padua and the National University of Quilmes Lecturer at the “3rd Quilmes School for Advanced Bioinformatics: 	<i>Quilmes, ARG</i> <i>Nov 2015</i>

Supervision and Mentoring

<ul style="list-style-type: none">• PhD supervisor, University of Padova, Dept. Biomedical Sciences<ul style="list-style-type: none">◦ Students: Martina Bevilacqua, Hamidreza Ghafouri, Jacopo Miotto	<i>Padua, IT 2019-now</i>
<ul style="list-style-type: none">• MSc supervisor, University of Padova<ul style="list-style-type: none">◦ Students: Davide Zago, Fatemeh Kordevani, Paolo Bonato, Arpad Goretity, Alessio Del Conte, Damiano Clementel, Adel Bouhraoua, Alberto Cocco, Mahta Mehdibadi, Riccardo Carangelo	<i>Padua, IT 2019-now</i>
<ul style="list-style-type: none">• PhD co-supervisor, University of Padova<ul style="list-style-type: none">◦ Students: Manuel Giollo, Layla Hirsh, Lisanna Paladin, Marco Necci, Andras Hatos, Federica Quaglia, Alessio Del Conte, Damiano Clementel, Mahta Mehdibadi, Adel Bouhraoua	<i>Padua, IT 2014-now</i>
<ul style="list-style-type: none">• MSc co-supervisor, International Bioinformatics Degree, University of Bologna<ul style="list-style-type: none">◦ Students: Lisanna Paladin	<i>Bologna, IT 2015</i>
<ul style="list-style-type: none">• BSc co-tutor, Biotechnology degree<ul style="list-style-type: none">◦ Students: Francesco Tabaro, Alessandra Di Lorenzo	<i>Bologna, IT 2010</i>

Education

University of Bologna PhD in Biotechnology, pharmacology and toxicology <ul style="list-style-type: none">• Thesis: A clustering method for robust and reliable large scale functional and structural protein sequence annotation	<i>Bologna, IT Oct 2009 - Apr 2013</i>
University of Bologna MSc in Bioinformatics <ul style="list-style-type: none">• Thesis: Contact map prediction with neural networks• Grade: 110/110 <i>cum laude</i>	<i>Bologna, IT Mar 2007 - Mar 2009</i>
University of Bologna BSc in Biotechnology <ul style="list-style-type: none">• Thesis: Modelling of the Voltage Dependent Anion Channel (VDAC)• Grade: 98/110	<i>Bologna, IT Sep 2003 - Mar 2007</i>
Additional experience EMBL Heidelberg <ul style="list-style-type: none">• EMBO Laboratory Management Course: Research Leadership for Postdocs	<i>Heidelberg, DE March 2017</i>

Language

- **Italian, native speaker**
- **English, C1 (TAL C1 certificate)**

Employment History

University of Padua, Department of Biomedical Sciences Associate professor (BIOS-07/A)	<i>Padua, IT</i> <i>Mar 2022 - Now</i>
University of Padua, Department of Biomedical Sciences Assistant professor (“RTDb”, BIOS-07/A) <ul style="list-style-type: none"> ● Co-lead of the Intrinsically Disordered Proteins Community of the ELIXIR Bioinformatic European Infrastructure 	<i>Padua, IT</i> <i>Mar 2019 - Feb 2022</i>
University of Padua, Department of Biomedical Sciences PostDoc researcher (“assegno di ricerca”, BIOS-07/A) <ul style="list-style-type: none"> ● Title “Towards the detailed typization of intrinsic disorder in proteins” ● Task leader for the integration of protein intrinsic disorder annotations into the ELIXIR Bioinformatic European Infrastructure 	<i>Padua, IT</i> <i>Feb 2018 - Mar 2019</i>
University of Padua, Department of Biomedical Sciences PostDoc researcher (“borsa di studio”, FIRC/AIRC Research Fellow) <ul style="list-style-type: none"> ● Title “Oxygen, HIF and friends: from oxygen sensing pathways to cancer development” ● Biological databases: pVHL mutations and interactions (VHLdb), intrinsic disorder (MobiDB, DisProt), protein signatures (InterPro), tandem repeat proteins (RepeatsDB) ● Bioinformatic software: intrinsic disorder (Mobi, MobiDB-lite, FIELDS), solubility (SODA), structural repetitions (ReUPred, RepeatsDB-lite) 	<i>Padua, IT</i> <i>Feb 2015 - Jan 2018</i>
University of Padua, Department of Biomedical Sciences PostDoc researcher (“assegno di ricerca”, BIOS-07/A) <ul style="list-style-type: none"> ● Title “Network-based analysis and prediction of function and folding rates from protein structures” ● Bioinformatic software: protein residue interaction network generator (RING), protein function (INGA) ● Biological databases: tandem repeat proteins (RepeatsDB) 	<i>Padua, IT</i> <i>May 2013 - Jan 2015</i>
University College London (UCL), Department of Computer Science Visiting PhD student <ul style="list-style-type: none"> ● Development of a library for the assessment of protein function predictors ● Implementation of the FFPred2.0 protein function prediction method 	<i>London, UK</i> <i>Aug 2012 - Dec 2012</i>
University of Bologna, Department of Experimental Evolutionary Biology PhD student <ul style="list-style-type: none"> ● Development of a tool for large-scale protein annotation (BAR+ database) ● Collaboration with the Department of Agricultural and Food Sciences at the University of Bologna for the analysis of the Sus Scrofa proteome (SUS-BAR database) ● Large scale prediction of Magnesium binding sites in proteins (BAR-hMG database) 	<i>Bologna, IT</i> <i>Oct 2009 - Apr 2013</i>

Editorial and review activity

Journal Editor

- Associate Editor
 - Frontiers in Bioinformatics (Q2, IF 2.8)
 - <https://loop.frontiersin.org/people/1053162/overview>
- Guest Editor
 - PLOS Computational Biology (Q1, IF 3.8)
 - <https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1010238>
- Frontiers Molecular Biosciences (Guest Editor)

Journal *ad hoc* Reviewer

- Nucleic Acid Research
- Bioinformatics
- Briefings in Bioinformatics
- PLOS Computational Biology
- BMC Supplements
- BMC Bioinformatics
- Frontiers Molecular Biosciences
- Amino Acids
- Plos ONE
- IEEE/ACM Transactions on Computational Biology and Bioinformatics

Organizational activity

- Co-organized of the BITS conference 2026, Padua, Italy
- Co-organizer of the Critical Assessment of Automatic Function (CAFA) prediction challenge, from 2019
- Co-organizer of the Function SIG at the ISMB 2023, Lyone, France
- Organizer of the ELIXIR IDP Community meetings and workshops, from 2019
- Organizer of the Continuous Assessment of protein Intrinsic Disorder (CAID) experiment (<http://disprotcentral.org/caid>), from 2018
- Organizer of the IDP-SIG meeting at the ECCB 2018 conference (Athens, Greece)
- Organizer of the NGP-net Winter School on computational methods for non-globular proteins (Brixen, 15-19 February 2016)
- As member of COST Action BM1405 (NGP-net), organizer of several workshops, conferences and training schools per year. (2015-2019)

Oral communications

- 2024
 - ELIXIR AHM, Uppsala, Sweden (**invited speaker**)
 - ISMB, Montreal, Canada (**selected abstract**)
- 2023
 - ISMB 2023, Lyone, France (**invited speaker**)
 - ML4NGP/ELIXIR-IDP Community, Bratislava, Slovakia (**invited speaker**)
 - ELIXIR AHM, Dublin, Ireland (**invited speaker**)
- 2022
 - CASP-15, Antalya, Turkey (**invited speaker**)
 - ELIXIR AHM, Amsterdam, Netherland (**invited speaker**)
- 2021
 - ISMB 2021, Virtual meeting (**selected abstract**)
- 2020
 - ISMB 2020, Virtual meeting, Toronto, Canada (**invited speaker**)
 - ELIXIR AHM, Virtual meeting, Barcelona, Spain (**invited speaker**)

- 2019
 - ISMB 2019, Basel, Switzerland (**invited speaker**)
 - ELIXIR AHM, Lisbon, Portugal (**invited speaker**)
- 2018
 - CASP 2018, Cancun, Mexico (**invited speaker**)
 - ECCB 2018, Athens, Greece (**highlight talk**)
 - IDP-SIG ECCB 2018, Athens, Greece (**invited speaker**)
 - Proteine 2018, Verona, Italy (**invited speaker**)
 - CeBiTec Symposium, Bielefeld, Germany (**invited speaker**)
 - EXCELERATE Workshop (ELIXIR), Barcelona, Spain (**invited speaker**)
 - DisProt Hackathon, Budapest, Hungary (**invited speaker**)
- 2017
 - Molecular and Causal Interactions Workshop (ELIXIR), Rome, Italy (**invited speaker**)
 - SIB Workshop, Bologna, Italy (**invited speaker**)
 - Proteomics Workshop (ELIXIR), Tübingen, Germany (**invited speaker**)
 - NGP-net Hackathon, Marseille, France (**invited speaker**)
 - NGP-net/ELIXIR Workshop, EMBL-EBI Hinxton, United Kingdom (**invited speaker**)
- 2015
 - Bioinformatics and Computational Biology, Bahia Blanca, Argentina (**invited speaker**)
- 2014
 - ISMB, Boston, USA (**invited speaker**)
- 2011
 - Bioinformatics Italian Society, Pisa, Italy (**selected abstract**)
- 2010
 - International Biotechnology Symposium and Exhibition, Rimini, Italy (**selected abstract**)
 - Congresso Nazionale SCI, San Vito di Cadore, Italy (**invited speaker**)

Scientific software development

Programming skills

<i>Language</i>	<i>Years' experience</i>	<i>Skill level</i>
Python	20	Expert
Bash	20	Expert
JavaScript	10	Expert
HTML/CSS	10	Expert
SQL	10	Expert
NoSQL	10	Expert
C++	5	Intermediate
Java	2	Novice

Developed biological software (described on the corresponding publication and URL)

<i>Name</i>	<i>Type</i>	<i>Contribution</i>	<i>URL</i>
Pfam	Database	Biocurator	pfam.xfam.org
PDBe-KB	Database	Back-end	www.ebi.ac.uk/pdbe/pdbe-kb
MobiDB	Database	Project Leader	mobidb.org
DisProt	Database	Project Leader	disprot.org
FuzDB	Database	Project Leader	fuzdb.org
RepeatsDB	Database	Back-end	repeatsdb.org
PlaToLoCo	Database	Front-end	platoloco.aei.polsl.pl/
VHLdb	Database	Biocurator	vhldb.bio.unipd.it
SUS-BAR	Database	Full-stack	bar.biocomp.unibo.it/pig
BAR-hMG	Database	Full-stack	bar.biocomp.unibo.it/mg
BAR+	Database	Full-stack	bar.biocomp.unibo.it/bar3
INGA 2.0	Software & WS	Full-stack	inga.bio.unipd.it
INGA	Software & WS	Full-stack	protein.bio.unipd.it/inga

RING	Software & WS	Full-stack	protein.bio.unipd.it/ring
FELLS	Software & WS	Full-stack	protein.bio.unipd.it/fells
SODA	Software & WS	Developer	protein.bio.unipd.it/soda
RepeatsDB-lite	Software & WS	Developer	protein.bio.unipd.it/repeatsdb-lite
CAID Portal	Software	Developer	caid.idpcentral.org/portal
ProtVista	Software	Developer	github.com/ebi-webcomponents/nightingale
ProSeqViewer	Software	Developer	github.com/BioComputingUP/ProSeqViewer
FLIPPER	Software	Developer	github.com/BioComputingUP/FLIPPER
Feature viewer	Software	Developer	github.com/BioComputingUP/feature-viewer-typescript
InterProScan	Software	Developer	www.ebi.ac.uk/interpro
MobiDB-lite	Software	Developer	protein.bio.unipd.it/mobidblite
Mobi	Software	Developer	protein.bio.unipd.it/mobi2
Victor	Software	Developer	protein.bio.unipd.it/victor
ReUPred	Software	Developer	protein.bio.unipd.it/reupred
FFPred	Software	Developer	bioinfadmin.cs.ucl.ac.uk/downloads/ffpred

Publications

Recent collaborators (evidenced by shared name on publication)

- **Silvio Tosatto**, University of Padova, Italy
- **Monika Fuxreiter**, University of Padova, Italy
- **Michele Vendruscolo**, University of Cambridge, United Kingdom
- **Zsuzsanna Dosztányi**, ELTE University, Hungary
- **Peter Tompa**, VIB, Belgium
- **Wim Vranken**, VIB, Belgium
- **Toby Gibson**, EMBL, Germany
- **Rob Finn**, EMBL-EBI, United Kingdom
- **Norman Davey**, ICR, United Kingdom
- **David T. Jones**, University College London, United Kingdom
- **Pedja Radivojac**, Northeastern University, USA

Statistics (SCOPUS, July 2024)

- Total citations: **8,205**
- H-index: **30**
- Total articles: **82** *69 with IF in 2023 + 11 without IF in 2023 + 2 corrections*
- Total Impact Factor: **734.9**

Aggregated statistics (SCOPUS, July 2024. Considering articles with an IF in 2023)

- Average Impact Factor per publication: **10.7**
- Average citations per publication: **119**
- Articles quartiles (1 - 4, %): **84%, 7%, 7%, 1%**
- First author: **21**
- Last author: **9**
- Corresponding author: **6**

Full list of publications on international, peer-reviewed journals

(^) first/co-first; (*) corresponding; (°) last author

2024

- [^] ^{*} **80** **Piovesan D.**, Zago D., Joshi P., De Paolis Kaluza M. C., Mehdiabadi M., Ramola R., Monzon A.M., Reade W., Friedberg I., Radivojac P., Tosatto S.C.E. *CAFA-evaluator: a Python tool for benchmarking ontological classification methods*. **Bioinformatics Advances** (2024) 4, 1, vbae043
- 79** Quaglia F., Chasapi A., Nugnes M.V., Aspromonte M.C., Leonardi E., Piovesan D., Tosatto S.C.E. *Best practices for the manual curation of intrinsically disordered proteins in DisProt Database* (2024) baae009
- [°] ^{*} **78** Aspromonte M.C., Nugnes M.V., Quaglia F., Bouharoua A., Tosatto S.C.E., **Piovesan D.** *DisProt in 2024: improving function annotation of intrinsically disordered proteins* **Nucleic Acids Research** (2024) 52, D1, D434-D441
- 77** Ghafouri H., Lazar T., Del Conte A., Tenorio Ku L.G., (...), **Piovesan D.**, (...), Tompa P., Tosatto S.C.E., Monzon A.M. *PED in 2024: improving the community deposition of structural ensembles for intrinsically disordered proteins* **Nucleic acids research** (2024) 52, D1, D536-D544
- 76** Del Conte A., Camagni G.F., Clementel D., Minervini G., Monzon A.M., Ferrari C., **Piovesan D.**, Tosatto S.C.E. *RING 4.0: faster residue interaction networks with novel interaction types across over 35,000 different chemical structures* **Nucleic Acids Research** (2024) gkae337

2023

- [^] **75** **Piovesan D.**, Del Conte A., Clementel D., Monzon A.M., Bevilacqua M., Aspromonte M.C., Iserte J. A., Orti F. E., Marino-Buslje C., Tosatto S.C.E. *MobiDB: 10 years of intrinsically disordered proteins* **Nucleic acids research** (2024) 51, D1, D438-D444
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