Curriculum Vitae - Damiano Piovesan

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Scientific Vision and Laboratory

Vision

My scientific work concentrates in the fields of bioinformatics and computational biology, with a special emphasis on the structural and mechanistic aspects of complex systems. Over the last ten years I focused on the development of tools for exploring and providing scientific significance to biological data. Recently, a focus is emerging on the structural and functional characterization of non-globular proteins.

Laboratory

As assistant professor (Italian RTDb) at the BioComputingUP laboratory (Department of Biomedical Sciences, University of Padua) I lead a team consisting on the following personnel:

- PostDocs (Federica Quaglia, Andras Hatos, Alexander Miguel Monzon, Edoardo Salladini)
- PhD students (Martina Bevilacqua, Alessio Del Conte, Damiano Clementel)
- Technician (Ivan Mičetić)
- Undergraduate students (Davide Zago, Fatemeh Kordevani)

Awards

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 in Biochemistry from June 2021 to May 2030 (05/E1-BIO/10, National Scientific Qualification examination, ASN)
- Qualified for Associate Professor in Biochemistry from August 2017 to July 2026 (05/E1-BIO/10, National Scientific Qualification examination, ASN)
- Co-lead of the Intrinsically Disordered Proteins Community of the ELIXIR Bioinformatic European Infrastructure (since 2019)

Grants

ELIXIR implementation study *Padua, IT*
- Title: APICURON integration with curation databases *2022 - 2023*
- Leader

ELIXIR implementation study *Padua, IT*
- Title: Improving IDP tools interoperability and integration into ELIXIR *2021 - 2022*
- Leader

ELIXIR implementation study   *Padua, IT*
- Title: Standardizing Intrinsically Disordered Proteins (IDPs) data   *2021 - 2022*
- Leader

Marie Skłodowska-Curie Actions Research and Innovation Staff Exchange   *Padua, IT*
(MSCA-RISE)   *2019 - 2022*
- Title: Repeat protein Function Refinement, Annotation and Classification of
  Topologies (REFRACT)
- Project writing, technical committee, collaborator

Marie Skłodowska-Curie Actions Research and Innovation Staff Exchange   *Padua, IT*
(MSCA-RISE)   *2018 - 2021*
- Title: Driving functional characterization of intrinsically disordered proteins
  (IDP-fun)
- Project writing, technical committee, collaborator

ELIXIR implementation study   *Padua, IT*
- Title: Integration and standardization of intrinsically disordered protein data *2018 - 2019*
- Project writing, collaborator, task leader

ELIXIR implementation study   *Padua, IT*
- Title: Integration of ELIXIR-IIB in ELIXIR Data Curation activities   *2017 - 2018*
- Participant, project writing, task leader

Italian Foundation for Cancer Research (FIRC)   *Padua, IT*
- Title: Oxygen, HIF and friends: from oxygen sensing pathways to cancer   *2015 – 2017*
  development. Project: 16621)
- Recipient of a 3 year fellowship

University of Padua, bilateral exchange of researchers and professors   *Padua, IT*
- Visiting researcher at the National University of Quilmes, Argentina   *2015*

Education

University of Bologna   *Bologna, IT*
PhD in Biotechnology, pharmacology and toxicology   *Oct 2009 - Apr 2013*
- Thesis: A clustering method for robust and reliable large scale functional and
  structural protein sequence annotation

University of Bologna   *Bologna, IT*
MSc in Bioinformatics   *Mar 2007 - Mar 2009*
- Thesis: Contact map prediction with neural networks
- Grade: 110/110 *cum laude*

University of Bologna   *Bologna, IT*
BSc in Biotechnology   *Sep 2003 - Mar 2007*
- Thesis: Modelling of the Voltage Dependent Anion Channel (VDAC)
- Grade: 98/110

Additional experience
EMBO Laboratory Management Course: Research Leadership for Postdocs, March 2017

Language
- Italian, native speaker
- English, C1

Teaching

University of Padua   *Padua, IT*
- Professor: MSc course of Structural Bioinformatics, Computer Science Degree   *May 2013 - now*
  (since 2019)
- Professor: MSc course of Biological data, Data Science Degree (since 2019)
- PhD supervisor (1 student: Martina Bevilacqua)
- MSc supervisor (Davide Zago, Fatemeh Kordevani, Paolo Bonato, Arpad
  Goretity, Alessio Del Conte, Damiano Clementel)
- PhD co-tutor (5 students: Manuel Giollo, Layla Hirsh, Lisanna Paladin, Marco
  Necci, Andras Hatos, Federica Quaglia, Alessio Del Conte, Damiano Clementel)
- MSc co-tutor, International Bioinformatics Degree (University of Bologna) (1
  student: Lisanna Paladin)
- Teaching assistant, MSc course of Structural bioinformatics, Computer Science
  Degree (3 courses since 2015)
- Teaching assistant, MSc course of Bioinformatics & Computational Biology,
  Pharmacy Degree (3 courses since 2015)

National University of Quilmes   *Quilmes, ARG*
- Researchers bilateral exchange ("accordi bilaterali"), lecturer at the "3rd Quilmes *Nov 2015*
  School for Advanced Bioinformatics: Computational methods for Protein
  Function Prediction" (http://ufq.unq.edu.ar/QuilmesSchool).

University of Bologna   *Bologna, IT*
- Teaching assistant ("tutor d'aula"), 3 contracts (2010, 2011, 2012), BSc   *2010 - 2012*
  Biotechnology degree
- BSc co-tutor, Biotechnology degree (2 students: Francesco Tabaro, Alessandra Di
  Lorenzo)
- Lecturer and practicum developer at the International Bioinformatics MSc Degree

Sultan Qaboos University   *Muscat, OM*
- Lecturer at the Bioinformatics Workshop   *Jan 2012*

Research Experience

University of Padua, Department of Biomedical Sciences   *Padua, IT*
Assistant professor ("RTDb", BIO/10)   *Mar 2019 - Feb 2022*
- Co-lead of the Intrinsically Disordered Proteins Community of the ELIXIR
  Bioinformatic European Infrastructure

University of Padua, Department of Biomedical Sciences   *Padua, IT*
PostDoc researcher ("assegno di ricerca", BIO/10)   *Feb 2018 - Mar 2019*
- 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

University of Padua, Department of Biomedical Sciences   *Padua, IT*
PostDoc researcher ("borsa di studio", FIRC/AIRC Research Fellow)   *Feb 2015 - Jan 2018*
- 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, FELLS),
  solubility (SODA), structural repetitions (ReUPred, RepeatsDB-lite)

University of Padua, Department of Biomedical Sciences *Padua, IT*

PostDoc researcher ("assegno di ricerca", BIO/10) *May 2013 - Jan 2015*

- 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)

University College London (UCL), Department of Computer Science *London, UK*

Visiting PhD student *Aug 2012 - Dec 2012*

- Development of a library for the assessment of protein function predictors
- Implementation of the FFPred2.0 protein function prediction method

University of Bologna, Department of Experimental Evolutionary Biology *Bologna, IT*

PhD student *Oct 2009 - Apr 2013*

- 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)

Editorial and review activity

Journal Editor

- Frontiers in Bioinformatics (Associate Editor)
- Frontiers Molecular Biosciences (Guest Editor)
- PLOS Computational Biology (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

Referee for grant proposal

- Progetti di Rilevante Interesse Nazionale (PRIN) 2020, Ministero dell'Università e della Ricerca, Italy
- FONDECYT Regular 2016 grant competition, Chilean National Science and Technology Commission (CONICYT - Chile)

Organizational activity

- Organizer of the ELIXIR IDP Community meetings and workshops, since 2019
- Organizer of the Continuous Assessment of protein Intrinsic Disorder (CAID) experiment (http://disprotcentral.org/caid), since 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)

Scientific dissemination

Oral communications

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**)
	● 12th CeBiTec Symposium: Big Data in Medicine and Biotechnology, Bielefeld, Germany (**invited speaker**)
	● Elixir-Excelerate WP3 (Task 3.3) workshop, Barcelona, Spain (**invited speaker**)
	● DisProt Hackathon on intrinsically disordered proteins, Budapest, Hungary (**invited speaker**)
2017	● Curation Workshop on Molecular and Causal Interactions (ELIXIR), Rome, Italy (**invited speaker**)
	● SIB workshop of the SIB Group "Computational and Systems Biology", Bologna, Italy (**invited speaker**)
	● Strategic workshop - "The future of proteomics in ELIXIR" in Tübingen, Germany (**invited speaker**)
	● 3rd NGP-net Hackathon on intrinsically disordered proteins, Marseille, France (**invited speaker**)
	● Joint NGP-net - ELIXIR workshop: coordinating intrinsic protein disorder across databases, EMBL-EBI Hinxton, United Kingdom (**invited speaker**)
2015	● VI Argentinian Conference on Bioinformatics and Computational Biology, Bahia Blanca, Argentina (**invited speaker**)
2014	● AFP, Automatic Function Prediction meeting (ISMB-Sig), Boston, USA (**invited speaker**)
2011	● Eighth Annual Meeting of the Bioinformatics Italian Society, Pisa, Italy
2010	● 14th International Biotechnology Symposium and Exhibition, Rimini, Italy
	● Congresso Nazionale della Divisione di Chimica dei Sistemi Biologici della SCI, San Vito di Cadore, Italy (**invited speaker**)

Posters

2018	● GRC-Intrinsically Disordered Proteins, Les Diablerets, Switzerland
2017	● ISMB/ECCB 2017, Prague, Czech Republic
2015	● Repetitive, Non-Globular Proteins: Nature to Nanotechnology, York, United Kingdom
2014	● Intelligent Systems for Molecular Biology (ISMB), Boston, USA
2011	● AFP, Automatic Function Prediction meeting (ISMB-Sig), Vienna, Austria
	● NETTAB workshop focused on Clinical Bioinformatics, Pavia, Italy
	● 2nd Euromag Meeting, Bologna, Italy

Scientific software development experience

Programming skills

Language	Years' experience	Skill level
Python	15	Expert
Bash	15	Expert
JavaScript	10	Expert
HTML	10	Expert
NoSQL	10	Expert
C++	5	Intermediate
SQL	5	Intermediate
Java	2	Novice

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

Name	Type	Contribution	URL
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
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 collaborations (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

Full list of publications on international, peer-reviewed journals

2021

61 Monzon A.M., **Piovesan D.**, Fuxreiter M. *Molecular Determinants of Selectivity in Disordered Complexes May Shed Light on Specificity in Protein Condensates* (2021) **Biomolecules**, 12(1), 92

60 Quaglia F., Lazar T., Hatos A., Tompa P., **Piovesan D.**, Tosatto S.C.E. *Exploring curated conformational ensembles of intrinsically disordered proteins in the protein ensemble database* (2021) **Current protocols**, e192,1

59 Varadi M., Anyango S., Armstrong D., Berrisford J., (...), **Piovesan D.**, (...), Thornton J., Sternberg M., Orengo C., Velankar S. *PDBe-KB: collaboratively defining the biological context of structural data* (2021) **Nucleic Acids Research**, 50,D1,D534–D542

58 Bevilacqua M., Paladin L., Tosatto S.C.E., **Piovesan D.** *ProSeqViewer: an interactive, responsive and efficient TypeScript library for visualization of sequences and alignments in web applications* (2021) **Bioinformatics**

57 Hatos A., Monzon A.M., Tosatto S.C.E., **Piovesan D.**, Fuxreiter M. *FuzDB: a new phase in understanding fuzzy interactions* (2021) **Nucleic Acids Research**, 50,D1,D509–D517

56 Quaglia F., Mészáros B., Salladini E., Hatos A., (...), Dosztányi Z., Tompa P., Tosatto S.C.E., **Piovesan D.** *DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation* (2021) **Nucleic Acids Research**, 50,D1,D480–D487

55 Necci M., **Piovesan D.**, CAID Predictors, DisProt Curators, Tosatto S.C.E. *Critical assessment of protein intrinsic disorder prediction* (2021) **Nature Methods**, 18,472-481

54 Monzon A.M., Bonato P., Necci M., Tosatto Silvio S.C.E., **Piovesan D.** *FLIPPER: Predicting and Characterizing Linear Interacting Peptides in the Protein Data Bank* (2021) **Journal of Molecular Biology,** 433,9,166900

53 Hatos A., Quaglia F., **Piovesan D.,** Tosatto S.C.E. *APICURON: a database to credit and acknowledge the work of biocurators* (2021) **Database**

52 Lazar T., Martínez-Pérez E., Quaglia F., Hatos A., (...), **Piovesan D.** *PED in 2021: a major update of the protein ensemble database for intrinsically disordered proteins* (2021) **Nucleic Acids Research**, 49,D1,D404-D411

51 **Piovesan D.,** Necci M., Escobedo N., Monzon A.M., Hatos A., Mičetić I., Quaglia F., (...), Tosatto S.C.E. *MobiDB: intrinsically disordered proteins in 2021* (2021) **Nucleic Acids Research**, 49,D1,D361-D367

50 Paladin L., Bevilacqua M., Errigo S., **Piovesan D.**, Mičetić I., Necci M., Monzon A.M., Fabre M.L., Lopez J.L., Nilsson J.F., (...), Tosatto S.C.E. *RepeatsDB in 2021: improved data and extended classification for protein tandem repeat structures* (2020) **Nucleic Acids Research**, 49,D1,D452-D457

2020

49 Necci M., **Piovesan D.**, Clementel D., Zsuzsanna D., Tosatto S.C.E. *MobiDB-lite 3.0: fast consensus annotation of intrinsic disorder flavors in proteins* (2020) **Bioinformatics,** 36,5533–5534

48 Quaglia F., Hatos A., **Piovesan D.**, Tosatto S.C.E. *Exploring Manually Curated Annotations of Intrinsically Disordered Proteins with DisProt* (2020) **Current Protocols in Bioinformatics**, 72,1,e107

47 Paladin L., Necci M., **Piovesan D.**, Pablo M., Andrade-Navarro M.A., Tosatto S.C.E. *A novel approach to investigate the evolution of structured tandem repeat protein families by exon duplication* (2020) **Journal of Structural Biology**, 212,2,107608

46 Falconieri A., Minervini G., Bortolotto R., **Piovesan D.**, Lopreiato R., Sartori G., Pennuto M., Tosatto S.C.E. *The E3 ubiquitin-protein ligase MDM2 is a novel interactor of the von Hippel-Lindau tumor suppressor* (2020) **Oncogene**

45 Jarnot P., (...), **Piovesan D.**, (...), Gruca A. *PlaToLoCo: the first web meta-server for visualization and annotation of low complexity regions in proteins* (2020) **Nucleic Acids Research**

44 Paladin L., Schaeffer M., Gaudet P., Zahn-Zabal M., Pierre-André M., **Piovesan D.**, Tosatto S.C.E., Bairoch A. *The Feature-Viewer: a visualization tool for positional annotations on a sequence* (2020). **Bioinformatics**

43 Hatos A., (...), **Piovesan D**. *DisProt: intrinsic protein disorder annotation in 2020* (2020) **Nucleic Acids Research,** 48(D1):D269-D276

42 **Piovesan D**., Hatos A., Minervini G., Quaglia F., Monzon A.M., Tosatto S.C.E. *Assessing predictors for new post translational modification sites: A case study on hydroxylation* (2020) **PLoS Comput Biol**

41 Monzon A.M., Hatos A., Necci M., **Piovesan D.**, Tosatto S.C.E. *Exploring Protein Intrinsic Disorder with MobiDB* (2020) **Methods Mol Biol,** 2141:127-143

40 Monzon A. M., Necci M., Quaglia F., Walsh I., Zanotti G., **Piovesan D.**, Tosatto S.C.E. *Experimentally determined long intrinsically disordered protein regions are now abundant in the Protein Data Bank* (2020) **International journal of molecular sciences**

2019

39 Zhou N., Jiang Y., (...), **Piovesan D.**, (...), Iddo Friedberg. *The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens* (2019) **Genome Biology**

38 **Piovesan D.** and Tosatto S.C.E. *INGA 2.0: improving protein function prediction for the dark proteome* (2019) **Nucleic Acids Research**

37 El-Gebali S., Mistry J., Bateman A., Eddy S.R., Luciani A., Potter S.C., Qureshi M., Richardson L.J., Salazar G.A., Smart A., Sonnhammer E.L.L., Hirsh L., Paladin L., **Piovesan, D.**, Tosatto S.C.E., Finn R.D. *The Pfam protein families database in 2019* (2019) **Nucleic Acids Research**, 47 (D1), pp. D427-D432

36 Davey N.E., Babu M.M., Blackledge M., Bridge A., Capella-Gutierrez S., Dosztanyi Z., Drysdale R., Edwards R.J., Elofsson A., (...), **Piovesan D.**, (...) and Tosatto S.C.E. *An intrinsically disordered proteins community for ELIXIR* (2019) **F1000Research**, 8

2018

35 Necci M., **Piovesan D.**, Micheletti D., Paladin L., Cestaro A., Tosatto S.C.E. *PhytoTypeDB: a database of plant protein inter-cultivar variability and function* (2018) **Database**

34 Necci M., **Piovesan D.**, Tosatto S.C.E. *Where differences resemble: sequence-feature analysis in curated databases of intrinsically disordered proteins* (2018) **Database**

33 Hirsh L., Paladin L., **Piovesan D.**, Tosatto S.C.E. *RepeatsDB-lite: a web server for unit annotation of tandem repeat proteins* (2018) **Nucleic Acids Research**

32 Necci, M., **Piovesan, D.**, Dosztányi, Z., Tompa, P., Tosatto, S.C.E. *A comprehensive assessment of long intrinsic protein disorder from the DisProt database* (2018) **Bioinformatics**, 34(3), pp. 445-452

31 **Piovesan, D.**, Tosatto, S.C.E. *Mobi 2.0: An improved method to define intrinsic disorder, mobility and linear binding regions in protein structures* (2018) **Bioinformatics**, 34 (1), pp. 122-123

30 **Piovesan, D**., Tabaro, F., Paladin, L., Necci, M., Mieti, I., Camilloni, C., Davey, N., Dosztányi, Z., Mészáros, B., Monzon, A.M., Parisi, G., Schad, E., Sormanni, P., Tompa, P., Vendruscolo, M., Vranken, W.F., Tosatto, S.C.E. *MobiDB 3.0: More annotations for intrinsic disorder, conformational diversity and interactions in proteins* (2018) **Nucleic Acids Research**, 46 (D1), pp. D471-D476

2017

29 Paladin, L., **Piovesan, D.**, Tosatto, S.C.E. *SODA: Prediction of protein solubility from disorder and aggregation propensity* (2017) **Nucleic Acids Research**, 45 (W1), pp. W236-W240

28 **Piovesan, D.**, Walsh, I., Minervini, G., Tosatto, S.C.E. *FELLS: Fast estimator of latent local structure* (2017) **Bioinformatics**, 33 (12), pp. 1889-1891

27 Necci, M., **Piovesan, D.**, Dosztanyi, Z., Tosatto, S.C.E. *MobiDB-lite: Fast and highly specific consensus prediction of intrinsic disorder in proteins* (2017) **Bioinformatics**, 33 (9), pp. 1402-1404

26 Sormanni, P., **Piovesan, D.**, Heller, G.T., Bonomi, M., Kukic, P., Camilloni, C., Fuxreiter, M., Dosztanyi, Z., Pappu, R.V., Babu, M.M., Longhi, S., Tompa, P., Dunker, A.K., Uversky, V.N., Tosatto, S.C.E., Vendruscolo, M. *Simultaneous quantification of protein order and disorder* (2017) **Nature Chemical Biology**, 13 (4), pp. 339-342

25 Paladin, L., Hirsh, L., **Piovesan, D.**, Andrade-Navarro, M.A., Kajava, A.V., Tosatto, S.C.E. *RepeatsDB 2.0: Improved annotation, classification, search and visualization of repeat protein structures* (2017) **Nucleic Acids Research**, 45 (D1), pp. D308-D312

24 Vizcaíno, J.A., Walzer, M., Jiménez, R.C., Bittremieux, W., Bouyssié, D., Carapito, C., Corrales, F., Ferro, M., Heck, A.J.R., Horvatovich, P., Hubalek, M., Lane, L., Laukens, K., Levander, F., Lisacek, F., Novak, P., Palmblad, M., **Piovesan, D.**, Pühler, A., Schwämmle, V., Valkenborg, D., van Rijswijk, M., Vondrasek, J., Eisenacher, M., Martens, L., Kohlbacher, O. *A community proposal to integrate proteomics activities in ELIXIR* (2017) **F1000Research**, 6, art. no. 875

23 **Piovesan, D.**, Tabaro, F., Mičetić, I., Necci, M., Quaglia, F., (...), Tompa, P., Tosatto, S.C.E. *DisProt 7.0: A major update of the database of disordered proteins* (2017) **Nucleic Acids Research**, 45 (D1), pp. D219-D227

22 Finn, R.D., Attwood, T.K., Babbitt, P.C., Bateman, A., Bork, P., (...), **Piovesan, D.**, (...), Mitchell, A.L. *InterPro in 2017-beyond protein family and domain annotations* (2017) **Nucleic Acids Research**, 45 (D1), pp.

2016

21 Necci, M., **Piovesan, D.**, Tosatto, S.C.E. *Large-scale analysis of intrinsic disorder flavors and associated functions in the protein sequence universe* (2016) **Protein Science**, 25 (12), pp. 2164-2174

20 Jiang, Y., Oron, T.R., Clark, W.T., Bankapur, A.R., (...), **Piovesan, D.**, (...), A., Babbitt, P.C., Brenner, S.E., Linial, M., Orengo, C.A., Rost, B., Greene, C.S., Mooney, S.D., Friedberg, I., Radivojac, P. *An expanded evaluation of protein function prediction methods shows an improvement in accuracy* (2016) **Genome Biology**, 17 (1), art. no. 184

19 Tabaro, F., Minervini, G., Sundus, F., Quaglia, F., Leonardi, E., **Piovesan, D.**, Tosatto, S.C.E. *VHLdb: A database of von Hippel-Lindau protein interactors and mutations* (2016) **Scientific Reports**, 6, art. no. 31128

18 **Piovesan, D.**, Minervini, G., Tosatto, S.C. *The RING 2.0 web server for high quality residue interaction networks* (2016) **Nucleic acids research**, 44 (W1), pp. W367-W374

17 Hirsh, L., Piovesan, D., Paladin, L., Tosatto, S.C.E. *Identification of repetitive units in protein structures with ReUPred* (2016) **Amino Acids**, 48 (6), pp. 1391-1400

2015

16 **Piovesan, D.**, Giollo, M., Ferrari, C., Tosatto, S.C.E. *Protein function prediction using guilty by association from interaction networks* (2015) **Amino Acids**, 47 (12), pp. 2583-2592

15 Profiti, G., Piovesan, D., Martelli, P.L., Fariselli, P., Casadio, R. *Protein sequence annotation by means of community detection* (2015) **Current Bioinformatics**, 10 (2), pp. 139-143

14 Hirsh, L., Piovesan, D., Giollo, M., Ferrari, C., Tosatto, S.C.E. *The Victor C++ library for protein representation and advanced manipulation* (2015) **Bioinformatics**, 31 (7), pp. 1138-1140

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2014

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