

An Engaged, Inclusive and Transparent EuPA for the European Proteomics Community

A Team of Candidates for the 2020 EuPA Executive Committee Elections

Dear Colleagues,

As you know, the 2020 EuPA Executive Committee elections will take place this fall, and these will considerably change the Executive Committee as many current members have reached term limits.

Because of this large change, **the seven of us have come together as a coordinated, well-integrated team of candidates**. Of course, the EuPA elections call for individual nominations for each position, but we nevertheless felt that presenting as a unified team with a joint vision provides a more solid foundation for EuPA's future, and allows us to share our joint vision with you more efficiently.

We would therefore ask that you **consider nominating (and, ultimately, voting for) all of us as a team, each candidate for their respective position**, rather than seeing us as independent candidates.

Our joint vision rests on the core goal of ensuring that EuPA will be an engaged, inclusive, and transparent organisation to foster and support the proteomics community in Europe.

An engaged EuPA means that representatives from our Young Proteomics Investigators Club (YPIC) and the European Bioinformatics Community for Mass Spectrometry (EuBIC) have a place at the Executive Committee table, and we will thus create such positions, guided by similar initiatives in several national societies. It also means updating EuPA's online presence, in the process helping national societies expand their online presence as well, as COVID-19 has shown us that excellent opportunities can be found online to create new and engaging community events. We are also envisioning an EuPA-facilitated, tailored mentoring system for young researchers, to help those at the most stressful and demanding stage of their career achieve their ambitions and dreams. In addition, we will actively pursue connections with emerging sub-communities within the European proteomics community, to support and boost their growth and their reach as potential EuPA Initiatives. Yet engagement cannot be restricted to our own community, and we will therefore connect to other life sciences communities through joint sessions at conferences and through dedicated workshops to explore promising and exciting interfaces between proteomics and the life sciences at large.

An inclusive EuPA means that we need to ensure that all proteomics researchers in Europe can feel part of a welcoming and nurturing community, regardless of career stage, background, gender, place of origin, or any other personal characteristics. We must therefore identify and address any barriers to participation as we move forward, and we will leverage our entire community to help us with this task. For instance, the COVID-19 pandemic demonstrated that, when used wisely, modern technology can allow us to eradicate many barriers to community membership and participation that researchers have struggled with in the past. We all feel very strongly that EuPA needs to represent and value everyone in our community, and our team is therefore dedicated to making sure that EuPA creates a welcoming and inclusive community for all.

A transparent EuPA means more open communication. This will be achieved through more frequent communication with the national societies through online general council meetings, complete with detailed agendas and early access to the necessary background information. It also means clear and consistent agreements that focus on win-win arrangements with our Initiatives, and with our conference and workshop organisers. And it requires a modernisation of our membership system, for which we will work with, and build on, the experiences and efforts of national societies to ensure ease of adoption, and compliance to all applicable privacy laws.

If you entrust us with your vote, you can rest assured that our team, introduced in the next pages, is fully committed to carry out these actions to deliver an engaged, inclusive, and transparent EuPA!

Candidate for EuPA President

Prof. Dr. Lennart Martens, Ghent University and VIB, Gent, Belgium

Candidate for EuPA Vice-President

Prof. Dr. Connie R. Jimenez, Amsterdam University Medical Center, Amsterdam, The Netherlands

Candidate for EuPA Conferences and Communication

Dr. Éva Csósz, University of Debrecen, Debrecen, Hungary

Candidate for EuPA Education

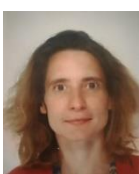
Dr. Christine Carapito, CNRS and University of Strasbourg, Strasbourg, France

Candidate for EuPA Journals

Prof. Dr. Stefan Tenzer, University Medical Center Mainz, Mainz, Germany

Candidate for EuPA Funding

Dr. Juan Antonio Vizcaíno, EMBL-EBI, Cambridge, United Kingdom

Candidate for EuPA Initiatives

Dr. Lydie Lane, University of Geneva and SIB, Geneva, Switzerland

Brief biography of Prof. Dr. Lennart Martens, candidate for EuPA President

Lennart Martens is Full Professor of Systems Biology at Ghent University, Group Leader of the Computational Omics and Systems Biology (CompOmics) group at VIB, and Associate Director of the VIB-UGent Center for Medical Biotechnology, all in Ghent, Belgium. He also holds a Visiting Group Leader position at EMBL-EBI in Cambridge, UK. He has been working in proteomics bioinformatics since his Master's degree, which focused on the computational interpretation of peptide mass spectra, and the sequence-dependent fragmentation of peptides. He then worked as a software developer and framework architect for a software company for a few years, before returning to Ghent University to pursue a Ph.D. in proteomics and proteomics informatics. During this time, he worked on the development of high-throughput peptide centric proteomics techniques and on bioinformatics tools to support these new approaches. In 2003 he started the PRIDE proteomics database at EMBL-EBI as a Marie Curie fellow of the European Commission. After obtaining his Ph.D., he rejoined EMBL-EBI to coordinate the newly created PRIDE group for the next three years, firmly establishing the system as the world's foremost public proteomics data repository. He then moved back to Ghent University to take up his current position, in which he focuses on novel machine learning algorithms for mass spectrometry data analysis, and their application to the large-scale reprocessing of public proteomics data.

Dr. Martens is active in several scientific organisations. He has been serving as a Board Member of the Belgian Proteomics Association (BePA) since its creation, has been elected to the Human Proteome Organisation (HUPO) Council in 2016, and has been elected Vice-President of the European Proteomics Association in 2017. He also served on the HUPO Executive Board from 2017 to 2019, is a co-founder and co-leader of the ELIXIR Proteomics Community, and has served as the President of the ABRF Proteomics Informatics Research Group (iPRG) in 2011. Dr. Martens has also been elected to the Young Academy of the Royal Belgian Academy of Sciences in 2013, and was admitted as a Fellow of the Royal Society for Chemistry in 2018. He received the 2014 Prometheus Award for Research Excellence from Ghent University, and the 2015 'Juan Pablo Albar' Proteomics Pioneer Award from the European Proteomics Association (EuPA). An author on more than 240 peer-reviewed papers, he has also co-written two popular Wiley textbooks on computational mass spectrometry.

Personal commitment

For me, the central role of EuPA is to support and connect the European proteomics community. As an international organisation, EuPA can provide community-wide connections and interactions that build upon and extend local networks established by the national societies. To do so effectively, EuPA needs to actively engage with the community, ensure full representation in its membership and in its support, and must communicate openly and frequently. Hence our team's slogan: **engaged, inclusive, transparent.**

Brief biography of Prof. Dr. Connie R. Jimenez, candidate for EuPA Vice-President

Connie Jimenez is Full Professor of Translational OncoProteomics, Group Leader of the OncoProteomics Laboratory and Director of Proteomics Core Facility, all at Amsterdam University Medical Center, Amsterdam, The Netherlands. She has been working on biological and biomedical applications of mass spectrometry and proteomics since her PhD studies. She pioneered single cell neuropeptide profiling by mass spectrometry at the Vrije Universiteit in Amsterdam (PhD, 1997) and neuroproteomics during her post-doc projects at UCSF, San Francisco and Vrije Universiteit. In 2006, she founded the OncoProteomics Laboratory with a start-up grant of the Cancer Center Amsterdam, to employ the power of mass spectrometry-

based proteomics to study cancer. Her lab's mission is to apply innovative mass spectrometry-based (phospho)proteomics and data analysis to improve (early) diagnostics and treatment of cancer and neurodegenerative disease (www.oncoproteomics.nl). Dr. Jimenez' multi-disciplinary team includes core members with expertise in mass spectrometry, biology, biochemistry, and bioinformatics, and post-docs and PhD students with life science and clinical backgrounds. Since its foundation, the OPL has acquired a strong reputation as clinical proteomics center.

In 2001 she started the Netherlands Proteomics Platform, for which she serves as member of the steering group. She has been active in various international proteomics networks, as general council member of the European Proteomics Association (2005-present), as HUPO council member (2013-2016), and as co-chair of the Cancer Initiative of the Human Proteome Organisation (2014-present). Furthermore, she is editorial board member of multiple proteomics journals: Journal of Proteomics (since 2007), Molecular and Cellular Proteomics (since 2010), Proteomics (since 2014), Proteomics Clinical Applications (since 2014) and Clinical Proteomics (since 2016). To date, Prof. Jimenez (co-)authored over 150 scientific peer reviewed articles, 11 book chapters and 8 articles in popular science and clinical journals and presented over 50 invited lectures at international meetings. Her research is funded by the Cancer Center Amsterdam, Dutch Cancer Society, Dutch Organisation for Scientific Research and the European Union.

Personal commitment

Since its foundation in 2001, I have been engaged in networking proteome researchers in The Netherlands through the organisation of annual meetings in which especially young researchers are given a chance to present their data. I see EuPA as the European network to connect proteome researchers and foster proteome science. Our team ambition is that this happens in an engaged, inclusive and transparent way, with awareness for optimal work environment conditions that support all, and especially young, proteome researchers in their careers.

Brief biography of Dr. Éva Csősz, candidate for EuPA Conferences and Communication

Dr. Éva Csősz is Associate Professor at the Department of Biochemistry and Molecular Biology, Faculty of Medicine, University of Debrecen, Debrecen, Hungary and is the leader of the Proteomics Core Facility at the University of Debrecen.

Dr. Csősz is devoted to proteomics method development and the application of quantitative proteomics to biomarker discovery from liquid biopsies, targeting mainly non-invasively accessible body fluids, such as tears, saliva and sweat. She works on the integration of data originating from different omics (proteomics, metabolomics, transcriptomics) or different modalities (clinical data, imaging, omics, etc.) in order to gain biologically relevant information. With a Master's degree in Biology with specialization in Biochemistry, and a PhD in Molecular Biology, Dr. Csősz has a wide perspective on the scientific problems that can be addressed with the help of proteomics. At the same time, as a Core Facility manager she had the possibility to learn the needs of scientists and clinicians willing to use the conceptual and technological possibilities provided by proteomics. With more than a decade experience in gel-based and gel-free proteomics and studies related to biochemistry and molecular biology, Dr. Csősz can help in creating interdisciplinary links among research groups in order to address the questions brought by life scientists with the full methodological arsenal of proteomics. Taking part in numerous national and international research projects she built up a research network and obtained extensive experience in scientific teamwork.

Dr. Csősz is the founder of the Proteomics Division of the Hungarian Molecular Biochemical Society and, as the president of the national organization, is an active organizer of conferences and meetings that aim to foster communication and interactions among the different proteomics labs. She helps the work of scientific communities in Hungary and abroad and is the author of more than 40 peer-reviewed papers. She teaches Biochemistry and Proteomics for BSc, MSc and PhD students at University of Debrecen, Hungary, and Babes-Bolyai University, Cluj Napoca, Romania on a regular basis, and is mentoring students at all levels of their scientific career.

Personal commitment

I envision EuPA as a network of people that are all devoted to science. A network in which information flows, where each node/person has his/her well-defined function, and which supports and takes care of its nodes. In this sense, EuPA as an organization should be welcoming and fully transparent. All who are interested in the functioning and activities of EuPA, as well as anyone who would like to join or to get involved in EuPA activities, should find relevant information in an easily accessible form. I believe that conferences, regular online meetings organized by the community, and opening up to other life science conferences (such as FEBS) will facilitate such a welcoming environment, in turn allowing EuPA members to build and maintain their important socio-scientific networks.

Brief biography of Dr. Christine Carapito, candidate for EuPA Education

Dr. Christine Carapito is a Senior Researcher at the French National Center for Scientific Research (CNRS) and University of Strasbourg.

She earned her PhD in Analytical Chemistry from the University of Strasbourg, France, focusing on the development of mass spectrometry-based proteomics and proteogenomics methods in 2006. After her PhD, she joined the laboratory of Prof. Ruedi Aebersold at the Institute of Molecular Systems Biology at ETH Zurich. There, she developed MS detection methods for the characterization of post-translational modifications and participated in the human SRM Atlas project.

In 2010, she became a Permanent Researcher of the French National Center for Scientific Research (CNRS) at the Hubert Curien Pluridisciplinary Institute in Strasbourg. Since then, she leads developments in proteomics and bioinformatics at the BioOrganic Mass Spectrometry laboratory. She defended her “Habilitation à Diriger des Recherches” in 2017, supervised seven PhD theses, is involved in teaching proteomics at the University of Strasbourg and holds editorial engagements. She has co-authored over 70 peer-reviewed articles. In 2018, she received the CNRS Bronze Medal and the award “Les Espoirs de l’Université de Strasbourg”.

She has been elected President of the French Proteomics Society (SFEAP) in 2017. In the meantime, she has become heavily involved in the scientific animation of the proteomics community by organizing congresses, meetings and thematic schools (SMAP 2019 congress, 16-19 September 2019 in Strasbourg, 400 attendees; Summerschool on PTMs, 24-28 June 2019 in Sète, >50 attendees from all over Europe, ...).

Personal commitment

I believe that the *raison d’être* of a community lies in its ability to accompany its scientific offspring, and allow them to grow into successful researchers. Promoting and providing access to training, courses, scientific exchanges and discussions to our young and “less young” members, whether through online or face-to-face means, therefore needs to be a central mission of EuPA!

Brief biography of Prof. Dr. Stefan Tenzer, candidate for EuPA Journals

Dr. Stefan Tenzer is Professor for Quantitative Proteomics at the Institute of Immunology, University Medical Center, Johannes-Gutenberg University Mainz, Mainz, Germany. He is head of the Core Facility for Mass Spectrometry at the Research Center for Immunotherapy and Coordinator of the Research Core “DIASyM”, which focuses on development and application of next generation data-independent acquisition mass spectrometric methods in Systems Medicine.

He earned his PhD in Biochemistry at the Department of Immunology at the Eberhard-Karls University, Tübingen, Germany. After his PhD, he moved to Mainz University where he established the Core Facility for Mass Spectrometry and

Protein at the Immunology Cluster of Excellence ‘Immunointervention’ University Medical Center Mainz in 2005.

His main interest is the development and application of methods for label-free quantitative proteomics using data-independent acquisition workflows. A special focus of the Tenzer Lab is the development of benchmarking methods and software for quantitative proteomics, which is also reflected in his role as an editor of the HUPO-PSI Quality Control Working Group. Dr. Tenzer teaches Biochemistry and Proteomics, Biochemistry and Immunology for BSc, MSc and PhD students at the Johannes-Gutenberg University Mainz and was a co-organizer of the 1st Human Immunopeptidomics Summer School in 2018. He is a member of several journal editorial boards and has co-authored over 120 peer reviewed publications. He was also elected as 2nd Vice-President of the German Society for Proteome Research in 2019.

Personal commitment

Journals constitute the major medium for the communication of results and novel methods in the scientific community. Many of us put major efforts not only into the writing, but also into reviewing manuscripts from our colleagues. Currently, the exchange between reviewers and authors is seldom revealed, even if it typically contains vital information to understand both strengths and limitations of novel approaches and results. Therefore, I strongly believe that transitioning towards open peer review formats will enhance transparency of the peer review process and enable us to see the important and often fascinating discussions between authors and reviewers, which are a vital aspect in shaping and improving our research.

Brief biography of Dr. Juan Antonio Vizcaíno, candidate for EuPA Funding

Dr. Juan Antonio Vizcaíno is leading the Proteomics Team at the EMBL-European Bioinformatics Institute (EMBL-EBI, Hinxton, Cambridge, UK). His team is responsible for the PRIDE database (<https://www.ebi.ac.uk/pride/>) and related software tools and resources. PRIDE is the most-prominent public repository for mass spectrometry (MS)-based proteomics data.

He earned undergraduate degrees in Pharmacy and Biochemistry, a Master's degree in Microbiology, and a doctoral degree in Molecular Biology from the University of Salamanca (Spain). Once he earned his Ph.D. he moved to bioinformatics. After working for one year as a postdoc in a functional genomics project in the University of Seville (Spain), he joined the PRIDE team at EMBL-EBI in 2006 as a postdoctoral fellow. At that point,

he started working in computational proteomics. He became PRIDE Group Coordinator in 2010 and Proteomics Team Leader in 2016. During these years, he has established PRIDE as the world-leading proteomics data depository. His overall goal is to help researchers to make the most of public proteomics data at different levels, including the integration of proteomics data with other omics data types.

He has been coordinating the International ProteomeXchange consortium of proteomics repositories (<http://www.proteomexchange.org/>) since its formal inception in 2011. At present, ProteomeXchange includes six members, including PRIDE, three resources in North America (PeptideAtlas, MassIVE and Panorama Public) and two in Asia (jPOST and iProX). He has also participated in the development of several open data standards and related software, as part of his contribution to the HUPO-Proteomics Standards Initiative (HUPO-PSI, <http://www.psidev.info/>), where he is currently the Chair of the Proteomics Informatics Working Group (since 2017). He is also currently one of the co-leaders of the ELIXIR Proteomics Community (since 2017, <https://elixir-europe.org/communities/proteomics>). Additionally, Dr. Vizcaíno has been a member of the management committee of the BSPR (British Society for Proteome Research) since 2016. It is important to highlight that due to his key roles, Dr. Vizcaíno has a close contact with many members of the proteomics community, both in Europe and worldwide.

In addition, he is quite experienced in providing training and support to users. Overall, he has co-authored over 120 peer-reviewed articles including some highly-cited ones in prominent journals.

Personal commitment

During my scientific career I have always invested in building and promoting activities in a community-wise manner. My work in HUPO-PSI, ProteomeXchange and ELIXIR all provide clear examples of this. I now want to use my experience to do the same across EuPA. In the specific context of EuPA finances, my key focus points will be rigour and transparency.

Brief biography of Dr. Lydie Lane, candidate for EuPA Initiatives

Dr. Lydie Lane co-directs the CALIPHO group at the SIB Swiss Institute of Bioinformatics and University of Geneva.

The CALIPHO group develops neXtProt, a knowledge platform on human proteins that integrates high quality datasets at the genomic, transcriptomic and proteomic levels and provides advanced semantic search tools to explore those. Since 2013 neXtProt is the reference knowledgebase for the HUPO Human Proteome Project (HPP); it integrates data generated by the project, develops specific analysis and visualisation tools and provides annual metrics.

Initially trained as a biochemist, Lydie Lane earned her PhD in Neurochemistry from the University of Orsay, France in 2002, by studying the impact of various post-translational modifications on the cholinergic metabolism. During her post-doc at the Institute of Developmental Biology in Marseille, she identified novel protein-protein interactions that are determinant for epithelial cell polarity. In 2004, she was hired by the SIB Swiss Institute of Bioinformatics as a biocurator for UniProtKB/Swiss-Prot. In charge of the curation of post-translational modifications, both from the literature and from proteomics datasets, she set up the very first UniProtKB pipeline for integration of mass spectrometry data. In 2009, together with Prof. Amos Bairoch, she created the CALIPHO group at University of Geneva and SIB Swiss Institute of Bioinformatics, with the aim to combine bioinformatics, curation, and experimental efforts to fill annotation gaps in the human proteome.

Lydie Lane is a long-term member of HUPO, has been playing key roles in the coordination of HPP projects since 2013 and serves on the HUPO Executive Board since 2019. She co-chairs the Swiss proteomics society and has been participating to various national and international initiatives to optimize proteomics data standardization and dissemination. She is a member of the Editorial Boards of the *Journal of Proteome Research* and *Expert Review of Proteomics*, has co-authored over 50 peer-reviewed articles and has supervised one master thesis and two PhD theses. In addition to provide training and support to neXtProt users, she teaches protein bioinformatics for BSc and MSc students at Geneva University and has created an innovative course that engages undergraduate students in research projects aimed at discovering the function of uncharacterized human proteins.

Personal commitment

In my scientific career, I have constantly been working at interfaces between various fields (e.g experimental cell biology, proteomics, bioinformatics) and I am convinced that collaboration between scientists from different backgrounds and disciplines is necessary to ask the right questions and reach appropriate solutions. For me, to make new ideas emerge, EuPA will need both to capitalize on the existing diversity of the European proteomics sub-communities and to better connect with other life science organisations. And this is precisely the purpose of EuPA Initiatives. Promoting and supporting existing Initiatives while encouraging the creation of interesting new Initiatives is therefore an exciting challenge for me, which I intend to take on based on engagement, inclusiveness and transparency!