

## PD Dr. rer. medic. Martin Eisenacher, 12<sup>th</sup> May 1973

Medical Bioinformatics at Medizinisches Proteom-Center  
Medical Faculty  
&  
Medical Proteome Analysis  
Center for Proteindiagnosics (PRODI)

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### SCIENTIFIC CAREER

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| since<br>01/2015     | Department leader of the “Medical Bioinformatics” at Medizinisches Proteom-Center, RUB<br>personnel responsibility for PostDocs, PhD / Master / Bachelor students, technical staff   |
| since<br>05/2014     | Consortium speaker and project leader of several running projects funded by BMBF, federal ministry for research and innovation, Deutsche Gesetzliche Unfallversicherung (DGUV);<br>Consortium speaker of the service center “Bioinformatics for Proteomics – BioInfra.Prot” within the BMBF funded “German Network for Bioinformatics Infrastructure – de.NBI” |
| 06/2014              | Habilitation (German qualification for higher education) in the medical faculty, RUB<br>Cumulative habilitation thesis: “Standard data formats, algorithms and analysis strategies for the bioinformatics of proteomics”<br>Habilitation colloquium at the faculty council: „Big data – chances and risks of personalised medicine“                            |
| since<br>05/2006     | Project leader and coordination of several finished projects funded by EU, BMBF, federal ministry for research and innovation, Deutsche Gesetzliche Unfallversicherung (DGUV), Cluster Industrielle Biotechnologie (CLIB), medical faculty RUB (FoRUM)   |
| 03/2012 –<br>12/2014 | Group leader of the work group “Bioinformatics / Biostatistics” at Medizinisches Proteom-Center, RUB<br>personnel responsibility for PostDocs, PhD / Master / Bachelor students, technical staff   |
| – 02/2012            | PostDoc at Medizinisches Proteom-Center, Ruhr-University Bochum (RUB), Germany   |
| 10/2000 –<br>05/2005 | PhD studies at the medical faculty, Westfälische Wilhelms-University Münster, Germany<br>PhD thesis: “intensity based quality control and scaling of gene expression data“   |
| 10/1992 –<br>09/1998 | Studies in computer science, university Dortmund, Germany<br>Degree: diploma in computer science   |

## PROFESSIONAL FUNCTIONS – SCIENTIFIC ACTIVITIES

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- 03/2018 – Member of Ethics Committee, RUB  
04/2019
- 06/2017 – Faculty coordinator for IT security and data privacy of the medical faculty, RUB  
01/2020
- 09/2016 Organisation, supervision of and lecturer at the de.NBI summer school „ From Big Data to Big Insights - Computational Methods for the analysis and interpretation of mass-spectrometric high-throughput data”, Leibniz-Zentrum für Informatik, Castle Dagstuhl, Germany
- since Member of the extended user council for the IT.Services department, RUB  
05/2016
- since 2015 Reviewer for conferences and funding institutions, e.g. German Research Society (“Deutsche Forschungsgemeinschaft” – DFG), German Conference for Bioinformatics (GCB), French Institute of Bioinformatics (IFB)
- since Editor of the Proteomics Standards Initiative (PSI) of the Human Proteome  
12/2014 Organization (HUPO): execution of the review process (“PSI document process”) for suggested standardisation documents
- since 2012 Member of the editorial board of the journal “BBA – Proteins and Proteomics”
- since 2006 Peer reviewer for scientific journals, e.g. *Bioinformatics*, *BMC Bioinformatics*, *Molecular and Cellular Proteomics*, *Proteomics*, *J Proteome Research*, *J Proteomics*, *BBA Proteins and Proteomics*

## PROFESSIONAL MEMBERSHIPS

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DGPF (German Society for Proteome Research)  
GI (Society for Informatics / Computer Science)  
Common work group of scientific societies “Bioinformatics” (FaBi, [www.bioinformatik.de](http://www.bioinformatik.de))  
Research Department Protein (Ruhr-University Bochum)

## IMPORTANT PUBLICATIONS

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1. Witzke KE, Großerueschkamp F, Jütte H, Horn M, Roghmann F, von Landenberg N, Bracht T, Kallenbach-Thieltges A, Käfferlein H, Brüning T, Schork K, **Eisenacher M**, Marcus K, Noldus J, Tannapfel A, Sitek B, Gerwert K (2019) Integrated Fourier Transform Infrared Imaging and Proteomics for Identification of a Candidate Histochemical Biomarker in Bladder Cancer. *Am J Pathol* 2019 Mar;189(3):619-631. doi: 10.1016/j.ajpath.2018.11.018. Epub 2019 Feb 12 (IF 2018: 3.8)
2. Mayer G, Quast C, Felden J, Lange M, Prinz M, Pühler A, Lawrenz C, Scholz U, Glöckner FO, Müller W, Marcus K, **Eisenacher M** (2019) A generally applicable lightweight method for calculating a value structure for tools and services in bioinformatics infrastructure projects. *Brief Bioinform* 2019 Jul 19;20(4):1215-1221. doi:10.1093/bib/bbx140. (IF 2018: 9.0)
3. Hoffmann N, Rein J, Sachsenberg T, Hartler J, Haug K, Mayer G, Alka O, Dayalan S, Pearce JTM, Rocca-Serra P, Qi D, **Eisenacher M**, Perez-Riverol Y, Vizcaino JA, Salek RM, Neumann S, Jones AR (2019) mzTab-M: A Data Standard for Sharing Quantitative Results in Mass Spectrometry Metabolomics. *Anal Chem* 2019 Mar 5;91(5):3302-3310. doi: 10.1021/acs.analchem.8b04310. Epub 2019 Feb 13 (IF 2018: 6.4)
4. Uszkoreit J, Perez-Riverol Y, Eggers B, Marcus K, **Eisenacher M** (2019) Protein Inference Using PIA Workflows and PSI Standard File Formats. *J Proteome Res* 2019 Feb 1;18(2):741-747. doi: 10.1021/acs.jproteome.8b00723. Epub 2018 Dec 5 (IF 2018: 3.8)
5. Perez-Riverol Y, Csordas A, Bai J, Bernal-Llinares M, Hewapathirana S, Kundu DJ, Inuganti A, Griss J, Mayer G, Eisenacher M, Pérez E, Uszkoreit J, Pfeuffer J, Sachsenberg T, Yilmaz S, Tiwary S, Cox J, Audain E, Walzer M, Jarnuczak AF, Ternent T, Brazma A, Vizcaino JA (2019) The PRIDE database and related tools and resources in 2019: improving support for quantification data. *Nucleic*

*Acids Res* 2019 Jan 8;47(D1):D442-D450. doi: 10.1093/nar/gky1106 [PMID: 30395289] (IF 2018: 11.1)

6. Turewicz M, Kohl M, Ahrens M, Mayer G, Uszkoreit J, Naboulsi W, Bracht T, Megger DA, Sitek B, Marcus K, **Eisenacher M** (2017) BioInfra.Prot: A comprehensive proteomics workflow including data standardization, protein inference, expression analysis and data publication. *J Biotechnol.* 2017 Nov 10;261:116-125 (IF 2.6)
7. Güttsches AK, Brady S, Krause K, Maerkens A, Uszkoreit J, **Eisenacher M**, Schreiner A, Galozzi S, Mertens-Rill J, Tegenthoff M, Holton JL, Harms MB, Lloyd TE, Vorgerd M, Wehl CC, Marcus K, Kley RA (2017) Proteomics of rimmed vacuoles define new risk allele in inclusion body myositis. *Ann Neurol* 2017 Feb;81(2):227-239 (IF 9.9)
8. Turewicz M, Ahrens M, May C, Marcus K, **Eisenacher M** (2016) PAA: an R/bioconductor package for biomarker discovery with protein microarrays. *Bioinformatics* 2016 May 15;32(10):1577-9 (IF 7.3)
9. Uszkoreit J, Maerkens A, Perez-Riverol Y, Meyer HE, Marcus K, Stephan C, Kohlbacher O, **Eisenacher M** (2015) PIA: An Intuitive Protein Inference Engine with a Web-Based User Interface. *J Proteome Res.* 2015 Jul 2;14(7):2988-97 (IF 4.2)
10. Vizcaíno JA, Deutsch EW, Wang R, Csordas A, Reisinger F, Ríos D, Dianes JA, Sun Z, Farrah T, Bandeira N, Binz PA, Xenarios I, **Eisenacher M**, Mayer G, Gatto L, Campos A, Chalkley RJ, Kraus HJ, Albar JP, Martinez-Bartolomé S, Apweiler R, Omenn GS, Martens L, Jones AR, Hermjakob H (2014) ProteomeXchange provides globally coordinated proteomics data submission and dissemination. *Nat Biotechnol* 2014 Mar 10;32(3):223-6 (IF 41.5)