

BIOGRAPHICAL SKETCH

NAME Henning Hermjakob	POSITION TITLE Team Leader Proteomics Services		
CURRENT AFFILIATION European Bioinformatics Institute, Hinxton, Cambridgeshire, UK			
EDUCATION/TRAINING <i>(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)</i>			
INSTITUTION AND LOCATION	DEGREE <i>(if applicable)</i>	YEAR(s)	FIELD OF STUDY
University of Bielefeld, Germany	MSc	1996	Bioinformatics

List of five recent publications by the candidate:

- Sandra Orchard, Lukasz Salwinski, Samuel Kerrien, Luisa Montecchi-Palazzi, Matthias Oesterheld, Volker Stümpflen, Arnaud Ceol, Andrew Chartrayamontri, John Armstrong, Peter Woollard, John J. Salama, Susan Moore, Jérôme Wojcik, Gary D. Bader, Marc Vidal, Michael E. Cusick, Mark Gerstein, Anne-Claude Gavin, Giulio Superti-Furga, Jack Greenblatt, Joel Bader, Peter Uetz, Mike Tyers, Pierre Legrain, Stan Fields, Nicola Mulder, Michael Gilson, Michael Niepmann, Lyle Burgoon, Javier De Las Rivas, Carlos Prieto, Victoria M. Perreau, Chris Hogue, Hans-Werner Mewes, Rolf Apweiler, Ioannis Xenarios, David Eisenberg, Gianni Cesareni, **Henning Hermjakob**: The Minimum Information required for reporting a Molecular Interaction Experiment (MIMIx). *Nat Biotechnol.* 2007 Aug, in press.
- Chris F Taylor, Norman W Paton, Kathryn S Lilley, Pierre-Alain Binz, Michael J Dunn, Randall K Julian Jr., Andrew R Jones, Weimin Zhu, Rolf Apweiler, Ruedi Aebersold, Eric W Deutsch, Albert JR Heck, Alexander Leitner, Marcus Macht, Matthias Mann, Lennart Martens, Thomas A Neubert, Scott D Patterson, Peipei Ping, Sean L Seymour, Puneet Souda, Akira Tsugita, Joel Vandekerckhove, Thomas M Vondriska, Julian P Whitelegge, Marc R Wilkins, Ioannis Xenarios, John R Yates III, **Henning Hermjakob**: The Minimum Information About a Proteomics Experiment (MIAPE). *Nat Biotechnol.* 2007 Aug, in press.
- Taussig MJ, Stoevesandt O, Borrebaeck CA, Bradbury AR, Cahill D, Cambillau C, de Daruvar A, Dubel S, Eichler J, Frank R, Gibson TJ, Gloriam D, Gold L, Herberg FW, **Hermjakob H**, Hoheisel JD, Joos TO, Kallioniemi O, Koegl M, Konthur Z, Korn B, Kremmer E, Krobitsch S, Landegren U, van der Maarel S, McCafferty J, Muyldermans S, Nygren PA, Palcy S, Pluckthun A, Polic B, Przybylski M, Saviranta P, Sawyer A, Sherman DJ, Skerra A, Templin M, Ueffing M, Uhlen M: ProteomeBinders: planning a European resource of affinity reagents for analysis of the human proteome. *Nat Methods.* 2007 Jan;4(1):13-7.
- Hermjakob H**, Apweiler R: The Proteomics Identifications Database (PRIDE) and the ProteomExchange Consortium: making proteomics data accessible. *Expert Rev Proteomics.* 2006 Feb;3(1):1-3.
- Hermjakob H**, Montecchi-Palazzi L, Bader G, Wojcik J, Salwinski L, Ceol A, Moore S, Orchard S, Sarkans U, von Mering C, Roechert B, Poux S, Jung E, Mersch H, Kersey P, Lappe M, Li Y, Zeng R, Rana D, Nikolski M, Husi H, Brun C, Shanker K, Grant SG, Sander C, Bork P, Zhu W, Pandey A, Brazma A, Jacq B, Vidal M, Sherman D, Legrain P, Cesareni G, Xenarios I, Eisenberg D, Steipe B, Hogue C, Apweiler R: The HUPO PSI's molecular interaction format--a community standard for the representation of protein interaction data. *Nat Biotechnol.* 2004 Feb;22(2):177-83.

Please indicate in 200 words or less the reason(s) why you would be a suitable candidate for the HUPO Council elections.

Henning Hermjakob is Team Leader for Proteomics Services at the European Bioinformatics Institute. Major resources provided by his team are the IntAct database for molecular interactions, the PRIDE database for protein identifications, and the ChEBI database for biochemical nomenclature. As founding member and current chair of the HUPO Proteomics Standards Initiative, member of the BSPR executive committee, and senior editor of the *PROTEOMICS* journal, he contributes to the standardization of data representation in proteomics. As a participant in the HUPO Brain, Liver, and Plasma proteome projects as well as the HUPO Antibody Initiative, he aims to ensure consistency in data management and data representation across HUPO projects. Current research interests include the comparative analysis of large scale proteomics datasets, and user-friendly approaches to data capture in systems biology.