

BIOGRAPHICAL SKETCH

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NAME Oliver Hofmann		POSITION TITLE Research Associate, Harvard School of Public Health	
eRA COMMONS USER NAME (credential, e.g., agency login)			
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 Cologne, Cologne, Germany	Diploma	1999	Biology
University of Cologne, Cologne Germany	PhD	2000-04	Biochemistry
SANBI, Cape Town, South Africa	Post Doctoral	2004-07	Bioinformatics
Harvard School of Public Health, Boston, MA	Post Doctoral	2007-08	

A. POSITIONS AND HONORSPositions and Employment

1999-2000 Ph.D. Student, University Clinic Cologne, Department of Dermatology
 2000-2001 Ph.D. Student, University of Cologne, Department of Biochemistry
 2001-2002 Research Fellow, Research stay at deCODE Genetics, Reykjavik, Iceland. Pattern analysis of gene families and cluster assembly algorithms.
 2002-2004 Ph.D. Student, University of Cologne, Department of Biochemistry
 2004-2007 Post Doctoral Research Fellow, South African National Bioinformatics Institute, University of the Western Cape
 2007-Present Research Associate, Department of Biostatistics, Harvard School of Public Health

B. SELECTED PEER REVIEWED PUBLICATIONS (in chronological order).

Oliver Hofmann (2000). Analysis of the human nidogen promotor. Diploma thesis, University of Cologne.
 Ida Schomburg, **Oliver Hofmann**, Claudia Bänsch, Antje Chang, Dietmar Schomburg. Enzyme data and metabolic information: \abk{brenda}, a resource for research in biology, biochemistry, and medicine. *Gene Function & Disease*, 2000;1(3-4):109.
 Ida Schomburg, Antje Chang, **Oliver Hofmann**, Christian Ebeling, Frank Ehrentreich, Dietmar Schomburg. BRENDA: a resource for enzyme data and metabolic information. *Trends Biochem Sci*, 2002;27(1):54. Review
Oliver Hofmann (2004). Determination of dependencies between enzymatic activities and disease related concepts by automatic evaluation of the scientific literature. PhD thesis, University of Cologne
Oliver Hofmann, Dietmar Schomburg. Concept-based annotation of enzyme classes. *Bioinformatics*, 2005;21(9):2059.
 A Mehrle, H Rosenfelder, I Schupp, C de Val, D Arlt, F Hahne, S Bechtel, J Simpson, **O Hofmann**, W Hide, KH Glatting, W Huber, R Pepperkok, A Poustka, S Wiemann (2006): The LifeDB database in. *Nucleic Acid Res*, 2006;1(34):415.
 Vladimir B Bajic, Sin Lam Tan, Alan Christoffels, Christian Schönbach, Leonard Lipovich, Liang Yang, Oliver Hofmann, Adele Kruger, Winston Hide, Chikatoshi Kai, Jun Kawai, David A Hume, Piero Carninci, Yoshihide Hayashizaki. Mice and men: their promoter properties. *PLoS Genet*, 2006;2:54

Program Director/Principal Investigator (Last, First, Middle):

- A. Kruger, **O. Hofmann**, P. Carninci, Y. Hayashizaki, and W. Hide. Simplified ontologies allowing comparison of developmental mammalian gene expression. *Genome Biol*, 2007; 8:R229.
- Z. Lombard, N. Tiffin, **O. Hofmann**, V. B. Bajic, W. Hide, and M. Ramsay. Computational selection and prioritization of candidate genes for fetal alcohol syndrome, *BMC Genomics*, 2007; 8:389.
- S. Mathivanan, M. Ahmed, N. G. Ahn, H. Alexandre, R. Amanchy, P. C. Andrews, et al (2008): Human proteinpedia enables sharing of human protein data, *Nat Biotechnol*, 2008; 26:164–7.
- M. Kaur, S. Schmeier, C.R. MacPherson, **O. Hofmann**, W.A. Hide, S. Taylor, N. Willcox and V.B. Bajic. Prioritizing genes of potential relevance to diseases affected by sex hormones: An example of Myasthenia Gravis. *BMC Genomics*, 2008; 9:481.
- G. Koscielnny, V. LeTexier, C. Gopalakrishnan, V. Kumanduri, J. Riethoven, F. Nardone, E. Whitfield, C. Fallsehr, **O. Hofmann**, M. Kull, H. E., S. Boue, E. Eyra, M. Plass, F. Lopez, W. Ritchie, V. Moucadel, T. Ara, H. Pospisil, A. Hermann, J. Reich, R. Guigo, P. Bork, M. von Knebel Doeberitz, J. Vilo, W. Hide, R. Apweiler, A. Thanaraj, and D. Gautheret. ASTD: the alternative splicing and transcript diversity database. *Genomics*, 2008; in press.
- Hofmann** et al. Genome-wide analysis of cancer/testis gene expression. *Proc Natl Acad Sci USA*, 2008; 105(51): 20422-7 .
- The Fantom4 consortium.** A complex transcriptional network controls growth arrest and differentiation in a human myeloid leukemia cell line. *Nat Genet*, (2009)