

**BIOGRAPHICAL SKETCH**

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NAME Burkhard Rost	POSITION TITLE Professor Bioinformatics, TUM Munich Associate Professor, Biochemistry, Columbia Univ.		
eRA COMMONS USER NAME (credential, e.g., agency login) rost_b			
EDUCATION/TRAINING (Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)			
INSTITUTION AND LOCATION	DEGREE (if applicable)	YEAR(s)	FIELD OF STUDY
Gießen University (Germany)	BS	1984	Physics
Heidelberg University (Germany)	BA	1988	Philosophy
Heidelberg University (Germany)	MS	1988	Physics
Heidelberg University (Germany)	Dr. rer. nat.	1994	Physics

**A. Positions and Honors.****Positions and Employment**

1986 - 1988 **Assistant** at Institute for Theoretical Physics, Heidelberg University (Germany)  
 1988 - 1990 Research fellow at Institute for Theoretical Physics, Heidelberg University (Germany)  
 1990 - 1992 Visitor at the European Molecular Biology Laboratory (EMBL), Heidelberg, Germany  
 1993 - 1994 Research fellow at the EMBL Heidelberg, Germany  
 1995 Scientist at the European Bioinformatics Institute (EBI), Hinxton, Cambridge, England  
 1996 - 1998 Scientist at EMBL Heidelberg, Germany  
 1998 Researcher at the company LION-Biosciences, Heidelberg, Germany  
 1999 - 2000 Assistant Professor at Columbia Univ., Dept. Biochemistry & Molecular Biophysics  
 2000 - 2010 **Associate Professor** at Columbia Univ., Dept. Biochemistry & Molecular Biophysics  
 2005 - 2010 Tenure at Columbia Univ., Dept. Biochemistry & Molecular Biophysics  
 2009/07 - now Professor for Bioinformatics at TU Munich, Germany, Dept. Computer Science  
 2009/09 - now Fellow at IAS TU Munich, Germany  
 2010/07 - now Adjunct Professor Columbia Univ., Dept. Biochemistry & Molecular Biophysics

**Other Experience and Professional Memberships**

1996 - now Member of ISCB (International Society for Computational Biology)  
 2002 - now Member of New York Academy of Sciences  
 1995 - now Program Committee of ISMB meetings (Intelligent Systems for Molecular Biology)  
 2002 - now Board of Directors ISCB  
 2004 - 2005 Vice President of ISCB (International Society for Computational Biology)  
 2005 - 2006 President Elect of ISCB (International Society for Computational Biology)  
 2006 - now President of ISCB (International Society for Computational Biology)  
 1992 - now Involved in organization of >41 international meetings, incl. the most important meeting in bioinformatics, namely the ISMB series (ISMB'02 Edmonton: Scientific Committee Co-Chair, ISMB'05 Detroit: Scientific Committee Co-chair; ISMB-ECCB'07/ISMB'08/ISMB-ECCB'11: Co-chair of meeting; ISMB'07-12: Chair of Highlights), the most important meeting for structure prediction (co-organizer at: CASP6-8), and several meetings outside the western hemisphere (ISCB-Africa: 2009: Bamako Mali, 2011: Cape Town; ISCB-Latin America: 2010: Montevideo Uruguay, 2012: Santiago Chile; ISCB-Asia: 2011: Kuala Lumpur Malaysia)  
 2001 - 2008 Ad hoc panels at NIH, including one as chair of the panel; Ad hoc panels for NSF; ad hoc panel for European Community  
 1999 - now Over 500 referee reports (112 in 2005) for peer-reviewed journals (incl. Science, Nature, Nature Structure, Nature Genetics, Cell, EMBO J, Structure, PNAS, JMB, Biochemistry)  
 2001 - 2007 Associate Editor Journal of Medical Informatics

2004 - 2006	Editorial Board Proteins: Structure, Function and Bioinformatics
2005 - 2006	Editorial Board Bioinformatics
2005 - now	Editorial Board FASEB
2006 - now	Editorial Board Journal of Structural and Functional Genomics
2005 - 2009	Associate Editor PLoS Computational Biology
2007 - now	Associate Editor Bioinformatics
2006 - now	Associate Editor Proteins: Structure, Function and Bioinformatics
2009 - now	Deputy Editor PLoS Computational Biology
1999 - now	Over 50 grant reviews from Austria, Denmark, England, Germany, Israel, Italy, Netherlands, Norway, Singapore, Spain, Sweden, Switzerland, USA; ad hoc panels for NIH and NSF
1988 - now	Over 140 invited talks at international meetings in 21 countries since 1988

**B. Selected peer-reviewed publications (in chronological order).**

(First- and last-author publications selected from 146 peer-reviewed publications)

- 8 **B Rost & C Sander** (1993) Prediction of protein secondary structure at better than 70% accuracy. **J Mol Biol** 232, 584-599.
- 17 **B Rost & C Sander** (1994) Conservation and prediction of solvent accessibility in protein families. **Proteins** 20, 216-26.
- 30 **B Rost, R Casadio & P Fariselli** (1996) Topology prediction for helical transmembrane proteins at 86% accuracy. **Protein Science** 5, 1704-1718.
- 36 **B Rost, R Schneider and C Sander** (1997) Protein fold recognition by prediction-based threading. **J Mol Biol** 270, 471-480.
- 41 **B Rost** (1999) Twilight zone of protein sequence alignments. **Prot Engng** 12, 85-94.
- 48 **M Cokol, R Nair & B Rost** (2000) Finding nuclear localisation signals. **EMBO Rep** 1, 411-415.
- 52 **D Przybylski & B Rost** (2002) Alignments grow, secondary structure prediction improves. **Proteins** 46, 195-205.
- 58 **B Rost** (2002) Enzyme function less conserved than anticipated. **J Mol Biol** 318, 595-608.
- 65 **J Liu, H Tan & B Rost** (2002) Loopy proteins appear conserved in evolution. **J Mol Biol** 322, 53-64.
- 70 **Y Ofran & B Rost** (2003) Analysing six types of protein-protein interfaces. **J Mol Biol** 325, 377-387.
- 88 **VA Eylich & B Rost** (2003) META-PP: single interface to crucial prediction servers. **NAR** 31, 3308-3310.
- 89 **P Carter, CAF Andersen, B Rost** (2003) DSSPcont: a database of continuous secondary structure assignments for proteins, **Nucl Acids Res** 31, 3308-3310.
- 97 **H Bigelow, D Petrey, J Liu, D Przybylski & B Rost** (2004) Predicting transmembrane beta-barrels for entire proteomes. **Nucl Acids Res** 32, 2566-2577.
- 101 **B Rost, G Yachdav & J Liu** (2004) The PredictProtein server. **Nucl Acids Res**, 32, W321-W326.
- 105 **S Mika & B Rost** (2004) Protein names peeled precisely off free text. **Bioinformatics**, 20 S1, I241-I247.
- 108 **D Przybylski & B Rost** (2004) Improving fold recognition without folds. **J Mol Biol** 341, 255-269.
- 110 **S Mika & B Rost** (2005) NMPdb: database of nuclear matrix proteins. **Nucl Acids Res** 33, D160-D163.
- 112 **R Nair & B Rost** (2005) Mimicking cellular sorting improves prediction of subcellular localization. **JMB** 348, 85-100.
- 113 **M Punta & B Rost** (2005) Protein folding rates estimated from contact predictions. **JMB** 348, 507-512.
- 117 **M Punta & B Rost** (2005) PROFcon: novel prediction of long-range contacts. **Bioinformatics** 21, 2960-2968.
- 125 **A Schlessinger, Y Ofran, G Yachdav & B Rost** (2006) Epitome: Database of structure-inferred antigenic epitopes. **Nucl Acids Res** 34 D777-D780.
- 126 **J Liu, J Gough & B Rost** (2006) Distinguish protein-coding from non-coding RNA using support vector machines. **PLoS Genetics** 2 (4):e29, DOI: 10.1371/journal.pgen.0020029.
- 128 **S Mika & B Rost** (2006) Model organisms pose problems for unraveling protein-protein interactions. **PLoS Comp Biol** 2, e79.
- 129 **Y Ofran, G Yachdav, E Mozes, T Soong & B Rost** (2006) Create and assess protein networks through molecular characteristics of individual proteins. **Bioinformatics (ISMB Proceedings)**, 22: e402-e407.
- 133 **Y Ofran & B Rost** (2007) ISIS: Interaction Sites Identified from Sequence. **Bioinformatics (ECCB'2006)**, 23, e5-e12.
- 135 **D Przybylski & B Rost** (2007) Consensus sequences improve PSI-BLAST searches. **NAR** 35, 2238-46.

- 138 **Y Bromberg & B Rost** (2007) SNAP: predict effect of non-synonymous polymorphisms on function. **Nucleic Acids Res** 35, 3823-3835.
- 139 **Y Ofran & B Rost** (2007) Protein-protein interaction hotspots carved into sequences. **PLoS Computational Biology** 3, e119.
- 141 **Y Ofran, V Mysore & B Rost** (2007) Prediction of DNA-binding residues from sequence. **Bioinformatics (ISMB Proceedings)** 23, i347-353.
- 142 **A Schlessinger, J Liu & B Rost** (2007) Natively unstructured loops differ from other loops. **PLoS Comp Biol** 3, e140.
- 143 **J Liu, GT Montelione & B Rost** (2007) Novel leverage of structural genomics. **Nature Biotech** 25,849-851.
- 144 **A Schlessinger, M Punta & B Rost** (2007) Natively unstructured regions in proteins identified from contact predictions. **Bioinformatics** 23, 2376-2384.
- 151 **Y Bromberg & B Rost** (2008) Comprehensive *in silico* mutagenesis highlights functionally important residues in proteins. **Bioinformatics (ECCB Proceedings)** 24, i207-i212.
- 154 **D Przybylski & B Rost** (2008) Powerful fusion: PSI-BLAST and consensus sequences. **Proteins** 24, 1987-1993.
- 155 **Y Ofran, A Schlessinger & B Rost** (2008) Automated Identification of Complementarity Determining Regions (CDRs) reveals peculiar characteristics of CDRs and B cell epitopes. **J Immunology** 181, 6230-6235.
- 156 **Y Bromberg & B Rost** (2008) SNAP predicts effect of mutations on protein function. **Bioinformatics** 24, 2397-2398.
- 157 **T-T Soong & B Rost** (2008) Physical protein-protein interactions predicted from microarrays. **Bioinformatics** 15, 2608-2614.
- 163 **A Schlessinger, M Punta, G Yachdav, L Kajan & B Rost** (2009) Improved disorder prediction by combination of orthogonal approaches. **PLoS ONE** 4, doi:10.1371/journal.pone.0004433.
- 164 **R Nair, J Liu, T-T Soong, TB Acton, J Everett, A Kouranov, A Fiser, A Godzik, L Jaroszewski, C Orengo, GT Montelione & B Rost** (2009) Structural genomics is the largest contributor of novel structural leverage. **J Structural Functional Genomics** 10:181-191.
- 165 **C Bertoni, M Punta, M Fischer, G Yachdav, F Frouhar, W Zhou, AP Kuzin, J Seetharaman, M Abashidze, TA Ramelot, MA Kennedy, JR Cort, A Belachew, JF Hunt, L Tong, GT Montelione & B Rost** (2009) Structural genomics reveals EVE as a new ASCH/PUA-related domain. **Proteins** 75, 760-773.
- 167 **A Kernytsky & B Rost** (2009) Using genetic algorithms to select most predictive protein features. **Proteins** 75, 75-88.
- 168 **Y Bromberg, G Yachdav, Y Ofran, R Schneider & B Rost** (2009) New in protein structure and function annotation: hotspots, single nucleotide polymorphisms and the Deep Web. **Curr Opin Drug Discov Devel** 12, 408-419.
- 174 **Y Bromberg, J Overton, RL Leibel & B Rost** (2009) *In silico* mutagenesis: a case study of the melanocortin 4 receptor. **FASEB J** 23, 3059-3069.
- 177 **C Schaefer, A Schlessinger & B Rost** (2010) Protein secondary structure appears to be robust under *in silico* evolution while protein disorder appears not to be. **Bioinformatics** 26, 625-631.
- 188 **S Rastogi & B Rost** (2011) LocDB: experimental annotations of localization for *Homo sapiens* and *Arabidopsis thaliana*. **NAR** 39, D230-234.
- 193 **A Schlessinger, C Schaefer, E Vicedo, M Schmidberger, M Punta, B Rost** (2011) Protein disorder - a breakthrough invention of evolution? **Current Opinion in Structural Biology**, 21: 412-418.

Note 1: numbers according to full publication list sorted by date (total incl. *in press* 197); members of my group in bold face.

Note 2: all first-/last-author papers have been quoted over 16,000 times (ISI, Aug. 2011); my personal impact factor over all publications (incl. those NOT quoted in ISI) is 14, i.e. higher than that of e.g. PNAS; my h-index was 52 in Aug. 2011 according to ISI and 62 in Aug. 2011 according to Google.