List of Publications

Florian Heinke

May 13, 2025

Journal Articles & Book Chapters

2025

Tommy Bergmann, Florian Heinke, Aurélien Thomas, Silke Grabherr, and Dirk Labudde. Modellierung der Hämoglobindegeneration im UV-Vis-Bereich als Unterstützung der forensischen Altersschätzung von Blutflecken. *Rechtsmedizin*, 2025

2023

Katrin Sophie Bohnsack, Julius Voigt, Marika Kaden, Florian Heinke, and Thomas Villmann. Multi-proximity based embedding scheme for learning vector quantization-based classification of biochemical structured data. *Neurocomputing*, 554:126632, 2023

2020

Michael Spranger, Kai-Jannis Hanke, Florian Heinke, and Dirk Labudde. Measuring competence: Improvements to determine the degree of opinion leadership in social networks. *International Journal on Advances in Internet Technology*, 13:97–109, 2020

2018

Adrie H. Westphal, Dirk Tischler, Florian Heinke, Sarah Hofmann, Janosch Alexander David Gröning, Dirk Labudde, and Willem J. H. van Berkel. Pyridine nucleotide coenzyme specificity of p-hydroxybenzoate hydroxylase and related flavoprotein monooxygenases. *Frontiers in Microbiology*, 9, 2018

Sven Becker, Michael Spranger, Florian Heinke, Steffen Grunert, and Dirk Labudde. A comprehensive framework for high resolution image-based 3d modeling and documentation of crime scenes and disaster sites. *International Journal on Advances in Systems and Measurements*, 11(1 & 2), 2018

2017

T. Bergmann, F. Heinke, and D. Labudde. Towards substrate-independent age estimation of blood stains based on dimensionality reduction and k-nearest neighbor classification of absorbance spectroscopic data. *Forensic science international*, 278:1, 2017

Michael Spranger, Hanna Siewerts, Joshua Hampl, Florian Heinke, and Dirk Labudde. Sona: A knowledge-based social network analysis framework for predictive policing. *International journal on advances in intelligent systems*, 10:147–156, 2017

Christoph Leberecht, Florian Heinke, and Dirk Labudde. Simulation of diffusion using a modular cell dynamic simulation system. *In silico biology*, 12(3-4):129–142, 2017

2016

F. Heinke, S. Bittrich, F. Kaiser, and D. Labudde. SequenceCEROSENE: A computational Method and Web Server to visualize spatial Residue Neighborhood. *BMC Biodata mining*, 2016

M. Spranger, F. Heinke, L. Appelt, M. Puder, and D. Labudde. MoNA: Automated Identification of Evidence in Forensic Short Messages. *Internation Journal on Advances in Security*, 2016

2015

A. Pflugbeil, S. Gross, J. Rothe, F. Heinke, H. Bruchhaus, J. Edelmann, D. Labudde, J. Dressler, and K. Thiele. Initial experience in the application of the PowerQuantTM system and the Investigator ESSplex SE QS kit for aDNA analysis. *Forensic Science International: Genetics*, 2015

M. Spranger, F. Heinke, and D. Labudde. Analyse von Kurznachrichten in der polizeilichen Fallarbeit. *Der Kriminalist*, 2015

2013

S. Grunert, F. Heinke, and D. Labudde. Structure Topology Prediction of Discriminative Sequence Motifs in Membrane Proteins with Domains of Unknown Function. *Structural Biology*, 2013, 2013

F. Heinke and D. Labudde. *Functional Analyses of Membrane Protein Mutants involved in Nephrogenic Diabetes insipidus: An Energy-based Approach - In: Research on Diabetes.* iConcept Press, 2013

F. Heinke, S. Schildbach, D. Stockmann, and D. Labudde. eProS– A Database and Toolbox for Investigating Protein Sequence-Structure-Function Relationships

through Energy Profiles. *Nucleic Acids Res*, 41(Database issue):D320–D326, Jan 2013

2012

F. Heinke and D. Labudde. Membrane protein stability analyses by means of protein energy profiles in case of nephrogenic diabetes insipidus. *Comput Math Methods Med*, 2012:790281, February 2012

M. Spranger, S. Schildbach, F. Heinke, S. Grunert, and D. Labudde. Semantic Tools for Forensics: A Highly Adaptable Framework. *IMMM2012*, pages 27 – 31, 2012

2011

F. Heinke, A. Tuukkanen, and D. Labudde. *Analysis of Membrane Protein Stability in Diabetes insipidus In: Diabetes insipidus.* InTech, 2011

Conference Papers

2025

Florian Heinke, Marie-Luise Heuschkel, and Dirk Labudde. Bildgestützte biometrische Personenidentifizierung anhand des digital-anthropometrischen Rigabgleichs: Quantitativer Vergleich mittels RWSD. In *Polizei-Informatik 2025 – 10. Jahrestagung*, 2025

2023

Florian Heinke, Marie-Luise Heuschkel, and Dirk Labudde. Analysing distributions of feature similarities in the context of digital anthropometric pattern matching probability. In *Lecture Notes in Informatics (LNI) – International Workshop on Digital Forensics 2023*, 2023

2022

Florian Heinke, Marie Heuschkel, and Dirk Labudde. A frequentist estimation of duplicate probability as a baseline for person identification from image and video material using anthropometric measurements. In *GI-Jahrestagung*, 2022

2020

Maik Benndorf, Gabriel Kind, Hanna Siewerts, Florian Heinke, and Uwe Schneider. Towards a better understanding of students in the entry phase of their studies. In *Proceedings of the 9th Computer Science Education Research Conference*, pages 1–7, 2020

2019

Florian Heinke, Lars Hempel, and Dirk Labudde. A novel approach for fast protein structure comparison and heuristic structure database searching based on residue eigenrank scores. In *International Conference -Beyond Databases, Architectures, and Structures*, 2019

2018

Michael Spranger, Florian Heinke, Hanna Siewerts, Joshua Hampl, and Dirk Labudde. Opinion leaders in star-like social networks: A simple case? 2018

2017

M. Spranger, S. Becker, F. Heinke, H. Siewerts, and D. Labudde. The Infiltration Game: Artificial Immune System for the Exploitation of Crime Relevant Information in Social Networks. In *IMMM 2017 : The Seventh International Conference on Advances in Information Mining and Management*, 2017

F. Heinke, R. Beier, T. Bergmann, H. Mixtacki, and D. Labudde. Novel Computational Techniques for Thin-Layer Chromatography (TLC) Profiling and TLC Profile Similarity Scoring. In *International Conference: Beyond Databases, Architectures and Structures*, pages 373–385. Springer, 2017

2016

S. Bittrich, F. Heinke, and D. Labudde. eQuant - A Server for fast Protein Model Quality assessment by integrating high-dimensional Data and Machine Learning. In S Kozielski, D. Mrozek, P. Kasprowski, B. Malysiak-Mrozek, and D. Kostrzewa, editors, *Proceedings of the IEEE Beyond Databases, Architectures and Structures 2016*. Springer, 2016

S. Schildbach, F. Heinke, and D. Labudde. Evaluation of Descriptor Algorithms of Biological Sequences and Distance Measures for the Intelligent Cluster Index (ICIx). In S Kozielski, D. Mrozek, P. Kasprowski, B. Malysiak-Mrozek, and D. Kostrzewa, editors, *Proceedings of the IEEE Beyond Databases, Architectures and Structures 2016*. Springer, 2016

M. Spranger, F. Heinke, S. Becker, and D. Labudde. Towards Drone-Assisted Large-scale Disaster Response and Recovery. In *The First Internation Conference on Advances in Computation, Communications and Services*, 2016

2015

F. Heinke, D. Stockmann, S. Schildbach, M. Langer, and D. Labudde. ePros - A Bioinformatics Knowledge Base, Toolbox and Database for Characterizing Protein

Function. In S Kozielski, D. Mrozek, P. Kasprowski, B. Malysiak-Mrozek, and D. Kostrzewa, editors, *Proceedings of the IEEE Beyond Databases, Architectures and Structures 2015*. Springer, 2015

S. Pflugbeil, A. Gross, J. Roth, F. Heinke, J. Bruchhaus, J. Edelmann, D. Labudde, J. Dressler, and K. Thiele. Initial Experience in the Application of the PowerquantTM system and the ESSplex SE QS Kit for ancient DNA analysis. In *Conference of the International Society of Forensics and Genetics 2015*, 2015

M. Spranger, F. Heinke, S. Grunert, and D. Labudde. Towards Predictive Policing: Knowledge-based Monitoring of Social Networks. In *The Fifth International Conference on Advances in Information Mining and Management (IMMM 2015)*, 2015

2014

F. Heinke and D. Labudde. Energy Profiling of Protein-Protein Interfaces: Toward the Understanding of biological Significance of near-native Protein complex structures. In *Proceedings of the GETGEOWEB Workshop 2014*, 2014

2013

F. Heinke, M. Langer, and D. Labudde. An Alternative View on the Evolutionary History of Tumour Suppressor Protein Domain BRCT. In *13. Nachwuchswissenschaftlerkonferenz*, 2013

F. Heinke, S. Schildbach, D. Stockmann, and D. Labudde. eProS - An online Toolbox, Knowledge Base and Repository for Protein Energy Profiling. In *Conference on Applied Informatics in Health and Life Sciences*, 2013

2012

F. Heinke and D. Labudde. Predicting functionality of the non-expressed putative human OHCU decarboxylase by means of novel protein energy profile-based methods. In W. Hohnekamp and P. Schindler, editors, *13. Nachwuchswissenschaftlerkonferenz*, 2012

M. Spranger, S. Schildbach, F. Heinke, S. Grunert, and D. Labudde. Semantic Tools for Forensics: A Highly Adaptable Framework. In *IMMM 2012: The Second International Confrence on Advances in Information Mining and Management*, 2012

Posters

2024

T. Bergmann, F. Heinke, A. Thomas, S. Grabherr, and D. Labudde. Modeling

bloodstain aging ex vivo based on spectroscopic data. In *103. Jahrestagungen der Deutschen Gesellschaft für Rechtsmedizin*, 2024

2017

F. Heinke and D. Labudde. The Concepts of Protein Energy Profiling - Deciphering Energy Fingerprints in Protein Structures. In *PTBI Symposium 2017*, 2017

2015

S. Bittrich, F. Heinke, and D. Labudde. eQuant: A novel statistics-based and parameter-free Approach for fast Protein Model Quality Assessment. In *9th CRTD Summer Conference on Regenerative Medicine*, 2015

C. Leberecht, F. Heinke, and D. Labudde. Basic Discrete Concepts for simulating biochemical Pathways using Graph Automata. In *9th CRTD Summer Conference on Regenerative Medicine*, 2015

F. Kaiser, A. Eisold, M. Kaden, F. Heinke, S.. Bittrich, C.. Leberecht, S.. Grunert, T. Villmann, and D. Labudde. Characterizing Protein Functions: Large-scale Screening and Classification of Structural Motifs. In *3DSIG: Structural Bioinformatics and Computational Biophysics*, 2015

2014

S. Bittrich, F. Heinke, S. Oswald, and D. Labudde. Applications of Energy Profiling - Assessing Protein Structures from a different Point of View. In *Saxon Biotechnology Symposium*, 2014

M. Langer, S. Oswald, F. Heinke, and D. Labudde. Identification of protein energy fingerprints that determine fold and function. In *Saxon Biotechnology Symposium*, 2014

F. Heinke and D. Labudde. Energy profiling of Protein-Protein Interfaces. In *Saxon Biotechnology Symposium*, 2014

M. Langer, F. Heinke, M. Garbe, and D. Labudde. A different Perspective on the Evolutionary History of BRCT. In *Saxon Biotechnology Symposium*, 2014

2013

F. Heinke, A. Marquardt, and D. Labudde. Predicting unfolding barriers in alpha-helical membrane proteins using coarse-grained representations of protein structures, dynamics, and single-molecule force spectroscopy. In *7th CRTD Summer Conference on Regenerative Medicine*, 2013

2012

S. Grunert, F. Heinke, and D. Labudde. Topology Separation of discriminative Sequence Motifs in Membrane Proteins with Domains of unknown Functions. In *The German Conference on Bioinformatics 2012*, 2012

F. Heinke, D. Stockmann, S. Schildbach, and D. Labudde. ePros - A Database and Toolbox for large-scale Analysis of energetic Properties that determine Protein Structure and Function. In *The German Conference on Bioinformatics 2012*, 2012

F. Heinke, S. Grunert, M. Spranger, and D. Labudde. Identifying functional synonymous and non-synonymous Mutations by means of coarse-grained energy-weighted Residue-Residue Contact Networks: A Case Study of human HGPRT mutations leading to Lesch-Nyhan disease. In *6th CRTD Summer Conference on Regenerative Medicine*, June 2012

F. Heinke, S. Grunert, and D. Labudde. eGOR - Predicting the total Potential Energy of a Protein's native State from Sequence. In *The Saxon Biotechnology Symposium 2012*, 2012

2011

F. Heinke and R. Brumm. Energieprofil-basierende Analysemethoden von Proteinfamilien. In F. Stolzenburg and F. Ruh, editors, *12. Nachwuchswissenschaftlerkonferenz*, 2011

F. Heinke, A. Tuukkanen, and D. Labudde. Analysis of Membrane Protein Stability in Diabetes insipidus by means of Protein Energy Profiling. In *5th CRTD Summer Conference on Regenerative Medicine*, 2011

A.M. Pflugbeil, F. Heinke, N. Heinig, and D. Labudde. The novel approach eHHM for analyzing membrane proteins in case of HP_0565. In M. Brand, M. Schroeder, R. Seidel, A.A. Robitzki, A. Reichenbacher, and N. Straeter, editors, *Saxon Biotechnology Symposium - Abstracts*, 2011

F. Heinke, S. Schildbach, and D. Labudde. Energy-based Prediction and Comparison of Protein Structures. In M. Brand, M. Schroeder, R. Seidel, A.A. Robitzki, A. Reichenbacher, and N. Straeter, editors, *Saxon Biotechnology Symposium*, 2011

F. Heinke, Tuukkanen A., and D. Labudde. Analysis of membrane protein stability in diabetes insipidus. In M. Brand, M. Schroeder, R. Seidel, A.A. Robitzki, A. Reichenbacher, and N. Straeter, editors, *Saxon Biotechnology Symposium*, 2011

R. Brumm, E. Frenzel, F. Heinke, and D. Labudde. Novel prediction algorithm eGOR - from sequence to stable regions in membrane proteins. In M. Brand, M. Schroeder, R. Seidel, A.A. Robitzki, A. Reichenbacher, and N. Straeter, editors, *Saxon Biotechnology Symposium*, 2011

2010

F. Heinke and D. Labudde. Energy-based Prediction and Comparison of Protein Structure. In D. Schomburg and A. Grote, editors, *Proceedings of the German Conference on Bioinformatics*, 2010