# Martin Hofmann-Apitius

List of Publications by Year
in descending order

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|---|---|---|---|
| 118<br>papers | 2,986<br>citations | 186265<br>28<br>h-index | 223800<br>46<br>g-index |
| 154<br>all docs | 154<br>docs citations | 154<br>times ranked | 4141<br>citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | GuiltyTargets: Prioritization of Novel Therapeutic Targets With Network Representation Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 491-500. | 3.0 | 9 |
| 2 | STonKGs: a sophisticated transformer trained on biomedical text and knowledge graphs. Bioinformatics, 2022, 38, 1648-1656. | 4.1 | 11 |
| 3 | A hybrid approach unveils drug repurposing candidates targeting an Alzheimer pathophysiology mechanism. Patterns, 2022, 3, 100433. | 5.9 | 13 |
| 4 | Deep Learning-based detection of psychiatric attributes from German mental health records. International Journal of Medical Informatics, 2022, 161, 104724. | 3.3 | 4 |
| 5 | On the influence of several factors on pathway enrichment analysis. Briefings in Bioinformatics, 2022, 23, . | 6.5 | 17 |
| 6 | Comparison and aggregation of event sequences across ten cohorts to describe the consensus biomarker evolution in Alzheimer's disease. Alzheimer's Research and Therapy, 2022, 14, 55. | 6.2 | 2 |
| 7 | Integrative data semantics through a model-enabled data stewardship. Bioinformatics, 2022, 38, 3850-3852. | 4.1 | 4 |
| 8 | Elucidating gene expression patterns across multiple biological contexts through a large-scale investigation of transcriptomic datasets. BMC Bioinformatics, 2022, 23, . | 2.6 | 3 |
| 9 | The COVID-19 Ontology. Bioinformatics, 2021, 36, 5703-5705. | 4.1 | 27 |
| 10 | Identifying multimodal signatures underlying the somatic comorbidity of psychosis: the COMMITMENT roadmap. Molecular Psychiatry, 2021, 26, 722-724. | 7.9 | 7 |
| 11 | COVID-19 Knowledge Graph: a computable, multi-modal, cause-and-effect knowledge model of COVID-19 pathophysiology. Bioinformatics, 2021, 37, 1332-1334. | 4.1 | 70 |
| 12 | OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2021, 2021, . | 3.0 | 0 |
| 13 | ANMerge: A Comprehensive and Accessible Alzheimer's Disease Patient-Level Dataset. Journal of Alzheimer's Disease, 2021, 79, 423-431. | 2.6 | 18 |
| 14 | A Systems Biology Approach for Hypothesizing the Effect of Genetic Variants on Neuroimaging Features in Alzheimer's Disease. Journal of Alzheimer's Disease, 2021, 80, 831-840. | 2.6 | 2 |
| 15 | Bridging Scales in Alzheimer's Disease: Biological Framework for Brain Simulation With The Virtual Brain. Frontiers in Neuroinformatics, 2021, 15, 630172. | 2.5 | 20 |
| 16 | Linking COVID-19 and Heme-Driven Pathophysiologies: A Combined Computational–Experimental Approach. Biomolecules, 2021, 11, 644. | 4.0 | 16 |
| 17 | CLEP: a hybrid data- and knowledge-driven framework for generating patient representations. Bioinformatics, 2021, 37, 3311-3318. | 4.1 | 6 |
| 18 | A method for the rational selection of drug repurposing candidates from multimodal knowledge harmonization. Scientific Reports, 2021, 11, 11049. | 3.3 | 12 |

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| 19 | Virtual connectomic datasets in Alzheimer's Disease and aging using whole-brain network dynamics modelling. ENeuro, 2021, 8, ENEURO.0475-20.2021. | 1.9 | 14 |
| 20 | DecoPath: a web application for decoding pathway enrichment analysis. NAR Genomics and Bioinformatics, 2021, 3, lqab087. | 3.2 | 3 |
| 21 | Towards a global investigation of transcriptomic signatures through co-expression networks and pathway knowledge for the identification of disease mechanisms. Nucleic Acids Research, 2021, 49, 7939-7953. | 14.5 | 3 |
| 22 | Using predictive machine learning models for drug response simulation by calibrating patient-specific pathway signatures. Npj Systems Biology and Applications, 2021, 7, 40. | 3.0 | 4 |
| 23 | MultiPaths: a Python framework for analyzing multi-layer biological networks using diffusion algorithms. Bioinformatics, 2021, 37, 137-139. | 4.1 | 3 |
| 24 | Realistic simulation of virtual multi-scale, multi-modal patient trajectories using Bayesian networks and sparse auto-encoders. Scientific Reports, 2020, 10, 10971. | 3.3 | 7 |
| 25 | Differences in cohort study data affect external validation of artificial intelligence models for predictive diagnostics of dementia - lessons for translation into clinical practice. EPMA Journal, 2020, 11, 367-376. | 6.1 | 34 |
| 26 | Data-Driven Modeling of Knowledge Assemblies in Understanding Comorbidity Between Type 2 Diabetes Mellitus and Alzheimer's Disease. Journal of Alzheimer's Disease, 2020, 78, 87-95. | 2.6 | 10 |
| 27 | Clustering of Alzheimer's and Parkinson's disease based on genetic burden of shared molecular mechanisms. Scientific Reports, 2020, 10, 19097. | 3.3 | 11 |
| 28 | PS4DR: a multimodal workflow for identification and prioritization of drugs based on pathway signatures. BMC Bioinformatics, 2020, 21, 231. | 2.6 | 11 |
| 29 | Variational Autoencoder Modular Bayesian Networks for Simulation of Heterogeneous Clinical Study Data. Frontiers in Big Data, 2020, 3, 16. | 2.9 | 12 |
| 30 | Data science in neurodegenerative disease: its capabilities, limitations, and perspectives. Current Opinion in Neurology, 2020, 33, 249-254. | 3.6 | 15 |
| 31 | A Computational Approach for Mapping Heme Biology in the Context of Hemolytic Disorders. Frontiers in Bioengineering and Biotechnology, 2020, 8, 74. | 4.1 | 16 |
| 32 | Drug2ways: Reasoning over causal paths in biological networks for drug discovery. PLoS Computational Biology, 2020, 16, e1008464. | 3.2 | 18 |
| 33 | Quantifying mechanisms in neurodegenerative diseases (NDDs) using candidate mechanism perturbation amplitude (CMPA) algorithm. BMC Bioinformatics, 2019, 20, 494. | 2.6 | 3 |
| 34 | Contribution of syndecans to cellular uptake and fibrillation of α-synuclein and tau. Scientific Reports, 2019, 9, 16543. | 3.3 | 44 |
| 35 | PathMe: merging and exploring mechanistic pathway knowledge. BMC Bioinformatics, 2019, 20, 243. | 2.6 | 42 |
| 36 | Re-curation and rational enrichment of knowledge graphs in Biological Expression Language. Database: the Journal of Biological Databases and Curation, 2019, 2019, . | 3.0 | 20 |

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| 37 | Contribution of syndecans to cellular internalization and fibrillation of amyloid-$\beta$(1–42). Scientific Reports, 2019, 9, 1393. | 3.3 | 33 |
| 38 | The Impact of Pathway Database Choice on Statistical Enrichment Analysis and Predictive Modeling. Frontiers in Genetics, 2019, 10, 1203. | 2.3 | 78 |
| 39 | Challenges of Integrative Disease Modeling in Alzheimer's Disease. Frontiers in Molecular Biosciences, 2019, 6, 158. | 3.5 | 13 |
| 40 | Converting Alzheimer's Disease Map into a Heavyweight Ontology: A Formal Network to Integrate Data. Lecture Notes in Computer Science, 2019, , 207-215. | 1.3 | 4 |
| 41 | Multi-omic approach decodes paradoxes of the triple-negative breast cancer: lessons for predictive, preventive and personalised medicine. Amino Acids, 2018, 50, 383-395. | 2.7 | 34 |
| 42 | BEL Commons: an environment for exploration and analysis of networks encoded in Biological Expression Language. Database: the Journal of Biological Databases and Curation, 2018, 2018, . | 3.0 | 17 |
| 43 | ComPath: an ecosystem for exploring, analyzing, and curating mappings across pathway databases. Npj Systems Biology and Applications, 2018, 4, 3. | 3.0 | 43 |
| 44 | Using Multi-Scale Genetic, Neuroimaging and Clinical Data for Predicting Alzheimer's Disease and Reconstruction of Relevant Biological Mechanisms. Scientific Reports, 2018, 8, 11173. | 3.3 | 59 |
| 45 | A systematic approach for identifying shared mechanisms in epilepsy and its comorbidities. Database: the Journal of Biological Databases and Curation, 2018, 2018, . | 3.0 | 7 |
| 46 | Novel approaches to develop community-built biological network models for potential drug discovery. Expert Opinion on Drug Discovery, 2017, 12, 1-9. | 5.0 | 13 |
| 47 | Knowledge-driven computational modeling in Alzheimer's disease research: Current state and future trends. Alzheimer's and Dementia, 2017, 13, 1292-1302. | 0.8 | 11 |
| 48 | A comprehensive, cell specific microRNA catalogue of human peripheral blood. Nucleic Acids Research, 2017, 45, 9290-9301. | 14.5 | 159 |
| 49 | Big data and data repurposing - using existing data to answer new questions in vascular dementia research. BMC Neurology, 2017, 17, 72. | 1.8 | 24 |
| 50 | Towards a 21st-century roadmap for biomedical research and drug discovery: consensus report and recommendations. Drug Discovery Today, 2017, 22, 327-339. | 6.4 | 64 |
| 51 | Analytical Strategy to Prioritize Alzheimer's Disease Candidate Genes in Gene Regulatory Networks Using Public Expression Data. Journal of Alzheimer's Disease, 2017, 59, 1237-1254. | 2.6 | 23 |
| 52 | Of Mice and Men: Comparative Analysis of Neuro-Inflammatory Mechanisms in Human and Mouse Using Cause-and-Effect Models. Journal of Alzheimer's Disease, 2017, 59, 1045-1055. | 2.6 | 18 |
| 53 | Comorbidity Analysis between Alzheimer's Disease and Type 2 Diabetes Mellitus (T2DM) Based on Shared Pathways and the Role of T2DM Drugs. Journal of Alzheimer's Disease, 2017, 60, 721-731. | 2.6 | 55 |
| 54 | Using Drugs as Molecular Probes: A Computational Chemical Biology Approach in Neurodegenerative Diseases. Journal of Alzheimer's Disease, 2017, 56, 677-686. | 2.6 | 14 |

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| 55 | Neuroimaging Feature Terminology: A Controlled Terminology for the Annotation of Brain Imaging Features. Journal of Alzheimer's Disease, 2017, 59, 1153-1169. | 2.6 | 11 |
| 56 | Multimodal mechanistic signatures for neurodegenerative diseases (NeuroMMSig): a web server for mechanism enrichment. Bioinformatics, 2017, 33, 3679-3681. | 4.1 | 39 |
| 57 | Towards a Pathway Inventory of the Human Brain for Modeling Disease Mechanisms Underlying Neurodegeneration. Journal of Alzheimer's Disease, 2016, 52, 1343-1360. | 2.6 | 14 |
| 58 | NeuroRDF: semantic integration of highly curated data to prioritize biomarker candidates in Alzheimer's disease. Journal of Biomedical Semantics, 2016, 7, 45. | 1.6 | 13 |
| 59 | Reasoning over genetic variance information in cause-and-effect models of neurodegenerative diseases. Briefings in Bioinformatics, 2016, 17, 505-516. | 6.5 | 10 |
| 60 | Construction of biological networks from unstructured information based on a semi-automated curation workflow. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav057. | 3.0 | 33 |
| 61 | Exploring novel mechanistic insights in Alzheimer's disease by assessing reliability of protein interactions. Scientific Reports, 2015, 5, 13634. | 3.3 | 9 |
| 62 | <i>NeuroTransDB</i>: highly curated and structured transcriptomic metadata for neurodegenerative diseases. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav099. | 3.0 | 8 |
| 63 | PDON: Parkinson's disease ontology for representation and modeling of the Parkinson's disease knowledge domain. Theoretical Biology and Medical Modelling, 2015, 12, 20. | 2.1 | 29 |
| 64 | Bioinformatics Mining and Modeling Methods for the Identification of Disease Mechanisms in Neurodegenerative Disorders. International Journal of Molecular Sciences, 2015, 16, 29179-29206. | 4.1 | 47 |
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| 66 | Knowledge Retrieval from PubMed Abstracts and Electronic Medical Records with the Multiple Sclerosis Ontology. PLoS ONE, 2015, 10, e0116718. | 2.5 | 26 |
| 67 | Boosting translational research on Alzheimer's disease in Europe: The Innovative Medicine Initiative AD research platform. Alzheimer's and Dementia, 2015, 11, 1121-1122. | 0.8 | 15 |
| 68 | Towards the taxonomy of human disease. Nature Reviews Drug Discovery, 2015, 14, 75-76. | 46.4 | 46 |
| 69 | Computable cause-and-effect models of healthy and Alzheimer's disease states and their mechanistic differential analysis. Alzheimer's and Dementia, 2015, 11, 1329-1339. | 0.8 | 46 |
| 70 | Systems approach for the selection of micro-RNAs as therapeutic biomarkers of anti-EGFR monoclonal antibody treatment in colorectal cancer. Scientific Reports, 2015, 5, 8013. | 3.3 | 6 |
| 71 | Identification of gene co-expression clusters in liver tissues from multiple porcine populations with high and low backfat androstenone phenotype. BMC Genetics, 2015, 16, 21. | 2.7 | 5 |
| 72 | Is dementia research ready for big data approaches?. BMC Medicine, 2015, 13, 145. | 5.5 | 11 |

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| 73 | Linking hypothetical knowledge patterns to disease molecular signatures for biomarker discovery in Alzheimer's disease. Genome Medicine, 2014, 6, 97. | 8.2 | 6 |
| 74 | Text mining for systems biology. Drug Discovery Today, 2014, 19, 140-144. | 6.4 | 31 |
| 75 | CSEO â€" the Cigarette Smoke Exposure Ontology. Journal of Biomedical Semantics, 2014, 5, 31. | 1.6 | 7 |
| 76 | A new optimization phase for scientific workflow management systems. Future Generation Computer Systems, 2014, 36, 352-362. | 7.5 | 16 |
| 77 | ADO: A disease ontology representing the domain knowledge specific to Alzheimer's disease. Alzheimer's and Dementia, 2014, 10, 238-246. | 0.8 | 77 |
| 78 | Linking hypothetical knowledge patterns to disease molecular signatures for biomarker discovery in Alzheimer's disease. Genome Medicine, 2014, 6, 97. | 8.2 | 6 |
| 79 | Detecting miRNA Mentions and Relations in Biomedical Literature. F1000Research, 2014, 3, 205. | 1.6 | 19 |
| 80 | Detecting miRNA Mentions and Relations in Biomedical Literature. F1000Research, 2014, 3, 205. | 1.6 | 22 |
| 81 | Pathway Based Analysis of Genes and Interactions Influencing Porcine Testis Samples from Boars with Divergent Androstenone Content in Back Fat. PLoS ONE, 2014, 9, e91077. | 2.5 | 9 |
| 82 | Challenges in mining the literature for chemical information. RSC Advances, 2013, 3, 16194. | 3.6 | 20 |
| 83 | A network model of genomic hormone interactions underlying dementia and its translational validation through serendipitous off-target effect. Journal of Translational Medicine, 2013, 11, 177. | 4.4 | 2 |
| 84 | HuPSON: the human physiology simulation ontology. Journal of Biomedical Semantics, 2013, 4, 35. | 1.6 | 7 |
| 85 | Challenges and opportunities for oncology biomarker discovery. Drug Discovery Today, 2013, 18, 614-624. | 6.4 | 44 |
| 86 | SVM Based Descriptor Selection and Classification of Neurodegenerative Disease Drugs for Pharmacological Modeling. Molecular Informatics, 2013, 32, 241-249. | 2.5 | 4 |
| 87 | â€˜HypothesisFinder:â€™ A Strategy for the Detection of Speculative Statements in Scientific Text. PLoS Computational Biology, 2013, 9, e1003117. | 3.2 | 37 |
| 88 | From integrative disease modeling to predictive, preventive, personalized and participatory (P4) medicine. EPMA Journal, 2013, 4, 23. | 6.1 | 46 |
| 89 | Biomarker-guided translation of brain imaging into disease pathway models. Scientific Reports, 2013, 3, 3375. | 3.3 | 6 |
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| 91 | Development of a benchmark corpus to support the automatic extraction of drug-related adverse effects from medical case reports. Journal of Biomedical Informatics, 2012, 45, 885-892. | 4.3 | 251 |
| 92 | Mining biomarker information in biomedical literature. BMC Medical Informatics and Decision Making, 2012, 12, 148. | 3.0 | 36 |
| 93 | Text mining in livestock animal science: Introducing the potential of text mining to animal sciences 1. Journal of Animal Science, 2012, 90, 3666-3676. | 0.5 | 5 |
| 94 | Challenges in the association of human single nucleotide polymorphism mentions with unique database identifiers. BMC Bioinformatics, 2011, 12, S4. | 2.6 | 33 |
| 95 | A UNICORE Plugin for HPC-Enabled Scientific Workflows in Taverna 2.2. , 2011, , . | | 6 |
| 96 | PLIO: an ontology for formal description of protein–ligand interactions. Bioinformatics, 2011, 27, 1684-1690. | 4.1 | 6 |
| 97 | An Improved Weighted–Residue Profile Based Method of Using Protein–Ligand Interaction Information in Increasing Hits Selection from Virtual Screening: A Study on Virtual Screening of Human GPCR A2A Receptor Antagonists. Molecular Informatics, 2010, 29, 781-791. | 2.5 | 2 |
| 98 | In Silico Drug Discovery Approaches on Grid Computing Infrastructures. Current Clinical Pharmacology, 2010, 5, 37-46. | 0.6 | 12 |
| 99 | DockFlow: Achieving interoperability of protein docking tools across heterogeneous Grid middleware. International Journal of Ad Hoc and Ubiquitous Computing, 2010, 6, 235. | 0.5 | 3 |
| 100 | Identification of histone modifications in biomedical text for supporting epigenomic research. BMC Bioinformatics, 2009, 10, S28. | 2.6 | 7 |
| 101 | WISDOM-II: Screening against multiple targets implicated in malaria using computational grid infrastructures. Malaria Journal, 2009, 8, 88. | 2.3 | 29 |
| 102 | Concept-Based Semi-Automatic Classification of Drugs. Journal of Chemical Information and Modeling, 2009, 49, 1986-1992. | 5.4 | 21 |
| 103 | A robust framework for rapid deployment of a virtual screening laboratory. Studies in Health Technology and Informatics, 2009, 147, 212-21. | 0.3 | 2 |
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| 105 | Grid-Added Value to Address Malaria. IEEE Transactions on Information Technology in Biomedicine, 2008, 12, 173-181. | 3.2 | 8 |
| 106 | OSIRISv1.2: A named entity recognition system for sequence variants of genes in biomedical literature. BMC Bioinformatics, 2008, 9, 84. | 2.6 | 31 |
| 107 | Detection of IUPAC and IUPAC-like chemical names. Bioinformatics, 2008, 24, i268-i276. | 4.1 | 102 |
| 108 | Knowledge environments representing molecular entities for the virtual physiological human. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2008, 366, 3091-3110. | 3.4 | 19 |

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| 109 | @neuLink: a service-oriented application for biomedical knowledge discovery. Studies in Health Technology and Informatics, 2008, 138, 165-72. | 0.3 | 11 |
| 110 | Reconstruction of Chemical Molecules from Images. , 2007, 2007, 4609-12. | | 15 |
| 111 | Identification of new drug classification terms in textual resources. Bioinformatics, 2007, 23, i264-i272. | 4.1 | 33 |
| 112 | IDENTIFYING GENE-SPECIFIC VARIATIONS IN BIOMEDICAL TEXT. Journal of Bioinformatics and Computational Biology, 2007, 05, 1277-1296. | 0.8 | 15 |
| 113 | Alternative to Consensus ScoringA New Approach Toward the Qualitative Combination of Docking Algorithms. Journal of Chemical Information and Modeling, 2007, 47, 1036-1044. | 5.4 | 28 |
| 114 | Virtual screening on large scale grids. Parallel Computing, 2007, 33, 289-301. | 2.1 | 27 |
| 115 | Design of New Plasmepsin Inhibitors:â€‰ A Virtual High Throughput Screening Approach on the EGEE Grid. Journal of Chemical Information and Modeling, 2007, 47, 1818-1828. | 5.4 | 46 |
| 116 | Integration and mining of malaria molecular, functional and pharmacological data: how far are we from a chemogenomic knowledge space?. Malaria Journal, 2006, 5, 110. | 2.3 | 18 |
| 117 | Hyaluronan-oligosaccharide-induced transcription of metalloproteases. Journal of Cell Science, 2004, 117, 359-367. | 2.0 | 149 |
| 118 | Detecting miRNA Mentions and Relations in Biomedical Literature. F1000Research, 0, 3, 205. | 1.6 | 17 |