

# Holger Fröhlich

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4946584/publications.pdf>

Version: 2024-02-01

134  
papers

4,642  
citations

117625

34  
h-index

155660

55  
g-index

146  
all docs

146  
docs citations

146  
times ranked

7460  
citing authors

#	ARTICLE	IF	CITATIONS
1	From hype to reality: data science enabling personalized medicine. BMC Medicine, 2018, 16, 150.	5.5	278
2	Modeling ERBB receptor-regulated G1/S transition to find novel targets for de novo trastuzumab resistance. BMC Systems Biology, 2009, 3, 1.	3.0	242
3	miR-155 regulates differentiation of brown and beige adipocytes via a bistable circuit. Nature Communications, 2013, 4, 1769.	12.8	225
4	Feature selection for support vector machines by means of genetic algorithm. , 0, , .		190
5	GOSim “an R-package for computation of information theoretic GO similarities between terms and gene products. BMC Bioinformatics, 2007, 8, 166.	2.6	168
6	Exosomal microRNA miR-92a concentration in serum reflects human brown fat activity. Nature Communications, 2016, 7, 11420.	12.8	137
7	Vibration-based Terrain Classification Using Support Vector Machines. , 2006, , .		101
8	Optimal assignment kernels for attributed molecular graphs. , 2005, , .		97
9	Integration of pathway knowledge into a reweighted recursive feature elimination approach for risk stratification of cancer patients. Bioinformatics, 2010, 26, 2136-2144.	4.1	94
10	Metabonomics in cancer diagnosis: mass spectrometry-based profiling of urinary nucleosides from breast cancer patients. Biomarkers, 2008, 13, 435-449.	1.9	81
11	Lâ€dopa increases <b> $\pm$ </b>â€synuclein DNA methylation in Parkinson's disease patients <i>in vivo</i> and <i>in vitro</i>. Movement Disorders, 2015, 30, 1794-1801.	3.9	81
12	The Impact of Pathway Database Choice on Statistical Enrichment Analysis and Predictive Modeling. Frontiers in Genetics, 2019, 10, 1203.	2.3	78
13	Crowdsourced estimation of cognitive decline and resilience in Alzheimer's disease. Alzheimer's and Dementia, 2016, 12, 645-653.	0.8	72
14	Caution, “œnormalâ€•BMI: health risks associated with potentially masked individual underweightâ€”EPMA Position Paper 2021. EPMA Journal, 2021, 12, 243-264.	6.1	70
15	Network and Data Integration for Biomarker Signature Discovery via Network Smoothed T-Statistics. PLoS ONE, 2013, 8, e73074.	2.5	63
16	Different MicroRNA Profiles in Chronic Epilepsy Versus Acute Seizure Mouse Models. Journal of Molecular Neuroscience, 2015, 55, 466-479.	2.3	63
17	Characterizing the genetic basis of innate immune response in TLR4-activated human monocytes. Nature Communications, 2014, 5, 5236.	12.8	61
18	DNA methylation signature in peripheral blood reveals distinct characteristics of human X chromosome numerical aberrations. Clinical Epigenetics, 2015, 7, 76.	4.1	59

#	ARTICLE	IF	CITATIONS
19	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
20	Feature Selection for Descriptor Based Classification Models. 2. Human Intestinal Absorption (HIA). Journal of Chemical Information and Computer Sciences, 2004, 44, 931-939.	2.8	56
21	Kernel Functions for Attributed Molecular Graphs – A New Similarity-Based Approach to ADME Prediction in Classification and Regression. QSAR and Combinatorial Science, 2006, 25, 317-326.	1.4	55
22	Premenopausal breast cancer: potential clinical utility of a multi-omics based machine learning approach for patient stratification. EPMA Journal, 2018, 9, 175-186.	6.1	54
23	Genome-wide CNV analysis in 221 unrelated patients and targeted high-throughput sequencing reveal novel causative candidate genes for colorectal adenomatous polyposis. International Journal of Cancer, 2015, 136, E578-89.	5.1	52
24	The EMT transcription factor Zeb2 controls adult murine hematopoietic differentiation by regulating cytokine signaling. Blood, 2017, 129, 460-472.	1.4	52
25	Susceptibility variants on chromosome 7p21.1 suggest HDAC9 as a new candidate gene for male-pattern baldness. British Journal of Dermatology, 2011, 165, 1293-1302.	1.5	50
26	Epigenome-wide DNA methylation analysis in siblings and monozygotic twins discordant for sporadic Parkinson's disease revealed different epigenetic patterns in peripheral blood mononuclear cells. Neurogenetics, 2017, 18, 7-22.	1.4	47
27	Towards realizing the vision of precision medicine: AI based prediction of clinical drug response. Brain, 2021, 144, 1738-1750.	7.6	47
28	Feature Selection for Descriptor Based Classification Models. 1. Theory and GA-SEC Algorithm. Journal of Chemical Information and Computer Sciences, 2004, 44, 921-930.	2.8	46
29	Efficient parameter selection for support vector machines in classification and regression via model-based global optimization. , 0, , .		45
30	Prognostic gene signatures for patient stratification in breast cancer - accuracy, stability and interpretability of gene selection approaches using prior knowledge on protein-protein interactions. BMC Bioinformatics, 2012, 13, 69.	2.6	45
31	Estimating large-scale signaling networks through nested effect models with intervention effects from microarray data. Bioinformatics, 2008, 24, 2650-2656.	4.1	44
32	Inter-locus as well as intra-locus heterogeneity in LINE-1 promoter methylation in common human cancers suggests selective demethylation pressure at specific CpGs. Clinical Epigenetics, 2015, 7, 17.	4.1	43
33	Bioinformatical evaluation of modified nucleosides as biomedical markers in diagnosis of breast cancer. Analytica Chimica Acta, 2008, 618, 29-34.	5.4	41
34	Hsp90 inhibition differentially destabilises MAP kinase and TGF-beta signalling components in cancer cells revealed by kinase-targeted chemoproteomics. BMC Cancer, 2012, 12, 38.	2.6	41
35	Benefits of a factorial design focusing on inclusion of female and male animals in one experiment. Journal of Molecular Medicine, 2019, 97, 871-877.	3.9	40
36	Large scale statistical inference of signaling pathways from RNAi and microarray data. BMC Bioinformatics, 2007, 8, 386.	2.6	39

#	ARTICLE	IF	CITATIONS
37	Comprehensive analysis of tumor necrosis factor receptor TNFRSF9 (4-1BB) DNA methylation with regard to molecular and clinicopathological features, immune infiltrates, and response prediction to immunotherapy in melanoma. EBioMedicine, 2020, 52, 102647.	6.1	38
38	PathME: pathway based multi-modal sparse autoencoders for clustering of patient-level multi-omics data. BMC Bioinformatics, 2020, 21, 146.	2.6	38
39	Towards Optimal Descriptor Subset Selection with Support Vector Machines in Classification and Regression. QSAR and Combinatorial Science, 2004, 23, 311-318.	1.4	36
40	Stimulation of MMP-1 and CCL2 by NAMPT in PDL Cells. Mediators of Inflammation, 2013, 2013, 1-12.	3.0	36
41	FEATURE SELECTION FOR SUPPORT VECTOR MACHINES USING GENETIC ALGORITHMS. International Journal on Artificial Intelligence Tools, 2004, 13, 791-800.	1.0	35
42	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
43	Gas source declaration with a mobile robot. , 2004, , .		33
44	TGF- $\beta$ 2 stimulation in human and murine cells reveals commonly affected biological processes and pathways at transcription level. BMC Systems Biology, 2014, 8, 55.	3.0	33
45	Genetic and epigenetic insights into uveal melanoma. Clinical Genetics, 2018, 93, 952-961.	2.0	33
46	Towards clinically more relevant dissection of patient heterogeneity via survival-based Bayesian clustering. Bioinformatics, 2017, 33, 3558-3566.	4.1	32
47	Changes in serum miRNAs following generalized convulsive seizures in human mesial temporal lobe epilepsy. Biochemical and Biophysical Research Communications, 2016, 481, 13-18.	2.1	31
48	Deep learning for clustering of multivariate clinical patient trajectories with missing values. GigaScience, 2019, 8, .	6.4	31
49	pathClass: an R-package for integration of pathway knowledge into support vector machines for biomarker discovery. Bioinformatics, 2011, 27, 1442-1443.	4.1	30
50	Biomarker Gene Signature Discovery Integrating Network Knowledge. Biology, 2012, 1, 5-17.	2.8	30
51	TGF-beta1 Does Not Induce Senescence of Multipotent Mesenchymal Stromal Cells and Has Similar Effects in Early and Late Passages. PLoS ONE, 2013, 8, e77656.	2.5	30
52	Key Players of Cisplatin Resistance: Towards a Systems Pharmacology Approach. International Journal of Molecular Sciences, 2018, 19, 767.	4.1	29
53	Multicenter Alzheimer's and Parkinson's disease immune biomarker verification study. Alzheimer's and Dementia, 2020, 16, 292-304.	0.8	29
54	Dynamic deterministic effects propagation networks: learning signalling pathways from longitudinal protein array data. Bioinformatics, 2010, 26, i596-i602.	4.1	28

#	ARTICLE	IF	CITATIONS
55	MCMC Techniques for Parameter Estimation of ODE Based Models in Systems Biology. <i>Frontiers in Applied Mathematics and Statistics</i> , 2019, 5, .	1.3	28
56	Remote monitoring technologies in Alzheimer's disease: design of the RADAR-AD study. <i>Alzheimer's Research and Therapy</i> , 2021, 13, 89.	6.2	28
57	Analyzing gene perturbation screens with nested effects models in R and bioconductor. <i>Bioinformatics</i> , 2008, 24, 2549-2550.	4.1	27
58	Fast and efficient dynamic nested effects models. <i>Bioinformatics</i> , 2011, 27, 238-244.	4.1	26
59	Joint Bayesian inference of condition-specific miRNA and transcription factor activities from combined gene and microRNA expression data. <i>Bioinformatics</i> , 2012, 28, 1714-1720.	4.1	25
60	Steiner tree methods for optimal sub-network identification: an empirical study. <i>BMC Bioinformatics</i> , 2013, 14, 144.	2.6	25
61	Optimal multiparametric set-up modelled for best survival outcomes in palliative treatment of liver malignancies: unsupervised machine learning and 3ÂPM recommendations. <i>EPMA Journal</i> , 2020, 11, 505-515.	6.1	25
62	Deterministic Effects Propagation Networks for reconstructing protein signaling networks from multiple interventions. <i>BMC Bioinformatics</i> , 2009, 10, 322.	2.6	24
63	Predicting Potent Compounds via Model-Based Global Optimization. <i>Journal of Chemical Information and Modeling</i> , 2013, 53, 553-559.	5.4	24
64	Evaluating the Alzheimer's disease data landscape. <i>Alzheimer's and Dementia: Translational Research and Clinical Interventions</i> , 2020, 6, e12102.	3.7	24
65	Nested effects models for learning signaling networks from perturbation data. <i>Biometrical Journal</i> , 2009, 51, 304-323.	1.0	23
66	netClass: an R-package for network based, integrative biomarker signature discovery. <i>Bioinformatics</i> , 2014, 30, 1325-1326.	4.1	22
67	Including network knowledge into Cox regression models for biomarker signature discovery. <i>Biometrical Journal</i> , 2014, 56, 287-306.	1.0	22
68	Utilising the EGFR interactome to identify mechanisms of drug resistance in non-small cell lung cancer – Proof of concept towards a systems pharmacology approach. <i>European Journal of Pharmaceutical Sciences</i> , 2016, 94, 20-32.	4.0	22
69	A Machine Learning Approach to Automated Gait Analysis for the Noldus Catwalk System. <i>IEEE Transactions on Biomedical Engineering</i> , 2018, 65, 1133-1139.	4.2	22
70	Unsupervised automated high throughput phenotyping of RNAi time-lapse movies. <i>BMC Bioinformatics</i> , 2013, 14, 292.	2.6	21
71	Network Based Consensus Gene Signatures for Biomarker Discovery in Breast Cancer. <i>PLoS ONE</i> , 2011, 6, e25364.	2.5	20
72	Learning (from) the errors of a systems biology model. <i>Scientific Reports</i> , 2016, 6, 20772.	3.3	20

#	ARTICLE	IF	CITATIONS
73	CADA: phenotype-driven gene prioritization based on a case-enriched knowledge graph. NAR Genomics and Bioinformatics, 2021, 3, lqab078.	3.2	20
74	Functional grouping of genes using spectral clustering and gene ontology. , 0, , .		19
75	Learning gene network structure from time laps cell imaging in RNAi Knock downs. Bioinformatics, 2013, 29, 1534-1540.	4.1	19
76	Voice perturbations under the stress overload in young individuals: phenotyping and suboptimal health as predictors for cascading pathologies. EPMA Journal, 2020, 11, 517-527.	6.1	19
77	Unraveling the heterogeneity in Alzheimer's disease progression across multiple cohorts and the implications for data-driven disease modeling. Alzheimer's and Dementia, 2022, 18, 251-261.	0.8	18
78	Integrating Heterogeneous omics Data via Statistical Inference and Learning Techniques. Genomics and Computational Biology, 2016, 2, 32.	0.7	18
79	Leveraging the Potential of Digital Technology for Better Individualized Treatment of Parkinson's Disease. Frontiers in Neurology, 2022, 13, 788427.	2.4	18
80	Predicting pathway membership via domain signatures. Bioinformatics, 2008, 24, 2137-2142.	4.1	17
81	Increasing the sensitivity of reverse phase protein arrays by antibody-mediated signal amplification. Proteome Science, 2010, 8, 36.	1.7	17
82	NEMix: Single-cell Nested Effects Models for Probabilistic Pathway Stimulation. PLoS Computational Biology, 2015, 11, e1004078.	3.2	17
83	Single nucleotide polymorphisms in the angiogenic and lymphangiogenic pathways are associated with lymphedema caused by Wuchereria bancrofti. Human Genomics, 2017, 11, 26.	2.9	17
84	Automated classification of the behavior of rats in the forced swimming test with support vector machines. Neural Networks, 2008, 21, 92-101.	5.9	16
85	MC EMINEM Maps the Interaction Landscape of the Mediator. PLoS Computational Biology, 2012, 8, e1002568.	3.2	16
86	A Geometric Method for Model Reduction of Biochemical Networks with Polynomial Rate Functions. Bulletin of Mathematical Biology, 2015, 77, 2180-2211.	1.9	16
87	A Bayesian approach to estimating hidden variables as well as missing and wrong molecular interactions in ordinary differential equation-based mathematical models. Journal of the Royal Society Interface, 2017, 14, 20170332.	3.4	16
88	Data and Graph Mining in Chemical Space for ADME and Activity Data Sets. QSAR and Combinatorial Science, 2006, 25, 205-220.	1.4	15
89	Evidence for contribution of epigenetic mechanisms in the pathogenesis of systemic mast cell activation disease. Immunogenetics, 2014, 66, 287-297.	2.4	15
90	Dynamic Bayesian Network Modeling of the Interplay between EGFR and Hedgehog Signaling. PLoS ONE, 2015, 10, e0142646.	2.5	15

#	ARTICLE	IF	CITATIONS
91	biRte: Bayesian inference of context-specific regulator activities and transcriptional networks. <i>Bioinformatics</i> , 2015, 31, 3290-3298.	4.1	15
92	Kit transduced signals counteract erythroid maturation by MAPK-dependent modulation of erythropoietin signaling and apoptosis induction in mouse fetal liver. <i>Cell Death and Differentiation</i> , 2015, 22, 790-800.	11.2	15
93	Epigenome-Wide Analysis of DNA Methylation in Parkinson's Disease Cortex. <i>Life</i> , 2022, 12, 502.	2.4	14
94	Inferring modulators of genetic interactions with epistatic nested effects models. <i>PLoS Computational Biology</i> , 2017, 13, e1005496.	3.2	13
95	Activation of AMP-activated protein kinase sensitizes lung cancer cells and H1299 xenografts to erlotinib. <i>Lung Cancer</i> , 2014, 86, 151-157.	2.0	12
96	Patients' perception of Parkinson's disease-associated pain following initiation of rotigotine: a multicenter non-interventional study. <i>Postgraduate Medicine</i> , 2017, 129, 46-54.	2.0	12
97	Molecular signatures in IASLC/ATS/ERS classified growth patterns of lung adenocarcinoma. <i>PLoS ONE</i> , 2018, 13, e0206132.	2.5	12
98	Variational Autoencoder Modular Bayesian Networks for Simulation of Heterogeneous Clinical Study Data. <i>Frontiers in Big Data</i> , 2020, 3, 16.	2.9	12
99	A method for the rational selection of drug repurposing candidates from multimodal knowledge harmonization. <i>Scientific Reports</i> , 2021, 11, 11049.	3.3	12
100	Skewed X-chromosome inactivation and XIST locus methylation levels do not contribute to the lower prevalence of Parkinson's disease in females. <i>Neurobiology of Aging</i> , 2017, 57, 248.e1-248.e5.	3.1	11
101	Drug repositioning of antiretroviral ritonavir for combinatorial therapy in glioblastoma. <i>European Journal of Cancer</i> , 2020, 140, 130-139.	2.8	11
102	Clustering of Alzheimer's and Parkinson's disease based on genetic burden of shared molecular mechanisms. <i>Scientific Reports</i> , 2020, 10, 19097.	3.3	11
103	An Explainable Multimodal Neural Network Architecture for Predicting Epilepsy Comorbidities Based on Administrative Claims Data. <i>Frontiers in Artificial Intelligence</i> , 2021, 4, 610197.	3.4	11
104	Boosting Probabilistic Graphical Model Inference by Incorporating Prior Knowledge from Multiple Sources. <i>PLoS ONE</i> , 2013, 8, e67410.	2.5	10
105	Linking metabolic network features to phenotypes using sparse group lasso. <i>Bioinformatics</i> , 2017, 33, 3445-3453.	4.1	10
106	Classic bladder exstrophy and adenocarcinoma of the bladder: Methylome analysis provide no evidence for underlying disease-mechanisms of this association. <i>Cancer Genetics</i> , 2019, 235-236, 18-20.	0.4	10
107	Feature subset selection for support vector machines by incremental regularized risk minimization. , 0, , .		9
108	GuiltyTargets: Prioritization of Novel Therapeutic Targets With Network Representation Learning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 491-500.	3.0	9

#	ARTICLE	IF	CITATIONS
109	Cross-talk between AMPK and EGFR dependent Signaling in Non-Small Cell Lung Cancer. Scientific Reports, 2016, 6, 27514.	3.3	8
110	A Bayesian Network View on Nested Effects Models. Eurasip Journal on Bioinformatics and Systems Biology, 2009, 2009, 195272.	1.4	8
111	Assignment kernels for chemical compounds. , 0, , .		7
112	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
113	Analysis of Reaction Network Systems Using Tropical Geometry. Lecture Notes in Computer Science, 2015, , 424-439.	1.3	7
114	Towards a Central Role of ISL1 in the Bladder Exstrophyâ€“Epispadias Complex (BEEC): Computational Characterization of Genetic Variants and Structural Modelling. Genes, 2018, 9, 609.	2.4	6
115	A Bayesian Network View on Nested Effects Models. Eurasip Journal on Bioinformatics and Systems Biology, 2009, 2009, 195272.	1.4	6
116	Machine Learning Based Prediction of COVID-19 Mortality Suggests Repositioning of Anticancer Drug for Treating Severe Cases. Artificial Intelligence in the Life Sciences, 2021, 1, 100020.	2.2	6
117	Expectation propagation for large scale Bayesian inference of non-linear molecular networks from perturbation data. PLoS ONE, 2017, 12, e0171240.	2.5	5
118	INFERRING GENE REGULATORY NETWORKS BY MACHINE LEARNING METHODS. , 2007, , .		4
119	A Simple 3-Parameter Model for Cancer Incidences. Scientific Reports, 2018, 8, 3388.	3.3	4
120	Comprehensive Profiling of Blood Coagulation and Fibrinolysis Marker Reveals Elevated Plasmin-Antiplasmin Complexes in Parkinsonâ€™s Disease. Biology, 2021, 10, 716.	2.8	4
121	Deep Learning-based detection of psychiatric attributes from German mental health records. International Journal of Medical Informatics, 2022, 161, 104724.	3.3	4
122	SEEDS: data driven inference of structural model errors and unknown inputs for dynamic systems biology. Bioinformatics, 2021, 37, 1330-1331.	4.1	2
123	A systems pharmacology approach to improve drug therapy in NSCLC: Establishing a CESAR network. International Journal of Clinical Pharmacology and Therapeutics, 2014, 52, 89-91.	0.6	2
124	Immune System Modeling and Related Pathologies. Computational and Mathematical Methods in Medicine, 2012, 2012, 1-2.	1.3	1
125	CD4+ T cell counts reflect the immunosuppressive state of CD4 helper cells in patients after allogeneic stem cell transplantation. Annals of Hematology, 2015, 94, 129-137.	1.8	1
126	Optimal Assignment Kernels for ADME in Silico Prediction. , 2011, , 16-34.		1



#	ARTICLE	IF	CITATIONS
127	NSCLC cells adapted to EGFR inhibition accumulate EGFR interacting proteins and down-regulate microRNA related to epithelial-mesenchymal transition. International Journal of Clinical Pharmacology and Therapeutics, 2014, 52, 92-94.	0.6	1
128	Which features trigger action potentials in cortical neurons in vivo?. , 0, , .		0
129	Modelling and mathematical analysis of the M <sub>2</sub> receptor-dependent joint signalling and secondary messenger network in CHO cells. Mathematical Medicine and Biology, 2018, 35, 279-297.	1.2	0
130	GENE REGULATORY NETWORK INFERENCE VIA REGRESSION BASED TOPOLOGICAL REFINEMENT. , 2007, , .		0
131	Molecular Characterization of F8 Secreting Cell. Blood, 2015, 126, 4671-4671.	1.4	0
132	Knowledge-based approach to identify key determinants of cisplatin sensitivity. International Journal of Clinical Pharmacology and Therapeutics, 2017, 55, 686-689.	0.6	0
133	Assessing the landscape of Alzheimer's disease cohort data. Alzheimer's and Dementia, 2020, 16, e043052.	0.8	0
134	Towards Realizing the Vision of Precision Medicine: AI Based Prediction of Clinical Drug Response. SSRN Electronic Journal, 0, , .	0.4	0