Holger Fröhlich

List of Publications by Year
in descending order

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	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	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
3	Leveraging the Potential of Digital Technology for Better Individualized Treatment of Parkinson's Disease. Frontiers in Neurology, 2022, 13, 788427.	2.4	18
4	Epigenome-Wide Analysis of DNA Methylation in Parkinson's Disease Cortex. Life, 2022, 12, 502.	2.4	14
5	Deep Learning-based detection of psychiatric attributes from German mental health records. International Journal of Medical Informatics, 2022, 161, 104724.	3.3	4
6	SEEDS: data driven inference of structural model errors and unknown inputs for dynamic systems biology. Bioinformatics, 2021, 37, 1330-1331.	4.1	2
7	Towards realizing the vision of precision medicine: AI based prediction of clinical drug response. Brain, 2021, 144, 1738-1750.	7.6	47
8	Remote monitoring technologies in Alzheimer's disease: design of the RADAR-AD study. Alzheimer's Research and Therapy, 2021, 13, 89.	6.2	28
9	A method for the rational selection of drug repurposing candidates from multimodal knowledge harmonization. Scientific Reports, 2021, 11, 11049.	3.3	12
10	An Explainable Multimodal Neural Network Architecture for Predicting Epilepsy Comorbidities Based on Administrative Claims Data. Frontiers in Artificial Intelligence, 2021, 4, 610197.	3.4	11
11	CADA: phenotype-driven gene prioritization based on a case-enriched knowledge graph. NAR Genomics and Bioinformatics, 2021, 3, lqab078.	3.2	20
12	Comprehensive Profiling of Blood Coagulation and Fibrinolysis Marker Reveals Elevated Plasmin-Antiplasmin Complexes in Parkinson's Disease. Biology, 2021, 10, 716.	2.8	4
13	Caution, "normal" BMI: health risks associated with potentially masked individual underweight—EPMA Position Paper 2021. EPMA Journal, 2021, 12, 243-264.	6.1	70
14	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
15	Multicenter Alzheimer's and Parkinson's disease immune biomarker verification study. Alzheimer's and Dementia, 2020, 16, 292-304.	0.8	29
16	Drug repositioning of antiretroviral ritonavir for combinatorial therapy in glioblastoma. European Journal of Cancer, 2020, 140, 130-139.	2.8	11
17	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
18	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

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19	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
20	Optimal multiparametric set-up modelled for best survival outcomes in palliative treatment of liver malignancies: unsupervised machine learning and 3ÂPM recommendations. EPMA Journal, 2020, 11, 505-515.	6.1	25
21	Clustering of Alzheimerâ€™s and Parkinsonâ€™s disease based on genetic burden of shared molecular mechanisms. Scientific Reports, 2020, 10, 19097.	3.3	11
22	Variational Autoencoder Modular Bayesian Networks for Simulation of Heterogeneous Clinical Study Data. Frontiers in Big Data, 2020, 3, 16.	2.9	12
23	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
24	PathME: pathway based multi-modal sparse autoencoders for clustering of patient-level multi-omics data. BMC Bioinformatics, 2020, 21, 146.	2.6	38
25	Evaluating the Alzheimer's disease data landscape. Alzheimer's and Dementia: Translational Research and Clinical Interventions, 2020, 6, e12102.	3.7	24
26	Assessing the landscape of Alzheimerâ€™s disease cohort data. Alzheimer's and Dementia, 2020, 16, e043052.	0.8	0
27	Classic bladder exstrophy and adenocarcinoma of the bladder: Methylome analysis provide no evidence for underlying disease-mechanisms of this association. Cancer Genetics, 2019, 235-236, 18-20.	0.4	10
28	MCMC Techniques for Parameter Estimation of ODE Based Models in Systems Biology. Frontiers in Applied Mathematics and Statistics, 2019, 5, .	1.3	28
29	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
30	Deep learning for clustering of multivariate clinical patient trajectories with missing values. GigaScience, 2019, 8, .	6.4	31
31	The Impact of Pathway Database Choice on Statistical Enrichment Analysis and Predictive Modeling. Frontiers in Genetics, 2019, 10, 1203.	2.3	78
32	A Machine Learning Approach to Automated Gait Analysis for the Noldus Catwalk System. IEEE Transactions on Biomedical Engineering, 2018, 65, 1133-1139.	4.2	22
33	A Simple 3-Parameter Model for Cancer Incidences. Scientific Reports, 2018, 8, 3388.	3.3	4
34	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
35	Genetic and epigenetic insights into uveal melanoma. Clinical Genetics, 2018, 93, 952-961.	2.0	33
36	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

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37	Molecular signatures in IASLC/ATS/ERS classified growth patterns of lung adenocarcinoma. PLoS ONE, 2018, 13, e0206132.	2.5	12
38	Modelling and mathematical analysis of the M_{2} receptor-dependent joint signalling and secondary messenger network in CHO cells. Mathematical Medicine and Biology, 2018, 35, 279-297.	1.2	0
39	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
40	Key Players of Cisplatin Resistance: Towards a Systems Pharmacology Approach. International Journal of Molecular Sciences, 2018, 19, 767.	4.1	29
41	From hype to reality: data science enabling personalized medicine. BMC Medicine, 2018, 16, 150.	5.5	278
42	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
43	Skewed X-chromosome inactivation and XIST locus methylation levels do not contribute to the lower prevalence of Parkinson's disease in females. Neurobiology of Aging, 2017, 57, 248.e1-248.e5.	3.1	11
44	The EMT transcription factor Zeb2 controls adult murine hematopoietic differentiation by regulating cytokine signaling. Blood, 2017, 129, 460-472.	1.4	52
45	Towards clinically more relevant dissection of patient heterogeneity via survival-based Bayesian clustering. Bioinformatics, 2017, 33, 3558-3566.	4.1	32
46	Linking metabolic network features to phenotypes using sparse group lasso. Bioinformatics, 2017, 33, 3445-3453.	4.1	10
47	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
48	Patients' perception of Parkinson's disease-associated pain following initiation of rotigotine: a multicenter non-interventional study. Postgraduate Medicine, 2017, 129, 46-54.	2.0	12
49	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
50	Expectation propagation for large scale Bayesian inference of non-linear molecular networks from perturbation data. PLoS ONE, 2017, 12, e0171240.	2.5	5
51	Inferring modulators of genetic interactions with epistatic nested effects models. PLoS Computational Biology, 2017, 13, e1005496.	3.2	13
52	Knowledge-based approach to identify key determinants of cisplatin sensitivity. International Journal of Clinical Pharmacology and Therapeutics, 2017, 55, 686-689.	0.6	0
53	Learning (from) the errors of a systems biology model. Scientific Reports, 2016, 6, 20772.	3.3	20
54	Crowdsourced estimation of cognitive decline and resilience in Alzheimer's disease. Alzheimer's and Dementia, 2016, 12, 645-653.	0.8	72

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55	Utilising the EGFR interactome to identify mechanisms of drug resistance in non-small cell lung cancer – Proof of concept towards a systems pharmacology approach. European Journal of Pharmaceutical Sciences, 2016, 94, 20-32.	4.0	22
56	Exosomal microRNA miR-92a concentration in serum reflects human brown fat activity. Nature Communications, 2016, 7, 11420.	12.8	137
57	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
58	Cross-talk between AMPK and EGFR dependent Signaling in Non-Small Cell Lung Cancer. Scientific Reports, 2016, 6, 27514.	3.3	8
59	Integrating Heterogeneous omics Data via Statistical Inference and Learning Techniques. Genomics and Computational Biology, 2016, 2, 32.	0.7	18
60	DNA methylation signature in peripheral blood reveals distinct characteristics of human X chromosome numerical aberrations. Clinical Epigenetics, 2015, 7, 76.	4.1	59
61	L–dopa increases **α**-synuclein DNA methylation in Parkinson's disease patients *in vivo* and *in vitro*. Movement Disorders, 2015, 30, 1794-1801.	3.9	81
62	Dynamic Bayesian Network Modeling of the Interplay between EGFR and Hedgehog Signaling. PLoS ONE, 2015, 10, e0142646.	2.5	15
63	Different MicroRNA Profiles in Chronic Epilepsy Versus Acute Seizure Mouse Models. Journal of Molecular Neuroscience, 2015, 55, 466-479.	2.3	63
64	A Geometric Method for Model Reduction of Biochemical Networks with Polynomial Rate Functions. Bulletin of Mathematical Biology, 2015, 77, 2180-2211.	1.9	16
65	biRte: Bayesian inference of context-specific regulator activities and transcriptional networks. Bioinformatics, 2015, 31, 3290-3298.	4.1	15
66	NEMix: Single-cell Nested Effects Models for Probabilistic Pathway Stimulation. PLoS Computational Biology, 2015, 11, e1004078.	3.2	17
67	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
68	Kit transduced signals counteract erythroid maturation by MAPK-dependent modulation of erythropoietin signaling and apoptosis induction in mouse fetal liver. Cell Death and Differentiation, 2015, 22, 790-800.	11.2	15
69	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
70	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
71	Analysis of Reaction Network Systems Using Tropical Geometry. Lecture Notes in Computer Science, 2015, , 424-439.	1.3	7
72	Molecular Characterization of F8 Secreting Cell. Blood, 2015, 126, 4671-4671.	1.4	0

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73	netClass: an R-package for network based, integrative biomarker signature discovery. Bioinformatics, 2014, 30, 1325-1326.	4.1	22
74	Activation of AMP-activated protein kinase sensitizes lung cancer cells and H1299 xenografts to erlotinib. Lung Cancer, 2014, 86, 151-157.	2.0	12
75	Characterizing the genetic basis of innate immune response in TLR4-activated human monocytes. Nature Communications, 2014, 5, 5236.	12.8	61
76	Including network knowledge into Cox regression models for biomarker signature discovery. Biometrical Journal, 2014, 56, 287-306.	1.0	22
77	Evidence for contribution of epigenetic mechanisms in the pathogenesis of systemic mast cell activation disease. Immunogenetics, 2014, 66, 287-297.	2.4	15
78	TGF-β 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
79	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
80	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
81	Steiner tree methods for optimal sub-network identification: an empirical study. BMC Bioinformatics, 2013, 14, 144.	2.6	25
82	Unsupervised automated high throughput phenotyping of RNAi time-lapse movies. BMC Bioinformatics, 2013, 14, 292.	2.6	21
83	Predicting Potent Compounds via Model-Based Global Optimization. Journal of Chemical Information and Modeling, 2013, 53, 553-559.	5.4	24
84	miR-155 regulates differentiation of brown and beige adipocytes via a bistable circuit. Nature Communications, 2013, 4, 1769.	12.8	225
85	Stimulation of MMP-1 and CCL2 by NAMPT in PDL Cells. Mediators of Inflammation, 2013, 2013, 1-12.	3.0	36
86	Learning gene network structure from time laps cell imaging in RNAi Knock downs. Bioinformatics, 2013, 29, 1534-1540.	4.1	19
87	Boosting Probabilistic Graphical Model Inference by Incorporating Prior Knowledge from Multiple Sources. PLoS ONE, 2013, 8, e67410.	2.5	10
88	Network and Data Integration for Biomarker Signature Discovery via Network Smoothed T-Statistics. PLoS ONE, 2013, 8, e73074.	2.5	63
89	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
90	MC EMiNEM Maps the Interaction Landscape of the Mediator. PLoS Computational Biology, 2012, 8, e1002568.	3.2	16

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91	Immune System Modeling and Related Pathologies. Computational and Mathematical Methods in Medicine, 2012, 2012, 1-2.	1.3	1
92	Joint Bayesian inference of condition-specific miRNA and transcription factor activities from combined gene and microRNA expression data. Bioinformatics, 2012, 28, 1714-1720.	4.1	25
93	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
94	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
95	Biomarker Gene Signature Discovery Integrating Network Knowledge. Biology, 2012, 1, 5-17.	2.8	30
96	Network Based Consensus Gene Signatures for Biomarker Discovery in Breast Cancer. PLoS ONE, 2011, 6, e25364.	2.5	20
97	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
98	<tt>pathClass</tt>: an R-package for integration of pathway knowledge into support vector machines for biomarker discovery. Bioinformatics, 2011, 27, 1442-1443.	4.1	30
99	Fast and efficient dynamic nested effects models. Bioinformatics, 2011, 27, 238-244.	4.1	26
100	Optimal Assignment Kernels for ADME in Silico Prediction. , 2011, , 16-34.		1
101	Increasing the sensitivity of reverse phase protein arrays by antibody-mediated signal amplification. Proteome Science, 2010, 8, 36.	1.7	17
102	Dynamic deterministic effects propagation networks: learning signalling pathways from longitudinal protein array data. Bioinformatics, 2010, 26, i596-i602.	4.1	28
103	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
104	Deterministic Effects Propagation Networks for reconstructing protein signaling networks from multiple interventions. BMC Bioinformatics, 2009, 10, 322.	2.6	24
105	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
106	Nested effects models for learning signaling networks from perturbation data. Biometrical Journal, 2009, 51, 304-323.	1.0	23
107	A Bayesian Network View on Nested Effects Models. Eurasip Journal on Bioinformatics and Systems Biology, 2009, 2009, 195272.	1.4	8
108	A Bayesian Network View on Nested Effects Models. Eurasip Journal on Bioinformatics and Systems Biology, 2009, 2009, 195272.	1.4	6

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109	Bioinformatical evaluation of modified nucleosides as biomedical markers in diagnosis of breast cancer. Analytica Chimica Acta, 2008, 618, 29-34.	5.4	41
110	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
111	Metabonomics in cancer diagnosis: mass spectrometry-based profiling of urinary nucleosides from breast cancer patients. Biomarkers, 2008, 13, 435-449.	1.9	81
112	Predicting pathway membership via domain signatures. Bioinformatics, 2008, 24, 2137-2142.	4.1	17
113	Estimating large-scale signaling networks through nested effect models with intervention effects from microarray data. Bioinformatics, 2008, 24, 2650-2656.	4.1	44
114	Analyzing gene perturbation screens with nested effects models in R and bioconductor. Bioinformatics, 2008, 24, 2549-2550.	4.1	27
115	INFERRING GENE REGULATORY NETWORKS BY MACHINE LEARNING METHODS. , 2007, , .		4
116	GOSim â€" an R-package for computation of information theoretic GO similarities between terms and gene products. BMC Bioinformatics, 2007, 8, 166.	2.6	168
117	Large scale statistical inference of signaling pathways from RNAi and microarray data. BMC Bioinformatics, 2007, 8, 386.	2.6	39
118	GENE REGULATORY NETWORK INFERENCE VIA REGRESSION BASED TOPOLOGICAL REFINEMENT. , 2007, , .		0
119	Data and Graph Mining in Chemical Space for ADME and Activity Data Sets. QSAR and Combinatorial Science, 2006, 25, 205-220.	1.4	15
120	Kernel Functions for Attributed Molecular Graphs â€" A New Similarity-Based Approach to ADME Prediction in Classification and Regression. QSAR and Combinatorial Science, 2006, 25, 317-326.	1.4	55
121	Vibration-based Terrain Classification Using Support Vector Machines. , 2006, , .		101
122	Optimal assignment kernels for attributed molecular graphs. , 2005, , .		97
123	Gas source declaration with a mobile robot. , 2004, , .		33
124	FEATURE SELECTION FOR SUPPORT VECTOR MACHINES USING GENETIC ALGORITHMS. International Journal on Artificial Intelligence Tools, 2004, 13, 791-800.	1.0	35
125	Towards Optimal Descriptor Subset Selection with Support Vector Machines in Classification and Regression. QSAR and Combinatorial Science, 2004, 23, 311-318.	1.4	36
126	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

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127	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
128	Feature selection for support vector machines by means of genetic algorithm. , 0, , .		190
129	Feature subset selection for support vector machines by incremental regularized risk minimization. , 0, , .		9
130	Assignment kernels for chemical compounds. , 0, , .		7
131	Which features trigger action potentials in cortical neurons in vivo?. , 0, , .		0
132	Efficient parameter selection for support vector machines in classification and regression via model-based global optimization. , 0, , .		45
133	Functional grouping of genes using spectral clustering and gene ontology. , 0, , .		19
134	Towards Realizing the Vision of Precision Medicine: AI Based Prediction of Clinical Drug Response. SSRN Electronic Journal, 0, , .	0.4	0