Stefan R Maetschke

List of Publications by Year
in descending order

21 papers	717 citations	759233 12 h-index	888059 17 g-index
21 all docs	21 docs citations	21 times ranked	1161 citing authors

#	Article	IF	Citations
1	Estimating Global Visual Field Indices in Glaucoma by Combining Macula and Optic Disc OCT Scans Using 3-Dimensional Convolutional Neural Networks. Ophthalmology Glaucoma, 2021, 4, 102-112.	1.9	23
2	Evaluation of artificial intelligence systems for assisting neurologists with fast and accurate annotations of scalp electroencephalography data. EBioMedicine, 2021, 66, 103275.	6.1	15
3	A feature agnostic approach for glaucoma detection in OCT volumes. PLoS ONE, 2019, 14, e0219126.	2.5	132
4	Automated summarisation of SDOCT volumes using deep learning: Transfer learning vs de novo trained networks. PLoS ONE, 2019, 14, e0203726.	2.5	5
5	Alignment-free inference of hierarchical and reticulate phylogenomic relationships. Briefings in Bioinformatics, 2019, 20, 426-435.	6.5	74
6	Semi-supervised Segmentation of Optic Cup in Retinal Fundus Images Using Variational Autoencoder. Lecture Notes in Computer Science, 2017, , 75-82.	1.3	23
7	A novel hybrid approach for severity assessment of Diabetic Retinopathy in colour fundus images. , 2017, , .		20
8	INsPeCT: INtegrative Platform for Cancer Transcriptomics. Cancer Informatics, 2014, 13, CIN.S13630.	1.9	9
9	Supervised, semi-supervised and unsupervised inference of gene regulatory networks. Briefings in Bioinformatics, 2014, 15, 195-211.	6.5	140
10	Characterizing cancer subtypes as attractors of Hopfield networks. Bioinformatics, 2014, 30, 1273-1279.	4.1	32
11	RMaNI: Regulatory Module Network Inference framework. BMC Bioinformatics, 2013, 14, S14.	2.6	6
12	Gene regulatory network inference: evaluation and application to ovarian cancer allows the prioritization of drug targets. Genome Medicine, 2012, 4, 41.	8.2	136
13	mCOPA: analysis of heterogeneous features in cancer expression data. Journal of Clinical Bioinformatics, 2012, 2, 22.	1.2	20
14	A visual framework for sequence analysis using n-grams and spectral rearrangement. Bioinformatics, 2010, 26, 737-744.	4.1	14
15	It's about time: Signal recognition in staged models of protein translocation. Pattern Recognition, 2009, 42, 567-574.	8.1	1
16	Detecting sequence and structure homology via an integrative kernel: A case-study in recognizing enzymes. , 2009, , .		0
17	A Comparison of Sequence Kernels for Localization Prediction of Transmembrane Proteins. , 2007, , .		0
18	Genome-wide analysis of chlamydiae for promoters that phylogenetically footprint. Research in Microbiology, 2007, 158, 685-693.	2.1	20

#	Article	IF	Citations
19	Identifying novel peroxisomal proteins. Proteins: Structure, Function and Bioinformatics, 2007, 69, 606-616.	2.6	22
20	Exploiting Sequence Dependencies in the Prediction of Peroxisomal Proteins. Lecture Notes in Computer Science, 2005, , 454-461.	1.3	3
21	BLOMAP: AN ENCODING OF AMINO ACIDS WHICH IMPROVES SIGNAL PEPTIDE CLEAVAGE SITE PREDICTION. , 2005, , .		22