Jan Grau

List of Publications by Year
in descending order

37 papers	2,824 citations	331670 21 h-index	315739 38 g-index
48 all docs	48 docs citations	48 times ranked	4499 citing authors

#	Article	IF	Citations
1	Flexible TALEs for an expanded use in gene activation, virulenceÂand scaffold engineering. Nucleic Acids Research, 2022, 50, 2387-2400.	14.5	1
2	Importance of RpoD- and Non-RpoD-Dependent Expression of Horizontally Acquired Genes in Cupriavidus metallidurans. Microbiology Spectrum, 2022, 10, e0012122.	3.0	3
3	Epigenetic features improve TALE target prediction. BMC Genomics, 2021, 22, 914.	2.8	0
4	Insights gained from a comprehensive all-against-all transcription factor binding motif benchmarking study. Genome Biology, 2020, 21, 114.	8.8	39
5	PrediTALE: A novel model learned from quantitative data allows for new perspectives on TALE targeting. PLoS Computational Biology, 2019, 15, e1007206.	3.2	12
6	Transcriptional Reprogramming of Rice Cells by Xanthomonas oryzae TALEs. Frontiers in Plant Science, 2019, 10, 162.	3.6	38
7	DepLogo: visualizing sequence dependencies in R. Bioinformatics, 2019, 35, 4812-4814.	4.1	4
8	GeMoMa: Homology-Based Gene Prediction Utilizing Intron Position Conservation and RNA-seq Data. Methods in Molecular Biology, 2019, 1962, 161-177.	0.9	165
9	Allele specific chromatin signals, 3D interactions, and motif predictions for immune and B cell related diseases. Scientific Reports, 2019, 9, 2695.	3.3	24
10	Accurate prediction of cell type-specific transcription factor binding. Genome Biology, 2019, 20, 9.	8.8	82
11	A conserved motif promotes HpaBâ€regulated export of type III effectors from <i>Xanthomonas</i>. Molecular Plant Pathology, 2018, 19, 2473-2487.	4.2	4
12	Combining RNA-seq data and homology-based gene prediction for plants, animals and fungi. BMC Bioinformatics, 2018, 19, 189.	2.6	192
13	Auxin-induced expression divergence between<i>Arabidopsis</i>species may originate within the TIR1/AFBâ€"AUX/IAAâ€"ARF module. Journal of Experimental Botany, 2017, 68, erw457.	4.8	13
14	InMoDe: tools for learning and visualizing intra-motif dependencies of DNA binding sites. Bioinformatics, 2017, 33, 580-582.	4.1	16
15	Evolution of Transcription Activator-Like Effectors in Xanthomonas oryzae. Genome Biology and Evolution, 2017, 9, 1599-1615.	2.5	56
16	Dissection of TALE-dependent gene activation reveals that they induce transcription cooperatively and in both orientations. PLoS ONE, 2017, 12, e0173580.	2.5	20
17	AnnoTALE: bioinformatics tools for identification, annotation and nomenclature of TALEs from Xanthomonas genomic sequences. Scientific Reports, 2016, 6, 21077.	3.3	119
18	Using intron position conservation for homology-based gene prediction. Nucleic Acids Research, 2016, 44, e89-e89.	14.5	449

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19	DiffLogo: a comparative visualization of sequence motifs. BMC Bioinformatics, 2015, 16, 387.	2.6	71
20	Genome-Wide Identification and Validation of Reference Genes in Infected Tomato Leaves for Quantitative RT-PCR Analyses. PLoS ONE, 2015, 10, e0136499.	2.5	54
21	Varying levels of complexity in transcription factor binding motifs. Nucleic Acids Research, 2015, 43, e119-e119.	14.5	66
22	PRROC: computing and visualizing precision-recall and receiver operating characteristic curves in R. Bioinformatics, 2015, 31, 2595-2597.	4.1	288
23	A TAL effector repeat architecture for frameshift binding. Nature Communications, 2014, 5, 3447.	12.8	45
24	Area under Precision-Recall Curves for Weighted and Unweighted Data. PLoS ONE, 2014, 9, e92209.	2.5	131
25	Evaluation of methods for modeling transcription factor sequence specificity. Nature Biotechnology, 2013, 31, 126-134.	17.5	341
26	TALENoffer: genome-wide TALEN off-target prediction. Bioinformatics, 2013, 29, 2931-2932.	4.1	89
27	A general approach for discriminative de novo motif discovery from high-throughput data. Nucleic Acids Research, 2013, 41, e197-e197.	14.5	44
28	DISPOM: A DISCRIMINATIVE DE-NOVO MOTIF DISCOVERY TOOL BASED ON THE JSTACS LIBRARY. Journal of Bioinformatics and Computational Biology, 2013, 11, 1340006.	0.8	1
29	Computational Predictions Provide Insights into the Biology of TAL Effector Target Sites. PLoS Computational Biology, 2013, 9, e1002962.	3.2	111
30	De-Novo Discovery of Differentially Abundant Transcription Factor Binding Sites Including Their Positional Preference. PLoS Computational Biology, 2011, 7, e1001070.	3.2	44
31	Apples and oranges: avoiding different priors in Bayesian DNA sequence analysis. BMC Bioinformatics, 2010, 11, 149.	2.6	9
32	Unifying generative and discriminative learning principles. BMC Bioinformatics, 2010, 11, 98.	2.6	4
33	Probabilistic Approaches to Transcription Factor Binding Site Prediction. Methods in Molecular Biology, 2010, 674, 97-119.	0.9	2
34	Recognition of AvrBs3-Like Proteins Is Mediated by Specific Binding to Promoters of Matching Pepper <i>Bs3</i> Alleles Â. Plant Physiology, 2009, 150, 1697-1712.	4.8	96
35	RECOGNITION OF CIS-REGULATORY ELEMENTS WITH VOMBAT. Journal of Bioinformatics and Computational Biology, 2007, 05, 561-577.	0.8	5
36	VOMBAT: prediction of transcription factor binding sites using variable order Bayesian trees. Nucleic Acids Research, 2006, 34, W529-W533.	14.5	13

#	Article	IF	Citations
37	Identification of transcription factor binding sites with variable-order Bayesian networks. Bioinformatics, 2005, 21, 2657-2666.	4.1	151