

# Jan Grau

## List of Publications by Year in descending order

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Version: 2024-02-01

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  | Using intron position conservation for homology-based gene prediction. <i>Nucleic Acids Research</i> , 2016, 44, e89-e89.  | 14.5 | 449       |
| 2  | Evaluation of methods for modeling transcription factor sequence specificity. <i>Nature Biotechnology</i> , 2013, 31, 126-134.   | 17.5 | 341       |
| 3  | PRROC: computing and visualizing precision-recall and receiver operating characteristic curves in R. <i>Bioinformatics</i> , 2015, 31, 2595-2597.                              | 4.1  | 288       |
| 4  | Combining RNA-seq data and homology-based gene prediction for plants, animals and fungi. <i>BMC Bioinformatics</i> , 2018, 19, 189.  | 2.6  | 192       |
| 5  | GeMoMa: Homology-Based Gene Prediction Utilizing Intron Position Conservation and RNA-seq Data. <i>Methods in Molecular Biology</i> , 2019, 1962, 161-177.                     | 0.9  | 165       |
| 6  | Identification of transcription factor binding sites with variable-order Bayesian networks. <i>Bioinformatics</i> , 2005, 21, 2657-2666.                                       | 4.1  | 151       |
| 7  | Area under Precision-Recall Curves for Weighted and Unweighted Data. <i>PLoS ONE</i> , 2014, 9, e92209.  | 2.5  | 131       |
| 8  | AnnoTALE: bioinformatics tools for identification, annotation and nomenclature of TALEs from <i>Xanthomonas</i> genomic sequences. <i>Scientific Reports</i> , 2016, 6, 21077. | 3.3  | 119       |
| 9  | Computational Predictions Provide Insights into the Biology of TAL Effector Target Sites. <i>PLoS Computational Biology</i> , 2013, 9, e1002962.                               | 3.2  | 111       |
| 10 | Recognition of AvrBs3-Like Proteins Is Mediated by Specific Binding to Promoters of Matching Pepper <i>Bs3</i> Alleles. <i>Plant Physiology</i> , 2009, 150, 1697-1712.        | 4.8  | 96        |
| 11 | TALenOffer: genome-wide TALEN off-target prediction. <i>Bioinformatics</i> , 2013, 29, 2931-2932.  | 4.1  | 89        |
| 12 | Accurate prediction of cell type-specific transcription factor binding. <i>Genome Biology</i> , 2019, 20, 9.   | 8.8  | 82        |
| 13 | DiffLogo: a comparative visualization of sequence motifs. <i>BMC Bioinformatics</i> , 2015, 16, 387.   | 2.6  | 71        |
| 14 | Varying levels of complexity in transcription factor binding motifs. <i>Nucleic Acids Research</i> , 2015, 43, e119-e119.  | 14.5 | 66        |
| 15 | Evolution of Transcription Activator-Like Effectors in <i>Xanthomonas oryzae</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 1599-1615.                                   | 2.5  | 56        |
| 16 | Genome-Wide Identification and Validation of Reference Genes in Infected Tomato Leaves for Quantitative RT-PCR Analyses. <i>PLoS ONE</i> , 2015, 10, e0136499.                 | 2.5  | 54        |
| 17 | A TAL effector repeat architecture for frameshift binding. <i>Nature Communications</i> , 2014, 5, 3447.   | 12.8 | 45        |
| 18 | De-Novo Discovery of Differentially Abundant Transcription Factor Binding Sites Including Their Positional Preference. <i>PLoS Computational Biology</i> , 2011, 7, e1001070.  | 3.2  | 44        |

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|----|--|------|-----------|
| 19 | A general approach for discriminative de novo motif discovery from high-throughput data. <i>Nucleic Acids Research</i> , 2013, 41, e197-e197.  | 14.5 | 44        |
| 20 | Insights gained from a comprehensive all-against-all transcription factor binding motif benchmarking study. <i>Genome Biology</i> , 2020, 21, 114.                                       | 8.8  | 39        |
| 21 | Transcriptional Reprogramming of Rice Cells by <i>Xanthomonas oryzae</i> TALEs. <i>Frontiers in Plant Science</i> , 2019, 10, 162.   | 3.6  | 38        |
| 22 | Allele specific chromatin signals, 3D interactions, and motif predictions for immune and B cell related diseases. <i>Scientific Reports</i> , 2019, 9, 2695.                             | 3.3  | 24        |
| 23 | Dissection of TALE-dependent gene activation reveals that they induce transcription cooperatively and in both orientations. <i>PLoS ONE</i> , 2017, 12, e0173580.                        | 2.5  | 20        |
| 24 | InMoDe: tools for learning and visualizing intra-motif dependencies of DNA binding sites. <i>Bioinformatics</i> , 2017, 33, 580-582.   | 4.1  | 16        |
| 25 | VOMBAT: prediction of transcription factor binding sites using variable order Bayesian trees. <i>Nucleic Acids Research</i> , 2006, 34, W529-W533.                                       | 14.5 | 13        |
| 26 | Auxin-induced expression divergence between <i>Arabidopsis</i> species may originate within the TIR1/AFBâ€AUX/IAAâ€ARF module. <i>Journal of Experimental Botany</i> , 2017, 68, erw457. | 4.8  | 13        |
| 27 | PrediTALE: A novel model learned from quantitative data allows for new perspectives on TALE targeting. <i>PLoS Computational Biology</i> , 2019, 15, e1007206.                           | 3.2  | 12        |
| 28 | Apples and oranges: avoiding different priors in Bayesian DNA sequence analysis. <i>BMC Bioinformatics</i> , 2010, 11, 149.  | 2.6  | 9         |
| 29 | RECOGNITION OF CIS-REGULATORY ELEMENTS WITH VOMBAT. <i>Journal of Bioinformatics and Computational Biology</i> , 2007, 05, 561-577.  | 0.8  | 5         |
| 30 | Unifying generative and discriminative learning principles. <i>BMC Bioinformatics</i> , 2010, 11, 98.  | 2.6  | 4         |
| 31 | A conserved motif promotes HpaBâ€regulated export of type III effectors from <i>Xanthomonas</i> . <i>Molecular Plant Pathology</i> , 2018, 19, 2473-2487.                                | 4.2  | 4         |
| 32 | DepLogo: visualizing sequence dependencies in R. <i>Bioinformatics</i> , 2019, 35, 4812-4814.  | 4.1  | 4         |
| 33 | Importance of RpoD- and Non-RpoD-Dependent Expression of Horizontally Acquired Genes in <i>Cupriavidus metallidurans</i> . <i>Microbiology Spectrum</i> , 2022, 10, e0012122.            | 3.0  | 3         |
| 34 | Probabilistic Approaches to Transcription Factor Binding Site Prediction. <i>Methods in Molecular Biology</i> , 2010, 674, 97-119.   | 0.9  | 2         |
| 35 | DISPOM: A DISCRIMINATIVE DE-NOVO MOTIF DISCOVERY TOOL BASED ON THE JSTACS LIBRARY. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1340006.                       | 0.8  | 1         |
| 36 | Flexible TALEs for an expanded use in gene activation, virulence and scaffold engineering. <i>Nucleic Acids Research</i> , 2022, 50, 2387-2400.  | 14.5 | 1         |

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|----|--|-----|-----------|
| 37 | Epigenetic features improve TALE target prediction. BMC Genomics, 2021, 22, 914. | 2.8 | 0         |