

# Jens Hollunder

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8729188/publications.pdf>

Version: 2024-02-01

19  
papers

1,884  
citations

567144

15  
h-index

839398

18  
g-index

20  
all docs

20  
docs citations

20  
times ranked

3101  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative transcriptomics as a tool for the identification of root branching genes in maize. Plant Biotechnology Journal, 2013, 11, 1092-1102.	4.1	54
2	Predicting Gene Function from Uncontrolled Expression Variation among Individual Wild-Type <i>Arabidopsis</i> Plants. Plant Cell, 2013, 25, 2865-2877.	3.1	50
3	CORNET 2.0: integrating plant coexpression, protein-protein interactions, regulatory interactions, gene associations and functional annotations. New Phytologist, 2012, 195, 707-720.	3.5	113
4	The Progeny of <i>Arabidopsis thaliana</i> Plants Exposed to Salt Exhibit Changes in DNA Methylation, Histone Modifications and Gene Expression. PLoS ONE, 2012, 7, e30515.	1.1	166
5	Specific Impact of Tobamovirus Infection on the <i>Arabidopsis</i> Small RNA Profile. PLoS ONE, 2011, 6, e19549.	1.1	70
6	Flexible network reconstruction from relational databases with Cytoscape and CytoSQL. BMC Bioinformatics, 2010, 11, 360.	1.2	0
7	Functional Modules in the <i>Arabidopsis</i> Core Cell Cycle Binary Protein-Protein Interaction Network. Plant Cell, 2010, 22, 1264-1280.	3.1	168
8	CORNET: A User-Friendly Tool for Data Mining and Integration. Plant Physiology, 2010, 152, 1167-1179.	2.3	62
9	DASS-GUI: a user interface for identification and analysis of significant patterns in non-sequential data. Bioinformatics, 2010, 26, 987-989.	1.8	5
10	Targeted interactomics reveals a complex core cell cycle machinery in <i>Arabidopsis thaliana</i> . Molecular Systems Biology, 2010, 6, 397.	3.2	315
11	Transgenerational Adaptation of <i>Arabidopsis</i> to Stress Requires DNA Methylation and the Function of Dicer-Like Proteins. PLoS ONE, 2010, 5, e9514.	1.1	416
12	DASS: efficient discovery and p-value calculation of substructures in unordered data. Bioinformatics, 2007, 23, 77-83.	1.8	21
13	Protein Subcomplexes-Molecular Machines With Highly Specialized Functions. IEEE Transactions on Nanobioscience, 2007, 6, 86-93.	2.2	3
14	Information theoretic description of networks. Physica A: Statistical Mechanics and Its Applications, 2007, 385, 385-396.	1.2	48
15	Integrated Assessment and Prediction of Transcription Factor Binding. PLoS Computational Biology, 2006, 2, e70.	1.5	82
16	Identification and characterization of protein subcomplexes in yeast. Proteomics, 2005, 5, 2082-2089.	1.3	22
17	Common patterns in type II restriction enzyme binding sites. Nucleic Acids Research, 2005, 33, 2726-2733.	6.5	11
18	Integrated Assessment and Prediction of Transcription Factor Binding. PLoS Computational Biology, 2005, preprint, e70.	1.5	0

#	ARTICLE	IF	CITATIONS
19	Post-transcriptional Expression Regulation in the Yeast <i>Saccharomyces cerevisiae</i> on a Genomic Scale. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 1083-1092.	2.5	217