Jens Hollunder

List of Publications by Year
in descending order

		566801	839053
19 papers	1,884 citations	15 h-index	18 g-index
20 all docs	20 docs citations	20 times ranked	3101 citing authors

#	ARTICLE	IF	CITATIONS
1	Transgenerational Adaptation of Arabidopsis to Stress Requires DNA Methylation and the Function of Dicer-Like Proteins. PLoS ONE, 2010, 5, e9514.	1.1	416
2	Targeted interactomics reveals a complex core cell cycle machinery in <i>Arabidopsis thaliana</i>. Molecular Systems Biology, 2010, 6, 397.	3.2	315
3	Post-transcriptional Expression Regulation in the Yeast Saccharomyces cerevisiae on a Genomic Scale. Molecular and Cellular Proteomics, 2004, 3, 1083-1092.	2.5	217
4	Functional Modules in the <i>Arabidopsis</i> Core Cell Cycle Binary Protein–Protein Interaction Network. Plant Cell, 2010, 22, 1264-1280.	3.1	168
5	The Progeny of Arabidopsis thaliana Plants Exposed to Salt Exhibit Changes in DNA Methylation, Histone Modifications and Gene Expression. PLoS ONE, 2012, 7, e30515.	1.1	166
6	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
7	Integrated Assessment and Prediction of Transcription Factor Binding. PLoS Computational Biology, 2006, 2, e70.	1.5	82
8	Specific Impact of Tobamovirus Infection on the Arabidopsis Small RNA Profile. PLoS ONE, 2011, 6, e19549.	1.1	70
9	CORNET: A User-Friendly Tool for Data Mining and Integration Â. Plant Physiology, 2010, 152, 1167-1179.	2.3	62
10	Comparative transcriptomics as a tool for the identification of root branching genes in maize. Plant Biotechnology Journal, 2013, 11, 1092-1102.	4.1	54
11	Predicting Gene Function from Uncontrolled Expression Variation among Individual Wild-Type <i>Arabidopsis</i> Plants. Plant Cell, 2013, 25, 2865-2877.	3.1	50
12	Information theoretic description of networks. Physica A: Statistical Mechanics and Its Applications, 2007, 385, 385-396.	1.2	48
13	Identification and characterization of protein subcomplexes in yeast. Proteomics, 2005, 5, 2082-2089.	1.3	22
14	DASS: efficient discovery and p-value calculation of substructures in unordered data. Bioinformatics, 2007, 23, 77-83.	1.8	21
15	Common patterns in type II restriction enzyme binding sites. Nucleic Acids Research, 2005, 33, 2726-2733.	6.5	11
16	DASS-GUI: a user interface for identification and analysis of significant patterns in non-sequential data. Bioinformatics, 2010, 26, 987-989.	1.8	5
17	Protein Subcomplexes-Molecular Machines With Highly Specialized Functions. IEEE Transactions on Nanobioscience, 2007, 6, 86-93.	2.2	3
18	Flexible network reconstruction from relational databases with Cytoscape and CytoSQL. BMC Bioinformatics, 2010, 11, 360.	1.2	0

#	Article	IF	Citations
19	Integrated Assessment and Prediction of Transcription Factor Binding. PLoS Computational Biology, 2005, preprint, e70.	1.5	0