

# Tobias Wittkop

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11840646/publications.pdf>

Version: 2024-02-01

15  
papers

906  
citations

1040056

9  
h-index

1058476

14  
g-index

15  
all docs

15  
docs citations

15  
times ranked

1752  
citing authors

#	ARTICLE	IF	CITATIONS
1	Density parameter estimation for finding clusters of homologous proteinsâ€”tracing actinobacterial pathogenicity lifestyles. <i>Bioinformatics</i> , 2013, 29, 215-222.	4.1	17
2	DEFOG: discrete enrichment of functionally organized genes. <i>Integrative Biology (United Kingdom)</i> , 2012, 4, 795.	1.3	3
3	Extension and Robustness of Transitivity Clustering for Proteinâ€™Protein Interaction Network Analysis. <i>Internet Mathematics</i> , 2011, 7, 255-273.	0.7	8
4	Comprehensive cluster analysis with Transitivity Clustering. <i>Nature Protocols</i> , 2011, 6, 285-295.	12.0	47
5	clusterMaker: a multi-algorithm clustering plugin for Cytoscape. <i>BMC Bioinformatics</i> , 2011, 12, 436.	2.6	541
6	Efficient Online Transcription Factor Binding Site Adjustment by Integrating Transitive Graph Projection with MoRAine 2.0. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.5	1
7	Partitioning biological data with transitivity clustering. <i>Nature Methods</i> , 2010, 7, 419-420.	19.0	84
8	Integrated analysis and reconstruction of microbial transcriptional gene regulatory networks using CoryneRegNet. <i>Nature Protocols</i> , 2009, 4, 992-1005.	12.0	39
9	MoRAine - A web server for fast computational transcription factor binding motif re-annotation. <i>Journal of Integrative Bioinformatics</i> , 2008, 5, .	1.5	5
10	MoRAine--a web server for fast computational transcription factor binding motif re-annotation. <i>Journal of Integrative Bioinformatics</i> , 2008, 5, .	1.5	6
11	CoryneRegNet 3.0â€™An interactive systems biology platform for the analysis of gene regulatory networks in corynebacteria and Escherichia coli. <i>Journal of Biotechnology</i> , 2007, 129, 279-289.	3.8	32
12	Large scale clustering of protein sequences with FORCE -A layout based heuristic for weighted cluster editing. <i>BMC Bioinformatics</i> , 2007, 8, 396.	2.6	56
13	EXACT AND HEURISTIC ALGORITHMS FOR WEIGHTED CLUSTER EDITING. , 2007, , .		43
14	Exact and heuristic algorithms for weighted cluster editing. <i>Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference</i> , 2007, 6, 391-401.	0.4	13
15	CoryneRegNet 2: An Integrative Bioinformatics Approach for Reconstruction and Comparison of Transcriptional Regulatory Networks in Prokaryotes. <i>Journal of Integrative Bioinformatics</i> , 2006, 3, 1-13.	1.5	11