

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