

# Vesna Memisevic

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11933603/publications.pdf>

Version: 2024-02-01

20  
papers

832  
citations

687363

13  
h-index

752698

20  
g-index

20  
all docs

20  
docs citations

20  
times ranked

844  
citing authors

#	ARTICLE	IF	CITATIONS
1	Topological network alignment uncovers biological function and phylogeny. <i>Journal of the Royal Society Interface</i> , 2010, 7, 1341-1354.	3.4	281
2	Systems-level cancer gene identification from protein interaction network topology applied to melanogenesis-related functional genomics data. <i>Journal of the Royal Society Interface</i> , 2010, 7, 423-437.	3.4	95
3	Dominating Biological Networks. <i>PLoS ONE</i> , 2011, 6, e23016.	2.5	85
4	C-GRAAL: Common-neighbors-based global GRAPh ALignment of biological networks. <i>Integrative Biology (United Kingdom)</i> , 2012, 4, 734.	1.3	79
5	Novel <i>Burkholderia mallei</i> Virulence Factors Linked to Specific Host-Pathogen Protein Interactions. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3036-3051.	3.8	38
6	Mining Host-Pathogen Protein Interactions to Characterize <i>Burkholderia mallei</i> Infectivity Mechanisms. <i>PLoS Computational Biology</i> , 2015, 11, e1004088.	3.2	34
7	Using host-pathogen protein interactions to identify and characterize <i>Francisella tularensis</i> virulence factors. <i>BMC Genomics</i> , 2015, 16, 1106.	2.8	33
8	Protein interaction network topology uncovers melanogenesis regulatory network components within functional genomics datasets. <i>BMC Systems Biology</i> , 2010, 4, 84.	3.0	32
9	Categorizing Biases in High-Confidence High-Throughput Protein-Protein Interaction Data Sets. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.012500.	3.8	25
10	Complementarity of network and sequence information in homologous proteins. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, 275-289.	1.5	20
11	Reconstituting protein interaction networks using parameter-dependent domain-domain interactions. <i>BMC Bioinformatics</i> , 2013, 14, 154.	2.6	17
12	Complementarity of network and sequence information in homologous proteins. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.5	17
13	An integrative approach to modeling biological networks. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.5	14
14	Mechanisms of action of <i>Coxiella burnetii</i> effectors inferred from host-pathogen protein interactions. <i>PLoS ONE</i> , 2017, 12, e0188071.	2.5	12
15	Tutorial on biological networks. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2012, 2, 298-325.	6.8	11
16	A reverse-phase protein microarray-based screen identifies host signaling dynamics upon <i>Burkholderia</i> spp. infection. <i>Frontiers in Microbiology</i> , 2015, 6, 683.	3.5	11
17	DBSecSys: a database of <i>Burkholderia mallei</i> secretion systems. <i>BMC Bioinformatics</i> , 2014, 15, 244.	2.6	9
18	An integrative approach to modeling biological networks. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.5	8

#	ARTICLE	IF	CITATIONS
19	Topological network alignment uncovers biological function and phylogeny. Nature Precedings, 2009, , .	0.1	7
20	DBSecSys 2.0: a database of Burkholderia mallei and Burkholderia pseudomallei secretion systems. BMC Bioinformatics, 2016, 17, 387.	2.6	4