

Vesna Memisevic

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

832
citations

686830

13
h-index

752256

20
g-index

20
all docs

20
docs citations

20
times ranked

844
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Mechanisms of action of <i>Coxiella burnetii</i> effectors inferred from host-pathogen protein interactions. <i>PLoS ONE</i> , 2017, 12, e0188071. | 1.1 | 12 |
| 2 | DBSecSys 2.0: a database of <i>Burkholderia mallei</i> and <i>Burkholderia pseudomallei</i> secretion systems. <i>BMC Bioinformatics</i> , 2016, 17, 387. | 1.2 | 4 |
| 3 | Using host-pathogen protein interactions to identify and characterize <i>Francisella tularensis</i> virulence factors. <i>BMC Genomics</i> , 2015, 16, 1106. | 1.2 | 33 |
| 4 | 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. | 1.5 | 11 |
| 5 | Mining Host-Pathogen Protein Interactions to Characterize <i>Burkholderia mallei</i> Infectivity Mechanisms. <i>PLoS Computational Biology</i> , 2015, 11, e1004088. | 1.5 | 34 |
| 6 | DBSecSys: a database of <i>Burkholderia mallei</i> secretion systems. <i>BMC Bioinformatics</i> , 2014, 15, 244. | 1.2 | 9 |
| 7 | Reconstituting protein interaction networks using parameter-dependent domain-domain interactions. <i>BMC Bioinformatics</i> , 2013, 14, 154. | 1.2 | 17 |
| 8 | Novel <i>Burkholderia mallei</i> Virulence Factors Linked to Specific Host-Pathogen Protein Interactions. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3036-3051. | 2.5 | 38 |
| 9 | C-GRAAL: Common-neighbors-based global GRAph ALignment of biological networks. <i>Integrative Biology (United Kingdom)</i> , 2012, 4, 734. | 0.6 | 79 |
| 10 | Tutorial on biological networks. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2012, 2, 298-325. | 4.6 | 11 |
| 11 | Dominating Biological Networks. <i>PLoS ONE</i> , 2011, 6, e23016. | 1.1 | 85 |
| 12 | Categorizing Biases in High-Confidence High-Throughput Protein-Protein Interaction Data Sets. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.012500. | 2.5 | 25 |
| 13 | Protein interaction network topology uncovers melanogenesis regulatory network components within functional genomics datasets. <i>BMC Systems Biology</i> , 2010, 4, 84. | 3.0 | 32 |
| 14 | Complementarity of network and sequence information in homologous proteins. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, 275-289. | 1.0 | 20 |
| 15 | An integrative approach to modeling biological networks. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, . | 1.0 | 14 |
| 16 | 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. | 1.5 | 95 |
| 17 | Topological network alignment uncovers biological function and phylogeny. <i>Journal of the Royal Society Interface</i> , 2010, 7, 1341-1354. | 1.5 | 281 |
| 18 | An integrative approach to modeling biological networks. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, . | 1.0 | 8 |

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|----|---|-----|-----------|
| 19 | Complementarity of network and sequence information in homologous proteins. Journal of Integrative Bioinformatics, 2010, 7, . | 1.0 | 17 |
| 20 | Topological network alignment uncovers biological function and phylogeny. Nature Precedings, 2009, , . | 0.1 | 7 |