

Nadezhda Tsankova Doncheva

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6609791/publications.pdf>

Version: 2024-02-01

22
papers

25,777
citations

471509

17
h-index

580821

25
g-index

28
all docs

28
docs citations

28
times ranked

39594
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. <i>Nucleic Acids Research</i> , 2019, 47, D607-D613. | 14.5 | 12,237 |
| 2 | The STRING database in 2017: quality-controlled protein-protein association networks, made broadly accessible. <i>Nucleic Acids Research</i> , 2017, 45, D362-D368. | 14.5 | 6,303 |
| 3 | The STRING database in 2021: customizable protein-protein networks, and functional characterization of user-uploaded gene/measurement sets. <i>Nucleic Acids Research</i> , 2021, 49, D605-D612. | 14.5 | 4,274 |
| 4 | Cytoscape StringApp: Network Analysis and Visualization of Proteomics Data. <i>Journal of Proteome Research</i> , 2019, 18, 623-632. | 3.7 | 1,228 |
| 5 | Topological analysis and interactive visualization of biological networks and protein structures. <i>Nature Protocols</i> , 2012, 7, 670-685. | 12.0 | 445 |
| 6 | Dense genotyping of immune-related disease regions identifies nine new risk loci for primary sclerosing cholangitis. <i>Nature Genetics</i> , 2013, 45, 670-675. | 21.4 | 339 |
| 7 | Analyzing and visualizing residue networks of protein structures. <i>Trends in Biochemical Sciences</i> , 2011, 36, 179-182. | 7.5 | 244 |
| 8 | Viruses.STRING: A Virus-Host Protein-Protein Interaction Database. <i>Viruses</i> , 2018, 10, 519. | 3.3 | 100 |
| 9 | Recent approaches to the prioritization of candidate disease genes. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2012, 4, 429-442. | 6.6 | 59 |
| 10 | Visualize omics data on networks with Omics Visualizer, a Cytoscape App. <i>F1000Research</i> , 2020, 9, 157. | 1.6 | 54 |
| 11 | Profiling of Parkin-Binding Partners Using Tandem Affinity Purification. <i>PLoS ONE</i> , 2013, 8, e78648. | 2.5 | 38 |
| 12 | NetworkPrioritizer: a versatile tool for network-based prioritization of candidate disease genes or other molecules. <i>Bioinformatics</i> , 2013, 29, 1471-1473. | 4.1 | 35 |
| 13 | Human pathways in animal models: possibilities and limitations. <i>Nucleic Acids Research</i> , 2021, 49, 1859-1871. | 14.5 | 35 |
| 14 | Visualize omics data on networks with Omics Visualizer, a Cytoscape App. <i>F1000Research</i> , 2020, 9, 157. | 1.6 | 35 |
| 15 | Consistent Prediction of Mutation Effect on Drug Binding in HIV-1 Protease Using Alchemical Calculations. <i>Journal of Chemical Theory and Computation</i> , 2018, 14, 3397-3408. | 5.3 | 24 |
| 16 | Astrocytic reactivity triggered by defective autophagy and metabolic failure causes neurotoxicity in frontotemporal dementia type 3. <i>Stem Cell Reports</i> , 2021, 16, 2736-2751. | 4.8 | 23 |
| 17 | setsApp: Set operations for Cytoscape Nodes and Edges. <i>F1000Research</i> , 2014, 3, 149. | 1.6 | 14 |
| 18 | Integrative visual analysis of protein sequence mutations. <i>BMC Proceedings</i> , 2014, 8, S2. | 1.6 | 13 |

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|----|--|-----|-----------|
| 19 | Non-active site mutants of HIV-1 protease influence resistance and sensitisation towards protease inhibitors. <i>Retrovirology</i> , 2020, 17, 13. | 2.0 | 12 |
| 20 | setsApp for Cytoscape: Set operations for Cytoscape Nodes and Edges. <i>F1000Research</i> , 2014, 3, 149. | 1.6 | 8 |
| 21 | Near-Neighbor Interactions in the NS3-4A Protease of HCV Impact Replicative Fitness of Drug-Resistant Viral Variants. <i>Journal of Molecular Biology</i> , 2019, 431, 2354-2368. | 4.2 | 3 |
| 22 | Epistatic interactions promote persistence of NS3-Q80K in HCV infection by compensating for protein folding instability. <i>Journal of Biological Chemistry</i> , 2021, 297, 101031. | 3.4 | 2 |