

Nadezhda Tsankova Doncheva

List of Publications by Year in descending order

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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	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
2	Human pathways in animal models: possibilities and limitations. <i>Nucleic Acids Research</i> , 2021, 49, 1859-1871.	14.5	35
3	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
4	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
5	Non-active site mutants of HIV-1 protease influence resistance and sensitisation towards protease inhibitors. <i>Retrovirology</i> , 2020, 17, 13.	2.0	12
6	Visualize omics data on networks with Omics Visualizer, a Cytoscape App. <i>F1000Research</i> , 2020, 9, 157.	1.6	54
7	Visualize omics data on networks with Omics Visualizer, a Cytoscape App. <i>F1000Research</i> , 2020, 9, 157.	1.6	35
8	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
9	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
10	Cytoscape StringApp: Network Analysis and Visualization of Proteomics Data. <i>Journal of Proteome Research</i> , 2019, 18, 623-632.	3.7	1,228
11	Viruses.STRING: A Virus-Host Protein-Protein Interaction Database. <i>Viruses</i> , 2018, 10, 519.	3.3	100
12	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
13	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
14	Integrative visual analysis of protein sequence mutations. <i>BMC Proceedings</i> , 2014, 8, S2.	1.6	13
15	setsApp: Set operations for Cytoscape Nodes and Edges. <i>F1000Research</i> , 2014, 3, 149.	1.6	14
16	setsApp for Cytoscape: Set operations for Cytoscape Nodes and Edges. <i>F1000Research</i> , 2014, 3, 149.	1.6	8
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	Profiling of Parkin-Binding Partners Using Tandem Affinity Purification. PLoS ONE, 2013, 8, e78648.	2.5	38
20	Topological analysis and interactive visualization of biological networks and protein structures. Nature Protocols, 2012, 7, 670-685.	12.0	445
21	Recent approaches to the prioritization of candidate disease genes. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2012, 4, 429-442.	6.6	59
22	Analyzing and visualizing residue networks of protein structures. Trends in Biochemical Sciences, 2011, 36, 179-182.	7.5	244