Nadezhda Tsankova Doncheva

List of Publications by Year
in descending order

22 papers	25,777 citations	471371 17 h-index	580701 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. Nucleic Acids Research, 2021, 49, D605-D612.	6.5	4,274
2	Human pathways in animal models: possibilities and limitations. Nucleic Acids Research, 2021, 49, 1859-1871.	6.5	35
3	Epistatic interactions promote persistence of NS3-Q80K inÂHCV infection by compensating for protein folding instability. Journal of Biological Chemistry, 2021, 297, 101031.	1.6	2
4	Astrocytic reactivity triggered by defective autophagy and metabolic failure causes neurotoxicity in frontotemporal dementia type 3. Stem Cell Reports, 2021, 16, 2736-2751.	2.3	23
5	Non-active site mutants of HIV-1 protease influence resistance and sensitisation towards protease inhibitors. Retrovirology, 2020, 17, 13.	0.9	12
6	Visualize omics data on networks with Omics Visualizer, a Cytoscape App. F1000Research, 2020, 9, 157.	0.8	54
7	Visualize omics data on networks with Omics Visualizer, a Cytoscape App. F1000Research, 2020, 9, 157.	0.8	35
8	Near-Neighbor Interactions in the NS3-4A Protease of HCV Impact Replicative Fitness of Drug-Resistant Viral Variants. Journal of Molecular Biology, 2019, 431, 2354-2368.	2.0	3
9	STRING v11: protein–protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. Nucleic Acids Research, 2019, 47, D607-D613.	6.5	12,237
10	Cytoscape StringApp: Network Analysis and Visualization of Proteomics Data. Journal of Proteome Research, 2019, 18, 623-632.	1.8	1,228
11	Viruses.STRING: A Virus-Host Protein-Protein Interaction Database. Viruses, 2018, 10, 519.	1.5	100
12	Consistent Prediction of Mutation Effect on Drug Binding in HIV-1 Protease Using Alchemical Calculations. Journal of Chemical Theory and Computation, 2018, 14, 3397-3408.	2.3	24
13	The STRING database in 2017: quality-controlled protein–protein association networks, made broadly accessible. Nucleic Acids Research, 2017, 45, D362-D368.	6.5	6,303
14	Integrative visual analysis of protein sequence mutations. BMC Proceedings, 2014, 8, S2.	1.8	13
15	setsApp: Set operations for Cytoscape Nodes and Edges. F1000Research, 2014, 3, 149.	0.8	14
16	setsApp for Cytoscape: Set operations for Cytoscape Nodes and Edges. F1000Research, 2014, 3, 149.	0.8	8
17	Dense genotyping of immune-related disease regions identifies nine new risk loci for primary sclerosing cholangitis. Nature Genetics, 2013, 45, 670-675.	9.4	339
18	NetworkPrioritizer: a versatile tool for network-based prioritization of candidate disease genes or other molecules. Bioinformatics, 2013, 29, 1471-1473.	1.8	35

#	Article	IF	Citations
19	Profiling of Parkin-Binding Partners Using Tandem Affinity Purification. PLoS ONE, 2013, 8, e78648.	1.1	38
20	Topological analysis and interactive visualization of biological networks and protein structures. Nature Protocols, 2012, 7, 670-685.	5.5	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.	3.7	244