Nadezhda Tsankova Doncheva

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

23	papers
12,260	citations
14	h-index
28	g-index
28	ext. papers
20,494	ext. citations
9.7	avg, IF
6.77	L-index

#	Paper	IF	Citations
23	Astrocytic reactivity triggered by defective autophagy and metabolic failure causes neurotoxicity in frontotemporal dementia type 3. *Stem Cell Reports*, **2021**, 16, 2736-2751	8	1
22	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	20.1	661
21	Human pathways in animal models: possibilities and limitations. *Nucleic Acids Research*, **2021**, 49, 1859-1871	20.1	7
20	Epistatic interactions promote persistence of NS3-Q80K in HCV infection by compensating for protein folding instability. *Journal of Biological Chemistry*, **2021**, 297, 101031	5.4	1
19	Non-active site mutants of HIV-1 protease influence resistance and sensitisation towards protease inhibitors. *Retrovirology*, **2020**, 17, 13	3.6	5
18	Visualize omics data on networks with Omics Visualizer, a Cytoscape App. *F1000Research*, **2020**, 9, 157	3.6	20
17	Visualize omics data on networks with Omics Visualizer, a Cytoscape App. *F1000Research*, **2020**, 9, 157	3.6	14
16	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	6.5	2
15	STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. *Nucleic Acids Research*, **2019**, 47, D607-D613	20.1	5966
14	Cytoscape StringApp: Network Analysis and Visualization of Proteomics Data. *Journal of Proteome Research*, **2019**, 18, 623-632	5.6	490
13	Viruses.STRING: A Virus-Host Protein-Protein Interaction Database. *Viruses*, **2018**, 10,	6.2	58
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	6.4	13
11	The STRING database in 2017: quality-controlled protein-protein association networks, made broadly accessible. *Nucleic Acids Research*, **2017**, 45, D362-D368	20.1	4068
10	Integrative visual analysis of protein sequence mutations. *BMC Proceedings*, **2014**, 8, S2	2.3	10
9	setsApp: Set operations for Cytoscape Nodes and Edges. *F1000Research*, **2014**, 3, 149	3.6	11
8	setsApp for Cytoscape: Set operations for Cytoscape Nodes and Edges. *F1000Research*, **2014**, 3, 149	3.6	6
7	Dense genotyping of immune-related disease regions identifies nine new risk loci for primary sclerosing cholangitis. *Nature Genetics*, **2013**, 45, 670-5	36.3	267

6	NetworkPrioritizer: a versatile tool for network-based prioritization of candidate disease genes or other molecules. *Bioinformatics*, **2013**, 29, 1471-3	7.2	31
5	Profiling of Parkin-binding partners using tandem affinity purification. *PLoS ONE*, **2013**, 8, e78648	3.7	32
4	Topological analysis and interactive visualization of biological networks and protein structures. *Nature Protocols*, **2012**, 7, 670-85	18.8	322
3	Recent approaches to the prioritization of candidate disease genes. *Wiley Interdisciplinary Reviews: Systems Biology and Medicine*, **2012**, 4, 429-42	6.6	45
2	Analyzing and visualizing residue networks of protein structures. *Trends in Biochemical Sciences*, **2011**, 36, 179-82	10.3	182
1	Cytoscape stringApp: Network analysis and visualization of proteomics data		5