

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

471061

17
h-index

580395

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.	6.5	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.	6.5	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.	6.5	4,274
4	Cytoscape StringApp: Network Analysis and Visualization of Proteomics Data. <i>Journal of Proteome Research</i> , 2019, 18, 623-632.	1.8	1,228
5	Topological analysis and interactive visualization of biological networks and protein structures. <i>Nature Protocols</i> , 2012, 7, 670-685.	5.5	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.	9.4	339
7	Analyzing and visualizing residue networks of protein structures. <i>Trends in Biochemical Sciences</i> , 2011, 36, 179-182.	3.7	244
8	Viruses.STRING: A Virus-Host Protein-Protein Interaction Database. <i>Viruses</i> , 2018, 10, 519.	1.5	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.	0.8	54
11	Profiling of Parkin-Binding Partners Using Tandem Affinity Purification. <i>PLoS ONE</i> , 2013, 8, e78648.	1.1	38
12	NetworkPrioritizer: a versatile tool for network-based prioritization of candidate disease genes or other molecules. <i>Bioinformatics</i> , 2013, 29, 1471-1473.	1.8	35
13	Human pathways in animal models: possibilities and limitations. <i>Nucleic Acids Research</i> , 2021, 49, 1859-1871.	6.5	35
14	Visualize omics data on networks with Omics Visualizer, a Cytoscape App. <i>F1000Research</i> , 2020, 9, 157.	0.8	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.	2.3	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.	2.3	23
17	setsApp: Set operations for Cytoscape Nodes and Edges. <i>F1000Research</i> , 2014, 3, 149.	0.8	14
18	Integrative visual analysis of protein sequence mutations. <i>BMC Proceedings</i> , 2014, 8, S2.	1.8	13

#	ARTICLE	IF	CITATIONS
19	Non-active site mutants of HIV-1 protease influence resistance and sensitisation towards protease inhibitors. <i>Retrovirology</i> , 2020, 17, 13.	0.9	12
20	setsApp for Cytoscape: Set operations for Cytoscape Nodes and Edges. <i>F1000Research</i> , 2014, 3, 149.	0.8	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.	2.0	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.	1.6	2