Natalia Maltsev

List of Publications by Year
in descending order

20 papers	1,097 citations	840776 11 h-index	713466 21 g-index
22 all docs	22 docs citations	22 times ranked	2161 citing authors

#	Article	IF	Citations
1	Unique somatic variants in DNA from urine exosomes of individuals with bladder cancer. Molecular Therapy - Methods and Clinical Development, 2021, 22, 360-376.	4.1	10
2	Exploring the functional impact of alternative splicing on human protein isoforms using available annotation sources. Briefings in Bioinformatics, 2019, 20, 1754-1768.	6.5	23
3	Chromosomal Heterogeneity of the G-401 Rhabdoid Tumor Cell Line: Unusual Partial 7p Trisomy. Frontiers in Medicine, 2019, 6, 187.	2.6	1
4	XPO1 Inhibitor Selinexor Overcomes Intrinsic Ibrutinib Resistance in Mantle Cell Lymphoma via Nuclear Retention of IκB. Molecular Cancer Therapeutics, 2018, 17, 2564-2574.	4.1	37
5	Chemokine expression in the early response to injury in human airway epithelial cells. PLoS ONE, 2018, 13, e0193334.	2.5	8
6	Strategic Integration of Multiple Bioinformatics Resources for System Level Analysis of Biological Networks. Methods in Molecular Biology, 2017, 1613, 85-99.	0.9	3
7	The functional domains for Baxâ†2 aggregate-mediated caspase 8-dependent cell death. Experimental Cell Research, 2017, 359, 342-355.	2.6	11
8	Extracellular vesicles in gastrointestinal cancer in conjunction with microbiota: On the border of Kingdoms. Biochimica Et Biophysica Acta: Reviews on Cancer, 2017, 1868, 372-393.	7.4	35
9	Lynx: a knowledge base and an analytical workbench for integrative medicine. Nucleic Acids Research, 2016, 44, D882-D887.	14.5	8
10	Disease Gene Prioritization Using Network and Feature. Journal of Computational Biology, 2015, 22, 313-323.	1.6	12
11	Lynx web services for annotations and systems analysis of multi-gene disorders. Nucleic Acids Research, 2014, 42, W473-W477.	14.5	5
12	Lynx: a database and knowledge extraction engine for integrative medicine. Nucleic Acids Research, 2014, 42, D1007-D1012.	14.5	40
13	An Integrative Computational Approach for Prioritization of Genomic Variants. PLoS ONE, 2014, 9, e114903.	2.5	7
14	Microvesicles and intercellular communication in the context of parasitism. Frontiers in Cellular and Infection Microbiology, 2013, 3, 49.	3.9	93
15	Prediction of candidate genes for neuropsychiatric disorders using feature-based enrichment. , 2012, , .		7
16	The BioPAX community standard for pathway data sharing. Nature Biotechnology, 2010, 28, 935-942.	17.5	613
17	Identification of *Francisella tularensis Himar1*-Based Transposon Mutants Defective for Replication in Macrophages. Infection and Immunity, 2007, 75, 5376-5389.	2.2	82
18	PUMA2--grid-based high-throughput analysis of genomes and metabolic pathways. Nucleic Acids Research, 2006, 34, D369-D372.	14.5	59

#	Article	IF	Citations
19	Molecular Mechanisms Involved in Robustness of Yeast Central Metabolism against Null Mutations. Journal of Biochemistry, 2005, 137, 177-187.	1.7	14
20	Sentra, a database of signal transduction proteins. Nucleic Acids Research, 2002, 30, 349-350.	14.5	16