

Mykyta Artomov

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/135389/publications.pdf>

Version: 2024-02-01

21
papers

2,221
citations

623734

14
h-index

713466

21
g-index

31
all docs

31
docs citations

31
times ranked

5503
citing authors

#	ARTICLE	IF	CITATIONS
1	Genotype imputation and polygenic score estimation in northwestern Russian population. PLoS ONE, 2022, 17, e0269434.	2.5	3
2	The 22q11.2 region regulates presynaptic gene-products linked to schizophrenia. Nature Communications, 2022, 13, .	12.8	22
3	Enhanced epigenetic profiling of classical human monocytes reveals a specific signature of healthy aging in the DNA methylome. Nature Aging, 2021, 1, 124-141.	11.6	30
4	Prioritization of disease genes from GWAS using ensemble-based positive-unlabeled learning. European Journal of Human Genetics, 2021, 29, 1527-1535.	2.8	19
5	Classifying Melanoma by TERT Promoter Mutational Status. Journal of Investigative Dermatology, 2020, 140, 390-394.e1.	0.7	16
6	Cancer risks associated with the germline MITF(E318K) variant. Scientific Reports, 2020, 10, 17051.	3.3	20
7	Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. Cell, 2020, 180, 568-584.e23.	28.9	1,422
8	Assessment of genetic variant burden in epilepsy-associated brain lesions. European Journal of Human Genetics, 2019, 27, 1738-1744.	2.8	12
9	Targeted gene sequencing in 6994 individuals with neurodevelopmental disorder with epilepsy. Genetics in Medicine, 2019, 21, 2496-2503.	2.4	45
10	Burden of unique and low prevalence somatic mutations correlates with cancer survival. Scientific Reports, 2019, 9, 4848.	3.3	49
11	Case-control analysis identifies shared properties of rare germline variation in cancer predisposing genes. European Journal of Human Genetics, 2019, 27, 824-828.	2.8	4
12	Use of Targeted Next-Generation Sequencing to Identify Activating Hot Spot Mutations in Cherry Angiomas. JAMA Dermatology, 2019, 155, 211.	4.1	22
13	Improving survival prediction for melanoma. ELife, 2019, 8, .	6.0	3
14	Haplotype Sharing Provides Insights into Fine-Scale Population History and Disease in Finland. American Journal of Human Genetics, 2018, 102, 760-775.	6.2	57
15	Germline Lysine-Specific Demethylase 1 (<i>LSD1/KDM1A</i>) Mutations Confer Susceptibility to Multiple Myeloma. Cancer Research, 2018, 78, 2747-2759.	0.9	56
16	Rare Variant, Gene-Based Association Study of Hereditary Melanoma Using Whole-Exome Sequencing. Journal of the National Cancer Institute, 2017, 109, .	6.3	32
17	Mosaic mutations in blood DNA sequence are associated with solid tumor cancers. Npj Genomic Medicine, 2017, 2, 22.	3.8	10
18	A role for genetic susceptibility in sporadic focal segmental glomerulosclerosis. Journal of Clinical Investigation, 2016, 126, 1067-1078.	8.2	41

#	ARTICLE	IF	CITATIONS
19	Gender Disparity and Mutation Burden in Metastatic Melanoma. Journal of the National Cancer Institute, 2015, 107, djv221.	6.3	114
20	Coordinate linkage of HIV evolution reveals regions of immunological vulnerability. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 11530-11535.	7.1	183
21	Only signaling modules that discriminate sharply between stimulatory and nonstimulatory inputs require basal signaling for fast cellular responses. Journal of Chemical Physics, 2010, 133, 105101.	3.0	5