Aleksandar Milosavljevic

List of Publications by Year
in descending order

49 papers	11,158 citations	201674 27 h-index	243625 44 g-index
57 all docs	57 docs citations	57 times ranked	26564 citing authors

#	Article	IF	Citations
1	MPAPASS software enables stitched multiplex, multidimensional EV repertoire analysis and a standard framework for reporting bead-based assays. Cell Reports Methods, 2022, 2, 100136.	2.9	8
2	Clinical diagnosis of metabolic disorders using untargeted metabolomic profiling and disease-specific networks learned from profiling data. Scientific Reports, 2022, 12, 6556.	3.3	15
3	A community approach to the cancer-variant-interpretation bottleneck. Nature Cancer, 2022, 3, 522-525.	13.2	3
4	Testicular germ cell tumors arise in the absence of sex-specific differentiation. Development (Cambridge), 2021, 148, .	2.5	12
5	ClinGen curation tools, web services and repository for clinical actionability assertions and supporting evidence. Molecular Genetics and Metabolism, 2021, 132, S121-S122.	1.1	0
6	Effective Aspirin Treatment of Women at Risk for Preeclampsia Delays the Metabolic Clock of Gestation. Hypertension, 2021, 78, 1398-1410.	2.7	10
7	Epigenetic and senescence markers indicate an accelerated ageing-like state in women with preeclamptic pregnancies. EBioMedicine, 2021, 70, 103536.	6.1	20
8	CTD: An information-theoretic algorithm to interpret sets of metabolomic and transcriptomic perturbations in the context of graphical models. PLoS Computational Biology, 2021, 17, e1008550.	3.2	8
9	Abstract PO-115: Effects of mesothelin exert on tumor microenvironment in pancreatic ductal adenocarcinoma. , 2021, , .		0
10	Abstract PO-004: Basal-like, Classical A, and Classical B subtypes of pancreatic cancer show distinct immuno-suppressive molecular profiles. , 2021, , .		0
11	Buffy Coat DNA Methylation Profile Is Representative of Methylation Patterns in White Blood Cell Types in Normal Pregnancy. Frontiers in Bioengineering and Biotechnology, 2021, 9, 782843.	4.1	1
12	Histoepigenetic analysis of the mesothelin network within pancreatic ductal adenocarcinoma cells reveals regulation of retinoic acid receptor gamma and AKT by mesothelin. Oncogenesis, 2020, 9, 62.	4.9	5
13	Glioma-Derived miRNA-Containing Extracellular Vesicles Induce Angiogenesis by Reprogramming Brain Endothelial Cells. Cell Reports, 2020, 30, 2065-2074.e4.	6.4	105
14	Guidelines for cell-type heterogeneity quantification based on a comparative analysis of reference-free DNA methylation deconvolution software. BMC Bioinformatics, 2020, 21, 16.	2.6	34
15	Untargeted metabolomic profiling reveals multiple pathway perturbations and new clinical biomarkers in urea cycle disorders. Genetics in Medicine, 2019, 21, 1977-1986.	2.4	47
16	Histoepigenetic analysis of HPV- and tobacco-associated head and neck cancer identifies both subtype-specific and common therapeutic targets despite divergent microenvironments. Oncogene, 2019, 38, 3551-3568.	5.9	20
17	exRNA Atlas Analysis Reveals Distinct Extracellular RNA Cargo Types and Their Carriers Present across Human Biofluids. Cell, 2019, 177, 463-477.e15.	28.9	228
18	The Extracellular RNA Communication Consortium: Establishing Foundational Knowledge and Technologies for Extracellular RNA Research. Cell, 2019, 177, 231-242.	28.9	152

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19	exceRpt: A Comprehensive Analytic Platform for Extracellular RNA Profiling. Cell Systems, 2019, 8, 352-357.e3.	6.2	118
20	ClinGen Allele Registry links information about genetic variants. Human Mutation, 2018, 39, 1690-1701.	2.5	48
21	ClinGen advancing genomic dataâ€sharing standards as a GA4GH driver project. Human Mutation, 2018, 39, 1686-1689.	2.5	15
22	Evidenceâ€based assessments of clinical actionability in the context of secondary findings: Updates from ClinGen's Actionability Working Group. Human Mutation, 2018, 39, 1677-1685.	2.5	34
23	Allele-specific epigenome maps reveal sequence-dependent stochastic switching at regulatory loci. Science, 2018, 361, .	12.6	87
24	ClinGen Pathogenicity Calculator: a configurable system for assessing pathogenicity of genetic variants. Genome Medicine, 2017, 9, 3.	8.2	59
25	Performance of ACMG-AMP Variant-Interpretation Guidelines among Nine Laboratories in the Clinical Sequencing Exploratory Research Consortium. American Journal of Human Genetics, 2016, 98, 1067-1076.	6.2	432
26	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	28.9	404
27	Epigenomic Deconvolution of Breast Tumors Reveals Metabolic Coupling between Constituent Cell Types. Cell Reports, 2016, 17, 2075-2086.	6.4	84
28	Extending gene ontology in the context of extracellular RNA and vesicle communication. Journal of Biomedical Semantics, 2016, 7, 19.	1.6	24
29	Integration of extracellular RNA profiling data using metadata, biomedical ontologies and Linked Data technologies. Journal of Extracellular Vesicles, 2015, 4, 27497.	12.2	48
30	Intermediate DNA methylation is a conserved signature of genome regulation. Nature Communications, 2015, 6, 6363.	12.8	91
31	Epigenomic footprints across 111 reference epigenomes reveal tissue-specific epigenetic regulation of lincRNAs. Nature Communications, 2015, 6, 6370.	12.8	77
32	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	27.8	5,653
33	CDKN2D-WDFY2 Is a Cancer-Specific Fusion Gene Recurrent in High-Grade Serous Ovarian Carcinoma. PLoS Genetics, 2014, 10, e1004216.	3.5	41
34	Confounding by Repetitive Elements and CpG Islands Does Not Explain the Association between Hypomethylation and Genomic Instability. PLoS Genetics, 2013, 9, e1003333.	3.5	3
35	Genomic Hypomethylation in the Human Germline Associates with Selective Structural Mutability in the Human Genome. PLoS Genetics, 2012, 8, e1002692.	3.5	80
36	An integrative variant analysis suite for whole exome next-generation sequencing data. BMC Bioinformatics, 2012, 13, 8.	2.6	252

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37	ReadDepth: A Parallel R Package for Detecting Copy Number Alterations from Short Sequencing Reads. PLoS ONE, 2011, 6, e16327.	2.5	193
38	Emerging patterns of epigenomic variation. Trends in Genetics, 2011, 27, 242-250.	6.7	33
39	Enabling Atlas2 personal genome analysis on the cloud. , 2011, , .		3
40	Pash 3.0: A versatile software package for read mapping and integrative analysis of genomic and epigenomic variation using massively parallel DNA sequencing. BMC Bioinformatics, 2010, 11, 572.	2.6	48
41	Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. Nature Biotechnology, 2010, 28, 1097-1105.	17.5	647
42	The NIH Roadmap Epigenomics Mapping Consortium. Nature Biotechnology, 2010, 28, 1045-1048.	17.5	1,705
43	Putting epigenome comparison into practice. Nature Biotechnology, 2010, 28, 1053-1056.	17.5	7
44	Proinflammatory Role for let-7 MicroRNAS in Experimental Asthma. Journal of Biological Chemistry, 2010, 285, 30139-30149.	3.4	222
45	Clinical Evaluation of a Custom Genome Wide 44K Oligoarray for Copy Number Changes in Acute Myeloid Leukemia. Blood, 2008, 112, 4869-4869.	1.4	0
46	Designing new microsatellite markers for linkage and population genetic analyses in rhesus macaques and other nonhuman primates. Genomics, 2006, 88, 706-710.	2.9	16
47	Comparative analysis for mapping and sequence assembly. , 2005, , .		0
48	Pooled genomic indexing of rhesus macaque. Genome Research, 2005, 15, 292-301.	5.5	14
49	Discovering simple DNA sequences by the algorithmic significance method. Bioinformatics, 1993, 9, 407-411.	4.1	33