

Arkadiusz Piotrowski

List of Publications by Year in descending order

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Version: 2024-02-01

62
papers

2,632
citations

201575

27
h-index

189801

50
g-index

66
all docs

66
docs citations

66
times ranked

4778
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive cancer-oriented biobanking resource of human samples for studies of post-zygotic genetic variation involved in cancer predisposition. <i>PLoS ONE</i> , 2022, 17, e0266111.	1.1	4
2	Regenerative Drug Discovery Using Ear Pinna Punch Wound Model in Mice. <i>Pharmaceuticals</i> , 2022, 15, 610.	1.7	2
3	High prevalence of somatic PIK3CA and TP53 pathogenic variants in the normal mammary gland tissue of sporadic breast cancer patients revealed by duplex sequencing. <i>Npj Breast Cancer</i> , 2022, 8, .	2.3	8
4	Immune cells lacking Y chromosome show dysregulation of autosomal gene expression. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 4019-4033.	2.4	54
5	PTD4 Peptide Increases Neural Viability in an In Vitro Model of Acute Ischemic Stroke. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6086.	1.8	5
6	Targeted massively parallel sequencing of candidate regions on chromosome 22q predisposing to multiple schwannomas: an analysis of 51 individuals in a single center experience. <i>Human Mutation</i> , 2021, , .	1.1	3
7	Development of a Peptide Derived from Platelet-Derived Growth Factor (PDGF-BB) into a Potential Drug Candidate for the Treatment of Wounds. <i>Advances in Wound Care</i> , 2020, 9, 657-675.	2.6	18
8	FRAX prognostic and intervention thresholds in the management of major bone fractures in hemodialysis patients: A two-year prospective multicenter cohort study. <i>Bone</i> , 2020, 133, 115188.	1.4	6
9	A vector-enzymatic DNA fragment amplification-expression technology for construction of artificial, concatemeric DNA, RNA and proteins for novel biomaterials, biomedical and industrial applications. <i>Materials Science and Engineering C</i> , 2020, 108, 110426.	3.8	8
10	Imunofanâ€”RDKVYR Peptideâ€”Stimulates Skin Cell Proliferation and Promotes Tissue Repair. <i>Molecules</i> , 2020, 25, 2884.	1.7	8
11	Data regarding a new, vector-enzymatic DNA fragment amplification-expression technology for the construction of artificial, concatemeric DNA, RNA and proteins, as well as biological effects of selected polypeptides obtained using this method. <i>Data in Brief</i> , 2020, 28, 105069.	0.5	4
12	Epigenetic inhibitor zebularine activates ear pinna wound closure in the mouse. <i>EBioMedicine</i> , 2019, 46, 317-329.	2.7	17
13	Draft Genome Sequence of <i>Paracoccus</i> sp. Strain 228, Isolated from Surface Water of the Gulf of GdaÅ„sk in the Baltic Sea. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
14	Immunophenotyping and transcriptional profiling of in vitro cultured human adipose tissue derived stem cells. <i>Scientific Reports</i> , 2018, 8, 11339.	1.6	31
15	High-Throughput Tabular Data Processor â€” Platform independent graphical tool for processing large data sets. <i>PLoS ONE</i> , 2018, 13, e0192858.	1.1	1
16	Alternative outcomes of pathogenic complex somatic structural variations in the genomes of NF1 and NF2 patients. <i>Neurogenetics</i> , 2017, 18, 169-174.	0.7	0
17	miR-200b downregulates Kruppel Like Factor 2 (KLF2) during acute hypoxia in human endothelial cells. <i>European Journal of Cell Biology</i> , 2017, 96, 758-766.	1.6	40
18	Mild hypothermia provides Treg stability. <i>Scientific Reports</i> , 2017, 7, 11915.	1.6	20

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19	Molecular bases of aberrant miR-182 expression in ovarian cancer. <i>Genes Chromosomes and Cancer</i> , 2016, 55, 877-889.	1.5	13
20	Draft Genome Sequence of <i>Flavobacterium</i> sp. 316, a Baltic Sea Isolate Exhibiting a High Level of Resistance to Marine Stress Conditions. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
21	Codon bias and the folding dynamics of the cystic fibrosis transmembrane conductance regulator. <i>Cellular and Molecular Biology Letters</i> , 2016, 21, 23.	2.7	32
22	miR-429 regulates the transition between Hypoxia-Inducible Factor (HIF)1A and HIF3A expression in human endothelial cells. <i>Scientific Reports</i> , 2016, 6, 22775.	1.6	55
23	Concurrent DNA Copy-Number Alterations and Mutations in Genes Related to Maintenance of Genome Stability in Uninvolved Mammary Glandular Tissue from Breast Cancer Patients. <i>Human Mutation</i> , 2015, 36, 1088-1099.	1.1	11
24	The hypoxia-inducible miR-429 regulates hypoxia-inducible factor-1 α expression in human endothelial cells through a negative feedback loop. <i>FASEB Journal</i> , 2015, 29, 1467-1479.	0.2	104
25	Decoding NF1 Intragenic Copy-Number Variations. <i>American Journal of Human Genetics</i> , 2015, 97, 238-249.	2.6	24
26	Signatures of post-zygotic structural genetic aberrations in the cells of histologically normal breast tissue that can predispose to sporadic breast cancer. <i>Genome Research</i> , 2015, 25, 1521-1535.	2.4	25
27	Palindrome-Mediated and Replication-Dependent Pathogenic Structural Rearrangements within the <i>NF1</i> Gene. <i>Human Mutation</i> , 2014, 35, 891-898.	1.1	13
28	The signal transducers Stat1 and Stat3 and their novel target <i>Jmjd3</i> drive the expression of inflammatory genes in microglia. <i>Journal of Molecular Medicine</i> , 2014, 92, 239-254.	1.7	158
29	Germline loss-of-function mutations in <i>LZTR1</i> predispose to an inherited disorder of multiple schwannomas. <i>Nature Genetics</i> , 2014, 46, 182-187.	9.4	242
30	Integration of genome-wide of Stat3 binding and epigenetic modification mapping with transcriptome reveals novel Stat3 target genes in glioma cells. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 1341-1350.	0.9	13
31	A genome-wide transcriptional profiling of sporulating <i>Bacillus subtilis</i> strain lacking PrpE protein phosphatase. <i>Molecular Genetics and Genomics</i> , 2013, 288, 469-481.	1.0	0
32	Regulation of the unfolded protein response by microRNAs. <i>Cellular and Molecular Biology Letters</i> , 2013, 18, 555-78.	2.7	49
33	Post-Zygotic and Inter-Individual Structural Genetic Variation in a Presumptive Enhancer Element of the Locus between the <i>IL10R1</i> and <i>IFNAR1</i> Genes. <i>PLoS ONE</i> , 2013, 8, e67752.	1.1	2
34	Structural Genetic Variation in the Context of Somatic Mosaicism. <i>Methods in Molecular Biology</i> , 2012, 838, 249-272.	0.4	34
35	Regeneration of comparative genomic hybridization oligonucleotide microarrays with dimethylurea. <i>Analytical Biochemistry</i> , 2012, 426, 91-93.	1.1	5
36	Age-Related Somatic Structural Changes in the Nuclear Genome of Human Blood Cells. <i>American Journal of Human Genetics</i> , 2012, 90, 217-228.	2.6	168

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37	Frequent genetic differences between matched primary and metastatic breast cancer provide an approach to identification of biomarkers for disease progression. <i>European Journal of Human Genetics</i> , 2010, 18, 560-568.	1.4	42
38	Recurrent genomic alterations in benign and malignant pheochromocytomas and paragangliomas revealed by whole-genome array comparative genomic hybridization analysis. <i>Endocrine-Related Cancer</i> , 2010, 17, 561-579.	1.6	29
39	Characterization of novel and complex genomic aberrations in glioblastoma using a 32K BAC array. <i>Neuro-Oncology</i> , 2009, 11, 803-818.	0.6	43
40	Profiling of copy number variations (CNVs) in healthy individuals from three ethnic groups using a human genome 32â€‰%K BAC-clone-based array. <i>Human Mutation</i> , 2008, 29, 398-408.	1.1	46
41	Somatic mosaicism for copy number variation in differentiated human tissues. <i>Human Mutation</i> , 2008, 29, 1118-1124.	1.1	184
42	Distal 22q11.2 microduplication encompassing the <i>BCR</i> gene. <i>American Journal of Medical Genetics, Part A</i> , 2008, 146A, 3075-3081.	0.7	30
43	Phenotypically Concordant and Discordant Monozygotic Twins Display Different DNA Copy-Number-Variation Profiles. <i>American Journal of Human Genetics</i> , 2008, 82, 763-771.	2.6	533
44	A segmental maximum a posteriori approach to genome-wide copy number profiling. <i>Bioinformatics</i> , 2008, 24, 751-758.	1.8	29
45	The Mechanism of Cystic Fibrosis Transmembrane Conductance Regulator Transcriptional Repression during the Unfolded Protein Response. <i>Journal of Biological Chemistry</i> , 2008, 283, 12154-12165.	1.6	66
46	Overlapping phenotype of Wolfâ€™Hirschhorn and Beckwithâ€™Wiedemann syndromes in a girl with der(4)t(4;11)(pter;pter). <i>American Journal of Medical Genetics, Part A</i> , 2007, 143A, 1760-1766.	0.7	5
47	A previously unrecognized microdeletion syndrome on chromosome 22 band q11.2 encompassing the <i>BCR</i> gene. <i>American Journal of Medical Genetics, Part A</i> , 2007, 143A, 2178-2184.	0.7	42
48	Comprehensive genetic and epigenetic analysis of sporadic meningioma for macro-mutations on 22q and micro-mutations within the NF2 locus. <i>BMC Genomics</i> , 2007, 8, 16.	1.2	67
49	Analysis of copy number variation in the normal human population within a region containing complex segmental duplications on 22q11 using high-resolution array-CGH. <i>Genomics</i> , 2006, 88, 152-162.	1.3	13
50	Chromosome 22 array-CGH profiling of breast cancer delimited minimal common regions of genomic imbalances and revealed frequent intra-tumoral genetic heterogeneity. <i>International Journal of Oncology</i> , 2006, 29, 935.	1.4	5
51	Microarray-based survey of CpG islands identifies concurrent hyper- and hypomethylation patterns in tissues derived from patients with breast cancer. <i>Genes Chromosomes and Cancer</i> , 2006, 45, 656-667.	1.5	40
52	Detailed assessment of chromosome 22 aberrations in sporadic pheochromocytoma using array-CGH. <i>International Journal of Cancer</i> , 2006, 118, 1159-1164.	2.3	24
53	The Phytochemical and Genetic Survey of Common and Dwarf Juniper (<i>Juniperus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 107 Tj <i>Planta Medica</i> , 2006, 72, 850-853.	0.7	23
54	Chromosome 22 array-CGH profiling of breast cancer delimited minimal common regions of genomic imbalances and revealed frequent intra-tumoral genetic heterogeneity. <i>International Journal of Oncology</i> , 2006, 29, 935-45.	1.4	15

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55	Two-Stage System for Micropropagation of Several Genista Plants Producing Large Amounts of Phytoestrogens. Zeitschrift Fur Naturforschung - Section C Journal of Biosciences, 2005, 60, 557-566.	0.6	12
56	Copy-number polymorphisms: mining the tip of an iceberg. Trends in Genetics, 2005, 21, 315-317.	2.9	45
57	Chromosome 22 tiling-path array-CGH analysis identifies germ-line- and tumor-specific aberrations in patients with glioblastoma multiforme. Genes Chromosomes and Cancer, 2005, 44, 161-169.	1.5	30
58	Identification of genetic aberrations on chromosome 22 outside theNF2locus in schwannomatosis and neurofibromatosis type 2. Human Mutation, 2005, 26, 540-549.	1.1	29
59	High-resolution array-CGH profiling of germline and tumor-specific copy number alterations on chromosome 22 in patients affected with schwannomas. Human Genetics, 2005, 118, 35-44.	1.8	19
60	Identification of novel deletion breakpoints bordered by segmental duplications in the NF1 locus using high resolution array-CGH. Journal of Medical Genetics, 2005, 43, 28-38.	1.5	49
61	Molecular Genetic Survey of European Mistletoe (<i>Viscum album</i>) Subspecies with Allele-Specific and dCAPS Type Markers Specific for Chloroplast and Nuclear DNA Sequences. Planta Medica, 2003, 69, 939-944.	0.7	3
62	Biologically active compounds from European mistletoe (<i>Viscum album</i> L.) ¹ . Canadian Journal of Plant Pathology, 2002, 24, 21-28.	0.8	29