Arkadiusz Piotrowski

List of Publications by Year
in descending order

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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	Phenotypically Concordant and Discordant Monozygotic Twins Display Different DNA Copy-Number-Variation Profiles. American Journal of Human Genetics, 2008, 82, 763-771.	2.6	533
2	Germline loss-of-function mutations in LZTR1 predispose to an inherited disorder of multiple schwannomas. Nature Genetics, 2014, 46, 182-187.	9.4	242
3	Somatic mosaicism for copy number variation in differentiated human tissues. Human Mutation, 2008, 29, 1118-1124.	1.1	184
4	Age-Related Somatic Structural Changes in the Nuclear Genome of Human Blood Cells. American Journal of Human Genetics, 2012, 90, 217-228.	2.6	168
5	The signal transducers Stat1 and Stat3 and their novel target Jmjd3 drive the expression of inflammatory genes in microglia. Journal of Molecular Medicine, 2014, 92, 239-254.	1.7	158
6	The hypoxiaâ€inducible miRâ€429 regulates hypoxiaâ€inducible factorâ€1Î± expression in human endothelial cells through a negative feedback loop. FASEB Journal, 2015, 29, 1467-1479.	0.2	104
7	Comprehensive genetic and epigenetic analysis of sporadic meningioma for macro-mutations on 22q and micro-mutations within the NF2 locus. BMC Genomics, 2007, 8, 16.	1.2	67
8	The Mechanism of Cystic Fibrosis Transmembrane Conductance Regulator Transcriptional Repression during the Unfolded Protein Response. Journal of Biological Chemistry, 2008, 283, 12154-12165.	1.6	66
9	miR-429 regulates the transition between Hypoxia-Inducible Factor (HIF)1A and HIF3A expression in human endothelial cells. Scientific Reports, 2016, 6, 22775.	1.6	55
10	Immune cells lacking Y chromosome show dysregulation of autosomal gene expression. Cellular and Molecular Life Sciences, 2021, 78, 4019-4033.	2.4	54
11	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
12	Regulation of the unfolded protein response by microRNAs. Cellular and Molecular Biology Letters, 2013, 18, 555-78.	2.7	49
13	Profiling of copy number variations (CNVs) in healthy individuals from three ethnic groups using a human genome 32â€‰K BAC-clone-based array. Human Mutation, 2008, 29, 398-408.	1.1	46
14	Copy-number polymorphisms: mining the tip of an iceberg. Trends in Genetics, 2005, 21, 315-317.	2.9	45
15	Characterization of novel and complex genomic aberrations in glioblastoma using a 32K BAC array. Neuro-Oncology, 2009, 11, 803-818.	0.6	43
16	A previously unrecognized microdeletion syndrome on chromosome 22 band q11.2 encompassing the BCR gene. American Journal of Medical Genetics, Part A, 2007, 143A, 2178-2184.	0.7	42
17	Frequent genetic differences between matched primary and metastatic breast cancer provide an approach to identification of biomarkers for disease progression. European Journal of Human Genetics, 2010, 18, 560-568.	1.4	42
18	Microarray-based survey of CpG islands identifies concurrent hyper- and hypomethylation patterns in tissues derived from patients with breast cancer. Genes Chromosomes and Cancer, 2006, 45, 656-667.	1.5	40

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19	miR-200b downregulates Kruppel Like Factor 2 (KLF2) during acute hypoxia in human endothelial cells. European Journal of Cell Biology, 2017, 96, 758-766.	1.6	40
20	Structural Genetic Variation in the Context of Somatic Mosaicism. Methods in Molecular Biology, 2012, 838, 249-272.	0.4	34
21	Codon bias and the folding dynamics of the cystic fibrosis transmembrane conductance regulator. Cellular and Molecular Biology Letters, 2016, 21, 23.	2.7	32
22	Immunophenotyping and transcriptional profiling of in vitro cultured human adipose tissue derived stem cells. Scientific Reports, 2018, 8, 11339.	1.6	31
23	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
24	Distal 22q11.2 microduplication encompassing the BCR gene. American Journal of Medical Genetics, Part A, 2008, 146A, 3075-3081.	0.7	30
25	Biologically active compounds from European mistletoe (Viscum albumL.)¹. Canadian Journal of Plant Pathology, 2002, 24, 21-28.	0.8	29
26	Identification of genetic aberrations on chromosome 22 outside theNF2locus in schwannomatosis and neurofibromatosis type 2. Human Mutation, 2005, 26, 540-549.	1.1	29
27	A segmental maximum a posteriori approach to genome-wide copy number profiling. Bioinformatics, 2008, 24, 751-758.	1.8	29
28	Recurrent genomic alterations in benign and malignant pheochromocytomas and paragangliomas revealed by whole-genome array comparative genomic hybridization analysis. Endocrine-Related Cancer, 2010, 17, 561-579.	1.6	29
29	Signatures of post-zygotic structural genetic aberrations in the cells of histologically normal breast tissue that can predispose to sporadic breast cancer. Genome Research, 2015, 25, 1521-1535.	2.4	25
30	Detailed assessment of chromosome 22 aberrations in sporadic pheochromocytoma using array-CGH. International Journal of Cancer, 2006, 118, 1159-1164.	2.3	24
31	Decoding NF1 Intragenic Copy-Number Variations. American Journal of Human Genetics, 2015, 97, 238-249.	2.6	24
32	The Phytochemical and Genetic Survey of Common and Dwarf Juniper (Juniperus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 227 Td (commun Planta Medica, 2006, 72, 850-853.	0.7	23
33	Mild hypothermia provides Treg stability. Scientific Reports, 2017, 7, 11915.	1.6	20
34	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
35	Development of a Peptide Derived from Platelet-Derived Growth Factor (PDGF-BB) into a Potential Drug Candidate for the Treatment of Wounds. Advances in Wound Care, 2020, 9, 657-675.	2.6	18
36	Epigenetic inhibitor zebularine activates ear pinna wound closure in the mouse. EBioMedicine, 2019, 46, 317-329.	2.7	17

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37	Chromosome 22 array-CGH profiling of breast cancer delimited minimal common regions of genomic imbalances and revealed frequent intra-tumoral genetic heterogeneity. International Journal of Oncology, 2006, 29, 935-45.	1.4	15
38	Analysis of copy number variation in the normal human population within a region containing complex segmental duplications on 22q11 using high-resolution array-CGH. Genomics, 2006, 88, 152-162.	1.3	13
39	Palindrome-Mediated and Replication-Dependent Pathogenic Structural Rearrangements within theNF1Gene. Human Mutation, 2014, 35, 891-898.	1.1	13
40	Integration of genome-wide of Stat3 binding and epigenetic modification mapping with transcriptome reveals novel Stat3 target genes in glioma cells. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2014, 1839, 1341-1350.	0.9	13
41	Molecular bases of aberrant miRâ€182 expression in ovarian cancer. Genes Chromosomes and Cancer, 2016, 55, 877-889.	1.5	13
42	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
43	Concurrent DNA Copy-Number Alterations and Mutations in Genes Related to Maintenance of Genome Stability in Uninvolved Mammary Glandular Tissue from Breast Cancer Patients. Human Mutation, 2015, 36, 1088-1099.	1.1	11
44	A vector-enzymatic DNA fragment amplification-expression technology for construction of artificial, concatemeric DNA, RNA and proteins for novel biomaterials, biomedical and industrial applications. Materials Science and Engineering C, 2020, 108, 110426.	3.8	8
45	Imunofanâ€”RDKVYR Peptideâ€”Stimulates Skin Cell Proliferation and Promotes Tissue Repair. Molecules, 2020, 25, 2884.	1.7	8
46	High prevalence of somatic PIK3CA and TP53 pathogenic variants in the normal mammary gland tissue of sporadic breast cancer patients revealed by duplex sequencing. Npj Breast Cancer, 2022, 8, .	2.3	8
47	FRAX prognostic and intervention thresholds in the management of major bone fractures in hemodialysis patients: A two-year prospective multicenter cohort study. Bone, 2020, 133, 115188.	1.4	6
48	Chromosome 22 array-CGH profiling of breast cancer delimited minimal common regions of genomic imbalances and revealed frequent intra-tumoral genetic heterogeneity. International Journal of Oncology, 2006, 29, 935.	1.4	5
49	Overlapping phenotype of Wolfâ€“Hirschhorn and Beckwithâ€“Wiedemann syndromes in a girl with der(4)t(4;11)(pter;pter). American Journal of Medical Genetics, Part A, 2007, 143A, 1760-1766.	0.7	5
50	Regeneration of comparative genomic hybridization oligonucleotide microarrays with dimethylurea. Analytical Biochemistry, 2012, 426, 91-93.	1.1	5
51	PTD4 Peptide Increases Neural Viability in an In Vitro Model of Acute Ischemic Stroke. International Journal of Molecular Sciences, 2021, 22, 6086.	1.8	5
52	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. Data in Brief, 2020, 28, 105069.	0.5	4
53	Comprehensive cancer-oriented biobanking resource of human samples for studies of post-zygotic genetic variation involved in cancer predisposition. PLoS ONE, 2022, 17, e0266111.	1.1	4
54	Molecular Genetic Survey of European Mistletoe (Viscum album) Subspecies with Allele-Specific and dCAPS Type Markers Specific for Chloroplast and Nuclear DNA Sequences. Planta Medica, 2003, 69, 939-944.	0.7	3

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55	Targeted massively parallel sequencing of candidate regions on chromosome 22q predisposing to multiple schwannomas: an analysis of 51 individuals in a single center experience. Human Mutation, 2021, , .	1.1	3
56	Post-Zygotic and Inter-Individual Structural Genetic Variation in a Presumptive Enhancer Element of the Locus between the IL10RÎ² and IFNAR1 Genes. PLoS ONE, 2013, 8, e67752.	1.1	2
57	Regenerative Drug Discovery Using Ear Pinna Punch Wound Model in Mice. Pharmaceuticals, 2022, 15, 610.	1.7	2
58	Draft Genome Sequence of Flavobacterium sp. 316, a Baltic Sea Isolate Exhibiting a High Level of Resistance to Marine Stress Conditions. Genome Announcements, 2016, 4, .	0.8	1
59	Draft Genome Sequence of Paracoccus sp. Strain 228, Isolated from Surface Water of the Gulf of GdaÅ„sk in the Baltic Sea. Microbiology Resource Announcements, 2019, 8, .	0.3	1
60	High-Throughput Tabular Data Processor â€“ Platform independent graphical tool for processing large data sets. PLoS ONE, 2018, 13, e0192858.	1.1	1
61	A genome-wide transcriptional profiling of sporulating Bacillus subtilis strain lacking PrpE protein phosphatase. Molecular Genetics and Genomics, 2013, 288, 469-481.	1.0	0
62	Alternative outcomes of pathogenic complex somatic structural variations in the genomes of NF1 and NF2 patients. Neurogenetics, 2017, 18, 169-174.	0.7	0