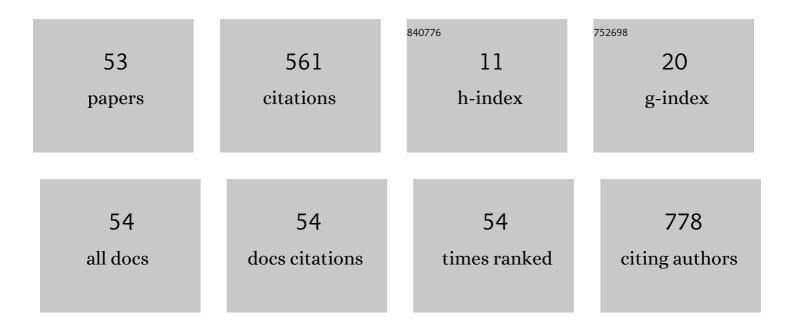
Tomasz SzmatoÅ,a

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7941548/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	MicroRNA gene methylation landscape in pediatric B-cell precursor acute lymphoblastic leukemia. Advances in Clinical and Experimental Medicine, 2022, 31, 0-0.	1.4	1
2	The Induced Expression of BPV E4 Gene in Equine Adult Dermal Fibroblast Cells as a Potential Model of Skin Sarcoid-like Neoplasia. International Journal of Molecular Sciences, 2022, 23, 1970.	4.1	7
3	Feeding pigs with coconut oil affects their adipose miRNA profile. Molecular Biology Reports, 2022, , 1.	2.3	Ο
4	Assessment of BPV-1 Mediated Matrix Metalloproteinase Genes Deregulation in the In Vivo and In Vitro Models Designed to Explore Molecular Nature of Equine Sarcoids. Cells, 2022, 11, 1268.	4.1	5
5	Tracking the Molecular Scenarios for Tumorigenic Remodeling of Extracellular Matrix Based on Gene Expression Profiling in Equine Skin Neoplasia Models. International Journal of Molecular Sciences, 2022, 23, 6506.	4.1	2
6	Maternal atopy and offspring epigenome-wide methylation signature. Epigenetics, 2021, 16, 629-641.	2.7	10
7	Suitability of Pedigree Information and Genomic Methods for Analyzing Inbreeding of Polish Cold-Blooded Horses Covered by Conservation Programs. Genes, 2021, 12, 429.	2.4	12
8	Transcriptome Profiling of the Retained Fetal Membranes—An Insight in the Possible Pathogenesis of the Disease. Animals, 2021, 11, 675.	2.3	1
9	Single Nucleotide Polymorphisms in Genes Encoding Toll-Like Receptors 7 and 8 and Their Association with Proviral Load of SRLVs in Goats of Polish Carpathian Breed. Animals, 2021, 11, 1908.	2.3	6
10	Single Nucleotide Polymorphism Discovery and Genetic Differentiation Analysis of Geese Bred in Poland, Using Genotyping-by-Sequencing (GBS). Genes, 2021, 12, 1074.	2.4	8
11	Evaluation of genetic differentiation and genome-wide selection signatures in Polish local sheep breeds. Livestock Science, 2021, 251, 104635.	1.6	7
12	The Identification of a Novel Fucosidosis-Associated FUCA1 Mutation: A Case of a 5-Year-Old Polish Girl with Two Additional Rare Chromosomal Aberrations and Affected DNA Methylation Patterns. Genes, 2021, 12, 74.	2.4	3
13	Pet ownership in pregnancy and methylation pattern in cord blood. Genes and Immunity, 2021, 22, 305-312.	4.1	0
14	Transcriptome Analysis for Genes Associated with Small Ruminant Lentiviruses Infection in Goats of Carpathian Breed. Viruses, 2021, 13, 2054.	3.3	8
15	Comparison of linkage disequilibrium, effective population size and haplotype blocks in Polish Landrace and Polish native pig populations. Livestock Science, 2020, 231, 103887.	1.6	11
16	Divergent selection signatures of phenotypic and production traits among conserved and commercial cattle breeds. Livestock Science, 2020, 239, 104174.	1.6	1
17	Runs of Homozygosity in Modern Chicken Revealed by Sequence Data. G3: Genes, Genomes, Genetics, 2020, 10, 4615-4623.	1.8	25
18	3′quant mRNA-Seq of Porcine Liver Reveals Alterations in UPR, Acute Phase Response, and Cholesterol and Bile Acid Metabolism in Response to Different Dietary Fats. Genes, 2020, 11, 1087.	2.4	3

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19	Detection of runs of homozygosity in conserved and commercial pig breeds in Poland. Journal of Animal Breeding and Genetics, 2020, 137, 571-580.	2.0	19
20	Identification of Molecular Mechanisms Related to Pig Fatness at the Transcriptome and miRNAome Levels. Genes, 2020, 11, 600.	2.4	9
21	Genetic Differentiation of the Two Types of Polish Cold-blooded Horses Included in the National Conservation Program. Animals, 2020, 10, 542.	2.3	4
22	A detailed characteristics of bias associated with long runs of homozygosity identification based on medium density SNP microarrays. Journal of Genomics, 2020, 8, 43-48.	0.9	3
23	Short communication: Locus-specific interrelations between gene expression and DNA methylation patterns in bovine mammary gland infected by coagulase-positive and coagulase-negative staphylococci. Journal of Dairy Science, 2020, 103, 10689-10695.	3.4	7
24	Mobility and Invasion Related Gene Expression Patterns in Equine Sarcoid. Animals, 2020, 10, 880.	2.3	1
25	MicroRNA profiling of the pig periaqueductal grey (PAG) region reveals candidates potentially related to sex-dependent differences. Biology of Sex Differences, 2020, 11, 67.	4.1	1
26	Identification of mRNA Degradome Variation Dependent on Divergent Muscle Mass in Different Pig Breeds. Annals of Animal Science, 2020, 20, 1241-1256.	1.6	0
27	The Blood and Muscle Expression Pattern of the Equine TCAP Gene during the Race Track Training of Arabian Horses. Animals, 2019, 9, 574.	2.3	2
28	The use of the SLC16A1 gene as a potential marker to predict race performance in Arabian horses. BMC Genetics, 2019, 20, 73.	2.7	8
29	An Evaluation of the Genetic Structure of Geese Maintained in Poland on the Basis of Microsatellite Markers. Animals, 2019, 9, 737.	2.3	6
30	Induced androgenetic development in rainbow trout and transcriptome analysis of irradiated eggs. Scientific Reports, 2019, 9, 8084.	3.3	7
31	Evaluation of genotyping by sequencing for population genetics of sibling and hybridizing birds: an example using Syrian and Great Spotted Woodpeckers. Journal of Ornithology, 2019, 160, 287-294.	1.1	5
32	Alterations in the rainbow trout (<i>Oncorhynchus mykiss</i>) eggs exposed to ionizing radiation during induced androgenesis. Reproduction in Domestic Animals, 2019, 54, 712-718.	1.4	6
33	A genome-wide scan for diversifying selection signatures in selected horse breeds. PLoS ONE, 2019, 14, e0210751.	2.5	52
34	A Comprehensive Analysis of Runs of Homozygosity of Eleven Cattle Breeds Representing Different Production Types. Animals, 2019, 9, 1024.	2.3	36
35	Source of Dietary Fat in Pig Diet Affects Adipose Expression of Genes Related to Cancer, Cardiovascular, and Neurodegenerative Diseases. Genes, 2019, 10, 948.	2.4	6
36	Genotyping-by-sequencing performance in selected livestock species. Genomics, 2019, 111, 186-195.	2.9	50

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37	Variant calling from RNA-seq data of the brain transcriptome of pigs and its application for allele-specific expression and imprinting analysis. Gene, 2018, 641, 367-375.	2.2	8
38	The distinguishable DNA whole genome methylation profile of 2 cases of pediatric precursor B acute lymphoblastic leukaemia (BCP ALL) with prodromal, preleukemic phase. Medicine (United States), 2018, 97, e12763.	1.0	0
39	A genome-wide detection of selection signatures in conserved and commercial pig breeds maintained in Poland. BMC Genetics, 2018, 19, 95.	2.7	31
40	Corn dried distillers grains with solubles (cDDGS) in the diet of pigs change the expression of adipose genes that are potential therapeutic targets in metabolic and cardiovascular diseases. BMC Genomics, 2018, 19, 864.	2.8	7
41	Transcriptome Analysis of Rainbow Trout (<i>Oncorhynchus mykiss</i>) Eggs Subjected to the High Hydrostatic Pressure Treatment. International Journal of Genomics, 2018, 2018, 1-7.	1.6	4
42	Evaluation of changes arising in the pig mesenchymal stromal cells transcriptome following cryopreservation and Trichostatin A treatment. PLoS ONE, 2018, 13, e0192147.	2.5	5
43	Genetic variability in equine GDF9 and BMP15 genes in Arabian and Thoroughbred mares. Annals of Animal Science, 2018, 18, 39-52.	1.6	2
44	The effect of histone deacetylase inhibitor trichostatin A on porcine mesenchymal stem cell transcriptome. Biochimie, 2017, 139, 56-73.	2.6	8
45	Comprehensive characteristics of microRNA expression profile of equine sarcoids. Biochimie, 2017, 137, 20-28.	2.6	16
46	Transcript variants of a region on SSC15 rich in QTLs associated with meat quality in pigs. Annals of Animal Science, 2017, 17, 703-715.	1.6	7
47	Genomic landscape of copy number variation and copy neutral loss of heterozygosity events in equine sarcoids reveals increased instability of the sarcoid genome. Biochimie, 2017, 140, 122-132.	2.6	5
48	Variation in TBX3 Gene Region in Dun Coat Color Polish Konik Horses. Journal of Equine Veterinary Science, 2017, 49, 60-62.	0.9	11
49	Whole-genome DNA methylation characteristics in pediatric precursor B cell acute lymphoblastic leukemia (BCP ALL). PLoS ONE, 2017, 12, e0187422.	2.5	8
50	The Genetic Structure of Five Pig Breeds Maintained in Poland. Annals of Animal Science, 2016, 16, 1019-1027.	1.6	2
51	Characteristics of runs of homozygosity in selected cattle breeds maintained in Poland. Livestock Science, 2016, 188, 72-80.	1.6	79
52	Shifts in rDNA levels act as a genome buffer promoting chromosome homeostasis. Cell Cycle, 2015, 14, 3475-3487.	2.6	11
53	The application of genome-wide SNP genotyping methods in studies on livestock genomes. Journal of Applied Genetics, 2014, 55, 197-208.	1.9	24