

# Artur Gurgul

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/468552/publications.pdf>

Version: 2024-02-01

87  
papers

1,038  
citations

516215

16  
h-index

525886

27  
g-index

90  
all docs

90  
docs citations

90  
times ranked

1313  
citing authors

#	ARTICLE	IF	CITATIONS
1	Investigation of genetic diversity and selection signatures in Czech cattle genetic resources revealed by genome-wide analysis. <i>Livestock Science</i> , 2022, 256, 104825.	0.6	2
2	MicroRNA gene methylation landscape in pediatric B-cell precursor acute lymphoblastic leukemia. <i>Advances in Clinical and Experimental Medicine</i> , 2022, 31, 0-0.	0.6	1
3	Another lesson from unmapped reads: in-depth analysis of RNA-Seq reads from various horse tissues. <i>Journal of Applied Genetics</i> , 2022, 63, 571-581.	1.0	2
4	Next-Generation Sequencing analysis discloses genes implicated in equine endometriosis that may lead to tumorigenesis. <i>Theriogenology</i> , 2022, 189, 158-166.	0.9	3
5	Maternal atopy and offspring epigenome-wide methylation signature. <i>Epigenetics</i> , 2021, 16, 629-641.	1.3	10
6	Common Myelin Regulatory Factor Gene Variants Predisposing to Excellence in Sports. <i>Genes</i> , 2021, 12, 262.	1.0	2
7	A genome-wide association study for prolificacy in three Polish sheep breeds. <i>Journal of Applied Genetics</i> , 2021, 62, 323-326.	1.0	11
8	Analysis of the Gut Mycobiome in Adult Patients with Type 1 and Type 2 Diabetes Using Next-Generation Sequencing (NGS) with Increased Sensitivityâ€”Pilot Study. <i>Nutrients</i> , 2021, 13, 1066.	1.7	16
9	Suitability of Pedigree Information and Genomic Methods for Analyzing Inbreeding of Polish Cold-Blooded Horses Covered by Conservation Programs. <i>Genes</i> , 2021, 12, 429.	1.0	12
10	Lipid droplets in mammalian eggs are utilized during embryonic diapause. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	37
11	Application of the targeted sequencing approach reveals the single nucleotide polymorphism (SNP) repertoire in microRNA genes in the pig genome. <i>Scientific Reports</i> , 2021, 11, 9848.	1.6	5
12	Single Nucleotide Polymorphism Discovery and Genetic Differentiation Analysis of Geese Bred in Poland, Using Genotyping-by-Sequencing (GBS). <i>Genes</i> , 2021, 12, 1074.	1.0	8
13	Peroxisome Proliferator-Activated Receptor $\beta$ , but Not $\alpha$ or G-Protein Coupled Estrogen Receptor Drives Functioning of Postnatal Boar Testisâ€”Next Generation Sequencing Analysis. <i>Animals</i> , 2021, 11, 2868.	1.0	1
14	Transcriptome analysis of human Leydig cell tumours reveals potential mechanisms underlying its development. <i>Andrologia</i> , 2021, 53, e14222.	1.0	1
15	Evaluation of genetic differentiation and genome-wide selection signatures in Polish local sheep breeds. <i>Livestock Science</i> , 2021, 251, 104635.	0.6	7
16	Pet ownership in pregnancy and methylation pattern in cord blood. <i>Genes and Immunity</i> , 2021, 22, 305-312.	2.2	0
17	Comparison of linkage disequilibrium, effective population size and haplotype blocks in Polish Landrace and Polish native pig populations. <i>Livestock Science</i> , 2020, 231, 103887.	0.6	11
18	Next-Generation Sequencing as a Tool to Detect Vaginal Microbiota Disturbances during Pregnancy. <i>Microorganisms</i> , 2020, 8, 1813.	1.6	14

#	ARTICLE	IF	CITATIONS
19	Divergent selection signatures of phenotypic and production traits among conserved and commercial cattle breeds. <i>Livestock Science</i> , 2020, 239, 104174.	0.6	1
20	Preliminary Identification of Candidate Genes Related to Survival of Gynogenetic Rainbow Trout ( <i>Oncorhynchus mykiss</i> ) Based on Comparative Transcriptome Analysis. <i>Animals</i> , 2020, 10, 1326.	1.0	7
21	Detection of runs of homozygosity in conserved and commercial pig breeds in Poland. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 571-580.	0.8	19
22	Mouse testicular transcriptome after modulation of non-canonical oestrogen receptor activity. <i>Reproduction, Fertility and Development</i> , 2020, 32, 903.	0.1	5
23	Genetic, historical and breeding aspects of the occurrence of the tobiano pattern and white markings in the Polish population of Hucul horses – a review. <i>Journal of Applied Animal Research</i> , 2020, 48, 21-27.	0.4	4
24	Genetic Differentiation of the Two Types of Polish Cold-blooded Horses Included in the National Conservation Program. <i>Animals</i> , 2020, 10, 542.	1.0	4
25	A detailed characteristics of bias associated with long runs of homozygosity identification based on medium density SNP microarrays. <i>Journal of Genomics</i> , 2020, 8, 43-48.	0.6	3
26	MicroRNA profiling of the pig periaqueductal grey (PAG) region reveals candidates potentially related to sex-dependent differences. <i>Biology of Sex Differences</i> , 2020, 11, 67.	1.8	1
27	Identification of mRNA Degradome Variation Dependent on Divergent Muscle Mass in Different Pig Breeds. <i>Annals of Animal Science</i> , 2020, 20, 1241-1256.	0.6	0
28	Methylation Marks of Blood Leukocytes of Native Hucul Mares Differentiated in Age. <i>International Journal of Genomics</i> , 2019, 2019, 1-9.	0.8	2
29	Diversifying selection signatures among divergently selected subpopulations of Polish Red cattle. <i>Journal of Applied Genetics</i> , 2019, 60, 87-95.	1.0	12
30	Induced androgenetic development in rainbow trout and transcriptome analysis of irradiated eggs. <i>Scientific Reports</i> , 2019, 9, 8084.	1.6	7
31	Evaluation of genotyping by sequencing for population genetics of sibling and hybridizing birds: an example using Syrian and Great Spotted Woodpeckers. <i>Journal of Ornithology</i> , 2019, 160, 287-294.	0.5	5
32	Alterations in the rainbow trout ( <i>Oncorhynchus mykiss</i> ) eggs exposed to ionizing radiation during induced androgenesis. <i>Reproduction in Domestic Animals</i> , 2019, 54, 712-718.	0.6	6
33	A genome-wide scan for diversifying selection signatures in selected horse breeds. <i>PLoS ONE</i> , 2019, 14, e0210751.	1.1	52
34	140 ASAS-EAAP Exchange Speaker Talk: Effects of different sources of fat in the diet of pigs on the liver transcriptome estimated by 3'RNA-sequencing. <i>Journal of Animal Science</i> , 2019, 97, 134-134.	0.2	0
35	A Comprehensive Analysis of Runs of Homozygosity of Eleven Cattle Breeds Representing Different Production Types. <i>Animals</i> , 2019, 9, 1024.	1.0	36
36	Genotyping-by-sequencing performance in selected livestock species. <i>Genomics</i> , 2019, 111, 186-195.	1.3	50

#	ARTICLE	IF	CITATIONS
37	The Genetic Basis of Piebald Coat Colour in Hucul Horses in the Context of White Markings and Crypto-Tobiano as a Breeding Problem in Poland. <i>Annals of Animal Science</i> , 2019, 19, 955-966.	0.6	0
38	Complete Genome Sequences of Three Fish-Associated <i>Streptococcus agalactiae</i> Isolates. <i>Genome Announcements</i> , 2018, 6, .	0.8	5
39	Complete Genome Sequences of Three <i>Streptococcus agalactiae</i> Serotype Ia Isolates Obtained from Disease Outbreaks in Nile Tilapia ( <i>Oreochromis niloticus</i> ). <i>Genome Announcements</i> , 2018, 6, .	0.8	2
40	Comparative analysis of DNA methylation patterns of equine sarcoid and healthy skin samples. <i>Veterinary and Comparative Oncology</i> , 2018, 16, 37-46.	0.8	9
41	The distinguishable DNA whole genome methylation profile of 2 cases of pediatric precursor B acute lymphoblastic leukaemia (BCP ALL) with prodromal, preleukemic phase. <i>Medicine (United States)</i> , 2018, 97, e12763.	0.4	0
42	A genome-wide detection of selection signatures in conserved and commercial pig breeds maintained in Poland. <i>BMC Genetics</i> , 2018, 19, 95.	2.7	31
43	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. <i>BMC Genomics</i> , 2018, 19, 864.	1.2	7
44	Transcriptome Analysis of Rainbow Trout ( <i>Oncorhynchus mykiss</i> ) Eggs Subjected to the High Hydrostatic Pressure Treatment. <i>International Journal of Genomics</i> , 2018, 2018, 1-7.	0.8	4
45	A comprehensive transcriptome analysis of skeletal muscles in two Polish pig breeds differing in fat and meat quality traits. <i>Genetics and Molecular Biology</i> , 2018, 41, 125-136.	0.6	42
46	Examining the Genetic Background of Porcine Muscle Growth and Development Based on Transcriptome and miRNAome Data. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1208.	1.8	20
47	DNA methylation patterns of the S100A14, POU2F3 and SFN genes in equine sarcoid tissues. <i>Research in Veterinary Science</i> , 2018, 119, 302-307.	0.9	5
48	Evaluation of changes arising in the pig mesenchymal stromal cells transcriptome following cryopreservation and Trichostatin A treatment. <i>PLoS ONE</i> , 2018, 13, e0192147.	1.1	5
49	Analysis of the Methylation Status of CpG Sites Within Cancer-Related Genes in Equine Sarcoids. <i>Annals of Animal Science</i> , 2018, 18, 907-918.	0.6	2
50	Transcriptomic gene profiling of porcine muscle tissue depending on histological properties. <i>Animal Science Journal</i> , 2017, 88, 1178-1188.	0.6	13
51	Transcriptome profiling of Arabian horse blood during training regimens. <i>BMC Genetics</i> , 2017, 18, 31.	2.7	27
52	The effect of histone deacetylase inhibitor trichostatin A on porcine mesenchymal stem cell transcriptome. <i>Biochimie</i> , 2017, 139, 56-73.	1.3	8
53	Comprehensive characteristics of microRNA expression profile of equine sarcoids. <i>Biochimie</i> , 2017, 137, 20-28.	1.3	16
54	Genomic landscape of copy number variation and copy neutral loss of heterozygosity events in equine sarcoids reveals increased instability of the sarcoid genome. <i>Biochimie</i> , 2017, 140, 122-132.	1.3	5

#	ARTICLE	IF	CITATIONS
55	Transcriptome analysis of equine sarcoids. <i>Veterinary and Comparative Oncology</i> , 2017, 15, 1370-1381.	0.8	11
56	Whole-genome DNA methylation characteristics in pediatric precursor B cell acute lymphoblastic leukemia (BCP ALL). <i>PLoS ONE</i> , 2017, 12, e0187422.	1.1	8
57	Panel of informative SNP markers for two genetic lines of European bison: Lowland and Lowlandâ€Caucasian. <i>Animal Biodiversity and Conservation</i> , 2017, 40, 17-25.	0.3	6
58	Identification of genomeâ€wide selection signatures in the <sc>L</sc>imousin beef cattle breed. <i>Journal of Animal Breeding and Genetics</i> , 2016, 133, 264-276.	0.8	27
59	The Use of SNP Microarrays for Biodiversity Studies of Sheep â€ A Review. <i>Annals of Animal Science</i> , 2016, 16, 975-987.	0.6	12
60	Characteristics of runs of homozygosity in selected cattle breeds maintained in Poland. <i>Livestock Science</i> , 2016, 188, 72-80.	0.6	79
61	Identification of Unbalanced Aberrations in the Genome of Equine Sarcoid Cells Using CGH Technique. <i>Annals of Animal Science</i> , 2016, 16, 79-85.	0.6	3
62	Effects of Different Sources of Fat in the Diet of Pigs on the Liver Transcriptome Estimated by RNA-Seq. <i>Annals of Animal Science</i> , 2016, 16, 1073-1090.	0.6	12
63	Genomeâ€wide <sc>RNA</sc>â€Seq analysis of breast muscles of two broiler chicken groups differing in shear force. <i>Animal Genetics</i> , 2016, 47, 68-80.	0.6	40
64	The use of runs of homozygosity for estimation of recent inbreeding in Holstein cattle. <i>Journal of Applied Genetics</i> , 2016, 57, 527-530.	1.0	58
65	The Relevance of Methylation Profiles of Equine <i>ITGAL</i> Gene. <i>Annals of Animal Science</i> , 2016, 16, 711-720.	0.6	0
66	Epigenetic structure and the role of polymorphism in the shaping of DNA methylation patterns of equine OAS1 locus. <i>Journal of Applied Genetics</i> , 2015, 56, 231-238.	1.0	4
67	Shifts in rDNA levels act as a genome buffer promoting chromosome homeostasis. <i>Cell Cycle</i> , 2015, 14, 3475-3487.	1.3	11
68	Genome-wide characteristics of copy number variation in Polish Holstein and Polish Red cattle using SNP genotyping assay. <i>Genetica</i> , 2015, 143, 145-155.	0.5	12
69	The characteristics of the porcine ( <i>Sus scrofa</i> ) liver miRNAome with the use of next generation sequencing. <i>Journal of Applied Genetics</i> , 2015, 56, 239-252.	1.0	5
70	Identification of differential selection traces in two <sc>P</sc>olish cattle breeds. <i>Animal Science Journal</i> , 2015, 86, 17-24.	0.6	5
71	Imputation accuracy of bovine spongiform encephalopathy-associated PRNP indel polymorphisms from middle-density SNPs arrays. <i>Czech Journal of Animal Science</i> , 2014, 59, 244-249.	0.5	2
72	Identification of a New Haplotype within the Promoter Region of the &lt;&gt;MSTN&lt;/&gt; Gene in Horses from Five of the most Common Breeds in Poland. <i>Folia Biologica</i> , 2014, 62, 219-222.	0.1	5

#	ARTICLE	IF	CITATIONS
73	Changes in DNA methylation patterns and repetitive sequences in blood lymphocytes of aged horses. <i>Age</i> , 2014, 36, 31-48.	3.0	14
74	General assessment of copy number variation in normal and tumor tissues of the domestic dog ( <i>Canis</i> ) <i>Tj ETQq0 0 0 rgBT /Overlock 10 T</i>	1.0	7
75	The application of genome-wide SNP genotyping methods in studies on livestock genomes. <i>Journal of Applied Genetics</i> , 2014, 55, 197-208.	1.0	24
76	Comprehensive analysis of the whole transcriptomes from two different pig breeds using <i>&lt;sc&gt;RNA&lt;/sc&gt;â€œSeq</i> method. <i>Animal Genetics</i> , 2014, 45, 674-684.	0.6	45
77	Mitochondrial D-loop mutations can be detected in sporadic malignant tumours in dogs. <i>Bulletin of the Veterinary Institute in Pulawy = Biuletyn Instytutu Weterynarii W Pulawach</i> , 2014, 58, 631-637.	0.4	10
78	Gene Mapping as a Method for Verifying Sequence Localization Based on Interspecific Chromosome Painting (ZOO-FISH). <i>Folia Biologica</i> , 2014, 62, 17-21.	0.1	0
79	The Effect of Using DNA Obtained from Blood of Cattle with Genetic Chimerism on Illuminaâ€™s Beadchip Assay Performance. <i>Annals of Animal Science</i> , 2014, 14, 279-286.	0.6	5
80	The evaluation of the usefulness of pedigree verification-dedicated SNPs for breed assignment in three polish cattle populations. <i>Molecular Biology Reports</i> , 2013, 40, 6803-6809.	1.0	3
81	The Evaluation of Bovine SNP50 BeadChip Assay Performance in Polish Red Cattle Breed. <i>Folia Biologica</i> , 2013, 61, 173-176.	0.1	1
82	PRNP and SPRN genes polymorphism in atypical bovine spongiform encephalopathy cases diagnosed in Polish cattle. <i>Journal of Applied Genetics</i> , 2012, 53, 337-342.	1.0	22
83	Polymorphism of the prion protein gene (PRNP) in Polish cattle affected by classical bovine spongiform encephalopathy. <i>Molecular Biology Reports</i> , 2012, 39, 5211-5217.	1.0	14
84	Characterization of PRNP and SPRN coding regions from atypical scrapie cases diagnosed in Poland. <i>Molecular Biology Reports</i> , 2012, 39, 2575-2583.	1.0	3
85	Characteristics of X- and Y-chromosome specific regions of the amelogenin gene and a PCR-based method for sex identification in red deer ( <i>Cervus elaphus</i> ). <i>Molecular Biology Reports</i> , 2010, 37, 2915-2918.	1.0	20
86	Identification of carriers of the mutation causing coagulation factor XI deficiency in Polish Holstein-Friesian cattle. <i>Journal of Applied Genetics</i> , 2009, 50, 149-152.	1.0	8
87	Effect of Bovine PRNP Gene Polymorphisms on BSE Susceptibility in Cattle. <i>Folia Biologica</i> , 2007, 55, 81-86.	0.1	2