

Igor Jasielczuk

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1716978/publications.pdf>

Version: 2024-02-01

30
papers

520
citations

840119

11
h-index

676716

22
g-index

31
all docs

31
docs citations

31
times ranked

706
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Maternal atopy and offspring epigenome-wide methylation signature. <i>Epigenetics</i> , 2021, 16, 629-641.	1.3	10
3	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
4	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
5	Evaluation of genetic differentiation and genome-wide selection signatures in Polish local sheep breeds. <i>Livestock Science</i> , 2021, 251, 104635.	0.6	7
6	Pet ownership in pregnancy and methylation pattern in cord blood. <i>Genes and Immunity</i> , 2021, 22, 305-312.	2.2	0
7	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
8	Divergent selection signatures of phenotypic and production traits among conserved and commercial cattle breeds. <i>Livestock Science</i> , 2020, 239, 104174.	0.6	1
9	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
10	Linkage disequilibrium, haplotype blocks and historical effective population size in Arabian horses and selected Polish native horse breeds. <i>Livestock Science</i> , 2020, 239, 104095.	0.6	7
11	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
12	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
13	Diversifying selection signatures among divergently selected subpopulations of Polish Red cattle. <i>Journal of Applied Genetics</i> , 2019, 60, 87-95.	1.0	12
14	Induced androgenetic development in rainbow trout and transcriptome analysis of irradiated eggs. <i>Scientific Reports</i> , 2019, 9, 8084.	1.6	7
15	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
16	A genome-wide scan for diversifying selection signatures in selected horse breeds. <i>PLoS ONE</i> , 2019, 14, e0210751.	1.1	52
17	A Comprehensive Analysis of Runs of Homozygosity of Eleven Cattle Breeds Representing Different Production Types. <i>Animals</i> , 2019, 9, 1024.	1.0	36
18	Genotyping-by-sequencing performance in selected livestock species. <i>Genomics</i> , 2019, 111, 186-195.	1.3	50

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	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
22	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
23	Identification of genome-wide selection signatures in the Limousin beef cattle breed. <i>Journal of Animal Breeding and Genetics</i> , 2016, 133, 264-276.	0.8	27
24	Characteristics of runs of homozygosity in selected cattle breeds maintained in Poland. <i>Livestock Science</i> , 2016, 188, 72-80.	0.6	79
25	Linkage disequilibrium and haplotype block structure in Limousin, Simmental and native Polish Red cattle. <i>Livestock Science</i> , 2016, 191, 57-63.	0.6	10
26	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
27	Shifts in rDNA levels act as a genome buffer promoting chromosome homeostasis. <i>Cell Cycle</i> , 2015, 14, 3475-3487.	1.3	11
28	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
29	General assessment of copy number variation in normal and tumor tissues of the domestic dog (<i>Canis</i>) Tj ETQq1 1 0,784314.rgBT /Over	1.0	10
30	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