

# Gregor Gorjanc

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1441030/publications.pdf>

Version: 2024-02-01

95  
papers

3,173  
citations

218677

26  
h-index

223800

46  
g-index

147  
all docs

147  
docs citations

147  
times ranked

3010  
citing authors

#	ARTICLE	IF	CITATIONS
1	Efficient ancestry and mutation simulation with msprime 1.0. <i>Genetics</i> , 2022, 220, .	2.9	133
2	Temporal and genomic analysis of additive genetic variance in breeding programmes. <i>Heredity</i> , 2022, 128, 21-32.	2.6	13
3	Rare and population-specific functional variation across pig lines. <i>Genetics Selection Evolution</i> , 2022, 54, .	3.0	9
4	Phasing and imputation of single nucleotide polymorphism data of missing parents of biparental plant populations. <i>Crop Science</i> , 2021, 61, 2243-2253.	1.8	5
5	Robust modeling of additive and nonadditive variation with intuitive inclusion of expert knowledge. <i>Genetics</i> , 2021, 217, .	2.9	4
6	Modeling Illustrates That Genomic Selection Provides New Opportunities for Intercrop Breeding. <i>Frontiers in Plant Science</i> , 2021, 12, 605172.	3.6	22
7	Genomic Selection for Any Dairy Breeding Program via Optimized Investment in Phenotyping and Genotyping. <i>Frontiers in Genetics</i> , 2021, 12, 637017.	2.3	10
8	AlphaPartâ€™R implementation of the method for partitioning genetic trends. <i>Genetics Selection Evolution</i> , 2021, 53, 30.	3.0	9
9	Novel combination of CRISPR-based gene drives eliminates resistance and localises spread. <i>Scientific Reports</i> , 2021, 11, 3719.	3.3	19
10	Genomic evaluation of Brown Swiss dairy cattle with limited national genotype data and integrated external information. <i>Journal of Dairy Science</i> , 2021, 104, 5738-5754.	3.4	3
11	Long-term comparison between index selection and optimal independent culling in plant breeding programs with genomic prediction. <i>PLoS ONE</i> , 2021, 16, e0235554.	2.5	11
12	Association of inbreeding and regional equine leucocyte antigen homozygosity with the prevalence of insect bite hypersensitivity in Old Kladruber horse. <i>Animal Genetics</i> , 2021, 52, 422-430.	1.7	4
13	Genetic variation in recombination rate in the pig. <i>Genetics Selection Evolution</i> , 2021, 53, 54.	3.0	17
14	A genome-wide association analysis for body weight at 35 days measured on 137,343 broiler chickens. <i>Genetics Selection Evolution</i> , 2021, 53, 70.	3.0	12
15	Genetic architecture and major genes for backfat thickness in pig lines of diverse genetic backgrounds. <i>Genetics Selection Evolution</i> , 2021, 53, 76.	3.0	35
16	AlphaSimR: an R package for breeding program simulations. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	109
17	A gene drive does not spread easily in populations of the honey bee parasite <i>Varroa destructor</i> . <i>Apidologie</i> , 2021, 52, 1112-1127.	2.0	10
18	Genomic evaluations using data recorded on smallholder dairy farms in low- to middle-income countries. <i>JDS Communications</i> , 2021, 2, 366-370.	1.5	2

#	ARTICLE	IF	CITATIONS
19	Spatial modelling improves genetic evaluation in smallholder breeding programs. <i>Genetics Selection Evolution</i> , 2020, 52, 69.	3.0	14
20	AlphaFamImpute: high-accuracy imputation in full-sib families from genotype-by-sequencing data. <i>Bioinformatics</i> , 2020, 36, 4369-4371.	4.1	12
21	Combining QTL Analysis and Genomic Predictions for Four Durum Wheat Populations Under Drought Conditions. <i>Frontiers in Genetics</i> , 2020, 11, 316.	2.3	24
22	On the origin of European sheep as revealed by the diversity of the Balkan breeds and by optimizing population-genetic analysis tools. <i>Genetics Selection Evolution</i> , 2020, 52, 25.	3.0	58
23	Origin Specific Genomic Selection: A Simple Process To Optimize the Favorable Contribution of Parents to Progeny. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2445-2455.	1.8	9
24	In silico simulation of future hybrid performance to evaluate heterotic pool formation in a self-pollinating crop. <i>Scientific Reports</i> , 2020, 10, 4037.	3.3	9
25	Extending long-range phasing and haplotype library imputation algorithms to large and heterogeneous datasets. <i>Genetics Selection Evolution</i> , 2020, 52, 38.	3.0	3
26	Accuracy of whole-genome sequence imputation using hybrid peeling in large pedigreed livestock populations. <i>Genetics Selection Evolution</i> , 2020, 52, 17.	3.0	30
27	Evaluation of sequencing strategies for whole-genome imputation with hybrid peeling. <i>Genetics Selection Evolution</i> , 2020, 52, 18.	3.0	17
28	Hierarchical Modelling of Haplotype Effects on a Phylogeny. <i>Frontiers in Genetics</i> , 2020, 11, 531218.	2.3	8
29	How Population Structure Impacts Genomic Selection Accuracy in Cross-Validation: Implications for Practical Breeding. <i>Frontiers in Plant Science</i> , 2020, 11, 592977.	3.6	39
30	Parentage assignment with genotyping-by-sequencing data. <i>Journal of Animal Breeding and Genetics</i> , 2019, 136, 102-112.	2.0	23
31	Family-specific genotype arrays increase the accuracy of pedigree-based imputation at very low marker densities. <i>Genetics Selection Evolution</i> , 2019, 51, 33.	3.0	9
32	The Fests Issue on Robin Thompson's contributions to statistics, genetics and animal/plant genetic improvement schemes. <i>Journal of Animal Breeding and Genetics</i> , 2019, 136, 229-229.	2.0	0
33	Flexible modelling of spatial variation in agricultural field trials with the R package INLA. <i>Theoretical and Applied Genetics</i> , 2019, 132, 3277-3293.	3.6	23
34	The effects of training population design on genomic prediction accuracy in wheat. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1943-1952.	3.6	63
35	Removal of alleles by genome editing (RAGE) against deleterious load. <i>Genetics Selection Evolution</i> , 2019, 51, 14.	3.0	44
36	Analysis of a large dataset reveals haplotypes carrying putatively recessive lethal and semi-lethal alleles with pleiotropic effects on economically important traits in beef cattle. <i>Genetics Selection Evolution</i> , 2019, 51, 9.	3.0	24

#	ARTICLE	IF	CITATIONS
37	Efficient use of genomic information for sustainable genetic improvement in small cattle populations. <i>Journal of Dairy Science</i> , 2019, 102, 9971-9982.	3.4	12
38	A Strategy To Exploit Surrogate Sire Technology in Livestock Breeding Programs. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 203-215.	1.8	26
39	Impact of index hopping and bias towards the reference allele on accuracy of genotype calls from low-coverage sequencing. <i>Genetics Selection Evolution</i> , 2018, 50, 64.	3.0	38
40	Hybrid peeling for fast and accurate calling, phasing, and imputation with sequence data of any coverage in pedigrees. <i>Genetics Selection Evolution</i> , 2018, 50, 67.	3.0	46
41	Sequence variation, evolutionary constraint, and selection at the CD163 gene in pigs. <i>Genetics Selection Evolution</i> , 2018, 50, 69.	3.0	11
42	Assessment of the performance of hidden Markov models for imputation in animal breeding. <i>Genetics Selection Evolution</i> , 2018, 50, 44.	3.0	14
43	A heuristic method for fast and accurate phasing and imputation of single-nucleotide polymorphism data in bi-parental plant populations. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2345-2357.	3.6	20
44	Improvement of pork characteristics under commercial conditions with small amount of straw or hay. <i>Journal of Applied Animal Research</i> , 2018, 46, 1317-1322.	1.2	6
45	Genomic Prediction Using Individual-Level Data and Summary Statistics from Multiple Populations. <i>Genetics</i> , 2018, 210, 53-69.	2.9	15
46	AlphaMate: a program for optimizing selection, maintenance of diversity and mate allocation in breeding programs. <i>Bioinformatics</i> , 2018, 34, 3408-3411.	4.1	36
47	Optimal cross selection for long-term genetic gain in two-part programs with rapid recurrent genomic selection. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1953-1966.	3.6	120
48	Potential of gene drives with genome editing to increase genetic gain in livestock breeding programs. <i>Genetics Selection Evolution</i> , 2017, 49, 3.	3.0	28
49	Genomic prediction unifies animal and plant breeding programs to form platforms for biological discovery. <i>Nature Genetics</i> , 2017, 49, 1297-1303.	21.4	263
50	Prospects for Cost-Effective Genomic Selection via Accurate Within-Family Imputation. <i>Crop Science</i> , 2017, 57, 216-228.	1.8	48
51	A hybrid method for the imputation of genomic data in livestock populations. <i>Genetics Selection Evolution</i> , 2017, 49, 30.	3.0	34
52	A method for the allocation of sequencing resources in genotyped livestock populations. <i>Genetics Selection Evolution</i> , 2017, 49, 47.	3.0	27
53	National single-step genomic method that integrates multi-national genomic information. <i>Journal of Dairy Science</i> , 2017, 100, 465-478.	3.4	16
54	A method for allocating low-coverage sequencing resources by targeting haplotypes rather than individuals. <i>Genetics Selection Evolution</i> , 2017, 49, 78.	3.0	34

#	ARTICLE	IF	CITATIONS
55	The potential of shifting recombination hotspots to increase genetic gain in livestock breeding. <i>Genetics Selection Evolution</i> , 2017, 49, 55.	3.0	18
56	A Two-Part Strategy for Using Genomic Selection to Develop Inbred Lines. <i>Crop Science</i> , 2017, 57, 2372-2386.	1.8	140
57	Potential of Low-Coverage Genotyping-by-Sequencing and Imputation for Cost-Effective Genomic Selection in Biparental Segregating Populations. <i>Crop Science</i> , 2017, 57, 1404-1420.	1.8	64
58	AlphaSim: Software for Breeding Program Simulation. <i>Plant Genome</i> , 2016, 9, plantgenome2016.02.0013.	2.8	105
59	Effect of manipulating recombination rates on response to selection in livestock breeding programs. <i>Genetics Selection Evolution</i> , 2016, 48, 44.	3.0	33
60	Promotion of alleles by genome editing in livestock breeding programmes. <i>Journal of Animal Breeding and Genetics</i> , 2016, 133, 83-84.	2.0	37
61	Initiating maize pre-breeding programs using genomic selection to harness polygenic variation from landrace populations. <i>BMC Genomics</i> , 2016, 17, 30.	2.8	92
62	Genetic identification of thiosulfate sulfurtransferase as an adipocyte-expressed antidiabetic target in mice selected for leanness. <i>Nature Medicine</i> , 2016, 22, 771-779.	30.7	57
63	Partition of genetic trends by origin in Landrace and Large-White pigs. <i>Animal</i> , 2015, 9, 1605-1609.	3.3	8
64	Imputation of Single Nucleotide Polymorphism Genotypes in Biparental, Backcross, and Topcross Populations with a Hidden Markov Model. <i>Crop Science</i> , 2015, 55, 1934-1946.	1.8	37
65	Reliability of pedigree-based and genomic evaluations in selected populations. <i>Genetics Selection Evolution</i> , 2015, 47, 65.	3.0	54
66	Potential of promotion of alleles by genome editing to improve quantitative traits in livestock breeding programs. <i>Genetics Selection Evolution</i> , 2015, 47, 55.	3.0	125
67	Potential of genotyping-by-sequencing for genomic selection in livestock populations. <i>Genetics Selection Evolution</i> , 2015, 47, 12.	3.0	107
68	Recovery of Native Genetic Background in Admixed Populations Using Haplotypes, Phenotypes, and Pedigree Information – Using Cika Cattle as a Case Breed. <i>PLoS ONE</i> , 2015, 10, e0123253.	2.5	19
69	Estimation of additive and dominance variance for litter size components in rabbits. <i>Czech Journal of Animal Science</i> , 2014, 59, 182-189.	1.3	15
70	Evaluation of Genomic Selection Training Population Designs and Genotyping Strategies in Plant Breeding Programs Using Simulation. <i>Crop Science</i> , 2014, 54, 1476-1488.	1.8	164
71	AlphaMPSim: flexible simulation of multi-parent crosses. <i>Bioinformatics</i> , 2014, 30, 2686-2688.	4.1	6
72	Genetic parameters for litter size in Black Slavonian pigs. <i>Spanish Journal of Agricultural Research</i> , 2014, 12, 89.	0.6	12

#	ARTICLE	IF	CITATIONS
73	Genetic prediction of complex traits: integrating infinitesimal and marked genetic effects. <i>Genetica</i> , 2013, 141, 239-246.	1.1	1
74	Comparison between sire-maternal grandsire and animal models for genetic evaluation of longevity in a dairy cattle population with small herds. <i>Journal of Dairy Science</i> , 2013, 96, 8002-8013.	3.4	15
75	Genomic evaluations using similarity between haplotypes. <i>Journal of Animal Breeding and Genetics</i> , 2013, 130, 259-269.	2.0	31
76	Accuracy of genomic prediction for milk production traits with different approaches in a small population of Slovenian Brown bulls. <i>Livestock Science</i> , 2013, 157, 421-426.	1.6	3
77	Genotype Imputation to Increase Sample Size in Pedigreed Populations. <i>Methods in Molecular Biology</i> , 2013, 1019, 395-410.	0.9	8
78	The contribution of dominance and inbreeding depression in estimating variance components for litter size in Pannon White rabbits. <i>Journal of Animal Breeding and Genetics</i> , 2013, 130, 303-311.	2.0	19
79	Genetic and environmental parameters estimation for milk traits in Slovenian dairy sheep using random regression model. <i>Czech Journal of Animal Science</i> , 2013, 58, 125-135.	1.3	6
80	Simulated Data for Genomic Selection and Genome-Wide Association Studies Using a Combination of Coalescent and Gene Drop Methods. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 425-427.	1.8	61
81	Lactation curves for milk yield, fat and protein content in Slovenian dairy sheep. <i>Czech Journal of Animal Science</i> , 2012, 57, 231-239.	1.3	12
82	Analysis of longevity in Slovenian holstein cattle. <i>Acta Agriculturae Slovenica</i> , 2011, 98, .	0.3	7
83	Effects of two probiotic additives containing <i>Bacillus</i> spores on carcass characteristics, blood lipids and cecal volatile fatty acids in meat type chickens. <i>Journal of Animal Physiology and Animal Nutrition</i> , 2011, 95, 424-433.	2.2	16
84	Congenic and bioinformatics analyses resolved a major-effect <i>Fob3b</i> QTL on mouse Chr 15 into two closely linked loci. <i>Mammalian Genome</i> , 2010, 21, 172-185.	2.2	22
85	Evaluation of different approaches for the estimation of daily yield from single milk testing scheme in cattle. <i>Journal of Dairy Research</i> , 2010, 77, 137-143.	1.4	6
86	Inference of genotype probabilities and derived statistics for PrP locus in the Jezersko "Solcava sheep. <i>Livestock Science</i> , 2010, 129, 232-236.	1.6	1
87	Simplereparameterization to improveconvergence in linearmixedmodels. <i>Acta Agriculturae Slovenica</i> , 2010, 96, .	0.3	0
88	Covariance components by a repeatability model in Slovenian dairy sheep using test-day records. <i>Czech Journal of Animal Science</i> , 2009, 54, 426-434.	1.3	14
89	Analysis of inbreeding in Slovenian Haflinger population. <i>Italian Journal of Animal Science</i> , 2009, 8, 128-130.	1.9	0
90	Growth performance of station tested rams in Slovenia. <i>Italian Journal of Animal Science</i> , 2009, 8, 74-76.	1.9	1

#	ARTICLE	IF	CITATIONS
91	Genotoxicity evaluation of water soil leachates by Ames test, comet assay, and preliminary Tradescantia micronucleus assay. Environmental Monitoring and Assessment, 2008, 139, 107-118.	2.7	58
92	Porous Concrete Block as an Environmental Enrichment Device Increases Activity of Laying Hens in Cages. Poultry Science, 2008, 87, 1714-1719.	3.4	2
93	Straw or hay as environmental improvement and its effect on behaviour and production traits of fattening pigs. Archives Animal Breeding, 2008, 51, 549-559.	1.4	9
94	Assessment of differential expression of oncogenes in adenocarcinoma of stomach with fluorescent labeling and simultaneous amplification of gene transcripts. Radiology and Oncology, 2007, 41, 174.	1.7	2
95	Comet Assay Assessment of Wastewater Genotoxicity Using Yeast Cells. Bulletin of Environmental Contamination and Toxicology, 2004, 72, 607-616.	2.7	24