

# Giuliano Galimberti

## List of Publications by Year in descending order

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Version: 2024-02-01

48  
papers

1,110  
citations

471061

17  
h-index

414034

32  
g-index

49  
all docs

49  
docs citations

49  
times ranked

1521  
citing authors

#	ARTICLE	IF	CITATIONS
1	European agricultural landscapes, common agricultural policy and ecosystem services: a review. <i>Agronomy for Sustainable Development</i> , 2014, 34, 309-325.	2.2	246
2	A genome wide association study for backfat thickness in Italian Large White pigs highlights new regions affecting fat deposition including neuronal genes. <i>BMC Genomics</i> , 2012, 13, 583.	1.2	80
3	Identification and association analysis of several hundred single nucleotide polymorphisms within candidate genes for back fat thickness in Italian Large White pigs using a selective genotyping approach <sup>1</sup> . <i>Journal of Animal Science</i> , 2012, 90, 2450-2464.	0.2	65
4	A genomewide association study for average daily gain in Italian Large White pigs <sup>1</sup> . <i>Journal of Animal Science</i> , 2014, 92, 1385-1394.	0.2	64
5	Genome-wide association studies for 30 haematological and blood clinical-biochemical traits in Large White pigs reveal genomic regions affecting intermediate phenotypes. <i>Scientific Reports</i> , 2019, 9, 7003.	1.6	55
6	A candidate gene association study for nine economically important traits in Italian Holstein cattle. <i>Animal Genetics</i> , 2014, 45, 576-580.	0.6	49
7	Combined use of principal component analysis and random forests identify population-informative single nucleotide polymorphisms: application in cattle breeds. <i>Journal of Animal Breeding and Genetics</i> , 2015, 132, 346-356.	0.8	38
8	A machine learning approach for the identification of population-informative markers from high-throughput genotyping data: application to several pig breeds. <i>Animal</i> , 2020, 14, 223-232.	1.3	37
9	Comparison of three patterns of feed supplementation with live <i>Saccharomyces cerevisiae</i> yeast on postweaning diarrhea, health status, and blood metabolic profile of susceptible weaning pigs orally challenged with <i>Escherichia coli</i> F4ac1. <i>Journal of Animal Science</i> , 2015, 93, 2225-2233.	0.2	35
10	A multivariate linear regression analysis using finite mixtures of $t$ distributions. <i>Computational Statistics and Data Analysis</i> , 2014, 71, 138-150.	0.7	32
11	Model-based methods to identify multiple cluster structures in a data set. <i>Computational Statistics and Data Analysis</i> , 2007, 52, 520-536.	0.7	30
12	Multivariate linear regression with non-normal errors: a solution based on mixture models. <i>Statistics and Computing</i> , 2011, 21, 523-536.	0.8	27
13	Copy number variants in Italian Large White pigs detected using high-density single nucleotide polymorphisms and their association with back fat thickness. <i>Animal Genetics</i> , 2014, 45, 745-749.	0.6	27
14	Preselection statistics and Random Forest classification identify population informative single nucleotide polymorphisms in cosmopolitan and autochthonous cattle breeds. <i>Animal</i> , 2018, 12, 12-19.	1.3	25
15	Metabolomics evidences plasma and serum biomarkers differentiating two heavy pig breeds. <i>Animal</i> , 2016, 10, 1741-1748.	1.3	24
16	A retrospective analysis of allele frequency changes of major genes during 20 years of selection in the Italian Large White pig breed. <i>Journal of Animal Breeding and Genetics</i> , 2015, 132, 239-246.	0.8	20
17	Penalized factor mixture analysis for variable selection in clustered data. <i>Computational Statistics and Data Analysis</i> , 2009, 53, 4301-4310.	0.7	19
18	Genome-wide association study for ham weight loss at first salting in Italian Large White pigs: towards the genetic dissection of a key trait for dry-cured ham production. <i>Animal Genetics</i> , 2017, 48, 103-107.	0.6	18

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19	Association between melanocortin 4 receptor (MC4R) gene haplotypes and carcass and production traits in Italian Large White pigs evaluated with a selective genotyping approach. <i>Livestock Science</i> , 2013, 157, 48-56.	0.6	17
20	Deconstructing the pig sex metabolome: Targeted metabolomics in heavy pigs revealed sexual dimorphisms in plasma biomarkers and metabolic pathways. <i>Journal of Animal Science</i> , 2015, 93, 5681-5693.	0.2	17
21	Twenty years of artificial directional selection have shaped the genome of the Italian Large White pig breed. <i>Animal Genetics</i> , 2016, 47, 181-191.	0.6	16
22	Genome-wide association studies for seven production traits highlight genomic regions useful to dissect dry-cured ham quality and production traits in Duroc heavy pigs. <i>Animal</i> , 2018, 12, 1777-1784.	1.3	16
23	Modelling the role of variables in model-based cluster analysis. <i>Statistics and Computing</i> , 2018, 28, 145-169.	0.8	16
24	Genome-wide association study for the level of serum electrolytes in Italian Large White pigs. <i>Animal Genetics</i> , 2016, 47, 597-602.	0.6	13
25	A comparative analysis of label-free liquid chromatography-mass spectrometry liver proteomic profiles highlights metabolic differences between pig breeds. <i>PLoS ONE</i> , 2018, 13, e0199649.	1.1	13
26	A genome-wide association study for a proxy of intermuscular fat level in the Italian Large White breed identifies genomic regions affecting an important quality parameter for dry-cured hams. <i>Animal Genetics</i> , 2017, 48, 459-465.	0.6	12
27	Quantifying API polymorphs in formulations using X-ray powder diffraction and multivariate standard addition method combined with net analyte signal analysis. <i>European Journal of Pharmaceutical Sciences</i> , 2019, 130, 36-43.	1.9	11
28	Using mixtures in seemingly unrelated linear regression models with non-normal errors. <i>Statistics and Computing</i> , 2016, 26, 1025-1038.	0.8	10
29	Evaluating patient satisfaction through latent class factor analysis. <i>Health and Place</i> , 2009, 15, 210-218.	1.5	9
30	Genetic markers associated with resistance to infectious diseases have no effects on production traits and haematological parameters in Italian Large White pigs. <i>Livestock Science</i> , 2019, 223, 32-38.	0.6	8
31	Regression Trees for Longitudinal Data with Time-Dependent Covariates. <i>Studies in Classification, Data Analysis, and Knowledge Organization</i> , 2002, , 391-398.	0.1	8
32	Variable Selection in Cell Classification Problems: A Strategy Based on Independent Component Analysis. , 2005, , 21-29.		6
33	Using conditional independence for parsimonious model-based Gaussian clustering. <i>Statistics and Computing</i> , 2013, 23, 625-638.	0.8	6
34	Microarray gene expression analysis of porcine skeletal muscle sampled at several post mortem time points. <i>Meat Science</i> , 2011, 88, 604-609.	2.7	5
35	Notes on the Robustness of Regression Trees Against Skewed and Contaminated Errors. <i>Studies in Classification, Data Analysis, and Knowledge Organization</i> , 2011, , 255-263.	0.1	5
36	Bayesian variable selection in linear regression models with non-normal errors. <i>Statistical Methods and Applications</i> , 2019, 28, 323-358.	0.7	4

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37	Seemingly unrelated clusterwise linear regression. <i>Advances in Data Analysis and Classification</i> , 2020, 14, 235-260.	0.9	4
38	Targeted metabolomic profiles of piglet plasma reveal physiological changes over the suckling period. <i>Livestock Science</i> , 2020, 231, 103890.	0.6	4
39	Latent Classes of Objects and Variable Selection. , 2008, , 373-383.		3
40	When size matters: The gonads of larger female yellowfin tuna ( <i>Thunnus albacares</i> ) have different fatty acid profiles compared to smaller individuals. <i>Fisheries Research</i> , 2020, 232, 105726.	0.9	3
41	Covariance matrix estimation of the maximum likelihood estimator in multivariate clusterwise linear regression. <i>Statistical Methods and Applications</i> , 2021, 30, 235-268.	0.7	3
42	Finite mixture models for clustering multilevel data with multiple cluster structures. <i>Statistical Modelling</i> , 2010, 10, 265-290.	0.5	2
43	A note on the consistency of the maximum likelihood estimator under multivariate linear cluster-weighted models. <i>Statistics and Probability Letters</i> , 2020, 157, 108630.	0.4	1
44	Identifying Multiple Cluster Structures Through Latent Class Models. , 2006, , 174-181.		1
45	Multivariate cluster-weighted models based on seemingly unrelated linear regression. <i>Computational Statistics and Data Analysis</i> , 2022, 171, 107451.	0.7	1
46	The FAGenomicH project: towards a whole candidate gene approach to identify markers associated with fatness and production traits in pigs and investigate the pig as a model for human obesity. <i>Italian Journal of Animal Science</i> , 2009, 8, 87-89.	0.8	0
47	Discussion of "Model-based clustering and classification with non-normal mixture distributions" by S.X. Lee and G.J. McLachlan. <i>Statistical Methods and Applications</i> , 2013, 22, 463-465.	0.7	0
48	Combining Regression Trees and Radial Basis Function Networks in Longitudinal Data Modelling. <i>Studies in Classification, Data Analysis, and Knowledge Organization</i> , 2003, , 83-91.	0.1	0