

Francesco Tiezzi

List of Publications by Year in descending order

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Version: 2024-02-01

93
papers

1,712
citations

293460

24
h-index

371746

37
g-index

98
all docs

98
docs citations

98
times ranked

1697
citing authors

#	ARTICLE	IF	CITATIONS
1	Exploring the role of gut microbiota in host feeding behavior among breeds in swine. BMC Microbiology, 2022, 22, 1.	1.3	34
2	Genotype by Environment Interactions in Livestock Farming. , 2022, , 1-21.		1
3	Genotype by Environment Interaction and Selection Response for Milk Yield Traits and Conformation in a Local Cattle Breed Using a Reaction Norm Approach. Animals, 2022, 12, 839.	1.0	1
4	Use of Host Feeding Behavior and Gut Microbiome Data in Estimating Variance Components and Predicting Growth and Body Composition Traits in Swine. Genes, 2022, 13, 767.	1.0	2
5	Use of Milk Infrared Spectral Data as Environmental Covariates in Genomic Prediction Models for Production Traits in Canadian Holstein. Animals, 2022, 12, 1189.	1.0	0
6	Genotyping and phenotyping strategies for genetic improvement of meat quality and carcass composition in swine. Genetics Selection Evolution, 2022, 54, .	1.2	4
7	Exploring methods to summarize gut microbiota composition for microbiability estimation and phenotypic prediction in swine. Journal of Animal Science, 2022, 100, .	0.2	2
8	Microbiability of meat quality and carcass composition traits in swine. Journal of Animal Breeding and Genetics, 2021, 138, 223-236.	0.8	24
9	Evidence for recombination variability in purebred swine populations. Journal of Animal Breeding and Genetics, 2021, 138, 259-273.	0.8	6
10	Gut microbiome mediates host genomic effects on phenotypes: a case study with fat deposition in pigs. Computational and Structural Biotechnology Journal, 2021, 19, 530-544.	1.9	17
11	Potential effects of hormonal synchronized breeding on genetic evaluations of fertility traits in dairy cattle: A simulation study. Journal of Dairy Science, 2021, 104, 4404-4412.	1.4	5
12	A combination of <i>Lactobacillus buchneri</i> and <i>Pediococcus pentosaceus</i> extended the aerobic stability of conventional and brown midrib mutants' corn hybrids ensiled at low dry matter concentrations by causing a major shift in their bacterial and fungal community. Journal of Animal Science, 2021, 99, .	0.2	8
13	Predicting body weight in growing pigs from feeding behavior data using machine learning algorithms. Computers and Electronics in Agriculture, 2021, 184, 106085.	3.7	19
14	Trends in genetic diversity and the effect of inbreeding in American Angus cattle under genomic selection. Genetics Selection Evolution, 2021, 53, 50.	1.2	22
15	Potential Use of Gut Microbiota Composition as a Biomarker of Heat Stress in Monogastric Species: A Review. Animals, 2021, 11, 1833.	1.0	26
16	Microbial composition differs between production systems and is associated with growth performance and carcass quality in pigs. Animal Microbiome, 2021, 3, 57.	1.5	7
17	PSIV-5 Definition of environmental variables and critical periods to evaluate heat tolerance in maternal-line pigs based on single-step genomic reaction norms. Journal of Animal Science, 2021, 99, 297-298.	0.2	0
18	53 Awardee Talk: Implications of the Gut Microbiome for Genetic Improvement of Swine. Journal of Animal Science, 2021, 99, 29-29.	0.2	0

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19	23 Exploring the Role of Gut Microbiota in Host Feeding Behavior Among Breeds in Swine. <i>Journal of Animal Science</i> , 2021, 99, 10-11.	0.2	0
20	25 Gut Microbiome Information Enables Additional Discovery in Genome-wide Association Studies in Swine. <i>Journal of Animal Science</i> , 2021, 99, 10-10.	0.2	0
21	Genetic diversity and population history of eight Italian beef cattle breeds using measures of autozygosity. <i>PLoS ONE</i> , 2021, 16, e0248087.	1.1	10
22	PSXII-12 Partitioning direct and maternal genetic effects into additive and non-additive components for growth and maternal traits in Yorkshire pigs. <i>Journal of Animal Science</i> , 2021, 99, 251-252.	0.2	0
23	29 Effects of Recent and Ancient Inbreeding on Growth in American Angus Cattle. <i>Journal of Animal Science</i> , 2021, 99, 14-14.	0.2	0
24	Definition of Environmental Variables and Critical Periods to Evaluate Heat Tolerance in Large White Pigs Based on Single-Step Genomic Reaction Norms. <i>Frontiers in Genetics</i> , 2021, 12, 717409.	1.1	10
25	The interaction between microbiome and pig efficiency: A review. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 4-13.	0.8	43
26	Analysis of milk leukocyte differential measures for use in management practices for decreased mastitis incidence. <i>Journal of Dairy Science</i> , 2020, 103, 572-582.	1.4	6
27	Genome-wide association study for carcass quality traits and growth in purebred and crossbred pigs1. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	23
28	Gut microbiome composition differences among breeds impact feed efficiency in swine. <i>Microbiome</i> , 2020, 8, 110.	4.9	108
29	Modeling host-microbiome interactions for the prediction of meat quality and carcass composition traits in swine. <i>Genetics Selection Evolution</i> , 2020, 52, 41.	1.2	14
30	Heritability of Teat Condition in Italian Holstein Friesian and Its Relationship with Milk Production and Somatic Cell Score. <i>Animals</i> , 2020, 10, 2271.	1.0	4
31	Integration of Wet-Lab Measures, Milk Infrared Spectra, and Genomics to Improve Difficult-to-Measure Traits in Dairy Cattle Populations. <i>Frontiers in Genetics</i> , 2020, 11, 563393.	1.1	9
32	Symposium review: Exploiting homozygosity in the era of genomicsâ€”Selection, inbreeding, and mating programs. <i>Journal of Dairy Science</i> , 2020, 103, 5302-5313.	1.4	30
33	Genomics of Heat Tolerance in Reproductive Performance Investigated in Four Independent Maternal Lines of Pigs. <i>Frontiers in Genetics</i> , 2020, 11, 629.	1.1	19
34	Heritability and genome-wide association of swine gut microbiome features with growth and fatness parameters. <i>Scientific Reports</i> , 2020, 10, 10134.	1.6	47
35	Tree species effects on understory forage productivity and microclimate in a silvopasture of the Southeastern USA. <i>Agriculture, Ecosystems and Environment</i> , 2020, 295, 106917.	2.5	22
36	Transcriptome analysis identifies genes and co-expression networks underlying heat tolerance in pigs. <i>BMC Genetics</i> , 2020, 21, 44.	2.7	12

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37	Genetic Parameters for Tolerance to Heat Stress in Crossbred Swine Carcass Traits. <i>Frontiers in Genetics</i> , 2020, 11, 612815.	1.1	21
38	Genetic parameters of weeping teats in Italian Saanen and Alpine dairy goats and their relationship with milk production and somatic cell score. <i>Journal of Dairy Science</i> , 2020, 103, 9167-9176.	1.4	10
39	43 Feed efficiency and behavior are associated with gut microbiome in three breeds of pigs. <i>Journal of Animal Science</i> , 2020, 98, 24-24.	0.2	1
40	30 Inbreeding in American Angus cattle before and after the implementation of genomic selection. <i>Journal of Animal Science</i> , 2020, 98, 14-14.	0.2	0
41	249 Predicting body weight of finishing pigs using machine and deep learning algorithms. <i>Journal of Animal Science</i> , 2020, 98, 176-176.	0.2	0
42	Genetic parameters of meat quality, carcass composition, and growth traits in commercial swine. <i>Journal of Animal Science</i> , 2019, 97, 3669-3683.	0.2	33
43	Predicting Growth and Carcass Traits in Swine Using Microbiome Data and Machine Learning Algorithms. <i>Scientific Reports</i> , 2019, 9, 6574.	1.6	38
44	381 Investigation of heat stress on differential gene expression in tolerant and susceptible pigs. <i>Journal of Animal Science</i> , 2019, 97, 144-144.	0.2	0
45	213 Genomic selection of carcass quality traits in crossbred pigs using a reference population. <i>Journal of Animal Science</i> , 2019, 97, 41-41.	0.2	1
46	215 Selection response for meat quality and carcass composition in commercial pigs using crossbred and purebred traits as predictors. <i>Journal of Animal Science</i> , 2019, 97, 45-45.	0.2	0
47	210 Genotype by environment interaction for pre-weaning survival in commercial crossbred pigs. <i>Journal of Animal Science</i> , 2019, 97, 40-41.	0.2	0
48	216 Contribution of host gut microbiome in prediction of meat quality and carcass composition traits in swine. <i>Journal of Animal Science</i> , 2019, 97, 44-45.	0.2	0
49	212 Genomic prediction of carcass average daily gain, fat and loin depth in three-way crossbred pigs including information collected on purebreds. <i>Journal of Animal Science</i> , 2019, 97, 40-40.	0.2	0
50	214 Correlation among host gut microbiome and their relationship with meat quality and carcass composition traits of swine. <i>Journal of Animal Science</i> , 2019, 97, 44-44.	0.2	0
51	The use of genomic information to improve selection response while controlling inbreeding in dairy cattle breeding programs. <i>Burleigh Dodds Series in Agricultural Science</i> , 2019, , 71-96.	0.1	0
52	Individual Variation in Social Behaviours of Male Lab-reared Prairie voles (<i>Microtus ochrogaster</i>) is Non-heritable and Weakly Associated with V1aR Density. <i>Scientific Reports</i> , 2018, 8, 1396.	1.6	15
53	Bacterial and fungal communities, fermentation, and aerobic stability of conventional hybrids and brown midrib hybrids ensiled at low moisture with or without a homo- and heterofermentative inoculant. <i>Journal of Dairy Science</i> , 2018, 101, 3057-3076.	1.4	36
54	A comparison of accuracy validation methods for genomic and pedigree-based predictions of swine litter size traits using Large White and simulated data. <i>Journal of Animal Breeding and Genetics</i> , 2018, 135, 5-13.	0.8	16

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55	Short communication: Association analysis of diacylglycerol acyltransferase (DGAT1) mutation on chromosome 14 for milk yield and composition traits, somatic cell score, and coagulation properties in Holstein bulls. <i>Journal of Dairy Science</i> , 2018, 101, 8087-8091.	1.4	9
56	Including gene networks to predict calving difficulty in Holstein, Brown Swiss and Jersey cattle. <i>BMC Genetics</i> , 2018, 19, 20.	2.7	4
57	Host contributes to longitudinal diversity of fecal microbiota in swine selected for lean growth. <i>Microbiome</i> , 2018, 6, 4.	4.9	90
58	Genotype by environment (climate) interaction improves genomic prediction for production traits in US Holstein cattle. <i>Journal of Dairy Science</i> , 2017, 100, 2042-2056.	1.4	44
59	Laboratory silo type and inoculation effects on nutritional composition, fermentation, and bacterial and fungal communities of oat silage. <i>Journal of Dairy Science</i> , 2017, 100, 1812-1828.	1.4	73
60	GenoDiver: A combined coalescence and forward-in-time simulator for populations undergoing selection for complex traits. <i>Journal of Animal Breeding and Genetics</i> , 2017, 134, 553-563.	0.8	8
61	Comparison of Bayesian regression models and partial least squares regression for the development of infrared prediction equations. <i>Journal of Dairy Science</i> , 2017, 100, 7306-7319.	1.4	29
62	Association of candidate gene polymorphisms with milk technological traits, yield, composition, and somatic cell score in Italian Holstein-Friesian sires. <i>Journal of Dairy Science</i> , 2017, 100, 7271-7281.	1.4	39
63	Rumination time as a potential predictor of common diseases in high-productive Holstein dairy cows. <i>Journal of Dairy Research</i> , 2017, 84, 385-390.	0.7	12
64	A heuristic method to identify runs of homozygosity associated with reduced performance in livestock. <i>Journal of Animal Science</i> , 2017, 95, 4318-4332.	0.2	15
65	The relationship between different measures of feed efficiency and feeding behavior traits in Duroc pigs1. <i>Journal of Animal Science</i> , 2017, 95, 3370-3380.	0.2	27
66	Food Production or Food Distribution: The Key to Global Food Security?. <i>Perspectives on Global Development and Technology</i> , 2017, 16, 666-682.	0.2	3
67	P1025 A method for the identification of unfavorable haplotypes contained within runs of homozygosity that impact fitness traits and its application to different swine nucleus lines. <i>Journal of Animal Science</i> , 2016, 94, 26-27.	0.2	0
68	028 The use of alternative genomic metrics in swine nucleus herds to manage the diversity of purebred and crossbred animals. <i>Journal of Animal Science</i> , 2016, 94, 13-13.	0.2	0
69	0301 A combined coalescence forward in time simulator software for pedigreed populations undergoing selection for complex traits. <i>Journal of Animal Science</i> , 2016, 94, 143-144.	0.2	0
70	0387 Daily rumination time in Italian Holstein cows: Heritability and correlation with milk production. <i>Journal of Animal Science</i> , 2016, 94, 187-188.	0.2	3
71	The use of multiple imputation for the accurate measurements of individual feed intake by electronic feeders. <i>Journal of Animal Science</i> , 2016, 94, 824-832.	0.2	3
72	029 Mitigating the effect of seasonality on sow reproductive performance using genetic selection. <i>Journal of Animal Science</i> , 2016, 94, 14-14.	0.2	0

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73	Causal relationships between clinical mastitis events, milk yields and lactation persistency in US Holsteins. <i>Livestock Science</i> , 2016, 189, 8-16.	0.6	8
74	Characterization and management of long runs of homozygosity in parental nucleus lines and their associated crossbred progeny. <i>Genetics Selection Evolution</i> , 2016, 48, 91.	1.2	25
75	Variance component estimates for alternative litter size traits in swine. <i>Journal of Animal Science</i> , 2015, 93, 5153-5163.	0.2	37
76	A Genome-Wide Association Study for Clinical Mastitis in First Parity US Holstein Cows Using Single-Step Approach and Genomic Matrix Re-Weighting Procedure. <i>PLoS ONE</i> , 2015, 10, e0114919.	1.1	113
77	Causal relationships between milk quality and coagulation properties in Italian Holstein-Friesian dairy cattle. <i>Genetics Selection Evolution</i> , 2015, 47, 45.	1.2	13
78	Genomic prediction of disease occurrence using producer-recorded health data: a comparison of methods. <i>Genetics Selection Evolution</i> , 2015, 47, 41.	1.2	3
79	Inferring causal relationships between reproductive and metabolic health disorders and production traits in first-lactation US Holsteins using recursive models. <i>Journal of Dairy Science</i> , 2015, 98, 2713-2726.	1.4	12
80	Genetics of milk fatty acid groups predicted during routine data recording in Holstein dairy cattle. <i>Livestock Science</i> , 2015, 173, 9-13.	0.6	23
81	Accounting for trait architecture in genomic predictions of US Holstein cattle using a weighted realized relationship matrix. <i>Genetics Selection Evolution</i> , 2015, 47, 24.	1.2	51
82	Short communication: Genomic selection for hoof lesions in first-parity US Holsteins. <i>Journal of Dairy Science</i> , 2015, 98, 3502-3507.	1.4	10
83	Genome-wide association study on legendre random regression coefficients for the growth and feed intake trajectory on Duroc Boars. <i>BMC Genetics</i> , 2015, 16, 59.	2.7	53
84	Comparison between different statistical models for the prediction of direct genetic component on embryo establishment and survival in Italian Brown Swiss dairy cattle. <i>Livestock Science</i> , 2015, 180, 6-13.	0.6	3
85	A comparison of the predicted coagulation characteristics and composition of milk from multi-breed herds of Holstein-Friesian, Brown Swiss and Simmental cows. <i>International Dairy Journal</i> , 2014, 35, 6-10.	1.5	45
86	Thin and fat cows, and the nonlinear genetic relationship between body condition score and fertility. <i>Journal of Dairy Science</i> , 2013, 96, 6730-6741.	1.4	16
87	Short communication: Genetic analysis of dairy bull fertility from field data of Brown Swiss cattle. <i>Journal of Dairy Science</i> , 2013, 96, 7325-7328.	1.4	9
88	Heritability and repeatability of milk coagulation properties predicted by mid-infrared spectroscopy during routine data recording, and their relationships with milk yield and quality traits. <i>Animal</i> , 2013, 7, 1592-1599.	1.3	46
89	Genetic parameters for fertility of dairy heifers and cows at different parities and relationships with production traits in first lactation. <i>Journal of Dairy Science</i> , 2012, 95, 7355-7362.	1.4	48
90	Factors affecting the incidence of first-quality wheels of Trentingrana cheese. <i>Journal of Dairy Science</i> , 2011, 94, 3700-3707.	1.4	49

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91	Monitoring of sensory attributes used in the quality payment system of Trentingrana cheese. Journal of Dairy Science, 2011, 94, 5699-5709.	1.4	41
92	Genetic analysis of fertility in the Italian Brown Swiss population using different models and trait definitions. Journal of Dairy Science, 2011, 94, 6162-6172.	1.4	27
93	Characterization of buffalo production of northeast of Italy. Italian Journal of Animal Science, 2009, 8, 160-162.	0.8	7