

# Mehdi Momen

## List of Publications by Year in descending order

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Version: 2024-02-01

20  
papers

302  
citations

1051969

10  
h-index

1051228

16  
g-index

27  
all docs

27  
docs citations

27  
times ranked

512  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genic and non-genic SNP contributions to additive and dominance genetic effects in purebred and crossbred pig traits. <i>Scientific Reports</i> , 2022, 12, 3795.	1.6	1
2	Predictive assessment of single-step BLUP with linear and non-linear similarity RKHS kernels: A case study in chickens. <i>Journal of Animal Breeding and Genetics</i> , 2022, 139, 247-258.	0.8	3
3	A selection signatures study among Middle Eastern and European sheep breeds. <i>Journal of Animal Breeding and Genetics</i> , 2021, 138, 574-588.	0.8	9
4	Biologically Enhanced Genome-Wide Association Study Provides Further Evidence for Candidate Loci and Discovers Novel Loci That Influence Risk of Anterior Cruciate Ligament Rupture in a Dog Model. <i>Frontiers in Genetics</i> , 2021, 12, 593515.	1.1	7
5	Prediction of biological age and evaluation of genome-wide dynamic methylomic changes throughout human aging. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	3
6	Modeling multiple phenotypes in wheat using data-driven genomic exploratory factor analysis and Bayesian network learning. <i>Plant Direct</i> , 2021, 5, e00304.	0.8	7
7	Neurofilament light plasma concentration positively associates with age and negatively associates with weight and height in the dog. <i>Neuroscience Letters</i> , 2021, 744, 135593.	1.0	6
8	Heritability and genetic variance estimation of Osteosarcoma (OSA) in Irish Wolfhound, using deep pedigree information. <i>Canine Medicine and Genetics</i> , 2021, 8, 9.	1.4	4
9	Structural equation modeling for investigating multi-trait genetic architecture of udder health in dairy cattle. <i>Scientific Reports</i> , 2020, 10, 7751.	1.6	18
10	Bayesian and Machine Learning Models for Genomic Prediction of Anterior Cruciate Ligament Rupture in the Canine Model. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2619-2628.	0.8	14
11	Integration of single nucleotide variants and whole-genome DNA methylation profiles for classification of rheumatoid arthritis cases from controls. <i>Heredity</i> , 2020, 124, 658-674.	1.2	10
12	Performance of pedigree and various forms of marker-derived relationship coefficients in genomic prediction and their correlations. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 423-437.	0.8	1
13	Multi-trait random regression models increase genomic prediction accuracy for a temporal physiological trait derived from high-throughput phenotyping. <i>PLoS ONE</i> , 2020, 15, e0228118.	1.1	18
14	Utilizing trait networks and structural equation models as tools to interpret multi-trait genome-wide association studies. <i>Plant Methods</i> , 2019, 15, 107.	1.9	25
15	Predicting Longitudinal Traits Derived from High-Throughput Phenomics in Contrasting Environments Using Genomic Legendre Polynomials and B-Splines. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3369-3380.	0.8	24
16	Leveraging Breeding Values Obtained from Random Regression Models for Genetic Inference of Longitudinal Traits. <i>Plant Genome</i> , 2019, 12, 180075.	1.6	37
17	Including Phenotypic Causal Networks in Genome-Wide Association Studies Using Mixed Effects Structural Equation Models. <i>Frontiers in Genetics</i> , 2018, 9, 455.	1.1	26
18	Quantifying genomic connectedness and prediction accuracy from additive and non-additive gene actions. <i>Genetics Selection Evolution</i> , 2018, 50, 45.	1.2	14

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19	Predictive ability of genome-assisted statistical models under various forms of gene action. Scientific Reports, 2018, 8, 12309.	1.6	38
20	A predictive assessment of genetic correlations between traits in chickens using markers. Genetics Selection Evolution, 2017, 49, 16.	1.2	30