

Stefano Capomaccio

List of Publications by Year in descending order

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Version: 2024-02-01

64
papers

1,674
citations

361413

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315739

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docs citations

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#	ARTICLE	IF	CITATIONS
1	mcr-1-Mediated Colistin Resistance and Genomic Characterization of Antimicrobial Resistance in ESBL-Producing Salmonella Infantis Strains from a Broiler Meat Production Chain in Italy. <i>Antibiotics</i> , 2022, 11, 728.	3.7	3
2	Differential Effects of Dietary Oregano Essential Oil on the Inflammation Related Gene Expression in Peripheral Blood Mononuclear Cells From Outdoor and Indoor Reared Pigs. <i>Frontiers in Veterinary Science</i> , 2021, 8, 602811.	2.2	8
3	Genetic Regulation of Biomarkers as Stress Proxies in Dairy Cows. <i>Genes</i> , 2021, 12, 534.	2.4	3
4	Differential Expression Pattern of Retroviral Envelope Gene in the Equine Placenta. <i>Frontiers in Veterinary Science</i> , 2021, 8, 693416.	2.2	0
5	Selective symmetrical necrotizing encephalopathy secondary to primary mitochondrial disorder in a cat. <i>Journal of Veterinary Internal Medicine</i> , 2021, 35, 2401-2408.	1.6	1
6	Transcriptomic Characterization of Cow, Donkey and Goat Milk Extracellular Vesicles Reveals Their Anti-Inflammatory and Immunomodulatory Potential. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12759.	4.1	27
7	Circulating Transcriptional Profile Modulation in Response to Metabolic Unbalance Due to Long-Term Exercise in Equine Athletes: A Pilot Study. <i>Genes</i> , 2021, 12, 1965.	2.4	5
8	Evaluation of circulating leukocyte transcriptome and its relationship with immune function and blood markers in dairy cows during the transition period. <i>Functional and Integrative Genomics</i> , 2020, 20, 293-305.	3.5	20
9	Shedding light on cashmere goat hair follicle biology: from morphology analyses to transcriptomic landscape. <i>BMC Genomics</i> , 2020, 21, 458.	2.8	8
10	PANEV: an R package for a pathway-based network visualization. <i>BMC Bioinformatics</i> , 2020, 21, 46.	2.6	15
11	Metabolic and Biomolecular Changes Induced by Incremental Long-Term Training in Young Thoroughbred Racehorses during First Workout Season. <i>Animals</i> , 2020, 10, 317.	2.3	16
12	Gallop Racing Shifts Mature mRNA towards Introns: Does Exercise-Induced Stress Enhance Genome Plasticity?. <i>Genes</i> , 2020, 11, 410.	2.4	7
13	MCSed (Methylation Context Sensitive Enzyme ddRAD): A New Method to Analyze DNA Methylation. <i>Methods in Molecular Biology</i> , 2020, 2093, 47-64.	0.9	4
14	Guanylin, Uroguanylin and Guanylate Cyclase-C Are Expressed in the Gastrointestinal Tract of Horses. <i>Frontiers in Physiology</i> , 2019, 10, 1237.	2.8	2
15	Methylation content sensitive enzyme ddRAD (MCSed): a reference-free, whole genome profiling system to address cytosine/adenine methylation changes. <i>Scientific Reports</i> , 2019, 9, 14864.	3.3	14
16	Equine Adipose-Derived Mesenchymal Stromal Cells Release Extracellular Vesicles Enclosing Different Subsets of Small RNAs. <i>Stem Cells International</i> , 2019, 2019, 1-12.	2.5	21
17	Different expression of Defensin-B gene in the endometrium of mares of different age during the breeding season. <i>BMC Veterinary Research</i> , 2019, 15, 465.	1.9	7
18	PDGFA in Cashmere Goat: A Motivation for the Hair Follicle Stem Cells to Activate. <i>Animals</i> , 2019, 9, 38.	2.3	9

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19	Gene co-expression networks in liver and muscle transcriptome reveal sex-specific gene expression in lambs fed with a mix of essential oils. <i>BMC Genomics</i> , 2018, 19, 236.	2.8	19
20	Genome-wide association study of milk fatty acid composition in Italian Simmental and Italian Holstein cows using single nucleotide polymorphism arrays. <i>Journal of Dairy Science</i> , 2018, 101, 11004-11019.	3.4	54
21	Dietary supplementation with olive mill wastewaters induces modifications on chicken jejunum epithelial cell transcriptome and modulates jejunum morphology. <i>BMC Genomics</i> , 2018, 19, 576.	2.8	22
22	Circulating miRNAs as Putative Biomarkers of Exercise Adaptation in Endurance Horses. <i>Frontiers in Physiology</i> , 2018, 9, 429.	2.8	10
23	Oregano dietary supplementation modifies the liver transcriptome profile in broilers: RNASeq analysis. <i>Research in Veterinary Science</i> , 2018, 117, 85-91.	1.9	19
24	Deep sequencing and variant analysis of an Italian pathogenic field strain of equine infectious anaemia virus. <i>Transboundary and Emerging Diseases</i> , 2017, 64, 2104-2112.	3.0	12
25	Splicing site disruption in the <i>KIT</i> gene as strong candidate for white dominant phenotype in an Italian Trotter. <i>Animal Genetics</i> , 2017, 48, 727-728.	1.7	12
26	Transcriptome Analysis of Canine Cutaneous Melanoma and Melanocytoma Reveals a Modulation of Genes Regulating Extracellular Matrix Metabolism and Cell Cycle. <i>Scientific Reports</i> , 2017, 7, 6386.	3.3	28
27	Genome assembly and transcriptome resource for river buffalo, <i>Bubalus bubalis</i> (2n = 50). <i>GigaScience</i> , 2017, 6, 1-6.	6.4	55
28	An Overview of Ten Italian Horse Breeds through Mitochondrial DNA. <i>PLoS ONE</i> , 2016, 11, e0153004.	2.5	30
29	High Expression of Endogenous Retroviral Envelope Gene in the Equine Fetal Part of the Placenta. <i>PLoS ONE</i> , 2016, 11, e0155603.	2.5	12
30	Sexual Polyploidization in <i>Medicago sativa</i> L.: Impact on the Phenotype, Gene Transcription, and Genome Methylation. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 925-938.	1.8	6
31	Detection of bacterial contamination and DNA quantification in stored blood units in 2 veterinary hospital blood banks. <i>Veterinary Clinical Pathology</i> , 2016, 45, 406-410.	0.7	16
32	Stored Canine Whole Blood Units: What is the Real Risk of Bacterial Contamination?. <i>Journal of Veterinary Internal Medicine</i> , 2016, 30, 1830-1837.	1.6	17
33	Phenotypic and genotypic characterization of canine pyoderma isolates of <i>Staphylococcus pseudintermedius</i> for biofilm formation. <i>Journal of Veterinary Medical Science</i> , 2015, 77, 945-951.	0.9	22
34	Searching new signals for production traits through gene-based association analysis in three Italian cattle breeds. <i>Animal Genetics</i> , 2015, 46, 361-370.	1.7	20
35	Assessment of Heat Shock Protein 70 Induction by Heat in Alfalfa Varieties and Constitutive Overexpression in Transgenic Plants. <i>PLoS ONE</i> , 2015, 10, e0126051.	2.5	12
36	Genetic and phenotypic characterization of the Maremmano horse stud in Castelporziano. <i>Rendiconti Lincei</i> , 2015, 26, 545-552.	2.2	2

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37	First report of junctional epidermolysis bullosa (JEB) in the Italian draft horse. BMC Veterinary Research, 2015, 11, 55.	1.9	8
38	MUGBAS: a species free gene-based programme suite for post-GWAS analysis. Bioinformatics, 2015, 31, 2380-2381.	4.1	6
39	Polysynovitis in a horse due to <i>Borrelia burgdorferi</i> sensu lato infection – Case study. Annals of Agricultural and Environmental Medicine, 2015, 22, 247-250.	1.0	17
40	Molecular analysis of genetic diversity, population structure and inbreeding level of the Italian Lipizzan horse. Livestock Science, 2013, 151, 124-133.	1.6	20
41	Effect of training status on immune defence related gene expression in Thoroughbred: Are genes ready for the sprint?. Veterinary Journal, 2013, 195, 373-376.	1.7	36
42	Genome-Wide Analysis Reveals Selection for Important Traits in Domestic Horse Breeds. PLoS Genetics, 2013, 9, e1003211.	3.5	240
43	RNA Sequencing of the Exercise Transcriptome in Equine Athletes. PLoS ONE, 2013, 8, e83504.	2.5	55
44	Mitochondrial genomes from modern horses reveal the major haplogroups that underwent domestication. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2449-2454.	7.1	198
45	Variation of DNA methylation and phenotypic traits following unilateral sexual polyploidization in Medicago. Euphytica, 2012, 186, 731-739.	1.2	3
46	Geographic structuring of global EIAV isolates: A single origin for New World strains?. Virus Research, 2012, 163, 656-659.	2.2	19
47	Detection, molecular characterization and phylogenetic analysis of full-length equine infectious anemia (EIAV) gag genes isolated from Shackleford Banks wild horses. Veterinary Microbiology, 2012, 157, 320-332.	1.9	27
48	A point mutation in the Medicago sativa GSA gene provides a novel, efficient, selectable marker for plant genetic engineering. Journal of Biotechnology, 2011, 156, 147-152.	3.8	19
49	Assessment of simple marker-free genetic transformation techniques in alfalfa. Plant Cell Reports, 2011, 30, 1991-2000.	5.6	15
50	Athletic humans and horses: Comparative analysis of interleukin-6 (IL-6) and IL-6 receptor (IL-6R) expression in peripheral blood mononuclear cells in trained and untrained subjects at rest. BMC Physiology, 2011, 11, 3.	3.6	40
51	Quantification of Equid herpesvirus 5 DNA in clinical and necropsy specimens collected from a horse with equine multinodular pulmonary fibrosis. Journal of Veterinary Diagnostic Investigation, 2011, 23, 802-806.	1.1	32
52	Molecular Detection, Epidemiology, and Genetic Characterization of Novel European Field Isolates of Equine Infectious Anemia Virus. Journal of Clinical Microbiology, 2011, 49, 27-33.	3.9	43
53	Polyploidization and Gene Expression in Medicago sativa. , 2010, , 397-401.		2
54	Age-dependent prevalence of equid herpesvirus 5 infection. Veterinary Research Communications, 2010, 34, 703-708.	1.6	40

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55	Transcription of <i>LINE-1</i> derived sequences in exercise-induced stress in horses. <i>Animal Genetics</i> , 2010, 41, 23-27.	1.7	22
56	Microarray analysis after strenuous exercise in peripheral blood mononuclear cells of endurance horses. <i>Animal Genetics</i> , 2010, 41, 166-175.	1.7	32
57	<i>Anaplasma phagocytophilum</i> in horses and ticks: A preliminary survey of Central Italy. <i>Comparative Immunology, Microbiology and Infectious Diseases</i> , 2010, 33, 73-83.	1.6	42
58	Isolation of genes from female sterile flowers in <i>Medicago sativa</i> . <i>Sexual Plant Reproduction</i> , 2009, 22, 97-107.	2.2	6
59	Exercise-induced up-regulation of MMP-1 and IL-8 genes in endurance horses. <i>BMC Physiology</i> , 2009, 9, 12.	3.6	14
60	Exercise induced stress in horses: Selection of the most stable reference genes for quantitative RT-PCR normalization. <i>BMC Molecular Biology</i> , 2008, 9, 49.	3.0	111
61	Clinical, serological and molecular investigations of <i>ehv-1</i> and <i>ehv-4</i> in 15 unweaned thoroughbred foals. <i>Veterinary Record</i> , 2008, 162, 337-341.	0.3	10
62	Analysis of peripheral blood mononuclear cells gene expression in endurance horses by cDNA-AFLP technique. <i>Research in Veterinary Science</i> , 2007, 82, 335-343.	1.9	20
63	Non-antibiotic, efficient selection for alfalfa genetic engineering. <i>Plant Cell Reports</i> , 2007, 26, 1035-1044.	5.6	46
64	cDNA AFLP-based techniques for studying transcript profiles in horses. <i>Research in Veterinary Science</i> , 2005, 79, 105-112.	1.9	9