Stefano Capomaccio

List of Publications by Year in descending order

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64 papers

1,674 citations

20 h-index 315739 38 g-index

67 all docs

67
does citations

times ranked

67

2298 citing authors

#	Article	IF	CITATIONS
1	Genome-Wide Analysis Reveals Selection for Important Traits in Domestic Horse Breeds. PLoS Genetics, 2013, 9, e1003211.	3.5	240
2	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
3	Exercise induced stress in horses: Selection of the most stable reference genes for quantitative RT-PCR normalization. BMC Molecular Biology, 2008, 9, 49.	3.0	111
4	RNA Sequencing of the Exercise Transcriptome in Equine Athletes. PLoS ONE, 2013, 8, e83504.	2.5	55
5	Genome assembly and transcriptome resource for river buffalo, Bubalus bubalis (2n = 50). GigaScience, 2017, 6, 1-6.	6.4	55
6	Genome-wide association study of milk fatty acid composition in Italian Simmental and Italian Holstein cows using single nucleotide polymorphism arrays. Journal of Dairy Science, 2018, 101, 11004-11019.	3.4	54
7	Non-antibiotic, efficient selection for alfalfa genetic engineering. Plant Cell Reports, 2007, 26, 1035-1044.	5.6	46
8	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
9	Anaplasma phagocytophilum in horses and ticks: A preliminary survey of Central Italy. Comparative Immunology, Microbiology and Infectious Diseases, 2010, 33, 73-83.	1.6	42
10	Age-dependent prevalence of equid herpesvirus 5 infection. Veterinary Research Communications, 2010, 34, 703-708.	1.6	40
11	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
12	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
13	Microarray analysis after strenuous exercise in peripheral blood mononuclear cells of endurance horses. Animal Genetics, 2010, 41, 166-175.	1.7	32
14	Quantification of <i>Equid herpesvirus 5</i> 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
15	An Overview of Ten Italian Horse Breeds through Mitochondrial DNA. PLoS ONE, 2016, 11, e0153004.	2.5	30
16	Transcriptome Analysis of Canine Cutaneous Melanoma and Melanocytoma Reveals a Modulation of Genes Regulating Extracellular Matrix Metabolism and Cell Cycle. Scientific Reports, 2017, 7, 6386.	3.3	28
17	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
18	Transcriptomic Characterization of Cow, Donkey and Goat Milk Extracellular Vesicles Reveals Their Anti-Inflammatory and Immunomodulatory Potential. International Journal of Molecular Sciences, 2021, 22, 12759.	4.1	27

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19	Transcription of <i>LINE</i> à€derived sequences in exerciseâ€induced stress in horses. Animal Genetics, 2010, 41, 23-27.	1.7	22
20	Phenotypic and genotypic characterization of canine pyoderma isolates of <i>Staphylococcus pseudintermedius</i> for biofilm formation. Journal of Veterinary Medical Science, 2015, 77, 945-951.	0.9	22
21	Dietary supplementation with olive mill wastewaters induces modifications on chicken jejunum epithelial cell transcriptome and modulates jejunum morphology. BMC Genomics, 2018, 19, 576.	2.8	22
22	Equine Adipose-Derived Mesenchymal Stromal Cells Release Extracellular Vesicles Enclosing Different Subsets of Small RNAs. Stem Cells International, 2019, 2019, 1-12.	2.5	21
23	Analysis of peripheral blood mononuclear cells gene expression in endurance horses by cDNA-AFLP technique. Research in Veterinary Science, 2007, 82, 335-343.	1.9	20
24	Molecular analysis of genetic diversity, population structure and inbreeding level of the Italian Lipizzan horse. Livestock Science, 2013, 151, 124-133.	1.6	20
25	Searching new signals for production traits through gene-based association analysis in three Italian cattle breeds. Animal Genetics, 2015, 46, 361-370.	1.7	20
26	Evaluation of circulating leukocyte transcriptome and its relationship with immune function and blood markers in dairy cows during the transition period. Functional and Integrative Genomics, 2020, 20, 293-305.	3.5	20
27	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
28	Geographic structuring of global EIAV isolates: A single origin for New World strains?. Virus Research, 2012, 163, 656-659.	2.2	19
29	Gene co-expression networks in liver and muscle transcriptome reveal sex-specific gene expression in lambs fed with a mix of essential oils. BMC Genomics, 2018, 19, 236.	2.8	19
30	Oregano dietary supplementation modifies the liver transcriptome profile in broilers: RNASeq analysis. Research in Veterinary Science, 2018, 117, 85-91.	1.9	19
31	Stored Canine Whole Blood Units: What is the Real Risk of Bacterial Contamination?. Journal of Veterinary Internal Medicine, 2016, 30, 1830-1837.	1.6	17
32	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
33	Detection of bacterial contamination and <scp>DNA</scp> quantification in stored blood units in 2 veterinary hospital blood banks. Veterinary Clinical Pathology, 2016, 45, 406-410.	0.7	16
34	Metabolic and Biomolecular Changes Induced by Incremental Long-Term Training in Young Thoroughbred Racehorses during First Workout Season. Animals, 2020, 10, 317.	2.3	16
35	Assessment of simple marker-free genetic transformation techniques in alfalfa. Plant Cell Reports, 2011, 30, 1991-2000.	5.6	15
36	PANEV: an R package for a pathway-based network visualization. BMC Bioinformatics, 2020, 21, 46.	2.6	15

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37	Exercise-induced up-regulation of MMP-1 and IL-8 genes in endurance horses. BMC Physiology, 2009, 9, 12.	3.6	14
38	Methylation content sensitive enzyme ddRAD (MCSeEd): a reference-free, whole genome profiling system to address cytosine/adenine methylation changes. Scientific Reports, 2019, 9, 14864.	3.3	14
39	Assessment of Heat Shock Protein 70 Induction by Heat in Alfalfa Varieties and Constitutive Overexpression in Transgenic Plants. PLoS ONE, 2015, 10, e0126051.	2.5	12
40	High Expression of Endogenous Retroviral Envelope Gene in the Equine Fetal Part of the Placenta. PLoS ONE, 2016, 11, e0155603.	2.5	12
41	Deep sequencing and variant analysis of an Italian pathogenic field strain of equine infectious anaemia virus. Transboundary and Emerging Diseases, 2017, 64, 2104-2112.	3.0	12
42	Splicing site disruption in the <i><scp>KIT</scp></i> gene as strong candidate for white dominant phenotype in an Italian Trotter. Animal Genetics, 2017, 48, 727-728.	1.7	12
43	Clinical, serological and molecular investigations of <scp>ehvâ€4 </scp> and <scp>ehvâ€4 </scp> in 15 unweaned thoroughbred foals. Veterinary Record, 2008, 162, 337-341.	0.3	10
44	Circulating miRNAs as Putative Biomarkers of Exercise Adaptation in Endurance Horses. Frontiers in Physiology, 2018, 9, 429.	2.8	10
45	cDNA AFLP-based techniques for studying transcript profiles in horses. Research in Veterinary Science, 2005, 79, 105-112.	1.9	9
46	PDGFA in Cashmere Goat: A Motivation for the Hair Follicle Stem Cells to Activate. Animals, 2019, 9, 38.	2.3	9
47	First report of junctional epidermolysis bullosa (JEB) in the Italian draft horse. BMC Veterinary Research, 2015, 11, 55.	1.9	8
48	Shedding light on cashmere goat hair follicle biology: from morphology analyses to transcriptomic landascape. BMC Genomics, 2020, 21, 458.	2.8	8
49	Differential Effects of Dietary Oregano Essential Oil on the Inflammation Related Gene Expression in Peripheral Blood Mononuclear Cells From Outdoor and Indoor Reared Pigs. Frontiers in Veterinary Science, 2021, 8, 602811.	2.2	8
50	Different expression of Defensin-B gene in the endometrium of mares of different age during the breeding season. BMC Veterinary Research, 2019, 15, 465.	1.9	7
51	Gallop Racing Shifts Mature mRNA towards Introns: Does Exercise-Induced Stress Enhance Genome Plasticity?. Genes, 2020, 11, 410.	2.4	7
52	Isolation of genes from female sterile flowers in Medicago sativa. Sexual Plant Reproduction, 2009, 22, 97-107.	2.2	6
53	MUGBAS: a species free gene-based programme suite for post-GWAS analysis. Bioinformatics, 2015, 31, 2380-2381.	4.1	6
54	Sexual Polyploidization in Medicago sativa L.: Impact on the Phenotype, Gene Transcription, and Genome Methylation. G3: Genes, Genomes, Genetics, 2016, 6, 925-938.	1.8	6

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55	Circulating Transcriptional Profile Modulation in Response to Metabolic Unbalance Due to Long-Term Exercise in Equine Athletes: A Pilot Study. Genes, 2021, 12, 1965.	2.4	5
56	MCSeEd (Methylation Context Sensitive Enzyme ddRAD): A New Method to Analyze DNA Methylation. Methods in Molecular Biology, 2020, 2093, 47-64.	0.9	4
57	Variation of DNA methylation and phenotypic traits following unilateral sexual polyploidization in Medicago. Euphytica, 2012, 186, 731-739.	1.2	3
58	Genetic Regulation of Biomarkers as Stress Proxies in Dairy Cows. Genes, 2021, 12, 534.	2.4	3
59	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. Antibiotics, 2022, 11, 728.	3.7	3
60	Polyploidization and Gene Expression in Medicago sativa. , 2010, , 397-401.		2
61	Genetic and phenotypic characterization of the Maremmano horse stud in Castelporziano. Rendiconti Lincei, 2015, 26, 545-552.	2.2	2
62	Guanylin, Uroguanylin and Guanylate Cyclase-C Are Expressed in the Gastrointestinal Tract of Horses. Frontiers in Physiology, 2019, 10, 1237.	2.8	2
63	Selective symmetrical necrotizing encephalopathy secondary to primary mitochondrial disorder in a cat. Journal of Veterinary Internal Medicine, 2021, 35, 2401-2408.	1.6	1
64	Differential Expression Pattern of Retroviral Envelope Gene in the Equine Placenta. Frontiers in Veterinary Science, 2021, 8, 693416.	2.2	O