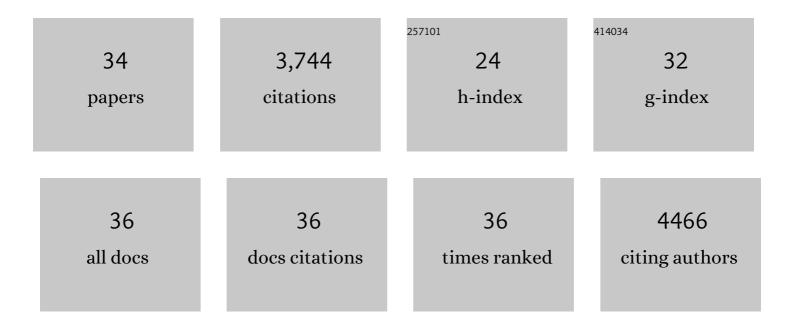
Elisabetta Giuffra

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Intestinal organoids in farm animals. Veterinary Research, 2021, 52, 33.	1.1	48
2	Tissue Resources for the Functional Annotation of Animal Genomes. Frontiers in Genetics, 2021, 12, 666265.	1.1	1
3	From FAANG to fork: application of highly annotated genomes to improve farmed animal production. Genome Biology, 2020, 21, 285.	3.8	74
4	An integrative atlas of chicken long non-coding genes and their annotations across 25 tissues. Scientific Reports, 2020, 10, 20457.	1.6	20
5	Distinctive Cellular and Metabolic Reprogramming in Porcine Lung Mononuclear Phagocytes Infected With Type 1 PRRSV Strains. Frontiers in Immunology, 2020, 11, 588411.	2.2	6
6	Macrophage-B Cell Interactions in the Inverted Porcine Lymph Node and Their Response to Porcine Reproductive and Respiratory Syndrome Virus. Frontiers in Immunology, 2019, 10, 953.	2.2	25
7	The miRNA-targeted transcriptome of porcine alveolar macrophages upon infection with Porcine Reproductive and Respiratory Syndrome Virus. Scientific Reports, 2019, 9, 3160.	1.6	9
8	Multi-species annotation of transcriptome and chromatin structure in domesticated animals. BMC Biology, 2019, 17, 108.	1.7	109
9	Functional Annotation of Animal Genomes (FAANG): Current Achievements and Roadmap. Annual Review of Animal Biosciences, 2019, 7, 65-88.	3.6	172
10	Porcine Reproductive and Respiratory Syndrome Virus Type 1.3 Lena Triggers Conventional Dendritic Cells 1 Activation and T Helper 1 Immune Response Without Infecting Dendritic Cells. Frontiers in Immunology, 2018, 9, 2299.	2.2	49
11	Long noncoding RNA repertoire in chicken liver and adipose tissue. Genetics Selection Evolution, 2017, 49, 6.	1.2	59
12	RNA-sequence analysis of gene expression from honeybees (Apis mellifera) infected with Nosema ceranae. PLoS ONE, 2017, 12, e0173438.	1.1	45
13	<scp>GO</scp> â€ <scp>FAANG</scp> meeting: a Gathering On Functional Annotation of <scp>An</scp> imal Genomes. Animal Genetics, 2016, 47, 528-533.	0.6	65
14	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. Genome Biology, 2015, 16, 57.	3.8	331
15	A 2.5-Kilobase Deletion Containing a Cluster of Nine MicroRNAs in the Latency-Associated-Transcript Locus of the Pseudorabies Virus Affects the Host Response of Porcine Trigeminal Ganglia during Established Latency. Journal of Virology, 2015, 89, 428-442.	1.5	24
16	RNA-Sequence Analysis of Primary Alveolar Macrophages after In Vitro Infection with Porcine Reproductive and Respiratory Syndrome Virus Strains of Differing Virulence. PLoS ONE, 2014, 9, e91918.	1.1	37
17	Structural and functional annotation of the porcine immunome. BMC Genomics, 2013, 14, 332.	1.2	203
18	Analyses of pig genomes provide insight into porcine demography and evolution. Nature, 2012, 491, 393-398.	13.7	1,190

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19	Prediction of Altered 3′- UTR miRNA-Binding Sites from RNA-Seq Data: The Swine Leukocyte Antigen Complex (SLA) as a Model Region. PLoS ONE, 2012, 7, e48607.	1.1	15
20	Co-Expression of Host and Viral MicroRNAs in Porcine Dendritic Cells Infected by the Pseudorabies Virus. PLoS ONE, 2011, 6, e17374.	1.1	40
21	Sensitive Detection and Quantification of Anisakid Parasite Residues in Food Products. Foodborne Pathogens and Disease, 2010, 7, 391-397.	0.8	27
22	Gene expression study of two widely used pig intestinal epithelial cell lines: IPEC-J2 and IPI-2I. Veterinary Immunology and Immunopathology, 2009, 131, 278-284.	0.5	83
23	Genome-wide transcriptional response of primary alveolar macrophages following infection with porcine reproductive and respiratory syndrome virus. Journal of General Virology, 2008, 89, 2550-2564.	1.3	100
24	Genetic analysis of anal atresia in pigs: evidence for segregation at two main loci. Mammalian Genome, 2005, 16, 164-170.	1.0	9
25	Haplotype Sharing Refines the Location of an Imprinted Quantitative Trait Locus With Major Effect on Muscle Mass to a 250-kb Chromosome Segment Containing the Porcine <i>IGF2</i> Gene. Genetics, 2003, 165, 277-285.	1.2	53
26	A large duplication associated with dominant white color in pigs originated by homologous recombination between LINE elements flanking KIT. Mammalian Genome, 2002, 13, 569-577.	1.0	149
27	Mapping loci causing susceptibility to anal atresia in pigs, using a resource pedigree. Journal of Pediatric Surgery, 2001, 36, 1370-1374.	0.8	15
28	Time-resolved fluorescence analysis of the recombinant photosystem II antenna complex CP29. FEBS Journal, 2001, 268, 260-267.	0.2	66
29	A paternally expressed QTL affecting skeletal and cardiac muscle mass in pigs maps to the IGF2 locus. Nature Genetics, 1999, 21, 157-158.	9.4	333
30	The Belt mutation in pigs is an allele at the Dominant white (I/KIT) locus. Mammalian Genome, 1999, 10, 1132-1136.	1.0	92
31	Zeaxanthin-induced fluorescence quenching in the minor antenna CP29. , 1998, , 333-336.		2
32	Analysis of Some Optical Properties of a Native and Reconstituted Photosystem II Antenna Complex, CP29:  Pigment Binding Sites Can Be Occupied by Chlorophyll a or Chlorophyll b and Determine Spectral Forms. Biochemistry, 1997, 36, 12984-12993.	1.2	76
33	A single point mutation (E166Q) prevents dicyclohexylcarbodiimide binding to the photosystem II subunit CP29. FEBS Letters, 1997, 402, 151-156.	1.3	74
34	Reconstitution and Pigment-Binding Properties of Recombinant CP29. FEBS Journal, 1996, 238, 112-120.	0.2	127