Fernando H Biase

List of Publications by Year
in descending order

21 papers	**1,647** citations	687363 **13** h-index	752698 **20** g-index
24 all docs	**24** docs citations	**24** times ranked	**2841** citing authors

#	Article	IF	Citations
1	Delayed processing of blood samples impairs the accuracy of mRNA-based biomarkers. Scientific Reports, 2022, 12, 8196.	3.3	6
2	Isolation of high-quality total RNA and RNA sequencing of single bovine oocytes. STAR Protocols, 2021, 2, 100895.	1.2	4
3	Beef heifer fertility: importance of management practices and technological advancements. Journal of Animal Science and Biotechnology, 2020, 11, 97.	5.3	26
4	Rewiring of gene expression in circulating white blood cells is associated with pregnancy outcome in heifers (Bos taurus). Scientific Reports, 2020, 10, 16786.	3.3	14
5	The blueprint of RNA storages relative to oocyte developmental competence in cattle (Bos taurus). Biology of Reproduction, 2020, 102, 784-794.	2.7	14
6	Evaluation of age, weaning weight, body condition score, and reproductive tract score in pre-selected beef heifers relative to reproductive potential. Journal of Animal Science and Biotechnology, 2019, 10, 18.	5.3	17
7	Fine-tuned adaptation of embryo–endometrium pairs at implantation revealed by transcriptome analyses in Bos taurus. PLoS Biology, 2019, 17, e3000046.	5.6	14
8	Extraction of total RNA from single-oocytes and single-cell mRNA sequencing of swine oocytes. BMC Research Notes, 2018, 11, 155.	1.4	5
9	Transcriptome data of peripheral white blood cells from beef heifers collected at the time of artificial insemination. Data in Brief, 2018, 18, 706-709.	1.0	10
10	Plasma metabolomic profiles differ at the time of artificial insemination based on pregnancy outcome, in Bos taurus beef heifers. Scientific Reports, 2018, 8, 13196.	3.3	17
11	Functional signaling and gene regulatory networks between the oocyte and the surrounding cumulus cells. BMC Genomics, 2018, 19, 351.	2.8	49
12	Rainbow-Seq: Combining Cell Lineage Tracing with Single-Cell RNA Sequencing in Preimplantation Embryos. IScience, 2018, 7, 16-29.	4.1	9
13	Transcriptome profiles in peripheral white blood cells at the time of artificial insemination discriminate beef heifers with different fertility potential. BMC Genomics, 2018, 19, 129.	2.8	30
14	Oocyte Developmental Competence: Insights from Cross-Species Differential Gene Expression and Human Oocyte-Specific Functional Gene Networks. OMICS A Journal of Integrative Biology, 2017, 21, 156-168.	2.0	22
15	Massive dysregulation of genes involved in cell signaling and placental development in cloned cattle conceptus and maternal endometrium. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14492-14501.	7.1	44
16	*In vitro* maturation alters gene expression in bovine oocytes. Zygote, 2016, 24, 624-633.	1.1	20
17	Time-variant clustering model for understanding cell fate decisions. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4797-806.	7.1	29
18	Cell fate inclination within 2-cell and 4-cell mouse embryos revealed by single-cell RNA sequencing. Genome Research, 2014, 24, 1787-1796.	5.5	263

#	Article	IF	Citations
19	Changes in WNT signaling–related gene expression associated with development and cloning in bovine extra–embryonic and endometrial tissues during the peri–implantation period. Molecular Reproduction and Development, 2013, 80, 977-987.	2.0	15
20	Nuclear and mitochondrial DNA markers in traceability of retail beef samples. Pesquisa Veterinaria Brasileira, 2010, 30, 783-786.	0.5	0
21	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. Science, 2009, 324, 522-528.	12.6	1,038