Fernando H Biase

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1386783/publications.pdf

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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	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. Science, 2009, 324, 522-528.	12.6	1,038
2	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
3	Functional signaling and gene regulatory networks between the oocyte and the surrounding cumulus cells. BMC Genomics, 2018, 19, 351.	2.8	49
4	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
5	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
6	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
7	Beef heifer fertility: importance of management practices and technological advancements. Journal of Animal Science and Biotechnology, 2020, 11, 97.	5.3	26
8	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
9	<i>In vitro</i> maturation alters gene expression in bovine oocytes. Zygote, 2016, 24, 624-633.	1.1	20
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	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
12	Changes in WNT signalingâ€related gene expression associated with development and cloning in bovine extraâ€embryonic and endometrial tissues during the periâ€implantation period. Molecular Reproduction and Development, 2013, 80, 977-987.	2.0	15
13	Fine-tuned adaptation of embryo–endometrium pairs at implantation revealed by transcriptome analyses in Bos taurus. PLoS Biology, 2019, 17, e3000046.	5.6	14
14	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
15	The blueprint of RNA storages relative to oocyte developmental competence in cattle (Bos taurus). Biology of Reproduction, 2020, 102, 784-794.	2.7	14
16	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
17	Rainbow-Seq: Combining Cell Lineage Tracing with Single-Cell RNA Sequencing in Preimplantation Embryos. IScience, 2018, 7, 16-29.	4.1	9
18	Delayed processing of blood samples impairs the accuracy of mRNA-based biomarkers. Scientific Reports, 2022, 12, 8196.	3.3	6

#	Article	IF	CITATIONS
19	Extraction of total RNA from single-oocytes and single-cell mRNA sequencing of swine oocytes. BMC Research Notes, 2018, 11, 155.	1.4	5
20	Isolation of high-quality total RNA and RNA sequencing of single bovine oocytes. STAR Protocols, 2021, 2, 100895.	1.2	4
21	Nuclear and mitochondrial DNA markers in traceability of retail beef samples. Pesquisa Veterinaria Brasileira, 2010, 30, 783-786.	0.5	0