

# Rocio M Rivera

## List of Publications by Year in descending order

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Version: 2024-02-01

44  
papers

1,615  
citations

331538

21  
h-index

315616

38  
g-index

47  
all docs

47  
docs citations

47  
times ranked

1782  
citing authors

#	ARTICLE	IF	CITATIONS
1	Manipulations of mouse embryos prior to implantation result in aberrant expression of imprinted genes on day 9.5 of development. <i>Human Molecular Genetics</i> , 2008, 17, 1-14.	1.4	303
2	Adverse impact of heat stress on embryo production: causes and strategies for mitigation. <i>Theriogenology</i> , 2001, 55, 91-103.	0.9	149
3	Large offspring syndrome. <i>Epigenetics</i> , 2013, 8, 591-601.	1.3	125
4	Characterization of global loss of imprinting in fetal overgrowth syndrome induced by assisted reproduction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4618-4623.	3.3	114
5	Epigenetics in fertilization and preimplantation embryo development. <i>Progress in Biophysics and Molecular Biology</i> , 2013, 113, 423-432.	1.4	68
6	Global assessment of imprinted gene expression in the bovine conceptus by next generation sequencing. <i>Epigenetics</i> , 2016, 11, 501-516.	1.3	65
7	Deleterious Actions of Gossypol on Bovine Spermatozoa, Oocytes, and Embryos <sup>1</sup> . <i>Biology of Reproduction</i> , 1997, 57, 901-907.	1.2	55
8	Alterations in Ultrastructural Morphology of Two-Cell Bovine Embryos Produced In Vitro and In Vivo Following a Physiologically Relevant Heat Shock <sup>1</sup> . <i>Biology of Reproduction</i> , 2003, 69, 2068-2077.	1.2	52
9	The effects of superovulation and reproductive aging on the epigenome of the oocyte and embryo. <i>Molecular Reproduction and Development</i> , 2018, 85, 90-105.	1.0	50
10	Expression of KCNQ1OT1, CDKN1C, H19, and PLAGL1 and the methylation patterns at the KvDMR1 and H19/IGF2 imprinting control regions is conserved between human and bovine. <i>Journal of Biomedical Science</i> , 2012, 19, 95.	2.6	48
11	Superovulation induces alterations in the epigenome of zygotes, and results in differences in gene expression at the blastocyst stage in mice. <i>Molecular Reproduction and Development</i> , 2015, 82, 207-217.	1.0	48
12	Epigenetics in humans: an overview. <i>Current Opinion in Endocrinology, Diabetes and Obesity</i> , 2010, 17, 493-499.	1.2	42
13	Heterogeneous distribution of histone methylation in mature human sperm. <i>Journal of Assisted Reproduction and Genetics</i> , 2014, 31, 45-49.	1.2	39
14	Production and Culture of the Bovine Embryo. <i>Methods in Molecular Biology</i> , 2019, 2006, 115-129.	0.4	39
15	Reorganization of Microfilaments and Microtubules by Thermal Stress in Two-Cell Bovine Embryos <sup>1</sup> . <i>Biology of Reproduction</i> , 2004, 70, 1852-1862.	1.2	33
16	Altered microRNA expression profiles in large offspring syndrome and Beckwith-Wiedemann syndrome. <i>Epigenetics</i> , 2019, 14, 850-876.	1.3	32
17	Colony-stimulating factor 2 acts from days 5 to 7 of development to modify programming of the bovine conceptus at day 86 of gestation <sup>â€</sup> . <i>Biology of Reproduction</i> , 2017, 96, 743-757.	1.2	30
18	Global misregulation of genes largely uncoupled to DNA methylome epimutations characterizes a congenital overgrowth syndrome. <i>Scientific Reports</i> , 2017, 7, 12667.	1.6	30

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19	Oxamflatin Treatment Enhances Cloned Porcine Embryo Development and Nuclear Reprogramming<sup />. Cellular Reprogramming, 2015, 17, 28-40.	0.5	29
20	Locus-Specific DNA Methylation Reprogramming During Early Porcine Embryogenesis1. Biology of Reproduction, 2013, 88, 48.	1.2	27
21	Genome-wide identification and analysis of A-to-I RNA editing events in bovine by transcriptome sequencing. PLoS ONE, 2018, 13, e0193316.	1.1	27
22	Overgrowth Syndrome. Veterinary Clinics of North America - Food Animal Practice, 2019, 35, 265-276.	0.5	25
23	Differences between Brahman and Holstein cows in response to estrus synchronization, superovulation and resistance of embryos to heat shock. Animal Reproduction Science, 2003, 78, 13-24.	0.5	22
24	Maternal Hyperleptinemia Is Associated with Male Offspring's Altered Vascular Function and Structure in Mice. PLoS ONE, 2016, 11, e0155377.	1.1	15
25	Consequences of assisted reproductive techniques on the embryonic epigenome in cattle. Reproduction, Fertility and Development, 2020, 32, 65.	0.1	14
26	Effects of the use of assisted reproduction and high-caloric diet consumption on body weight and cardiovascular health of juvenile mouse offspring. Reproduction, 2014, 147, 111-123.	1.1	12
27	Short Communication: Seasonal Effects on Development of Bovine Embryos Produced by In Vitro Fertilization in a Hot Environment. Journal of Dairy Science, 2000, 83, 305-307.	1.4	11
28	Epigenetic Aspects of Fertilization and Preimplantation Development in Mammals: Lessons from the Mouse. Systems Biology in Reproductive Medicine, 2010, 56, 388-404.	1.0	11
29	Effects of the Use of Assisted Reproductive Technologies and an Obesogenic Environment on Resistance Artery Function and Diabetes Biomarkers in Mice Offspring. PLoS ONE, 2014, 9, e112651.	1.1	8
30	Bovine preimplantation embryo development is affected by the stiffness of the culture substrate. Molecular Reproduction and Development, 2013, 80, 184-184.	1.0	7
31	Determination of Allelic Expression of H19 in Pre- and Peri-Implantation Mouse Embryos1. Biology of Reproduction, 2013, 88, 97.	1.2	7
32	Modeling allele-specific expression at the gene and SNP levels simultaneously by a Bayesian logistic mixed regression model. BMC Bioinformatics, 2019, 20, 530.	1.2	7
33	Conditions of embryo culture from days 5 to 7 of development alter the DNA methylome of the bovine fetus at day 86 of gestation. Journal of Assisted Reproduction and Genetics, 2020, 37, 417-426.	1.2	7
34	The effects of biological aging on global DNA methylation, histone modification, and epigenetic modifiers in the mouse germinal vesicle stage oocyte. Animal Reproduction, 2018, 15, 1253-1267.	0.4	7
35	Serum supplementation during bovine embryo culture affects their development and proliferation through macroautophagy and endoplasmic reticulum stress regulation. PLoS ONE, 2021, 16, e0260123.	1.1	7
36	Spontaneous and ART-induced large offspring syndrome: similarities and differences in DNA methylome. Epigenetics, 2022, 17, 1477-1496.	1.3	7

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37	A Bayesian Hidden Markov Model for Detecting Differentially Methylated Regions. <i>Biometrics</i> , 2019, 75, 663-673.	0.8	6
38	Allele-specific aberration of imprinted domain chromosome architecture associates with large offspring syndrome. <i>IScience</i> , 2022, 25, 104269.	1.9	6
39	Identification of large offspring syndrome during pregnancy through ultrasonography and maternal blood transcriptome analyses. <i>Scientific Reports</i> , 2022, 12, .	1.6	6
40	Characterization of tRNA expression profiles in large offspring syndrome. <i>BMC Genomics</i> , 2022, 23, 273.	1.2	5
41	Maternal DHA supplementation influences sex-specific disruption of placental gene expression following early prenatal stress. <i>Biology of Sex Differences</i> , 2021, 12, 10.	1.8	4
42	Detecting differentially expressed genes for syndromes by considering change in mean and dispersion simultaneously. <i>BMC Bioinformatics</i> , 2018, 19, 330.	1.2	2
43	Using online tools at the Bovine Genome Database to manually annotate genes in the new reference genome. <i>Animal Genetics</i> , 2020, 51, 675-682.	0.6	2
44	When six is not a half dozen: Representation of changes in H4K5ac during meiotic progression in mouse oocytes. <i>Molecular Reproduction and Development</i> , 2015, 82, 1-1.	1.0	1