

Ransom L Baldwin Vi

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2755547/publications.pdf>

Version: 2024-02-01

38
papers

1,437
citations

471509

17
h-index

330143

37
g-index

38
all docs

38
docs citations

38
times ranked

1701
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Functional annotation of regulatory elements in cattle genome reveals the roles of extracellular interaction and dynamic change of chromatin states in rumen development during weaning. <i>Genomics</i> , 2022, 114, 110296. | 2.9 | 4 |
| 2 | Characterization of Accessible Chromatin Regions in Cattle Rumen Epithelial Tissue during Weaning. <i>Genes</i> , 2022, 13, 535. | 2.4 | 4 |
| 3 | The Dynamics of Chromatin Accessibility Prompted by Butyrate-Induced Chromatin Modification in Bovine Cells. <i>Ruminants</i> , 2022, 2, 226-243. | 1.1 | 2 |
| 4 | Single-cell transcriptomic analyses of dairy cattle ruminal epithelial cells during weaning. <i>Genomics</i> , 2021, 113, 2045-2055. | 2.9 | 16 |
| 5 | Transcriptional Reprogramming in Rumen Epithelium during the Developmental Transition of Pre-Ruminant to the Ruminant in Cattle. <i>Animals</i> , 2021, 11, 2870. | 2.3 | 1 |
| 6 | PSVIII-25 Transcriptional reprogramming in rumen epithelium during the developmental transition of pre-ruminant to the ruminant in cattle. <i>Journal of Animal Science</i> , 2021, 99, 355-356. | 0.5 | 0 |
| 7 | Data of epigenomic profiling of histone marks and CTCF binding sites in bovine rumen epithelial primary cells before and after butyrate treatment. <i>Data in Brief</i> , 2020, 28, 104983. | 1.0 | 3 |
| 8 | The Profiling of DNA Methylation and Its Regulation on Divergent Tenderness in Angus Beef Cattle. <i>Frontiers in Genetics</i> , 2020, 11, 939. | 2.3 | 13 |
| 9 | Establishment and transcriptomic analyses of a cattle rumen epithelial primary cells (REPC) culture by bulk and single-cell RNA sequencing to elucidate interactions of butyrate and rumen development. <i>Heliyon</i> , 2020, 6, e04112. | 3.2 | 8 |
| 10 | Synthetic Alkaloid Treatment Influences the Intestinal Epithelium and Mesenteric Adipose Transcriptome in Holstein Steers. <i>Frontiers in Veterinary Science</i> , 2020, 7, 615. | 2.2 | 4 |
| 11 | Comparative whole genome DNA methylation profiling across cattle tissues reveals global and tissue-specific methylation patterns. <i>BMC Biology</i> , 2020, 18, 85. | 3.8 | 34 |
| 12 | Transcriptomic Profiling of Duodenal Epithelium Reveals Temporally Dynamic Impacts of Direct Duodenal Starch-Infusion During Dry Period of Dairy Cattle. <i>Frontiers in Veterinary Science</i> , 2019, 6, 214. | 2.2 | 2 |
| 13 | Functional annotation of the cattle genome through systematic discovery and characterization of chromatin states and butyrate-induced variations. <i>BMC Biology</i> , 2019, 17, 68. | 3.8 | 48 |
| 14 | Temporal dynamics in meta longitudinal RNA-Seq data. <i>Scientific Reports</i> , 2019, 9, 763. | 3.3 | 4 |
| 15 | Comparative whole genome DNA methylation profiling of cattle sperm and somatic tissues reveals striking hypomethylated patterns in sperm. <i>GigaScience</i> , 2018, 7, . | 6.4 | 60 |
| 16 | Transcriptomic Impacts of Rumen Epithelium Induced by Butyrate Infusion in Dairy Cattle in Dry Period. <i>Gene Regulation and Systems Biology</i> , 2018, 12, 117762501877479. | 2.3 | 12 |
| 17 | Effect of consuming endophyte-infected fescue seed on transcript abundance in the mammary gland of lactating and dry cows, as assessed by RNA sequencing. <i>Journal of Dairy Science</i> , 2018, 101, 10478-10494. | 3.4 | 8 |
| 18 | Assembly and Analysis of Changes in Transcriptomes of Dairy Cattle Rumen Epithelia during Lactation and Dry Periods. <i>Agricultural Sciences</i> , 2018, 09, 619-638. | 0.3 | 1 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 19 | Rumen Function and Development. <i>Veterinary Clinics of North America - Food Animal Practice</i> , 2017, 33, 427-439. | 1.2 | 53 |
| 20 | Selection of internal reference genes for normalization of reverse transcription quantitative polymerase chain reaction (RT-qPCR) analysis in the rumen epithelium. <i>PLoS ONE</i> , 2017, 12, e0172674. | 2.5 | 15 |
| 21 | The effect of helminth infection on the microbial composition and structure of the caprine abomasal microbiome. <i>Scientific Reports</i> , 2016, 6, 20606. | 3.3 | 129 |
| 22 | Transcriptomic Sequencing Reveals a Set of Unique Genes Activated by Butyrate-Induced Histone Modification. <i>Gene Regulation and Systems Biology</i> , 2016, 10, GRSB.S35607. | 2.3 | 18 |
| 23 | Consumption of endophyte-infected fescue seed during the dry period does not decrease milk production in the following lactation. <i>Journal of Dairy Science</i> , 2016, 99, 7574-7589. | 3.4 | 12 |
| 24 | Hot topic: Brown marmorated stink bug odor compounds do not transfer into milk by feeding bug-contaminated corn silage to lactating dairy cattle. <i>Journal of Dairy Science</i> , 2014, 97, 1877-1884. | 3.4 | 11 |
| 25 | Functional proteomic and interactome analysis of proteins associated with beef tenderness in Angus cattle. <i>Livestock Science</i> , 2014, 161, 201-209. | 1.6 | 35 |
| 26 | Gene expression in bovine rumen epithelium during weaning identifies molecular regulators of rumen development and growth. <i>Functional and Integrative Genomics</i> , 2013, 13, 133-142. | 3.5 | 118 |
| 27 | Characterization of the longissimus lumborum transcriptome response to adding propionate to the diet of growing Angus beef steers. <i>Physiological Genomics</i> , 2012, 44, 543-550. | 2.3 | 20 |
| 28 | Quantification of Transcriptome Responses of the Rumen Epithelium to Butyrate Infusion using RNA-seq Technology. <i>Gene Regulation and Systems Biology</i> , 2012, 6, GRSB.S9687. | 2.3 | 51 |
| 29 | Characterization of the rumen microbiota of pre-ruminant calves using metagenomic tools. <i>Environmental Microbiology</i> , 2012, 14, 129-139. | 3.8 | 311 |
| 30 | Muscle transcriptomic analyses in Angus cattle with divergent tenderness. <i>Molecular Biology Reports</i> , 2012, 39, 4185-4193. | 2.3 | 40 |
| 31 | Perturbation Dynamics of the Rumen Microbiota in Response to Exogenous Butyrate. <i>PLoS ONE</i> , 2012, 7, e29392. | 2.5 | 103 |
| 32 | The Bacterial Community Composition of the Bovine Rumen Detected Using Pyrosequencing of 16S rRNA Genes. <i>Metagenomics (Cairo, Egypt)</i> , 2012, 1, 1-11. | 1.2 | 91 |
| 33 | Enhanced mitochondrial complex gene function and reduced liver size may mediate improved feed efficiency of beef cattle during compensatory growth. <i>Functional and Integrative Genomics</i> , 2010, 10, 39-51. | 3.5 | 99 |
| 34 | Glutamate Is the Major Anaplerotic Substrate in the Tricarboxylic Acid Cycle of Isolated Rumen Epithelial and Duodenal Mucosal Cells from Beef Cattle. <i>Journal of Nutrition</i> , 2009, 139, 869-875. | 2.9 | 27 |
| 35 | Predicting Perchlorate Exposure in Milk from Concentrations in Dairy Feed. <i>Journal of Agricultural and Food Chemistry</i> , 2007, 55, 8806-8813. | 5.2 | 17 |
| 36 | Intestinal Protein Supply Alters Amino Acid, but Not Glucose, Metabolism by the Sheep Gastrointestinal Tract. <i>Journal of Nutrition</i> , 2006, 136, 1261-1269. | 2.9 | 44 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 37 | Isolation and characterization of a cDNA clone encoding ovine type I carbonic anhydrase.. Journal of Animal Science, 1996, 74, 345. | 0.5 | 8 |
| 38 | Identification of two cDNA clones encoding small proline-rich proteins expressed in sheep ruminal epithelium. Biochemical Journal, 1996, 317, 225-233. | 3.7 | 11 |