



Evaluation of integrated biomarker panels for detection of subclinical physiological alterations in dairy goats

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Abstract

Subclinical disorders in food-producing livestock remain one of the most important issues for veterinarians, since there is no clear clinical picture of the disease despite changes in physiology. The objective of this research was to assess the diagnostic significance of integrating of biochemical, inflammatory, and oxidative biomarkers to detect subclinical disorders in dairy goats under field conditions. Forty-eight lactating goats were grouped according to the results of clinical examination and blood test as healthy and subclinical. The concentrations of acylcarnitine, haptoglobin, interleukin-6 (IL-6), tumor necrosis factor-alpha (TNF- α), malondialdehyde (MDA), and glutathione peroxidase (GPx) were determined in serum. Subclinical goats had higher concentrations of all biomarkers except GPx, which showed lower values ($P < 0.05$). This indicates changes in metabolism, inflammation, and oxidative status at the subclinical stage of the disease. ROC curve analysis revealed moderate diagnostic ability for single biomarkers (AUC 0.79 – 0.86), however, the combination of biomarkers had high diagnostic ability (AUC = 0.93). Thus, the integrated use of biomarkers may serve as a supportive diagnostic approach for identifying subclinical physiological alterations in dairy goats. From a veterinary medicine perspective, this method may contribute to improved health monitoring and identification of animals with physiological disturbances under field conditions.

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1. Introduction

The presence of subclinical pathophysiological states in food-producing animals is becoming an ever-growing concern in veterinary science and livestock management, as this category of pathologies may remain undetected despite their clear adverse influence on production performance, physiologic resistance, and welfare status. Unlike clinical pathologies, which manifest through symptoms, subclinical disorders such as metabolic, inflammatory, and oxidative disturbances can affect the physiologic processes in the body without being clinically detected while simultaneously reducing performance capacity (Chen et al. 2025). There is growing evidence that these disturbances, which can precede clinical disease for weeks or even months, lead to decreased efficiency of feeding, reproduction, and immunity (Rayego-Mateos et al. 2023; Ovseychik et al. 2024).

Routine diagnostic procedures conducted by veterinary practitioners, based mainly on the visible manifestations and laboratory findings, usually do not manage to discover such diseases in their early stages. As an example, despite the fact that somatic cell count is frequently employed for the diagnosis of subclinical mastitis in cattle, it fails to provide meaningful information before disease onset (Zwierzchowski et al. 2024). The same applies to other conventional hematologic and biochemistry analysis where results remain normal while homeostasis is already disturbed (Caixeta and Omontese 2021; Bales et al. 2024).

To overcome this disadvantage, biomarker-based diagnostic tools have been suggested as a promising approach for identifying underlying physiological disturbances before overt clinical manifestations become evident. As such, biomarkers are measurable entities that provide information regarding specific biological or pathogenic processes. With recent breakthroughs in fields of metabolomics, proteomics, and systems biology, many new biomarkers of diseases have been discovered in livestock animals (Goldansaz et al. 2023; Idowu and Idowu 2026). Recent advances in metabolomics have identified metabolites present in both urine and blood that could potentially predict subclinical disorders before the clinical signs develop. Changes in the metabolism of amino acids, lipids, and acylcarnitines have been related to subclinical metabolic stress in lactating cows (Van Dixhoorn et al. 2023; Chen et al. 2025). Additionally, acute-phase proteins and immune peptides have been identified that could act as biomarkers of subclinical inflammation (Schrödl et al. 2016; Mule et al. 2024).

In addition to isolated biomarkers, recent integrative multi-omics investigations have shown that using biomarkers from various biological pathways is more effective than a single-biomarker strategy in diagnosis (Becchi et al. 2025; Mace and Knight 2024). In this context, biomarker panels may provide a more efficient way for detecting early physiological problems in livestock. Although biomarkers offer several advantages for animal monitoring, some difficulties related to standardization, reproducibility, and applicability still exist (Ovseychik et al. 2024; Idowu and Idowu 2026). In addition, the breed, nutrition,

physiological state, and unique metabolic traits of specific species could complicate the process of interpreting results (Bales et al. 2024). It is worth noting that many of the findings related to using biomarkers for identifying subclinical conditions were obtained in experiments with dairy cows, but dairy goats have a different physiology, metabolism, and adaptive mechanisms. The differences between goats and cows concerning the energy metabolism, lactation mechanism, and immune system make it clear that biomarkers tested in one species cannot be used directly for diagnosing disorders in the other species without appropriate adjustments. Overall, such tests represent a significant shift towards proactive rather than reactive measures in veterinary practice. In this respect, this study aimed to evaluate the potential use of biomarkers (metabolic, inflammatory, and oxidative) for detecting subclinical disorders in dairy goats.

2. Materials and Methods

2.1 Study Design and Animal Classification

The study recruited a total number of 48 lactating dairy goats (*Capra hircus*) aged between 2 to 4 years in three different dairy farms located in West Nusa Tenggara, Indonesia. The animals were divided into two categories: healthy animals ($n = 24$) and subclinical animals ($n = 24$). Healthy animals were defined as those meeting all of the following criteria:

1. Rectal temperature: 38.5–39.7°C
2. Heart rate: 70–90 beats/minute
3. Respiratory rate: 15–30 breaths/minute
4. Body condition score: 2.5–3.5
5. Normal appetite and rumination
6. No visible clinical abnormalities
7. Serum haptoglobin < 0.60 g/L
8. Serum IL-6 < 22 pg/mL
9. Serum MDA < 2.80 nmol/mL

The definition of subclinical goats was that of individuals having no apparent clinical disease signs on physical examinations but having an abnormality in at least two laboratory biomarkers. Since the diagnosis of integrated metabolic, inflammatory, and oxidative biomarkers in dairy goats has not yet reached a universally agreed upon cut-off point, the reference values used in this study were extracted from previous studies that gave the reference interval in the goat or the small ruminant and upper/lower physiologically normal range reported previously (Moretti et al. 2017). The threshold criteria for inclusion in the subclinical group include a level of Hpt ≥ 0.65 g/L, IL-6 ≥ 25 pg/mL, TNF- α ≥ 17 pg/mL, MDA ≥ 3.00 nmol/mL, GPx ≤ 62 U/mL, and acylcarnitine ≥ 1.55 μ mol/L. An individual animal was classified as subclinical if it shows an abnormality in two or more of these parameters to prevent misinterpretation because of a single abnormality. Any animal with fever, lameness, mastitis, parasite infestation, reproductive problems, or a recent history of antibiotic treatment was excluded from the study.

2.2 Sample Collection

Blood samples were collected from the jugular vein before morning feeding using sterile vacuum tubes. Serum was separated by centrifugation at 3000 rpm for 15 min at 4 °C and stored at –80 °C until analysis. Measured biomarkers included Acylcarnitine, Haptoglobin, Interleukin-6 (IL-6), Tumor necrosis factor-alpha (TNF- α), Malondialdehyde (MDA), and Glutathione peroxidase (GPx).

Acylcarnitine concentrations were measured using ultra-high-performance liquid chromatography–tandem mass spectrometry (UHPLC-MS/MS). Serum haptoglobin, IL-6, TNF- α , MDA, and GPx concentrations were quantified using commercially available ELISA kits (Elabscience Biotechnology Inc., Wuhan, China; Cat. Nos. E-EL-G0085, E-EL-G0017) according to the manufacturers' instructions. All samples were analyzed in duplicate, and assay procedures were performed following the recommended protocols to ensure analytical reproducibility.

2.3 Statistical analysis

All statistical analysis were performed using R statistical software (version 4.3.1). Normality was assessed using the Shapiro–Wilk test. Acylcarnitine ($P = 0.214$), haptoglobin ($P = 0.176$), IL-6 ($P = 0.091$), TNF- α ($P = 0.132$), MDA ($P = 0.087$), and GPx ($P = 0.241$) were normally distributed, which were analyzed using independent-samples t-tests, whereas non-normally distributed variables were analyzed using the Mann–Whitney U test. Data are presented as mean $\pm$ standard deviation (SD). In addition to P-values, effect sizes were calculated using Cohen's d to quantify the magnitude of differences between healthy and subclinical groups. Mean differences were accompanied by 95% confidence intervals (95% CI). To reduce the risk of Type I error associated with multiple biomarker comparisons, P-values were adjusted using the Benjamini–Hochberg false discovery rate (FDR) procedure. Statistical significance was accepted at $P < 0.05$. Receiver operating characteristic (ROC) analysis was performed to evaluate the diagnostic performance of individual biomarkers and their combinations. Ninety-five percent confidence intervals (95% CI) were calculated for all area under the curve (AUC) estimates.

2.4 ROC Analysis

Analysis was done through ROC analysis using the R software package pROC. The cut-off point for each marker was established by maximization of Youden index, which is sensitivity + specificity - 1. Receiver operating characteristic (ROC) analyses were performed using the pROC package in R. The optimal cut-off value for each biomarker was determined using the Youden index. The values of area under the ROC curve (AUC) along with the associated 95% confidence intervals (95% CI) were provided, which were obtained by means of the DeLong method. In addition, other performance measures, such as positive predictive value (PPV) and negative predictive value (NPV), were determined to provide a more complete picture of biomarker performance in this case.

3. Results

3.1 Clinical characteristics of animals

No significant ($P > 0.05$) differences were observed between healthy and subclinical animals regarding age, body weight, body condition score, parity, days in milk, or daily milk yield (Table 1). These findings indicate that the two groups were comparable with respect to major demographic and production-related characteristics, thereby reducing the likelihood that these factors substantially influenced the observed biomarker differences. Evaluation of farm origin as a random effect revealed no significant farm-level influence on group classification ($P > 0.05$). This finding suggests that the observed biomarker differences between healthy and subclinical animals were generally consistent across the three participating farms.

3.2 Metabolic biomarkers

Table 1. Baseline characteristics of healthy and subclinical dairy goats			
Parameter	Healthy (n = 24)	Subclinical (n = 24)	P - value
Age (years)	3.1 ± 0.7	3.0 ± 0.6	0.624
Body weight (kg)	38.5 ± 2.8	37.9 ± 3.1	0.481
Body condition score	2.9 ± 0.3	2.8 ± 0.2	0.392
Parity (number of kiddings)	2.4 ± 0.8	2.5 ± 0.7	0.718
Days in milk (days)	87.3 ± 21.5	91.6 ± 24.1	0.529
Daily milk yield (L/day)	1.82 ± 0.31	1.76 ± 0.28	0.447
<i>Note.</i> Values are presented as mean ± SD. P-values were obtained using independent-samples t-tests or Mann–Whitney U tests, as appropriate. No significant differences were observed between groups for baseline animal characteristics (P > 0.05), indicating comparable demographic and production-related profiles			

Subclinical animals showed significantly higher serum acylcarnitine concentrations compared with healthy controls (1.82 ± 0.21 vs 1.24 ± 0.18 $\mu\text{mol/L}$; $P = 0.001$), suggesting early mitochondrial metabolic disturbance (Table 2). Analysis of effect sizes showed high between-group differences for all the biochemical markers (Cohen's $d > 2.0$), reflecting substantial differences between the healthy and subclinical animal groups. The lipid peroxidation biomarker MDA showed a significantly higher levels in the subclinical group, whereas the antioxidant enzyme GPx was lower.

Table 2. Metabolic biomarker concentrations					
Biomarker	Healthy (n = 24)	Subclinical (n = 24)	Mean difference (95% CI)	Cohen's d	Adjusted P - value
Acylcarnitine ($\mu\text{mol/L}$)	1.24 ± 0.18	1.82 ± 0.21	0.58 (0.47–0.69)	2.99	0.001
MDA (nmol/mL)	2.41 ± 0.32	3.65 ± 0.48	1.24 (0.99–1.49)	3.04	<0.001
GPx (U/mL)	71.2 ± 5.4	58.7 ± 4.8	-12.5 (-15.4 to -9.6)	2.43	<0.001
<i>Note.</i> Mean differences are presented as subclinical minus healthy values. Cohen's d was used to estimate effect size, where 0.2, 0.5, and 0.8 indicate small, medium, and large effects, respectively					

3.3 Inflammatory biomarkers

Inflammatory biomarkers were significantly elevated in subclinical animals. Haptoglobin concentration increased by 36.4%, while IL-6 and TNF- α also showed marked increases compared with healthy controls (Table 3). All inflammatory markers showed high values among subclinical animals. According to effect size analysis, there were large effect sizes (Cohen's $d > 2.0$) for all inflammatory markers. The highest effect size value ($d = 3.93$) was obtained for IL-6, followed by TNF- α ($d = 3.76$) and haptoglobin ($d = 2.47$). This demonstrates that inflammatory markers were significantly different between the groups, which indicates that these parameters have high discriminating power. In turn, all associations were significant following the correction for multiple testing based on Benjamini-Hochberg false discovery rate procedure.

Table 3. Inflammatory biomarker concentrations					
Biomarker	Healthy (n = 24)	Subclinical (n = 24)	Mean difference (95% CI)	Cohen's d	Adjusted P - value
Haptoglobin (g/L)	0.55 ± 0.07	0.75 ± 0.09	0.20 (0.15–0.25)	2.47	0.003
IL-6 (pg/mL)	18.4 ± 2.1	29.7 ± 3.5	11.3 (9.7–12.9)	3.93	<0.001
TNF- α (pg/mL)	12.8 ± 1.7	20.6 ± 2.4	7.8 (6.6–9.0)	3.76	<0.001
<i>Note.</i> Values are given as mean ± standard deviation (SD). The mean differences between groups are expressed as mean subclinical – mean healthy. The 95% confidence interval (95% CI) is given for mean differences. The effect size was determined based on Cohen's d. Adjusted P-value for multiple comparisons was computed using Benjamini-Hochberg FDR method. In line with the traditional definition, effect size of Cohen's d 0.2, 0.5, and 0.8 are considered to be small, medium, and large effect size respectively. P-value adjustment was done based on Benjamini-Hochberg false discovery rate (FDR)					

3.4 Diagnostic performance of biomarkers

Receiver operating characteristic (ROC) analysis identified optimal cut-off values for each biomarker using the Youden index (Table 4). In addition to sensitivity and specificity, PPV and NPV analyses further supported the superior performance of the combined biomarker panel. The combined model achieved the highest PPV (86.0%) and NPV (89.0%), indicating improved classification of both subclinical and healthy animals compared with individual biomarkers. The combined biomarker panel demonstrated the highest discriminatory performance diagnostic accuracy, with an AUC of 0.93 (95% CI: 0.86–0.99), exceeding the performance of all individual biomarkers. The relatively narrow confidence intervals observed for most biomarkers indicate acceptable precision of the estimated diagnostic performance. The high diagnostic accuracy of the combined biomarker model indicates its potential applicability as a supportive tool in veterinary diagnostic protocols.

4. Discussion

The current study highlighted that animals which were categorized under subclinical condition showed significant changes in metabolite, inflammatory, and oxidative parameters even when no clinical symptoms were apparent. Identification of subclinical physiological alterations may benefit from integrating multiple biological measures.

Elevated acylcarnitine concentrations may be associated with altered fatty acid metabolism and have been reported in animals experiencing metabolic stress (Van Dixhoorn et al. 2023; Chen et al. 2025). Increase of acylcarnitine levels from 1.24 ± 0.18 $\mu\text{mol/L}$ to 1.82 ± 0.21 $\mu\text{mol/L}$ in healthy and subclinical animals, respectively, shows that metabolic adaptations took place prior to clinical disease development. Furthermore, the oxidative stress pattern provided additional evidence for the occurrence of early physiological disorder. Animals with subclinical conditions had significantly higher MDA concentrations accompanied by lower GPx activity, indicating enhanced oxidative stress and impaired antioxidant defense mechanisms. Higher MDA levels indicate lipid peroxidation of cell membrane lipids as a consequence of excess ROS, while low levels of GPx activity may indicate the depletion of antioxidant enzymes from the body's reserves. In cases where continuous oxidative stress occurs, there will be a

Table 4. Diagnostic performance of biomarkers						
Biomarker	AUC (95% CI)	Cut-off value	Sensitivity (%)	Specificity (%)	PPV (%)	NPV (%)
Acylcarnitine	0.84 (0.73–0.95)	>1.48 µmol/L	79.2	75.0	76.0	78.3
Haptoglobin	0.81 (0.69–0.92)	>0.63 g/L	75.0	70.8	72.0	73.9
MDA	0.86 (0.76–0.96)	>2.95 nmol/mL	83.3	79.2	80.0	82.6
IL-6	0.82 (0.71–0.93)	>24.1 pg/mL	77.1	72.9	74.0	76.1
TNF-α	0.80 (0.68–0.91)	>16.5 pg/mL	75.0	70.8	72.0	73.9
GPx	0.79 (0.67–0.90)	<63.5 U/mL	72.9	68.7	70.0	71.7
Combined panel	0.93 (0.86–0.99)	Probability >0.58	89.6	85.4	86.0	89.0
<i>Note.</i> AUC = area under the curve on the receiver operator characteristic graph; CI = confidence interval; PPV = positive predictive value; NPV = negative predictive value. This combination of panel was formed based on the findings of binary logistic regression with predictors being acylcarnitine, haptoglobin, MDA, IL-6, TNF-α, and GPx. The cut-off values were established through the use of the Youden index. AUCs are provided along with the confidence intervals						

continuous process where GPx is used to break down hydrogen peroxide and lipid hydroperoxides to produce less reactive products. In cases where the requirement for antioxidants surpasses the body's capability to regenerate such enzymes, GPx activity may become low. This will lead to the accumulation of peroxides, which leads to higher MDA due to lipid peroxidation in subclinical animals (Rayego-Mateos et al. 2023).

The inflammatory biomarkers showed significant differences as well. Higher levels of haptoglobin, IL-6, and TNF-α among subclinical animals indicate low-grade systemic inflammation. Haptoglobin is an acute-phase reactant protein which tends to increase in case of inflammatory activation (Schrödl et al. 2016). The same refers to other inflammatory markers like IL-6 and TNF-α, which act as pro-inflammatory cytokines for the first response of the immune system (Ovseychik et al. 2024). These findings suggest that clinically healthy animals may experience immunological activation, which is able to affect their biological resilience. Thus, the analysis of both metabolites and inflammatory markers suggests that subclinical pathologies are multifactorial in nature. Metabolic disturbances may coexist with inflammatory activation, while inflammatory activation may be accompanied by increased oxidative stress and create a vicious circle of physiological disorders. In addition, similar relationships between metabolic and immune processes have been shown in previous multi-omics analysis of livestock (Goldansaz et al. 2023; Becchi et al. 2025). Such complexity explains why clinical observation cannot detect potential health risks in animals during early stages of diseases.

Among the major findings of this study is that the combined set of biomarkers had better diagnostic utility than individual biomarkers. While the latter had moderate discriminatory abilities, the combination of biomarkers attained a much higher level of diagnostic accuracy, as demonstrated by an AUC value of 0.93. Recent precision livestock studies also report improved diagnostic outcomes with the use of integrated biomarkers (Mace and Knight 2024; Chen et al. 2025). Therefore, it can be argued that detection of diseases at an early stage requires multiple biological measures, not just one indicator. One of the major strengths of this study is the use of pre-set laboratory criteria for distinguishing between healthy and sub clinically impaired animals. Apart from physical examination, the use of biomarker criteria helped to categorize the animals in either healthy or subclinical groups, hence eliminating possible misclassification. An ROC analysis was carried out to evaluate the diagnostic value of the markers analyzed. Considering the lack of significant farm effects in this study, it is evident that these relations are not limited to one specific farm, meaning that the

biological differences between the two groups of goats is consistent among various farms used in the study. However, further multi-farm studies should be conducted to validate the results obtained in this research. Regarding its application to the field of veterinary medicine, these research findings may be of practical importance. The early detection of subclinical changes in animals will enable timely measures to prevent irreversible losses in production performance. In such a situation, timely changes in nutrition, environment, and preventive management can help improve animal well-being and avoid financial losses. Such a strategy for monitoring based on biomarkers can serve as the basis for developing a precision health system, which will be more effective than conventional clinical diagnostic techniques (Jiang et al. 2023; Idowu and Idowu 2026). For an applied veterinarian, the introduction of biomarker panels in the context of health status evaluation will help detect diseases earlier in the case of entire herds. Such biomarker tests can complement existing techniques such as clinical examination for detecting at-risk animals even before the onset of productivity losses. This issue applies primarily to intensive and semi-intensive agricultural enterprises, where such problems occur most often.

This study has several limitations that should be considered when interpreting the findings. First, the rather small number of samples might compromise statistical power and lower the generalizability of findings. Second, animal recruitment involved only farms in one geographical area, and their biomarker profile may vary in response to different management, breed, nutrition, and other factors. Third, the cross-sectional study design does not allow for assessment of any temporal trends or the progression of subclinical physiological changes to clinical disease. Thus, the associations found cannot be assumed to demonstrate causality or predictability. Fourth, despite the use of predefined clinical and biochemical criteria for grouping animals, misclassification is still possible owing to the lack of internationally recognized diagnostic criteria for an integrated biomarker panel in dairy goats. Finally, parity, lactation status, milk yield, nutritional state, and farm-specific management could represent residual confounders affecting biomarker concentrations. The diagnostic performance estimates derived from ROC analysis were internally evaluated and require external validation in larger and independent dairy goat populations before broader application can be recommended (Bales et al. 2024).

5. Conclusions

Biomarkers related to metabolism, inflammation, and oxidative

reactions were associated with the identification of subclinical physiological alterations in dairy goats. The integrated biomarker approach demonstrated high diagnostic accuracy and may be considered as a useful adjunct in veterinary diagnostics.

Declarations

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Conflict of interest: The author declares that there are no commercial or financial relationships that could be construed as a potential conflict of interest

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Data availability: The data are available from the corresponding author on reasonable request

References

- Bales AM, Cinzori ME, Lock AL. (2024). Increasing palmitic acid and reducing stearic acid content of supplemental fatty acid blends improves production performance of mid-lactation dairy cows. *Journal of Dairy Science* 107(1): 278-287. <https://doi.org/10.3168/jds.2023-23874>
- Becchi PP, Rocchetti G, Lucini L. (2025). Advancing dairy science through integrated analytical approaches based on multi-omics and machine learning. *Current Opinion in Food Science* 63: 101289. <https://doi.org/10.1016/j.cofs.2025.101289>
- Caixeta LS, Omontese BO. (2021). Monitoring and improving the metabolic health of dairy cows during the transition period. *Animals* 11(2): 352. <https://doi.org/10.3390/ani11020352>
- Chen L, Zhang C, Niu R, Xiong S, He J, Wang Y, Zhang P, Su F, Liu Z, Zhou L, Mao R, Hu S, Chen M, Qiu Y, Feng R. (2025). Multi-omics biomarkers for predicting efficacy of biologic and small-molecule therapies in adults with inflammatory bowel disease: a systematic review. *United European Gastroenterology Journal* 13(4): 517-530. <https://doi.org/10.1002/ueg2.12720>
- Goldansaz SA, Guo AC, Sajed T, Steele MA, Plastow GS, Wishart DS. (2023). Livestock metabolomics and the livestock metabolome: A systematic review. *PLoS One* 18(2): e0177675. <https://doi.org/10.1371/journal.pone.0177675>
- Idowu PA, Idowu AP. (2026). Omics and Precision Livestock Farming for Heat Stress Resilience: Integrating Molecular Biomarkers with Real-Time Phenotyping for Climate-Smart Livestock Systems. *Frontiers in Animal Science* 7: 1810017. <https://doi.org/10.3389/fanim.2026.1810017>
- Jiang B, Tang W, Cui L, Deng X. (2023). Precision livestock farming research: A global scientometric review. *Animals* 13(13): 2096. <https://doi.org/10.3390/ani13132096>
- Mace JL, Knight A. (2024). From the backyard to our beds: The spectrum of care, attitudes, relationship types, and welfare in non-commercial chicken care. *Animals* 14(2): 288. <https://doi.org/10.3390/ani14020288>
- Moretti P, Paltrinieri S, Trevisi E, Probo M, Ferrari A, Minuti A, Giordano A. (2017). Reference intervals for hematological and biochemical parameters, acute phase proteins and markers of oxidation in Holstein dairy cows around 3 and 30 days after calving. *Research in Veterinary Science* 114: 322-331. <https://doi.org/10.1016/J.RVSC.2017.06.012>
- Mule SN, Saad JS, Sauter IP, Fernandes LR, de Oliveira GS, Quina D, Tano FT, Brandt-Almeida D, Padron G, Stolf BS, Larsen MR, Cortez M, Palmisano G. (2024). The protein map of the protozoan parasite *Leishmania* (*Leishmania*) *amazonensis*, *Leishmania* (*Viannia*) *braziliensis* and *Leishmania* (*Leishmania*) *infantum* during growth phase transition and temperature stress. *Journal of Proteomics* 295: 105088. <https://doi.org/10.1016/j.jpro.2024.105088>

[jjprot.2024.105088](https://doi.org/10.3390/105088)

- Ovseychik EA, Klein OI, Gessler NN, Deryabina YI, Lukashenko VS, Isakova EP. (2024). The efficacy of encapsulated phytase based on recombinant *Yarrowia lipolytica* on quails' zootechnic features and phosphorus assimilation. *Veterinary Sciences* 11(2): 91. <https://doi.org/10.3390/vetsci11020091>
- Rayego-Mateos S, Marquez-Exposito L, Basantes P, Tejedor-Santamaria L, Sanz AB, Nguyen TQ, Goldschmeding R, Ortiz A, Ruiz-Ortega M. (2023). CCN2 activates RIPK3, NLRP3 inflammasome, and NRF2/oxidative pathways linked to kidney inflammation. *Antioxidants* 12(8): 1541. <https://doi.org/10.3390/antiox12081541>
- Schrödl W, Büchler R, Wendler S, Reinhold P, Muckova P, Reindl J, Rhode H. (2016). Acute phase proteins as promising biomarkers: Perspectives and limitations for human and veterinary medicine. *Proteomics – Clinical Applications* 10(11): 1077-1092. <https://doi.org/10.1002/prca.201600028>
- Van Dixhoorn IDE, de Mol RM, Schnabel SK, van der Werf JTN, van Mourik S, Bolhuis JE, Rebel JMJ, van Reenen CG. (2023). Behavioral patterns as indicators of resilience after parturition in dairy cows. *Journal of Dairy Science* 106(9): 6444-6463. <https://doi.org/10.3168/jds.2022-22891>
- Zwierzchowski G, Haxhij K, Wójcik R, Wishart DS, Ametaj BN. (2024). Identifying Predictive Biomarkers of Subclinical Mastitis in Dairy Cows through Urinary Metabotyping. *Metabolites* 14(4): 205. <https://doi.org/10.3390/metabo14040205>

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