# Complex Analysis of Follicular Fluid of Patients Undergoing Artificial Reproduction Technologies

Doctoral (Ph.D.) Thesis

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## 1. Introduction

Infertility is a growing global health problem affecting approximately 10–15% of couples of reproductive age. Despite major advances in assisted reproductive technologies (ART), overall success rates remain limited, indicating that key biological determinants of reproductive success are still incompletely understood.

Among the factors influencing ART outcome, oocyte quality plays a central role. Oocyte competence determines fertilization potential, implantation, early embryonic development, and ultimately, the success of pregnancy. Beyond genetic factors, the developmental potential of the oocyte is strongly influenced by its surrounding microenvironment during folliculogenesis. This microenvironment provides metabolic substrates, signaling molecules, antioxidants, and hormonal regulation required for proper oocyte maturation.

Follicular fluid (FF) constitutes the immediate biochemical environment of the oocyte and cumulus–oocyte complex. FF is formed through the transudation of blood plasma across the blood–follicle barrier and by active secretion from granulosa and theca cells. Importantly, FF is not a passive ultrafiltrate of plasma but a highly regulated biological matrix with a distinct molecular composition shaped by selective transport mechanisms and local ovarian regulatory processes. Alterations in FF composition have been associated with impaired oocyte maturation, reduced fertilization rates, poor embryo quality, and unsuccessful ART outcomes. Clinical conditions such as endometriosis, insulin resistance, obesity, and thyroid disorders are known to affect follicular physiology and are frequently accompanied by changes in the molecular composition of FF.

Traditional research approaches have often focused on individual biomarkers in FF; however, such strategies provide limited information on the complex molecular interactions underlying follicular function. The follicular microenvironment is regulated by interconnected networks of proteins, lipids, and metabolites, which cannot be adequately characterized by single-parameter analyses. In this context, multi-omics approaches integrating proteomics, lipidomics, and metabolomics offer a powerful framework for system-level characterization of FF.

The present doctoral work applies a comprehensive multi-omics approach to the analysis of FF obtained from patients undergoing assisted reproductive treatment. By integrating proteomic, lipidomic, and targeted metabolomic data, this work aims to provide deeper information on the molecular mechanisms shaping the follicular microenvironment and to identify potential biomarkers relevant for reproductive success.

## 2. Literature Overview

### 2.1. Follicular fuid formation and its role in oocyte development

Follicular fluid represents the immediate microenvironment of the developing oocyte and plays a fundamental role in regulating oocyte growth and fertilization competence. The formation of FF is a highly regulated process involving both passive and active mechanisms. During folliculogenesis, plasma components cross the blood–follicle barrier through selective transudation, while granulosa and theca cells actively secrete proteins, lipids, metabolites, hormones, and growth factors into the follicular antrum. The blood–follicle barrier plays a central role in FF formation by controlling molecular transport based on size and charge. While small molecules and water-soluble metabolites may diffuse relatively freely, the transport of larger proteins and lipoprotein particles is tightly regulated. In addition to passive transfer, granulosa cells contribute substantially to FF composition through de novo synthesis and metabolic transformation of circulating molecules.

As follicular development progresses, dynamic changes occur in FF composition reflecting follicle size, hormonal stimulation, and oocyte maturation stage. These changes include alterations in protein abundance, lipid classes, antioxidant capacity, and metabolite concentrations. Consequently, FF represents a temporally and functionally dynamic microenvironment rather than a static fluid compartment.

Several studies have demonstrated that FF is not a passive ultrafiltrate of plasma but a highly regulated biological matrix. Comparative analyses between serum and FF have revealed selective enrichment or depletion of specific proteins, lipids, and metabolites, highlighting the importance of local ovarian regulation. Alterations in FF composition have been associated with impaired oocyte quality, reduced fertilization rates, and poor ART outcomes.

### 2.1. Role of proteins in the follicular microenvironment

Proteins present in FF are involved in diverse biological processes, including lipid transport, immune regulation, coagulation, protease inhibition, and antioxidant defense. Proteomic studies have identified albumin, apolipoproteins, complement factors, and acute-phase proteins as major components of FF. These proteins contribute to maintaining osmotic balance, transporting lipids and hormones, and protecting the oocyte from oxidative and inflammatory damage.

Recent proteomic investigations have emphasized the importance of lipoprotein-associated proteins, particularly apolipoprotein A1 and high-density lipoprotein (HDL), in follicular

physiology. HDL particles are the main cholesterol carriers in FF and provide cholesterol for steroidogenesis while simultaneously exerting antioxidant and anti-inflammatory effects. Altered abundance of HDL-associated proteins has been linked to impaired oocyte maturation and reduced pregnancy rates.

### 2.2. Lipid metabolism and oxidative stress in follicular fluid

Lipids play essential roles in follicular development by serving as structural components of cell membranes, signaling molecules, and energy substrates. Phospholipids, sphingolipids, and cholesterol esters are among the most abundant lipid classes in FF. Balanced lipid composition is required for membrane fluidity, mitochondrial function, and signal transduction in both oocytes and surrounding cumulus cells.

Accumulating evidence suggests that dysregulated lipid metabolism contributes to oxidative stress and inflammation within the follicular environment. Increased levels of ceramides and oxidized lipids have been associated with apoptosis, mitochondrial dysfunction, and reduced oocyte competence. Conversely, HDL-associated lipids have been shown to protect against lipid peroxidation and oxidative damage, underscoring the importance of lipid transport and remodeling in FF.

### 2.3. Amino acid metabolism in follicular fluid

Amino acids are essential substrates for protein synthesis, energy metabolism, redox balance, and epigenetic regulation during oocyte maturation and early embryonic development. FF amino acid composition reflects both systemic nutritional status and local metabolic activity of ovarian cells.

Several studies have reported associations between specific amino acids in FF and oocyte quality or embryo development. Glycine, histidine, and glutamine are involved in antioxidant defense and nitrogen balance, while branched-chain amino acids are linked to energy metabolism and insulin sensitivity. Alterations in FF amino acid profiles have been described in metabolic disorders such as insulin resistance, endometriosis, and thyroid dysfunction, conditions frequently associated with reduced ART success.

## 2.4. Multi-omics studies of follicular fluid

Although numerous studies have investigated individual molecular components of FF, single-omics approaches provide limited information on the complex interactions governing follicular physiology. Proteins, lipids, and metabolites are functionally interconnected, and alterations in one molecular layer often propagate across others.

Multi-omics strategies enable integrated analysis of these molecular networks and facilitate the identification of key pathways rather than isolated biomarkers. Applying proteomic, lipidomic, and metabolomic analyses to FF allows a comprehensive characterization of the follicular microenvironment and provides a mechanistic framework for understanding differences in oocyte competence and ART outcomes.

## 3. Aims

Given the central role of the follicular microenvironment in determining oocyte competence and assisted reproductive technology outcomes, the overall aim of this doctoral work was to characterize follicular fluid using an integrated multi-omics approach. By combining proteomic, lipidomic, and targeted metabolomic analyses, the study seeks to identify molecular mechanisms, pathways, and potential biomarkers associated with reproductive outcome and disease-specific alterations.

The specific objectives of the study were defined to address distinct but interconnected molecular levels of the follicular microenvironment.

### 3.1. Proteomics

- To comprehensively characterize the protein composition of FF using high-resolution liquid chromatography-tandem mass spectrometry.
- To compare protein profiles between pregnant and non-pregnant ART patients to identify outcome-associated proteins.
- To construct protein-protein interaction networks and perform functional enrichment analyses to reveal key biological processes and regulatory hubs involved in follicular physiology.
- To select lipid and transport-related proteins for targeted quantitative validation and evaluate their potential role as biomarkers of reproductive success.

### 3.2. Lipidomics

- To investigate the lipid composition of FF using untargeted high-resolution liquid chromatography-tandem mass spectrometry-based lipidomic profiling.
- To identify lipid classes and individual lipid species associated with oocyte competence and pregnancy outcome.
- To assess alterations in lipid metabolism and lipid signaling pathways related to oxidative stress and inflammation within the follicular environment.
- To provide mechanistic information on the role of lipid transport and remodeling in ART success.

### 3.3. Metabolomics

- To perform targeted quantitative analysis of the twenty main amino acids in FF.
- To compare amino acid profiles among different clinical subgroups, including control patients and patients with endometriosis, insulin resistance, or thyroid disease.
- To identify amino acid related metabolic pathways associated with altered follicular physiology and impaired reproductive outcome.
- To evaluate the biomarker potential of selected amino acids using statistical and pathway-based approaches.

## 4. Materials and Methods

### 4.1. Study design and ethical approval

This study was conducted between May 2021 and March 2025 at the University of Pécs. FF sampling was performed at the Department of Obstetrics and Gynecology, while the analytical work was carried out at the Department of Biochemistry and Medical Chemistry, at the Department of Laboratory Medicine and at the National Laboratory on Human Reproduction in the Szentágothai Research Center. All procedures involving human participants were performed in accordance with the ethical standards of the institutional research committee and the Declaration of Helsinki. Written informed consent was obtained from all patients prior to sample collection.

Patients undergoing assisted reproductive treatment were enrolled and grouped according to pregnancy outcome or underlying clinical conditions, depending on the specific analytical objective. Clinical data including age, body mass index (BMI), number of retrieved and fertilized oocytes, and treatment outcomes were recorded.

### 4.1. Sample collection and processing

Follicular fluid samples were collected during transvaginal ultrasound-guided oocyte retrieval. Only clear FF samples free of visible blood contamination were included in the analysis. Samples were centrifuged to remove cellular debris and stored at -80 °C until further processing.

Peripheral venous blood samples were obtained on the day of oocyte retrieval to allow serum-FF comparisons in selected analyses. Serum samples were processed according to standard clinical laboratory procedures and stored under identical conditions.

### 4.2. Multi-omic analysis

Proteomic analysis of FF was performed using liquid chromatography-tandem mass spectrometry (LC-MS/MS). Proteins were extracted, denatured, reduced, alkylated, and enzymatically digested prior to analysis. Peptides were separated by reverse-phase liquid chromatography and analyzed using a high-resolution mass spectrometer. Label-free quantification was applied to compare protein abundance between study groups. Identified proteins were functionally annotated, and protein-protein interaction networks were constructed using publicly available databases. Functional enrichment analyses were performed to identify overrepresented biological processes and pathways.

Lipidomic profiling of FF was carried out using an untargeted UHPLC-MS/MS approach following Bligh–Dyer lipid extraction. Lipid species were identified based on accurate mass, retention time, and fragmentation patterns using reference databases. Multivariate statistical analyses were applied to identify lipid classes and species associated with ART outcome.

Targeted metabolomic analysis focused on the quantification of twenty proteinogenic amino acids in FF. Amino acids were derivatized and analyzed using UHPLC with fluorescence detection. Statistical analyses included group comparisons, correlation analyses with clinical parameters, pathway enrichment, and biomarker evaluation.

### 4.3. Quantitative analysis of lipid-related proteins

Selected lipid-related proteins and lipoprotein parameters, including apolipoprotein A1, HDL-cholesterol, total cholesterol, LDL-cholesterol, triglycerides, and lipoprotein(a) were quantified in matched serum and FF samples using validated clinical chemistry methods. Serum-to-follicular fluid ratios were calculated to assess selective transport across the blood-follicle barrier.

### 4.4. Statistical analysis and data processing

Statistical analyses were performed using SPSS. Group comparisons were conducted using parametric or non-parametric tests as appropriate, while associations between molecular and clinical parameters were assessed using Spearman's correlation. Correction for multiple testing was applied where necessary, and statistical significance was set at $p < 0.05$.

Proteomic data were processed using dedicated mass spectrometry software and curated protein databases. Functional annotation, pathway analysis, and protein-protein interaction network construction were performed using STRING and PANTHER software to identify key functional modules and hub proteins. Lipidomic data were analyzed using vendor-specific software for peak detection and normalization, followed by statistical evaluation of lipid classes and targeted lipid parameters. Amino acid metabolomic data were analyzed using MetaboAnalyst, including statistical testing, principal component analysis (PCA), enrichment and pathway analysis, as well as biomarker analysis.

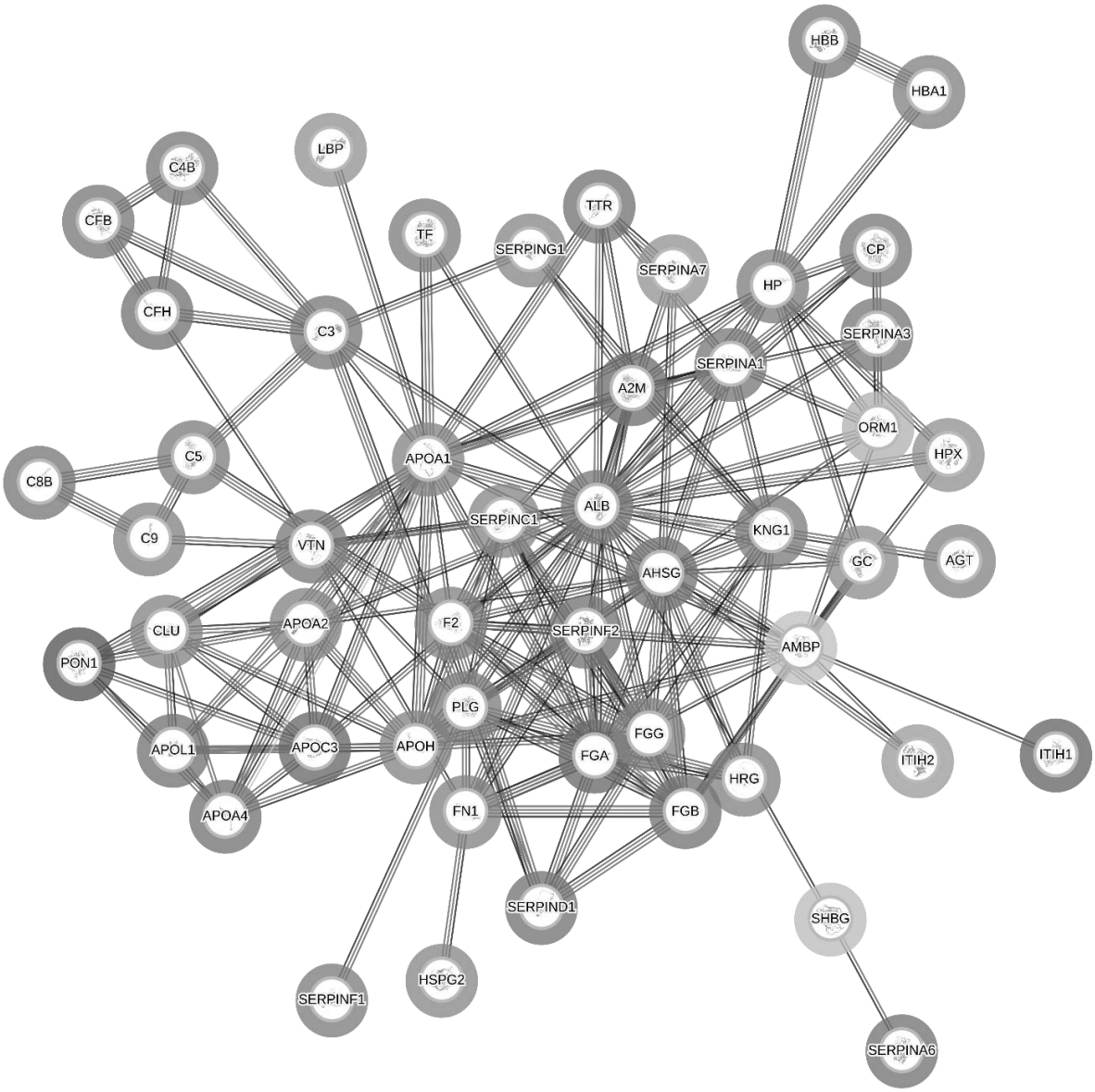
## 5. Main Results

### 5.1. Proteomic results

Using high-resolution proteomic analysis, a total of 131 individual proteins were identified in the FF samples, and they were classified according to biological processes, functional protein classes, and associated pathways. Functional annotation revealed that the FF proteome is dominated by proteins involved in cellular and metabolic processes as well as biological regulation, indicating intensive local metabolic and regulatory activity within the follicular microenvironment. Classification based on protein function showed that defense and immunity-related proteins constituted the largest group, followed by protein-binding activity modulators and transport/carrier proteins. Pathway enrichment analysis identified blood coagulation and the plasminogen activation cascade as the most prominently represented pathways. Further enriched pathways included B cell activation, angiogenesis, integrin signaling, vitamin D metabolism, and serine-glycine biosynthesis, reflecting the complex regulatory network governing follicular homeostasis.

Comparative quantitative analysis revealed that 77 proteins showed significantly different abundance between pregnant and non-pregnant ART patients, indicating that the follicular proteome is closely associated with reproductive outcome. Functional enrichment analysis demonstrated that proteins associated with lipid metabolism, cholesterol transport, and inflammatory regulation were overrepresented among the differentially abundant proteins.

Protein-protein interaction network analysis identified albumin and apolipoprotein A1 as central hub proteins, characterized by high connectivity within the network as presented in Figure 1. Functional enrichment analysis highlighted HDL-related pathways, cholesterol transport, and serine protease inhibition, indicating a key role of lipid-associated proteins in reproductive outcome.




*1. Figure: Protein-protein interaction network of the identified proteins. The network includes only high-confidence interactions (minimum required interaction score: 0.9). Nodes represent the identified proteins, while edges indicate protein–protein interactions.*

## 5.2. Quantitative analysis of lipid-related proteins

Based on proteomic findings, targeted quantitative analyses were performed to further investigate lipid transport-related parameters. Concentrations of apolipoprotein A1, HDL-cholesterol, total cholesterol, LDL-cholesterol, triglycerides, and lipoprotein(a) were measured in matched serum and FF samples.

As expected, serum concentrations of cholesterol-related parameters were markedly higher than those measured in FF, reflecting the selective permeability of the blood-follicle barrier. However, outcome-related differences were primarily observed within the FF rather than in serum. Follicular fluid samples obtained from pregnant patients exhibited significantly lower concentrations of ApoA1 and total cholesterol compared to samples from non-pregnant patients, with similar trends observed for HDL-C and lipoprotein(a).

Analysis of serum-to-follicular fluid ratios revealed distinct outcome-dependent patterns, indicating that lipid transport into the follicular compartment is a regulated process rather than passive diffusion. These findings suggest that efficient HDL remodeling and controlled cholesterol utilization within the follicular environment are associated with successful ART outcomes. The altered distribution of HDL-related proteins further supports the central role of ApoA1-mediated lipid transport in maintaining follicular homeostasis and optimizing conditions for oocyte maturation.

### 5.3. Lipidomic profiling of follicular fluid

Untargeted UHPLC-MS/MS-based lipidomic analysis revealed distinct lipid signatures associated with ART outcome. Several lipid classes, including phosphatidylcholines, lysophosphatidylcholines, and sphingomyelins, showed significantly lower abundance in FF of pregnant patients. In contrast, FF samples from non-pregnant patients exhibited elevated levels of cholesteryl esters and ceramides. These lipid species are known to be involved in pro-inflammatory signaling pathways and oxidative stress responses. The observed lipidomic alterations indicate a shift toward a pro-inflammatory and metabolically unfavorable follicular environment in unsuccessful ART cycles.

### 5.4. Amino acid profiling of the follicular fluid

Targeted metabolomic profiling of FF focused on the quantitative analysis of twenty proteinogenic amino acids, providing information on the metabolic state of the follicular microenvironment. Comparative analysis revealed significant differences in amino acid composition between pregnant and non-pregnant ART patients, indicating that amino acid availability and metabolism are closely linked to reproductive outcome.

Follicular fluid samples from pregnant patients showed significantly higher concentrations of asparagine, histidine, glycine, and threonine. These amino acids are involved in key

biological processes including protein synthesis, nitrogen metabolism, antioxidant defense, and cellular redox balance, all of which are essential for oocyte maturation and early embryonic development. Glycine and histidine have been associated with protection against oxidative stress, suggesting a more favorable redox environment in follicles leading to successful ART outcomes.

Correlation analyses further demonstrated associations between specific amino acids and clinical parameters. Tyrosine and leucine concentrations showed significant correlations with body mass index, reflecting the influence of systemic metabolic status on follicular amino acid composition. In addition, several amino acids exhibited correlations with the number of retrieved and fertilized oocytes, supporting their functional relevance to oocyte competence.

Disease-specific subgroup analyses identified characteristic amino acid alterations in patients with endometriosis and insulin resistance. PCA based on FF amino acid profiles demonstrated partial separation of patient groups. In patients with endometriosis, altered concentrations of amino acids involved in energy metabolism and redox regulation were observed, consistent with increased oxidative stress and inflammatory activity described in this condition. Similarly, patients with insulin resistance displayed characteristic amino acid patterns related to disturbed metabolic homeostasis. These findings indicate that different pathological conditions are associated with distinct metabolic signatures in FF. Pathway enrichment analysis of significantly altered amino acids highlighted metabolic pathways related to amino acid biosynthesis, nitrogen metabolism, and antioxidant defense.

Together, these results demonstrate that targeted amino acid profiling provides sensitive indicators of follicular metabolic status and contributes to understanding the metabolic determinants of oocyte quality and ART success.

## 6. Conclusion

This work demonstrates that follicular fluid is a highly regulated and biologically active microenvironment that plays a decisive role in determining oocyte competence and assisted reproductive technology outcomes. The integrative analysis of proteomic, lipidomic, and metabolomic data reveals that reproductive success is not driven by isolated molecular changes but by the coordinated regulation of interconnected metabolic and signaling networks within the follicular compartment.

The results indicate that lipid transport and cholesterol homeostasis represent central regulatory mechanisms in follicular physiology. Alterations in HDL-associated proteins, lipid species, and amino acid composition collectively reflect oxidative stress, inflammatory activity, and metabolic imbalance, which are detrimental to oocyte maturation and fertilization potential. Conversely, successful pregnancy outcomes are associated with a more balanced follicular environment characterized by efficient lipid remodeling, preserved antioxidant capacity, and optimized metabolic support.

Disease-specific analyses further demonstrate that systemic metabolic and inflammatory conditions such as insulin resistance and endometriosis profoundly reshape the follicular microenvironment. These alterations manifest as characteristic amino acid and lipid signatures linked to mitochondrial dysfunction, oxidative stress, and disturbed energy metabolism, providing mechanistic insight into the reduced fertility observed in these patient populations.

Overall, the findings emphasize that follicular fluid composition reflects both systemic metabolic health and local ovarian regulation. Comprehensive multi-omics profiling of follicular fluid therefore represents a powerful approach for understanding reproductive physiology and identifying molecular determinants of ART success.

## 7. Summary and Novel Findings

This doctoral work presents a comprehensive multi-omics characterization of follicular fluid and its relationship with reproductive outcome and disease-associated metabolic alterations. By integrating proteomic, lipidomic, and targeted amino acid analyses, the study identifies molecular signatures associated with pregnancy success and reveals condition-specific disturbances affecting follicular homeostasis.

**Novel scientific findings of this dissertation include:**

- Demonstration that follicular fluid is not a passive ultrafiltrate of serum but a dynamically regulated biological matrix with distinct proteomic, lipidomic, and metabolomic profiles.
- Identification of albumin and apolipoprotein A1 as central hub proteins within the follicular fluid protein-protein interaction network, highlighting their integrative role in lipid transport, antioxidant defense, and immune regulation.
- Evidence that successful pregnancy is associated with efficient HDL-mediated lipid remodeling and regulated cholesterol utilization within the follicular compartment.
- Integration of lipidomic and metabolomic data revealing oxidative stress and inflammation-related molecular signatures characteristic of unsuccessful ART outcomes.
- Identification of disease-specific follicular fluid metabolic phenotypes in insulin resistance and endometriosis, reflecting impaired energy metabolism and reduced antioxidant capacity.

Together, these results advance the understanding of follicular biology and demonstrate that multi-omics analysis of follicular fluid provides clinically relevant information on the molecular determinants of oocyte quality. The identified biomarkers and pathways offer promising opportunities for future diagnostic and therapeutic strategies aimed at improving assisted reproductive treatment outcomes.

## 8. List of Publications

### 8.1. Publications related to the dissertation

- **Kurdi, C**.; Schmidt, J.; Horváth-Szalai, Z.; Mauchart, P.; Gödöny, K.; Várnagy, Á.; Kovács, G. L.; Kőszegi, T.; Follicular Fluid Proteomic Analysis of Women Undergoing Assisted Reproduction Suggests That Apolipoprotein A1 Is a Potential Fertility Marker, INTERNATIONAL JOURNAL OF MOLECULAR SCIENCES 25 : 1 Paper: 486 , 15 p. (2024); **IF:4.9, Q1**
- **Kurdi, C.;** Lelovics, V.; Hesszenberger, D.; Lajtai, A.; Lakatos, Á.; Herczeg, R.; Gödöny, K.; Mauchart, P.; Várnagy, Á.; Kovács, G.L.; Kőszegi, T.; Amino Acid Profiling of Follicular Fluid in Assisted Reproduction Reveals Important Roles of Several Amino Acids in Patients with Insulin Resistance; INTERNATIONAL JOURNAL OF MOLECULAR SCIENCES 24 : 15 Paper: 12458 , 15 p. (2023); **IF:4.9, Q1**
- **Kurdi, C**.; Hesszenberger, D.; Csabai, D.; Lajtai, A.; Lakatos, Á.; Jakabfi-Csepregi, R.; Gödöny, K.; Mauchart, P.; Várnagy, Á.; Kovács, G. L.; Kőszegi, T.; Follicular Fluid Amino Acid Alterations in Endometriosis: Evidence for Oxidative Stress and Metabolic Dysregulation, BIOMEDICINES : 13 Paper: 2634, 15 p (2025); **IF: 3.9, Q1**

  **The cumulative impact factor: 13.7**

### 8.2. Other publications not directly related to the dissertation

- Suthar, Sharad K.; Jernei, T.; **Kurdi, C.**; Horváth, Á.I. ; Rauscher, A.Á.; Gyimesi, M.; Málnási-Csizmadia, A.; Fragment-based structure-activity relationship analysis of CK-571 reveals non-interacting groups drive smooth muscle myosin selectivity.; EUROPEAN JOURNAL OF MEDICINAL CHEMISTRY 305 Paper: 118476 (2025); **IF: 5.9, Q1**
- Suthar, Sharad K.; Szimler, T.; Pénzes, M.; Chandrabhas, S.; Rauscher, A. Á.; Lőrincz, I.; Hegyi, G..; **Kurdi, C.**; Glatz, G.; Szőnyegi, Z. et al.; Comprehensive SAR analysis of actomyolytics, drug candidates targeting the actomyosin complex; EUROPEAN JOURNAL OF MEDICINAL CHEMISTRY 299 Paper: 117999 (2025); **IF: 5.9, Q1**
- Gergics, M.; Pham-Dobor, G.; **Kurdi, C.;** Montskó, G.; Mihályi, K.; Bánfai, G.; Kanizsai, P.; Kőszegi, T.; Mezősi, E.; Bajnok, L.; Apelin-13 as a Potential Biomarker in Critical Illness; JOURNAL OF CLINICAL MEDICINE 12: 14 Paper: 4801, 11 p. (2023), **IF:2.9 Q1**

- Kőszegi, T.; Horváth-Szalai, Z.; Ragán, D.; Kósa, B.; Szirmay, B.; **Kurdi, C.;** Kovács, G.L. ; Mühl, D.; Measurement of Urinary Gc-Globulin by a Fluorescence ELISA Technique: Method Validation and Clinical Evaluation in Septic Patients—A Pilot Study; MOLECULES 28 : 19 Paper: 6864 , 15 p. (2023), **IF:4.2 ,Q1**
- Gyimesi, M.; Horváth, Á.I.; Túrós, D.; Suthar, Sharad K.; Pénzes, M.; **Kurdi, C.;** Canon, L.; Kikuti, C.; Ruppel, K. M.; Trivedi, D.V. et al., Single Residue Variation in Skeletal Muscle Myosin Enables Direct and Selective Drug Targeting for Spasticity and Muscle Stiffness, CELL 183 : 2 pp. 335-346.e13., 12 p. (2020), **IF: 41.584, Q1**

**The cumulative impact factor of the publications: 13.7**
**The total impact factor of all publications: 74.284**
**Independent citations: 36**
**Hirsch index: 3**

### 8.3. Book chapters not related to this thesis

- **Csilla K.**; Tamás K.; CIRCULATING TUMOR CELLS IN MEDICAL RESEARCH, In: Tamás Kőszegi; Antonella Chesca; LABORATORY TECHNIQUES WITH APPLICABILITY IN MEDICAL PRACTICE; Saarbrücken: Lambert Academic Publishing (LAP), pp 135-144 (2015)

### 8.4. Conference presentations and posters not related to the thesis

- Temesfői V.; **Kurdi C.**; Kőszegi T.; Fibrin alapú három dimenziós szövettenyésztési eljárás fejlesztése; In: IDK 2015 - IV. Interdiszciplináris Doktorandusz Konferencia 2015 : Abstract
- **Csilla K.**; Viktória T.; Tamás K.; Possible method for tumor cell isolation from whole blood; 4th Interdisciplinary Doctoral Conference 2015
- **Csilla K.**; Viktoria T.; Tamás K.; Development of 3D tissue culturing method for investigation of circulating tumor cells; In: Semmelweis Egyetem PhD : PhD Scientific Days 2015
- Temesfői V.; **Kurdi C.**; Szálig Á.Gy.; Laki A: J.; Kőszegi T.; Bemeneti minta optimalizálása keringő tumorsejtek kinyeréséhez; mikrofluidikai eszköz fejlesztése; Doktoranduszok a Klinikai Kutatásokban; Pécs, 28$^{th}$ October, 2017

- R. Csepregi; V. Temesfői; **C. Kurdi**; Á.G. Szélig; A.J. Laki; T. Kőszegi; DETECTION AND IDENTIFICATION OF CULTURED TUMOR CELLS IN MICROFLUIDIC DEVICE; 3rd ACTC Advances in Circulating Tumour Cells Liquid Biopsy in Clinical Practice, (ACTC 2017); October 4th - 7th, 2017, Rhodes, Greece
- **Kurdi C.**: Temesfői V.; Szélig Á.Gy.; Kőszegi T.; Laki A: J.; Mikrofluidikai eszköz tesztelése keringő tumorsejtek izolálása céljából; Doktoranduszok a Klinikai Kutatásokban; 28th October 2017
- Suthar Sharad K.; Gyimesi M.; **Kurdi C.**; Malnasi-Csizmadia A.; SAR Analysis of Linker Derivatives of the Smooth Muscle Myosin Specific CK-571 Compound; BIOPHYSICAL JOURNAL (0006-3495 1542-0086): 118 3 pp 495A-495A (2020)

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