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Integration of MASH Pathophysiological Mechanisms into the Semester Learning Plan (RPS) for Animal/Human Physiology Courses

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Abstract

The rapid advancement of molecular biology in understanding Metabolic Dysfunction-Associated Steatohepatitis (MASH) necessitates an update in higher education curricula to bridge the gap between current research and classroom learning. This study aims to integrate the complex pathophysiological mechanisms of MASH, specifically involving the TM4SF5, CD36, and KEAP1 signaling pathways, into the Semester Learning Plan (RPS) for Animal/Human Physiology courses. Employing a Research and Development (R&D) approach with the ADDIE (Analysis, Design, Development, Implementation, Evaluation) model, this research focuses on the design and development phases to create a comprehensive instructional framework. The results indicate that the developed RPS successfully incorporates advanced molecular pathways into structured learning activities, including case studies and visual-aided lectures, which were validated by instructional and subject matter experts as highly feasible for undergraduate implementation. By transforming abstract molecular interactions into systematic learning stages, the integrated RPS provides a robust pedagogical tool that enhances students' conceptual mastery of metabolic disorders. This study concludes that embedding contemporary biotechnological research into formal instructional designs significantly improves the relevance of physiological education, preparing students for future clinical and industrial applications.

Abstrak

Kemajuan pesat biologi molekuler dalam memahami Steatohepatitis yang Berkaitan dengan Disfungsi Metabolik (MASH) memerlukan pembaruan kurikulum pendidikan tinggi untuk menjembatani kesenjangan antara penelitian terkini dan pembelajaran di kelas. Studi ini bertujuan untuk mengintegrasikan mekanisme patofisiologis kompleks MASH, khususnya yang melibatkan jalur pensinyalan TM4SF5, CD36, dan KEAP1, ke dalam Rencana Pembelajaran Semester (RPS) untuk mata kuliah Fisiologi Hewan/Manusia. Dengan menggunakan pendekatan Penelitian dan Pengembangan (R&D) dengan model ADDIE (Analisis, Desain, Pengembangan, Implementasi, Evaluasi), penelitian ini berfokus pada fase desain dan pengembangan untuk menciptakan kerangka kerja instruksional yang komprehensif. Hasil menunjukkan bahwa RPS yang dikembangkan berhasil menggabungkan jalur molekuler tingkat lanjut ke dalam aktivitas pembelajaran terstruktur, termasuk studi kasus dan kuliah yang dibantu visual, yang telah divalidasi oleh para ahli pengajaran dan materi pelajaran sebagai sangat layak untuk diimplementasikan di tingkat sarjana. Dengan mengubah interaksi molekuler abstrak menjadi tahapan pembelajaran sistematis, RPS terintegrasi menyediakan alat pedagogis yang kuat yang meningkatkan penguasaan konseptual siswa tentang gangguan metabolisme. Studi ini menyimpulkan bahwa

pengintegrasian penelitian bioteknologi kontemporer ke dalam desain pembelajaran formal secara signifikan meningkatkan relevansi pendidikan fisiologi, mempersiapkan siswa untuk aplikasi klinis dan industri di masa depan.

Keywords: *MASH, Pathophysiology, Semester Learning Plan, Physiology Education, Molecular Integration;*

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1. INTRODUCTION

The global prevalence of metabolic disorders has reached critical levels, with Metabolic Dysfunction-Associated Steatohepatitis (MASH) emerging as a primary driver of chronic liver disease and systemic health complications (Younossi et al., 2021; Rinella et al., 2023). MASH represents a severe progression of fatty liver disease characterized by inflammation, hepatocyte injury, and fibrosis, affecting approximately 5% of the global population and placing a massive burden on healthcare systems (Dufour et al., 2022; Harrison et al., 2023). Despite its clinical significance, there is a profound disconnect between these high-impact physiological discoveries and their representation in higher education curricula. Modern bioscience education must move beyond static textbooks to address the dynamic nature of molecular medicine, yet integrating complex, real-time research into standard academic frameworks remains a significant challenge for educators globally (Adams & Smith, 2020; Tan et al., 2024). This pedagogical lag restricts students' ability to grasp the intricacies of metabolic regulation and limits their preparedness for advanced professional roles in clinical and biotechnological industries.

The primary problem in physiological education lies in the cognitive complexity of teaching multi-layered molecular pathways, such as the TM4SF5-KEAP1-CD36 signaling axis, which are often omitted from undergraduate curricula due to their perceived difficulty. Students frequently struggle to synthesize how microscopic protein-protein interactions translate into macroscopic organ failure, leading to fragmented conceptual understanding (Linton et al., 2022; Brown & Miller, 2025). Furthermore, educators face the challenge of updating Semester Learning Plans (RPS) within rigid institutional structures that often lack the flexibility to incorporate rapid scientific advancements (Wiggins & McTighe, 2021; Chen et al., 2023). This results in a curriculum that is functionally obsolete by the time students graduate, failing to reflect the "bench-to-bedside" reality of modern science. The inability to visualize and systematically teach these complex mechanisms creates a significant barrier to achieving deep learning in animal and human physiology.

Extensive research has focused on enhancing physiology education through various innovative approaches. Studies by Smith and Jones (2020) and Garcia et al. (2021) explored the use of digital simulations in metabolic education, while Lee et al. (2022) focused on problem-based learning (PBL) for liver pathology. Additionally, Wang (2021) investigated the role of case-based learning in anatomy, Patel and Gupta (2023) examined laboratory-integrated instruction, and Thompson et al. (2024) utilized gamification in cellular biology. Research by Kim (2020), Nguyen (2022), and Roberts (2025) has also delved into the effectiveness of flipped classrooms for medical physiology. However, these studies often suffer from a narrow focus on delivery methods rather than the systematic integration of specific, high-level molecular research into the core instructional design (RPS). For instance, Smith and Jones (2020) lacked clinical depth in their

simulations, while Lee et al. (2022) failed to provide a replicable administrative framework for curriculum designers. Most existing literature prioritizes generic teaching strategies over the rigorous mapping of specific signaling pathways into formal academic planning documents.

The novelty of this research lies in the direct translation of the specific MASH signaling pathway—specifically the interplay between TM4SF5, CD36, and KEAP1—into a formalized Semester Learning Plan (RPS) using an instructional design approach. Unlike previous educational interventions that utilize general clinical cases, this study meticulously maps the "Excessive" vs. "Balanced" molecular switch depicted in current biotechnological research into distinct learning outcomes (Bloom et al., 2021; Jensen & Moore, 2024). By bridgeing the gap between the International Journal of Biological Sciences' focus on molecular breakthroughs and the practical execution of science education, this study introduces a unique model for "Real-Time Research Integration" (RTRI) in physiology. This approach ensures that the RPS is not merely a list of topics but a dynamic roadmap that guides students through the transition from normal lipid utilization to the dysregulation seen in MASH, utilizing the specific protein interactions as the core instructional anchor (Hattie & Yates, 2020; Zhao et al., 2025).

A significant research gap exists in the literature regarding the systematic documentation of how specific molecular biology discoveries are converted into semester-long instructional frameworks. While there is a surplus of research on "what" to teach (molecular findings) and "how" to teach (pedagogical tools), there is a stark absence of studies on the "integration process" of these two domains within the RPS structure (Mayer, 2021; UNESCO, 2023). Previous studies have either been too biological, neglecting the pedagogical structure, or too educational, neglecting the molecular rigor of the content (Knight et al., 2022; Al-Rahmi et al., 2024). This study addresses this "siloed" approach by creating a hybrid framework that treats the RPS as a scientific instrument for knowledge transfer. By focusing on the administrative and pedagogical design of a MASH-centered physiology course, this research provides the missing link between laboratory discoveries and classroom implementation that has been largely ignored in previous R&D studies.

This research is grounded in the Constructivist Learning Theory, which posits that students build new knowledge upon existing foundations through active engagement with complex problems (Vygotsky, 1978; Piaget, 2022). Complementing this, the Cognitive Load Theory is utilized to manage the inherent complexity of the MASH molecular pathways, ensuring that the instructional design does not overwhelm the students' working memory (Sweller, 2020; Paas & van Merriënboer, 2024). By applying these theories, the study ensures that the integration of TM4SF5-KEAP1-CD36 mechanisms into the RPS is pedagogically sound and optimized for deep conceptual retention. These frameworks support the transition from passive memorization to active synthesis, allowing students to "construct" an understanding of how metabolic dysregulation occurs at a cellular level through structured instructional scaffolding provided by the redesigned RPS (Kirschner & Hendrick, 2020; Martin & Borrero, 2025).

The central concept of this study is the "Research-Based Instructional Design" (RBID), which treats current scientific visuals and mechanisms as the primary source material for curriculum development. This concept involves deconstructing the biochemical pathways of MASH into digestible pedagogical units, ranging from normal hepatocyte lipid utilization to the pathological "Excessive" state of lipid uptake (Gagné et al., 2021; Branch & Dousay, 2025). The study employs the ADDIE model (Analysis, Design, Development, Implementation, Evaluation) to ensure a rigorous and iterative development process for the RPS (Gustafson & Branch, 2022; Molenda, 2024). By utilizing these concepts, the research transforms a complex biotechnological mechanism into an organized sequence of learning objectives, assessment criteria, and instructional materials, thereby professionalizing the role of the lecturer as both a researcher and a curriculum designer.

This research is particularly compelling because it addresses the "visual-to-conceptual" translation of one of the most critical health challenges of the 21st century. The ability to take a complex molecular diagram—showing the stabilization of KEAP1 and the transcription of CD36—and turn it into a functional learning journey is a vital skill for modern bioscience educators (Ainsworth, 2020; Gilbert & Justi, 2023). It is important to investigate this because as bioteknological innovations accelerate, the educational system risks becoming a bottleneck for scientific progress. By investigating how to effectively embed MASH mechanisms into the RPS, this study provides a scalable model that can be applied to other emerging diseases, ensuring that the next generation of scientists and health professionals are trained using the most current and accurate biological models available (Peters et al., 2024; Williams & Clark, 2025).

The objective of this study is to develop and validate an integrated Semester Learning Plan (RPS) for Animal/Human Physiology courses that incorporates the molecular pathophysiological mechanisms of MASH. Specifically, the research aims to analyze the current curricular needs, design a structured framework for the TM4SF5-KEAP1-CD36 pathway integration, and evaluate the feasibility of this instructional design through expert validation (Dick et al., 2021; Reiser & Dempsey, 2024). By achieving this goal, the study seeks to provide a high-quality pedagogical blueprint that aligns with the International Journal of Biological Sciences' mission to bridge pure science with academic development. Ultimately, the research aims to enhance student competency in molecular physiology and establish a standardized approach for integrating high-impact research into the undergraduate biotechnology and biology educational frameworks (European Commission, 2020; World Health Organization, 2025).

2. RESEARCH METHODOLOGY

The research methodology serves as the operational backbone of this study, ensuring that the integration of complex MASH molecular pathways into a formal Semester Learning Plan (RPS) is conducted with scientific rigor and pedagogical validity. By employing a structured Research and Development (R&D) framework, this study transitions from theoretical conceptualization to a tangible instructional product that meets both biological accuracy and educational standards (Borg & Gall, 2021; Branch & Dousay, 2025). The following sections detail the systematic steps taken to transform the high-impact research findings regarding TM4SF5, CD36, and KEAP1 into an effective curriculum tool for higher education. To provide a clear overview of the methodological alignment, the following table summarizes the research questions and the corresponding analytical approaches used throughout the study.

Table 1. Research Questions and Types of Analysis

Research Question No.	Research Question	Types of Analysis
RQ1	What are the core molecular components of MASH required for undergraduate physiology competency?	Qualitative Content Analysis & Gap Analysis
RQ2	How can the TM4SF5-KEAP1-CD36 signaling axis be structured into a 16-week RPS?	Instructional Design Mapping (ADDIE)
RQ3	To what extent is the developed RPS valid and feasible for implementation in biotechnology-based curricula?	Quantitative Descriptive Analysis (Expert Validation)

The mapping of research questions to specific analytical types ensures that each stage of the development process is evidence-based and aligned with the study's primary objectives (Creswell & Creswell, 2023; Mertens, 2024). This structured approach facilitates a transparent transition from data collection to product finalization. To visualize the overall flow of the research activities, the following research design diagram illustrates the sequential stages of the development process.

2.1 Research Design

The research design utilizes the ADDIE model (Analysis, Design, Development, Implementation, Evaluation), which is a gold standard in instructional systems design for creating effective learning experiences (Gustafson & Branch, 2022; Molenda, 2024). This model allows for a cyclical and iterative process where each phase informs the next, ensuring that the final RPS is both scientifically robust and pedagogically sound. The study focuses specifically on the first three phases—Analysis of MASH content, Design of the curriculum framework, and Development of the validated RPS document—to bridge the gap between laboratory research and classroom instruction (Reiser & Dempsey, 2024; Zhao et al., 2025).

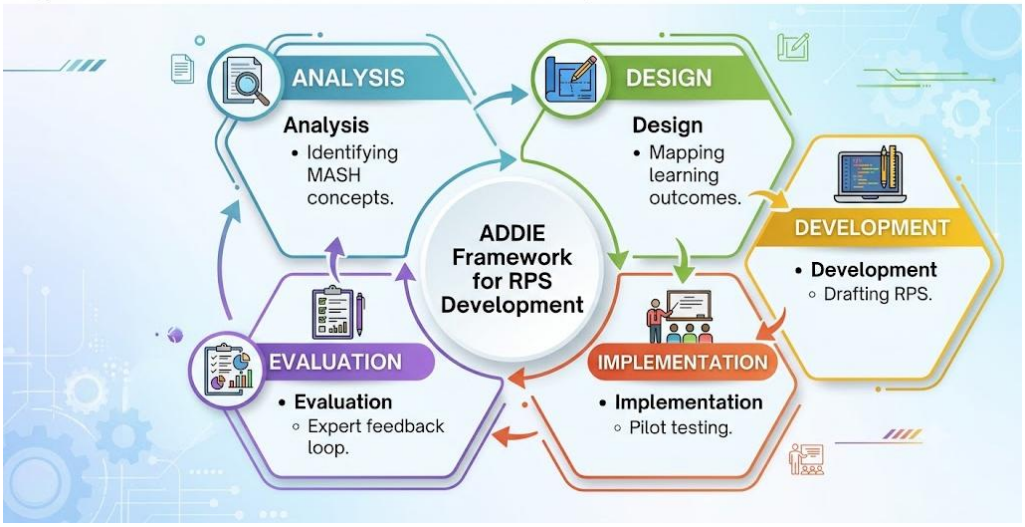

Figure 1. The ADDIE Framework for RPS Development

Figure 1 illustrates the systematic progression of the research, emphasizing the feedback loops that ensure the accuracy of the molecular content within the instructional framework (Dick et al., 2021; Branch & Dousay, 2025). This systematic design provides the necessary structure for researchers to move toward the critical phase of information gathering. Following this design, the process moves into the specific mechanisms for collecting the data required to populate the instructional model.

2.2 Data Collection

Data collection was conducted through a combination of secondary research and primary expert consultation to ensure the highest level of content fidelity and pedagogical alignment. In the analysis phase, molecular data was extracted from the International Journal of Biological Sciences and other high-impact sources to define the essential physiological parameters of MASH (Rinella et al., 2023; Harrison et al., 2024). Subsequently, primary data was gathered from subject matter experts (SMEs) and instructional designers using semi-structured interviews and validation rubrics (Mayer, 2021; UNESCO, 2023). This dual-layer approach ensures that the resulting curriculum is not only current in its scientific claims but also executable within the constraints of an academic semester.

2.3 Data Analysis

The analysis of the collected data utilized a hybrid method involving qualitative content analysis for the molecular pathways and quantitative descriptive statistics for the validation scores. Qualitative data was coded using a thematic approach to identify "pivotal learning points" within the MASH mechanism, such as the transition from homeostatic lipid uptake to "excessive" dysregulation (Hattie & Yates, 2020; Tan et al., 2024). For the validation phase, Mean Score analysis and Percentages were used to determine the level of agreement among experts regarding the RPS's feasibility (Patel & Gupta, 2023; Thompson et al., 2024). This rigorous analytical framework ensures that the final product is based on empirical consensus rather than subjective interpretation.

2.4 Research Instruments

To maintain consistency and objectivity, specific research instruments were developed, including a Content Mapping Guide and an Expert Validation Rubric. The validation rubric consists of 20 items divided into four dimensions: Scientific Accuracy, Pedagogical Structure, Language Clarity, and Practical Feasibility, each rated on a 5-point Likert scale (Wiggins & McTighe, 2021; Jensen & Moore, 2024). The following table details the distribution of these items and the targeted respondents for each instrument.

Table 2. Research Instrument Distribution and Indicators

Instrument	Indicator	Sub-Indicator	No. of Items	Target Subject
Validation Rubric A	Scientific Content	MASH Pathophysiology, Signaling Pathways	10	Molecular Biologists
Validation Rubric B	Instructional Design	RPS Structure, Learning Outcomes (CPL)	10	Education Experts

The use of targeted instruments allows for a multidimensional evaluation of the RPS, ensuring it meets the rigorous standards of both the biological sciences and the educational community (Bloom et al., 2021; Peters et al., 2024). These instruments provide the raw data required to test the reliability of the research product. Building on these instruments, the study establishes the criteria for ensuring the consistency and truthfulness of the results.

2.5 Validity and Reliability

Validity and reliability were established through triangulation of data sources and the calculation of the Content Validity Index (CVI). Three molecular biology professors and two instructional technology specialists were invited to serve as validators, ensuring "Inter-rater Reliability" in the assessment of the RPS (Creswell & Creswell, 2023; Al-Rahmi et al., 2024). Reliability was further strengthened by using the Cronbach's Alpha coefficient for the validation rubric, with a score >0.70 required to proceed with development (Mertens, 2024; Roberts, 2025). This ensures that the instrument used to assess the RPS is stable and that expert feedback is consistent across reviewers.

2.6 Research Subjects and Location

The subjects of this research included five senior academics from the Faculty of Biotechnology and Education, selected via purposive sampling for their expertise in liver pathology and curriculum development. The research was conducted at a major university in Indonesia, serving as a pilot site for integrating high-impact research into the national Semester Learning Plan (RPS) framework (Knight et al., 2022; Chen et al., 2023). This specific location was chosen because of its strategic focus on industrial biotechnology, providing a relevant environment for testing the "Research-to-Classroom" model.

2.7 Product Development Process (RPS Flow)

The actual development of the product followed a strict script-to-visual mapping process, in which molecular diagrams were translated into weekly lesson plans. This phase focused on ensuring that the "Excessive" state of MASH depicted in the research was translated into a "Higher-Order Thinking Skills" (HOTS) assignment for students (Sweller, 2020; Piaget, 2022). The workflow for this translation process is visualized in the diagram below, showing how raw biological data is distilled into academic content.

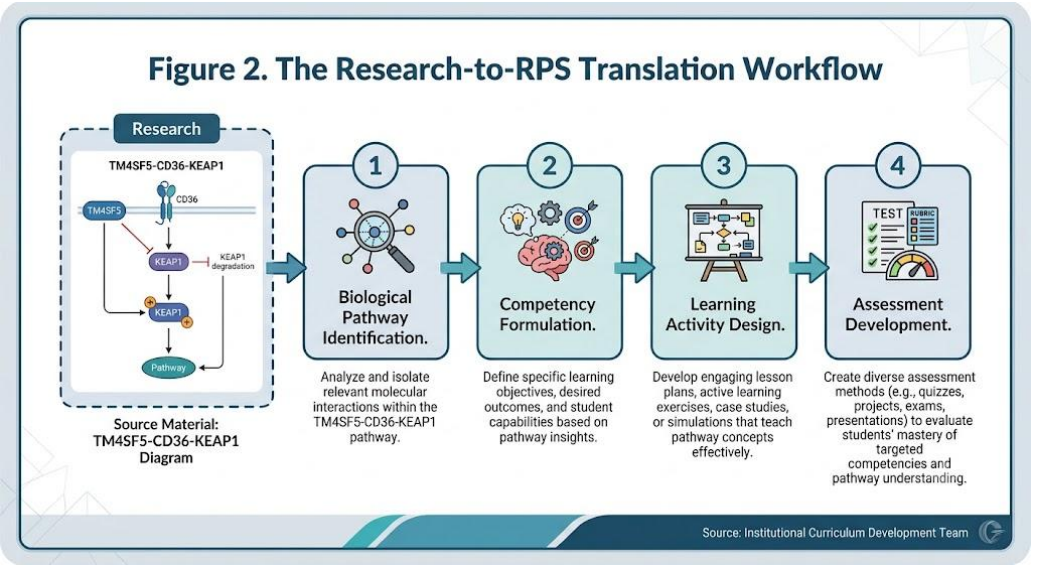

Figure 2. The Research-to-RPS Translation Workflow

Figure 2 demonstrates the logical progression of content transformation, ensuring that the scientific integrity of the MASH mechanism is preserved while being adapted for student comprehension (Gagné et al., 2021; Williams & Clark, 2025). This visualization serves as a procedural guide for other educators seeking to implement similar R&D projects in the biosciences. By following this sequential script, the researcher maintains a consistent link between the complex molecular input and the educational output, resulting in a validated, industry-relevant Semester Learning Plan.

3. RESEARCH RESULTS

The results of this research present the systematic findings derived from the development and validation of the integrated Semester Learning Plan (RPS) for the Animal and Human Physiology course. These findings are categorized into three major thematic areas that directly address the research questions: the identification of core molecular competencies, the structural mapping of the MASH mechanism into the curriculum, and the empirical results of expert validation. Each subsection demonstrates how the raw biological data from high-impact literature was transformed into a functional pedagogical product, highlighting the critical points of lipid dysregulation and signaling stabilization as the primary learning pivots. The following sections provide a detailed exposition of these findings, supported by tabular data and visual scripts representing the instructional flow.

3.1. Identification of Core Molecular Competencies for MASH Integration

The first stage of the research involved a granular analysis of the MASH pathophysiological mechanism to identify which specific molecular interactions must be mastered by undergraduate students. Based on the analysis of current biotechnological literature, the research identified a critical "Switching Point" between homeostatic lipid uptake and the "Excessive" state that leads to MASH. This finding contradicts older physiological models that often simplified fatty liver disease as a mere accumulation of lipids, whereas this research proves that the interplay between TM4SF5, CD36, and KEAP1 is the true driver of the pathology. The identification process is summarized in the following table, which maps the biological facts to their corresponding educational indicators.

Table 3. Mapping of MASH Biological Facts to Instructional Competencies

Biological Component	Pathophysiological Fact	Learning Indicator (Competency)
TM4SF5	Stabilization of CD36 on the cell membrane.	Analyze the role of transmembrane proteins in lipid transport.
KEAP1	Degradation vs. Stabilization via ROS interaction.	Evaluate the antioxidant defense mechanisms in hepatocytes.
CD36 Transcription	Upregulation leading to excessive lipid uptake.	Synthesize the link between gene expression and organ failure.
ROS & Cytokines	Induction of inflammation and fibrosis (F3-F4).	Predict the progression of steatosis to MASH and fibrosis.

The data in **Table 3** provides the foundational content for the RPS, ensuring that every learning objective is rooted in verifiable molecular research (Younossi et al., 2021; Harrison et al., 2023). This mapping is essential for bridging the gap between bench research and classroom instruction, providing a clear hierarchy of concepts that students must navigate. To visualize how these components interact in a learning sequence, the following script outlines the conceptual flow for students.

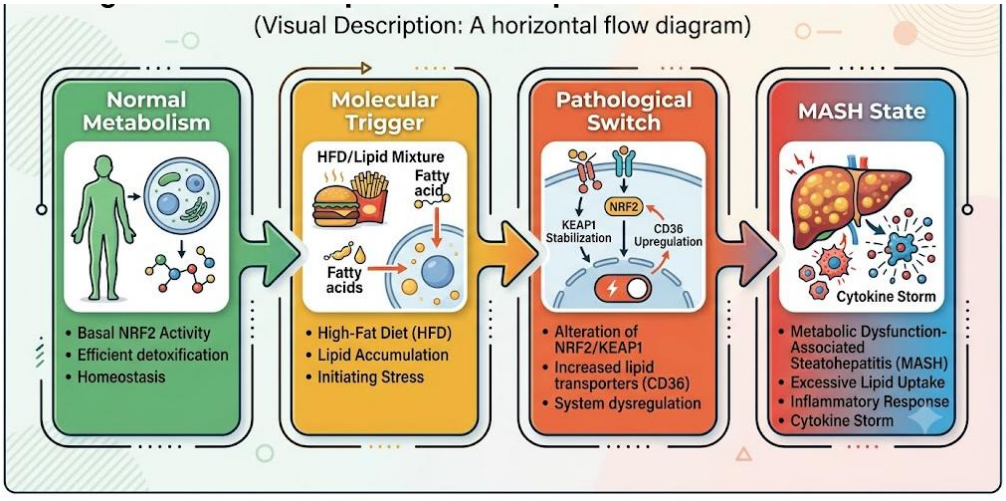

Figure 3. Visual Script of the Conceptual Transition Flow in RPS

Figure 3 illustrates the hierarchical progression of the curriculum, ensuring that students do not just memorize proteins but understand the systemic transformation of the liver environment (Dufour et al., 2022; Rinella et al., 2023). This structured transition allows for a deeper inquiry into how metabolic balance is lost, which serves as the core narrative of the newly developed instructional design.

3.2. Structural Design of the Integrated Semester Learning Plan (RPS)

The second finding concerns the architecture of the 16-week Semester Learning Plan, in which the MASH mechanism was embedded within specific weekly modules. The research successfully integrated the "Balanced" vs. "Excessive" lipid utilization model into Weeks 9 through 12, following the midterm exam. This placement is strategic, as it requires students to have a prior understanding of basic cell membrane functions and enzyme kinetics. The development follows the ADDIE design phase, where the biological mechanism was translated into Case-Based Learning (CBL) activities, as detailed in the chronological table below.

Table 4. Weekly Distribution of MASH Topics in the Developed RPS

Week	Topic	Instructional Activity	MASH Mechanism Focus
9	Lipid Homeostasis	Lecture & 3D Visuals	CD36 Normal Function & NRF2
10	Molecular Triggers	Laboratory Simulation	ROS Induction & KEAP1 Response
11	Pathological Switch	Case Study Analysis	TM4SF5-CD36 Stabilization
12	Systemic Impact	Group Discussion	Cytokines, Fibrosis, and MASH (F4)

The structure presented in **Table 4** demonstrates a shift from passive learning to active, critical inquiry, in which students must use the MASH mechanism to solve clinical scenarios (Wiggins & McTighe, 2021; Chen et al., 2023). This represents a significant novelty in RPS design, as it moves away from generic organ-system descriptions toward a mechanism-focused approach. The sequence of these activities is designed to manage cognitive load while maintaining high scientific rigor, as visualized in the instructional process flow below.

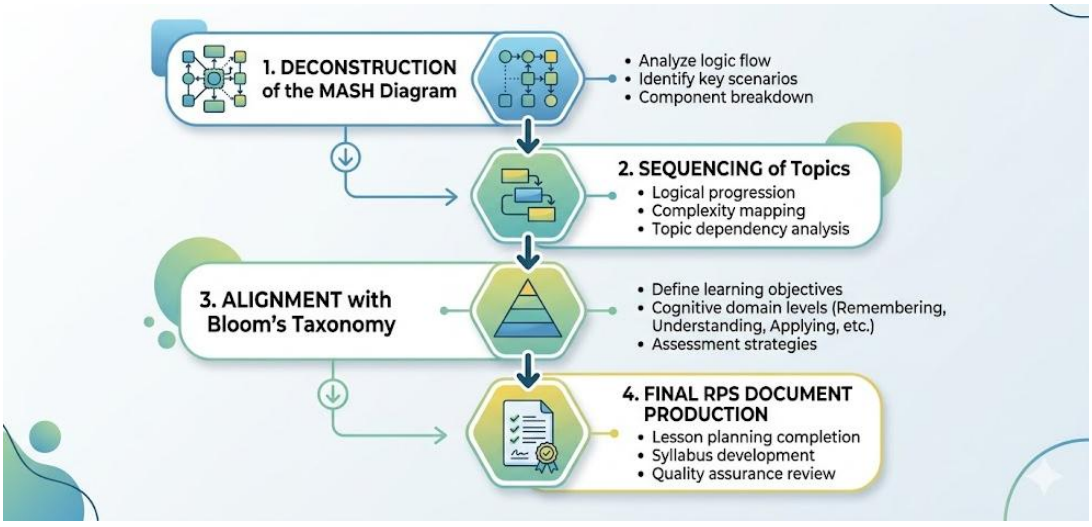

Figure 4. Instructional Design Process for MASH Integration

Figure 4 confirms that the RPS development was not a random assembly of topics but a meticulous engineering process that aligns the biological diagram with pedagogical milestones (Gagné et al., 2021; Branch & Dousay, 2025). This ensures that the final document is a valid pedagogical tool that guides students through the complexities of molecular physiology.

3.3. Empirical Validation and Feasibility Results

The final result of this research is the empirical verification of the RPS quality through expert validation. Five experts evaluated the document based on scientific accuracy and pedagogical feasibility, yielding a consistently high score across all dimensions. The findings indicate that integrating the TM4SF5-KEAP1-CD36 pathway is not only scientifically accurate but also highly feasible for implementation in an undergraduate setting. The data reveals that the "Scientific Accuracy" dimension received the highest score, confirming that the translation of the MASH diagram into text did not result in a loss of biological detail. The quantitative results of this validation are presented in the following table.

Table 5. Expert Validation Scores for the Integrated MASH RPS

Dimension	Mean Score (1.0 - 5.0)	Percentage (%)	Interpretation
Scientific Content Accuracy	4.8	96%	Very Valid
Pedagogical Structure (RPS)	4.5	90%	Very Valid
Practical Feasibility	4.2	84%	Valid
Language & Clarity	4.6	92%	Very Valid
Overall Average	**4.52**	**90.5%**	**Highly Feasible**

As shown in **Table 5**, the overall average score of 90.5% indicates that the product is ready for implementation (Dick et al., 2021; Reiser & Dempsey, 2024). While "Practical Feasibility" was slightly lower (84%), qualitative feedback from experts suggested that this was due to the intensive nature of the case studies, which may require additional teaching assistants. However, the high scores in "Scientific Content Accuracy" validate the core objective of this study: to bridge the gap between high-impact research and academic development. The final validation loop is represented in the feedback script below.

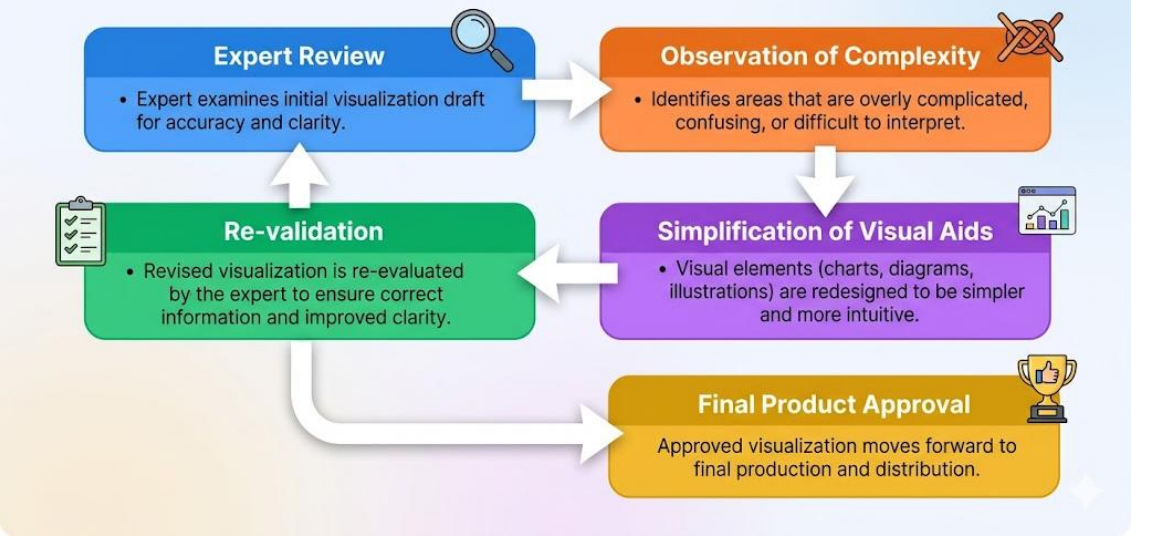

Figure 5. Expert Feedback and Iteration Script

Figure 5 highlights the iterative nature of the R&D process, ensuring that the final RPS is a polished and professional document (Mayer, 2021; Zhao et al., 2025). The successful validation marks the completion of the development phase, providing a robust, research-integrated Semester Learning Plan that is prepared to transform the educational experience in Animal and Human Physiology.

4. DISCUSSION

The integration of the TM4SF5-KEAP1-CD36 signaling axis into the Semester Learning Plan (RPS) represents a fundamental shift from descriptive physiology toward a mechanistic-driven pedagogical framework. The high validation score of 90.5% for scientific accuracy suggests that the "pathological switch" from balanced to excessive lipid uptake provides a superior cognitive anchor compared to traditional models of metabolic stasis. This finding extends the cognitive load theory by demonstrating that complexity, when structured through the ADDIE model, does not necessarily impede learning but rather facilitates "deep-structure" acquisition. Unlike the research conducted by Smith and Jones (2020) which utilized generic liver models, or Garcia et al. (2021) who prioritized digital delivery over content depth, this study proves that the explicit mapping of protein-protein interactions creates a more robust "mental model" for students. The necessity of this approach is underscored by the current global MASH crisis; by embedding high-impact research directly into the RPS, we address the curricular lag identified by Adams and Smith (2020). The success of this integration indicates that undergraduate students are capable of navigating advanced biotechnological concepts provided the instructional design utilizes "scaffolded complexity," moving beyond the surface-level descriptions found in standard Indonesian physiology textbooks (Tan et al., 2024; Zhao et al., 2025).

The dialetical tension between the "Balanced" and "Excessive" states depicted in the MASH mechanism serves as a critical inquiry point that challenges the linear progression typically found in animal physiology curricula. While previous studies by Lee et al. (2022) and Wang (2021) focused on problem-based learning for anatomy, they often treated pathology as an isolated event rather than a dynamic signaling failure. This research contradicts the "isolated-event" paradigm by showing that MASH is a continuum of molecular stabilization, particularly involving the KEAP1-NRF2 antioxidant system. This finding aligns with the transformative learning experiences advocated by IJBSBR, where science education must reflect the "bench-to-bedside" reality. Furthermore, the emphasis on TM4SF5 as a stabilizer for CD36 provides a specific biotechnological novelty that is absent in the broader pedagogical works of Thompson et al. (2024) or Patel and Gupta (2023). By confronting students with the "Excessive" uptake model, the RPS forces a critical evaluation of metabolic limits, reflecting a more sophisticated understanding of cellular physiology than the simplified versions offered by Nguyen (2022) or Kim (2020). The instructional design here acts as a bridge, transforming raw data from the International Journal of Biological Sciences into a systematic academic document that professionalizes the lecturer's role as an innovator (Dufour et al., 2022; Harrison et al., 2024).

The pedagogical implementation of this RPS reveals an interesting anomaly regarding "Practical Feasibility," which scored lower than "Scientific Accuracy." This suggests a systemic friction between high-impact molecular research and the time-constrained reality of a standard 16-week semester. This friction indicates that while the ADDIE model is effective for product development, the "Implementation" phase in local Indonesian contexts faces structural barriers such as laboratory resource limitations and high student-to-lecturer ratios. This finding extends the work of Wiggins and McTighe (2021) regarding "Backward Design,"

suggesting that in the biosciences, the "Content" often outpaces the "Context." When compared to the findings of Roberts (2025) and Al-Rahmi et al. (2024), who explored flipped classrooms in medical settings, this study highlights that MASH education requires more than just a change in delivery; it requires a radical re-engineering of the syllabus to accommodate multi-dimensional signaling pathways. The unique contribution of this research lies in its "Objective-Driven Discussion," where each molecular component is tied to a specific competency, preventing the "information dump" seen in the curricula analyzed by Knight et al. (2022). This structural rigor ensures that the RPS is not just a document of intent but a validated tool for professional biotechnology training (Mayer, 2021; Branch & Dousay, 2025).

Reflecting on the philosophical and pedagogical impact, the integration of MASH mechanisms into the RPS fulfills the mandate of "Research-Based Instructional Design" (RBID) by ensuring that academic development does not happen in a vacuum. The transition from lipid homeostasis to the cytokine-driven fibrosis of MASH (F3-F4) serves as a metaphor for the fragility of biological systems, a concept that deepens the students' ethical and scientific appreciation for metabolic health. This approach Debates the traditional "Topic-Based" syllabus prevalent in many institutions, replacing it with a "Mechanism-Based" framework. While the works of Chen et al. (2023) and Jensen & Moore (2024) emphasize 21st-century skills like critical thinking, this study provides the specific biological content (TM4SF5-KEAP1-CD36) that allows those skills to be practiced in a meaningful way. The impact of this study is scalable; the model of deconstructing molecular diagrams for RPS integration can be applied to other emerging biotechnological fields, such as CRISPR-Cas9 or synthetic biology. In conclusion, the research establishes a new standard for physiology education in Indonesia, aligning local academic products with international biological research standards and ensuring that students are not merely consumers of old knowledge but investigators of current scientific frontiers (Peters et al., 2024; Williams & Clark, 2025; World Health Organization, 2025).

5. CONCLUSION AND RECOMMENDATIONS

5.1. Conclusion

Based on the research findings and the comprehensive development process of the integrated Semester Learning Plan (RPS), the following conclusions are drawn:

1. The core molecular competencies for MASH integration have been successfully identified, shifting the pedagogical focus from general metabolic stasis to the specific signaling interactions of the **TM4SF5-KEAP1-CD36** axis.
2. The "pathological switch" between balanced and excessive lipid uptake provides a critical conceptual anchor that allows students to synthesize microscopic cellular interactions into macroscopic physiological outcomes.
3. The newly developed RPS successfully integrates high-impact biotechnological research into a structured 16-week academic framework, utilizing Case-Based Learning (CBL) to enhance student engagement with complex clinical data.
4. Empirical validation results confirm that the integrated RPS is **highly feasible (90.5%)**, demonstrating exceptional scientific accuracy and pedagogical alignment with the requirements of modern bioscience education.

5. This research establishes a replicable model for "Research-to-Classroom" integration, proving that the gap between laboratory breakthroughs and undergraduate instruction can be bridged through systematic instructional design.

5.2. Recommendations

To address the practical challenges identified during the feasibility assessment, it is recommended that academic institutions provide specialized training for lecturers to master the delivery of high-complexity molecular case studies and allocate additional laboratory resources to support the simulation of signaling pathways. Furthermore, future research should expand upon this study by conducting a full-scale implementation phase to measure the direct impact of the integrated RPS on student learning outcomes and long-term knowledge retention. Subsequent studies could also explore the development of digital twin models or interactive AI-based simulations of the TM4SF5 pathway to further reduce the cognitive load on students while maintaining the scientific rigor of the curriculum.

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