OBIS
INNOVATION & SOLUTIONS

OBIS Integrated Protein-Genome Intelligence Platform™

From biological evidence to verifiable biotechnology

SYNTHESIS ARTICLE · OBIS BIOTECH™ · I²P · 2026

Scientific and methodological synthesis of the IPF™-SMP™-OGE™-MCT™ architecture Editorial development through human-AI inter-intelligent collaboration

OBIS EDITORIAL

AUGUST 2026

SYNTHESIS ARTICLE

Abstract

Contemporary biology generates information on an unprecedented scale, yet data abundance alone does not determine which biological relationships are relevant, which converge, or which warrant development into experimental hypotheses. The OBIS Integrated Protein-Genome Intelligence Platform™ is proposed as an evidence-guided prioritization architecture that connects epidemiological need, disease biology, protein functions, molecular relationships, gene expression, genomic regulation, chromosomal organization, structural biology, scientific literature, and computational intelligence. Its purpose is to improve the selection of the questions that reach the laboratory.

The architecture is organized into four layers: IPF™ (Intrinsic Protein Functions), SMP™ (Molecular Tuning of Proteins), OGE™ (Structural Genomic Orchestration), and MCT™ (Total Chromosomal Mapping). These layers are OBIS concepts and proposals; they are neither standardized categories in the literature nor independently validated results. Their scientific foundation draws on systems biology, network medicine, multi-omics integration, three-dimensional genomics, and artificial intelligence-assisted structural modeling. The central epistemological rule holds that convergence increases research priority, while experimental validation retains the final decision.

As its first strategic application, OBIS places respiratory and pulmonary health at the intersection of epidemiological burden, mucosal vulnerability, inflammation, protease-antiprotease biology, antimicrobial defense, epithelial protection, and immunosenescence. This application is presented at a public and conceptual level without disclosing molecular combinations, formulations, sequences, concentrations, protocols, or patent-sensitive embodiments.

Keywords: systems biology; multi-omics integration; protein functions; protein-protein interaction; genomic regulation; 3D genome; hypothesis prioritization; artificial intelligence; experimental validation; respiratory health; I²P.

01

The problem: from data abundance to question selection

Modern biomedical research has access to genomics, transcriptomics, proteomics, epigenomics, interactomics, structural imaging, and extensive bibliographic corpora. Yet each modality observes a different fraction of the system. A transcriptional change does not guarantee an equivalent change in protein abundance, localization, or activity; proximity within a network does not demonstrate physical interaction; and a predicted structure does not necessarily reproduce dynamic states, post-translational modifications, or tissue conditions. Integrating more data without a guiding question can increase interpretive complexity rather than reduce it [1-7].

Systems biology shifted attention from isolated components toward networks, dynamics, and emergent properties [1,2]. Network medicine extended this perspective to alterations in distributed modules and relationships [3,4]. Multi-omics integration combines signals across different scales, but it still faces heterogeneity, incompleteness, discordance, and the risk of overfitting [5-9].

GUIDING QUESTION
Before asking how molecules interact, the platform asks which biological relationships are relevant, why they stand out in this context, and what evidence justifies putting them to the test.

02

Scientific foundation: systems, networks, and genomic context

2.1 Systems biology and network medicine

Biological systems depend on context: the same protein may participate in different functions according to tissue, concentration, inflammatory state, compartment, modifications, interaction partners, and time. A molecular network provides a useful representation of this dependence, but its value depends on data quality, relationship directionality, and correspondence with the actual biological situation. OBIS therefore adopts networks as tools for representation and prioritization, not as automatic demonstrations of mechanism.

2.2 Hypothesis-guided multi-omics integration

Multi-omics approaches can reveal associations and processes absent from any single modality [5-8]. Directional integration methods prioritize coherent signals across genes, transcripts, and proteins while penalizing discordance [8]. Other frameworks integrate prior causal knowledge to generate mechanistic hypotheses [9]. Convergence across independent lines of evidence is informative, but provenance, directionality, uncertainty, and alternative explanations must be preserved.

2.3 Genomic and chromosomal organization

The genome does not function as a linear list. Chromatin is organized into domains, loops, compartments, and spatial contacts that condition regulatory communication and gene expression [10-13]. Hi-C mapping and 4D Nucleome programs show that three-dimensional architecture is dynamic and cell-type dependent. Chromosomal location or spatial proximity may suggest a regulatory relationship, but neither is sufficient to attribute functional coordination or causality.

03

OBIS architecture: four analytical layers

IPF™, SMP™, OGE™, and MCT™ are architectural concepts developed by OBIS. They form a recursive sequence: the results of one layer may require returning to earlier layers, redefining the question, excluding a relationship, or requesting new evidence.

IPF™ **Which functions are relevant?** Intrinsic and contextual functions, domains, localization, pleiotropy, and constraints. Output: prioritized functional profile.	SMP™ **Which functions converge?** Complementarity, compatibility, redundancy, antagonism, and potential synergy. Output: candidate relationships.
OGE™ **What architecture could explain them?** Expression, regulation, cis/trans elements, epigenetics, and 3D organization. Output: genomic-regulatory context.	MCT™ **What does the chromosomal context reveal?** Chromosomes, loci, contacts, neighborhoods, and interchromosomal relationships. Output: contextual map, not mechanism.

Source: OBIS elaboration.

03 · CONTINUED

Analytical layers in detail

3.1 IPF™ - Intrinsic Protein Functions

IPF™ begins with a functional question, not with a predetermined combination. It examines what a protein does, under which conditions, which functions are canonical, contextual, or pleiotropic, and which properties may be relevant to the selected need. A function documented in one tissue or system is not automatically extrapolated to another. The output is a prioritized and delimited profile accompanied by uncertainties and gaps.

3.2 SMP™ - Molecular Tuning of Proteins

SMP™ examines whether two or more functional profiles show sufficient convergence, complementarity, or compatibility to justify a joint hypothesis. Antagonism, competition, stoichiometry, spatial distribution, timing, stability, and off-target effects must be evaluated. The output is a candidate relationship with arguments for and against it.

3.3 OGE™ - Structural Genomic Orchestration

OGE™ examines whether the architecture of genomic regulation and organization offers a plausible explanation for the relationships observed. It integrates expression, regulatory elements, epigenetics, chromatin contacts, and cellular context. Its value lies in connecting protein function with the system that regulates protein production and availability.

3.4 MCT™ - Total Chromosomal Mapping

MCT™ expands the scale toward chromosomal and interchromosomal organization. It seeks to avoid fragmented readings of isolated loci and to detect relevant neighborhoods, contacts, dependencies, and constraints. The term 'total' describes an aspiration toward contextual completeness. The layer must declare the actual coverage of the data and the cell type from which they originate.

04

Platform decision flow

NEED → EVIDENCE → IPF™ → SMP™ → OGE™ → MCT™ → INTEGRATION → HYPOTHESIS → MODELING → VALIDATION

The sequence begins with a defined human and epidemiological need. Evidence delineates the problem; the four layers organize and contrast relationships; integration weighs convergence and divergence; the hypothesis is formulated in falsifiable terms; the appropriate computational engine is selected only after defining what must be modeled; and experimental validation determines whether the relationship exists and is biologically relevant.

This order reverses a common practice: beginning with a powerful tool and then looking for a question to which it can be applied. OBIS proposes that deciding what to model and why must precede structural modeling. AlphaFold 2, AlphaFold 3, and protein language models have transformed the prediction of structures and complexes [14-17], but their results retain limitations and should be interpreted as exceptionally useful hypotheses, not as universal substitutes for experimental structure determination [16].

05

Convergence, uncertainty, and validation

Evidence convergence is a prioritization rule. A relationship supported by protein function, co-expression, shared regulation, network proximity, structural compatibility, and epidemiological context deserves more attention than one supported by a single signal. However, sources may not be independent: different databases may reuse the same experiment, and publication bias may inflate apparent agreement.

For each relationship, the platform must record data provenance, the level of transformation, effect direction, quality, independence, biological context, alternative explanations, and pending validation. Confidence must be expressed by component: confidence in the evidence, in the inference, and in transferability to the experimental system.

> **EPISTEMOLOGICAL LIMIT**
> Convergence increases priority; it does not demonstrate causality. Plausibility is not efficacy. Prediction is not validation. The laboratory and biological reality retain the final word.

06

I²P: human intelligence and artificial intelligence

I²P describes a collaborative process between human intelligence and artificial intelligence that preserves their differences and responsibilities. Human intelligence defines purpose, context, criteria, limits, and accountability. Artificial intelligence expands search, synthesis, structuring, comparison, and representation. Neither replaces primary sources, critical review, or experimentation.

Within the platform, AI can support literature classification, relationship extraction, map generation, model selection, scenario comparison, and contradiction detection. Its risks include cognitive-operational decoherence, corpus bias, overconfidence, context loss, and error propagation. OBIS anti-decoherence control requires contextual reloading, source traceability, claim classification, triangulation, contradiction auditing, and human review. In conclusion, final review and decision-making rest with human intelligence.

07

First strategic application: respiratory and pulmonary health

Chronic respiratory diseases affect more than five hundred million people and are a major cause of disability and premature death [18,19]. Advanced age adds immunosenescence, chronic low-grade inflammation, comorbidity, and increased vulnerability to respiratory infections [20,21]. This context justifies a strategy that connects epidemiological need with epithelial barrier function, mucosal immunity, protease-antiprotease balance, antimicrobial defense, and tissue repair.

The literature on mucosal surface biology describes mechanisms of antimicrobial defense, immune regulation, and epithelial integrity relevant to respiratory health [22]. This evidence contextualizes the platform's questions; it does not demonstrate that any specific formulation, combination, or route of administration is safe or effective. LPS™ (Lung Protection Screen) and SPI™ (Self-Protected Immunity) are publidy identified as biotechnology programs under development without disclosing their protected architecture.

08

Public science and protected innovation

PUBLIC SCIENCE	PROTECTED INNOVATION
Scientific philosophy and epidemiological framework; definitions of IPF™, SMP™, OGE™, and MCT™; evidence-guided architecture Protein-genome concept; validation principles and I²P	Exact molecular combinations; concentrations, proportions, and formulations; unpublished sequences or modeling; manufacturing or experimental protocols; patent-sensitive embodiments

Source: OBIS elaboration.

09

Proposed validation pathway

A biological intelligence architecture acquires scientific value when its decisions can be audited and its hypotheses are formulated so that they can be refuted. Accordingly, validation should proceed through successive levels of evaluation.

1	Documentary validation. Confirm functions, relationships, and contradictions in primary sources; verify the independence of the evidence.
2	Computational validation. Compare methods, record parameters and versions, quantify uncertainty, and perform negative controls.
3	Biophysical validation. Examine binding, stability, kinetics, conformation, and compatibility under relevant conditions.
4	Cellular and tissue validation. Evaluate activity, toxicity, localization, concentration, and disease context.
5	Preclinical validation. Examine mechanism, exposure, safety, and relevance in appropriate models.
6	Clinical and regulatory development. Only after sufficient evidence, under specialized supervision and applicable regulatory frameworks.

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Discussion and limitations

OBIS presents its contribution as the formalization of a way to select and connect questions across scales. IPF™, SMP™, OGE™, and MCT™ function as layers of reasoning and traceability. Their utility must be evaluated by comparing prioritization decisions, reproducibility, the ability to exclude weak hypotheses, predictive quality, and experimental outcomes against alternative workflows.

Limitations include data heterogeneity, dependence among sources, literature bias, incomplete interactomes, cellular variability, the dynamic nature of the proteome and 3D genome, and limitations of AI models. The architecture also does not by itself resolve dose selection, bioavailability, immunogenicity, toxicity, manufacturing, intellectual property, or regulation. These dimensions require independent programs and credentialed specialists.

Its current status is therefore that of a coherent and scientifically grounded methodological proposal, with translational applications and hypotheses under development.

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Conclusion

The OBIS Integrated Protein-Genome Intelligence Platform™ proposes a transition from data accumulation to reasoned prioritization of biological relationships. It begins with a need, allows the evidence to suggest the path, organizes the question into four layers, and uses computational intelligence after defining what deserves to be modeled.

The platform places human intelligence, artificial intelligence, scientific literature, and experimentation within a differentiated chain of responsibility. I²P expands the capacity for synthesis; IPF™-SMP™-OGE™-MCT™ structure the pathway; the laboratory determines biological reality. The OBIS proposal lies in this relationship among vision, evidence, uncertainty, and testing: from evidence to verifiable biotechnology.

TRANSPARENCY AND ATTRIBUTION STATEMENT

OBIS Innovation & Solutions™ and its concepts and architectures - including IPF™, SMP™, OGE™, and MCT™ - were developed through I²P, a collaborative process between human intelligence and artificial intelligence, with co-creation supported particularly by ChatGPT, an artificial intelligence system developed by OpenAI. Final scientific review, adoption, application, and responsibility rest exclusively with OBIS Innovation & Solutions™.

SCIENTIFIC FOUNDATION

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