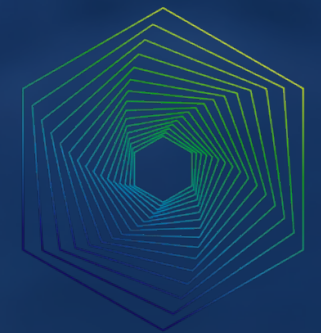


Use case

LENS<sup>ai</sup>™ Integrated Intelligence Technology  
powered by HYFTs®

# Solving the Information Integration Dilemma (IID) in life sciences



# Disclosures

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The forward-looking statements that are contained in this presentation involve a number of risks and uncertainties and are based on certain assumptions, including: the progress, timing and costs related to the execution of the Company’s business plan and strategy; estimates and projections regarding the industry in which the Company operates; the future success of research and development activities; the absence of material changes in general business and economic conditions; estimates regarding the future financing and capital requirements; and the absence of adverse changes in relevant laws and regulations. As a consequence, actual results might differ materially from results forecast or suggested in these forward-looking statements. Further information on risks and uncertainties may be found in the Company’s Management Discussion & Analysis which may be obtained from SEDAR at [www.sedar.com](http://www.sedar.com) and SEC at [www.sec.gov](http://www.sec.gov).

Furthermore, forward-looking statements contained herein are made as of the date of this MD&A and the Company disclaims any obligation to update any forward-looking statements, whether as a result of new information, future events or results or otherwise. There can be no assurance that forward-looking statements will prove to be accurate, as actual results and future events could differ materially from those anticipated in such statements. Accordingly, readers should not place undue reliance on forward-looking statements.



In our increasingly data-driven world, integrating and harnessing vast amounts of information effectively is a challenge.

The complexity of biological information is that it relates to multiple dimensions such as functions of proteins, 3D structures of molecules, genetic information involving the whole process of translating DNA code into RNA and proteins, and much more.

Collectively these dimensions need to be captured to understand biological systems and create meaningful predictions and insights.

**Information Integration Dilemma (IID)** refers to the complex task of integrating, consolidating, analyzing, and utilizing these diverse data, data sources, and formats.



# The IID challenges in omics data analysis

- **Data Silos:**  
Data that are biologically interconnected are stored and accumulated as isolated data sources, hindering collaboration, data sharing and the development of accurate and reliable analytical insights.
- **Data Inconsistency:**  
Diverse data formats, structures, and quality levels make it challenging to reconcile and merge information accurately.
- **Integration Complexity:**  
Merging data from disparate sources with varying schemas, standards, and semantics requires substantial effort.
- **Security and Privacy:**  
Protecting sensitive information while ensuring data integration introduces additional complexities.
- **Scalability:**  
As data volumes grow, integration solutions must handle the increasing load without sacrificing performance or reliability.



## Our solution

# Introducing LENS<sup>ai</sup><sup>™</sup> integrated intelligence platform powered by HYFT<sup>®</sup> technology:

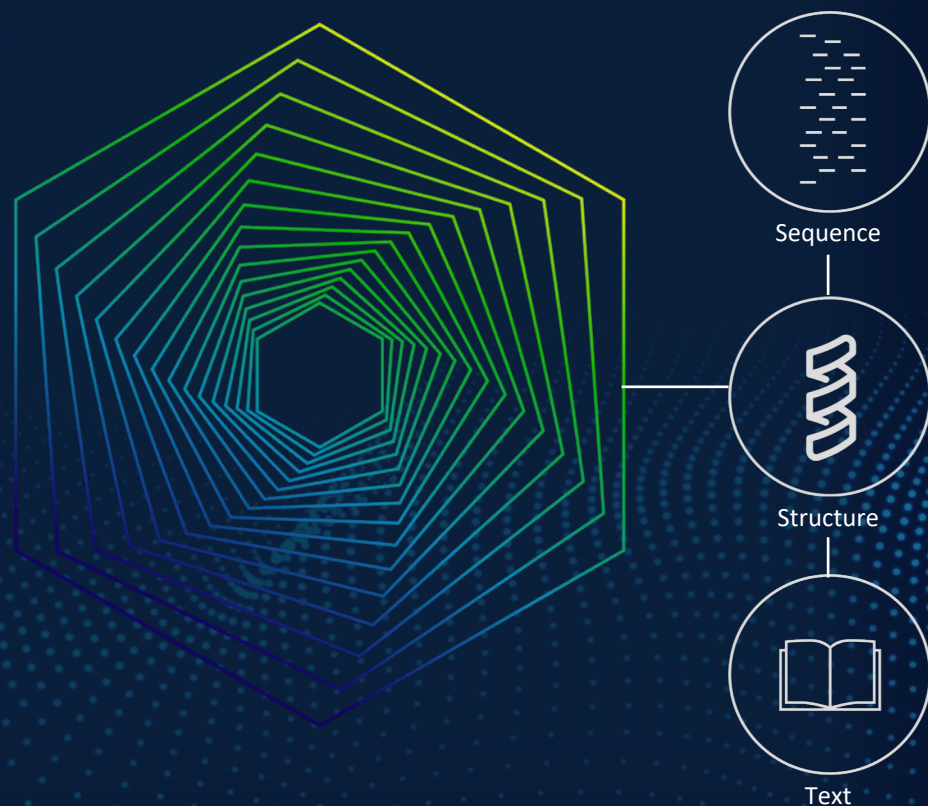
Step into the future of biotherapeutic discovery with LENS<sup>ai</sup>. Our powerful technology is at the forefront of healthcare innovation, accelerating drug discovery through scalable data analysis and insights.

- Patented technology
- Unprecedented data integration and fusion
- Seamless integration through one AI framework
- Create actionable data through infinite scalability
- Understand the specific context and connections in biology
- Make valuable predictions and uncover new information and insights



The differentiator for life science discovery

# One revolutionary framework seamlessly integrates mass amounts of multi-omics data



**LENS<sup>ai</sup> powered by HYFTs<sup>™</sup> technology**

Unparalleled technology to connect the biosphere's fundamental pillars into one framework: sequence, structure and function.

- Sequence: DNA-RNA-Protein
- Structure: Alpha Fold, ESM-2, Rosetta Fold, Cryo-EM, Crystallography
- Text: Peer-Reviewed Literature, Patents, Clinical Trials



# Solving the IID by utilizing the power of LENS<sup>ai</sup> HYFTs

## Reducing noise to make data meaningful

### What are HYFTs?

Universal Fingerprint™ patterns found across the entire biosphere.

### How do HYFTs serve us?

1. HYFTs function as encapsulated tokens “words” carrying information and knowledge, to provide context and meaning
2. HYFTs are foundational anchor points. They eliminate the background noise inherent in all data (structured and unstructured)
3. HYFTs capture cross data relationships to deduce meaningful and actionable insights

### How are HYFTs used?

#### Process Data

- 1000x more efficient

#### Analyze data

- Discovery, development and translational strategies
  - Integration of all data set types
  - Hypothesis generation

#### Act on data

- Improve wet-lab drug discovery

# The IID challenge in a researcher's daily life today

Use case:

Biotherapeutic analysis currently requires multiple search queries from several sources and involves heterogeneous AI models.

What it takes today:

- Consulting back and forth on numerous databases, data types and AI models
- Knowledge gathering is a scattered and time-consuming process
- Ultimately, a limited amount of information can be gathered and consumed

The collage consists of four overlapping screenshots from scientific databases:

- Top Left:** A screenshot of the NCBI BLAST search results page. It shows a search for 'Protein Sequence' with job title 'BLASTP' and query ID 'iQuery\_61226'. The results section shows 'Putative conserved domains have been detected' with a bar chart indicating domain scores.
- Top Right:** A screenshot of the RCSB PDB (Protein Data Bank) search results page. It shows a search for '4N9L' (Crystal structure of adalimumab FAB fragment) with a 3D ribbon diagram of the protein structure.
- Bottom Left:** A screenshot of the PubMed search results page. It shows a search for 'Zolbetuximab' with a bar chart showing the number of results by year (2013 to 2023).
- Bottom Right:** A screenshot of a bioRxiv preprint titled 'FAST: a randomised phase II study of zolbetuximab (IMAB362) plus EOX versus EOX alone for first-line treatment of advanced CLDN18.2-positive gastric and gastro-oesophageal adenocarcinoma'.





From a disconnected IID experience to fully integrated biotherapeutic intelligence

# LENS<sup>ai</sup> seamlessly integrates sequence, structure, and text

1.

**One comprehensive integrated view:**

Explore sequence, structure and textual information concurrently and swiftly

2.

**A layered view into insight foundations:**

The HYFTs encapsulate the sequential and structural context to guide AI understanding of the biological sequence function

3.

**Access deeper analysis through additional AI algorithms:**

Explore further meaningful insight and hidden relationships

# 1. Comprehensive integrated views

## • Sequence-structure-text in one graph

One framework connecting information on (sub)sequence-structure-text: full comprehensive insight, easily accessible, ready for in-depth exploration and AI analysis

Data below represented in graph

Antibodies **Antibody (18)** and hotspots **Hotspot (44)** have syntactical representations via

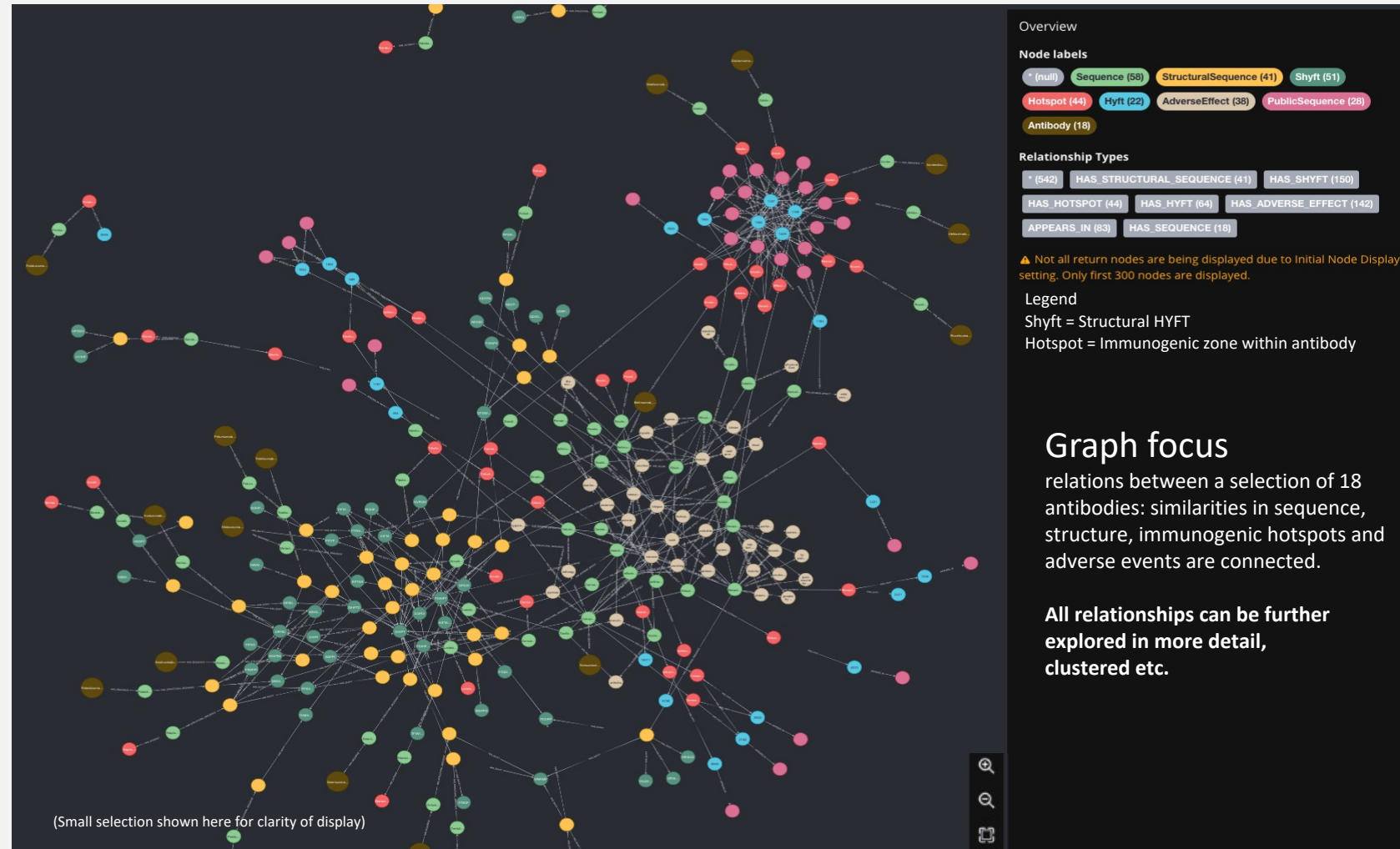
**Sequence (58)** **Hyft (22)**

and a structural representation via

**StructuralSequence (41)** **Shyft (51)**

Textual information derived through our proprietary NLP technology is represented in **AdverseEffect (38)**

Adverse effect node is a higher order symptomatology clustering used to give a first broader overview of the information gathered out of all Pubmed abstracts



Sequence



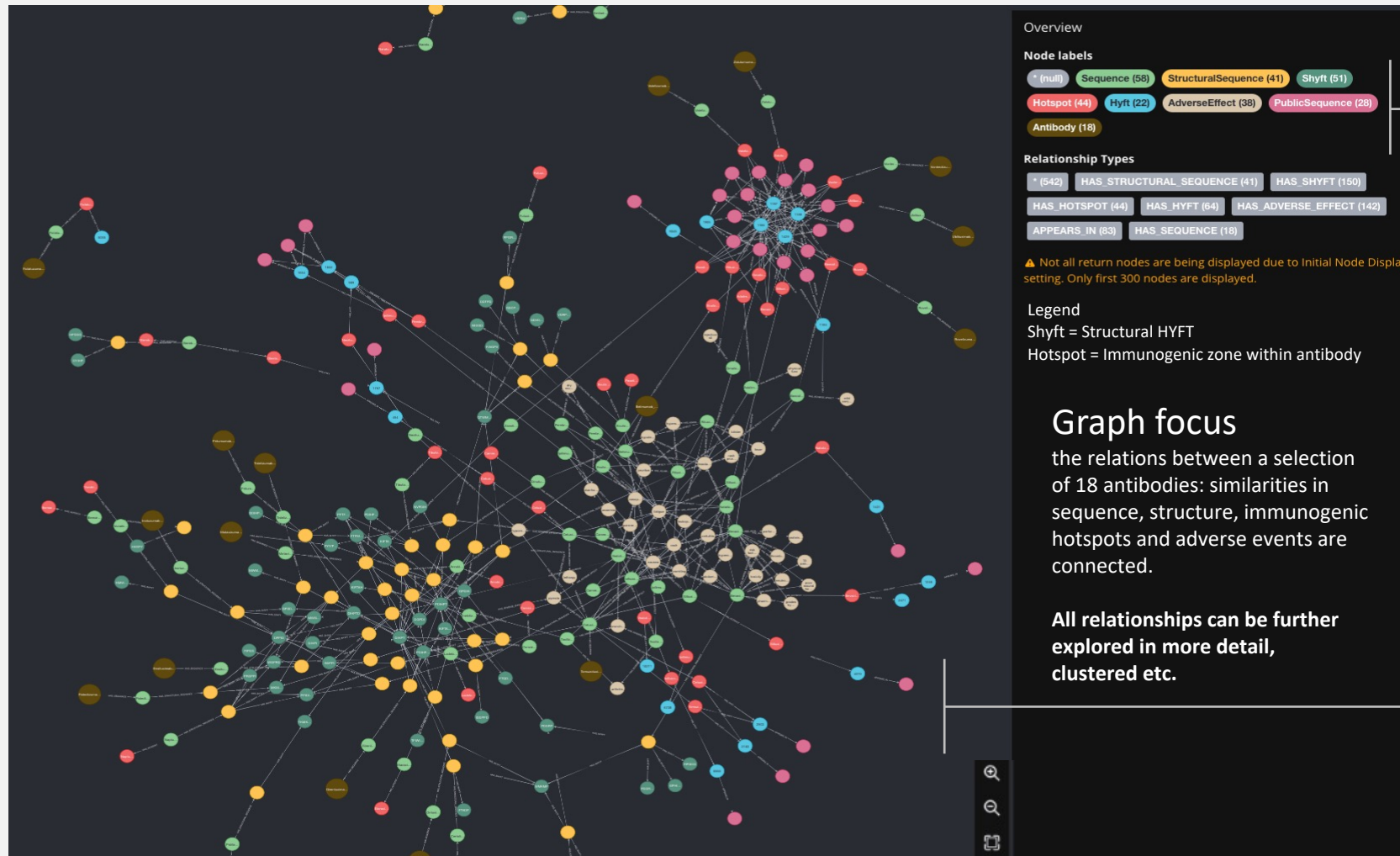
Structure



Text



# 1. Comprehensive integrated views — key features



## White box AI approach:

Concepts and relations are traceable

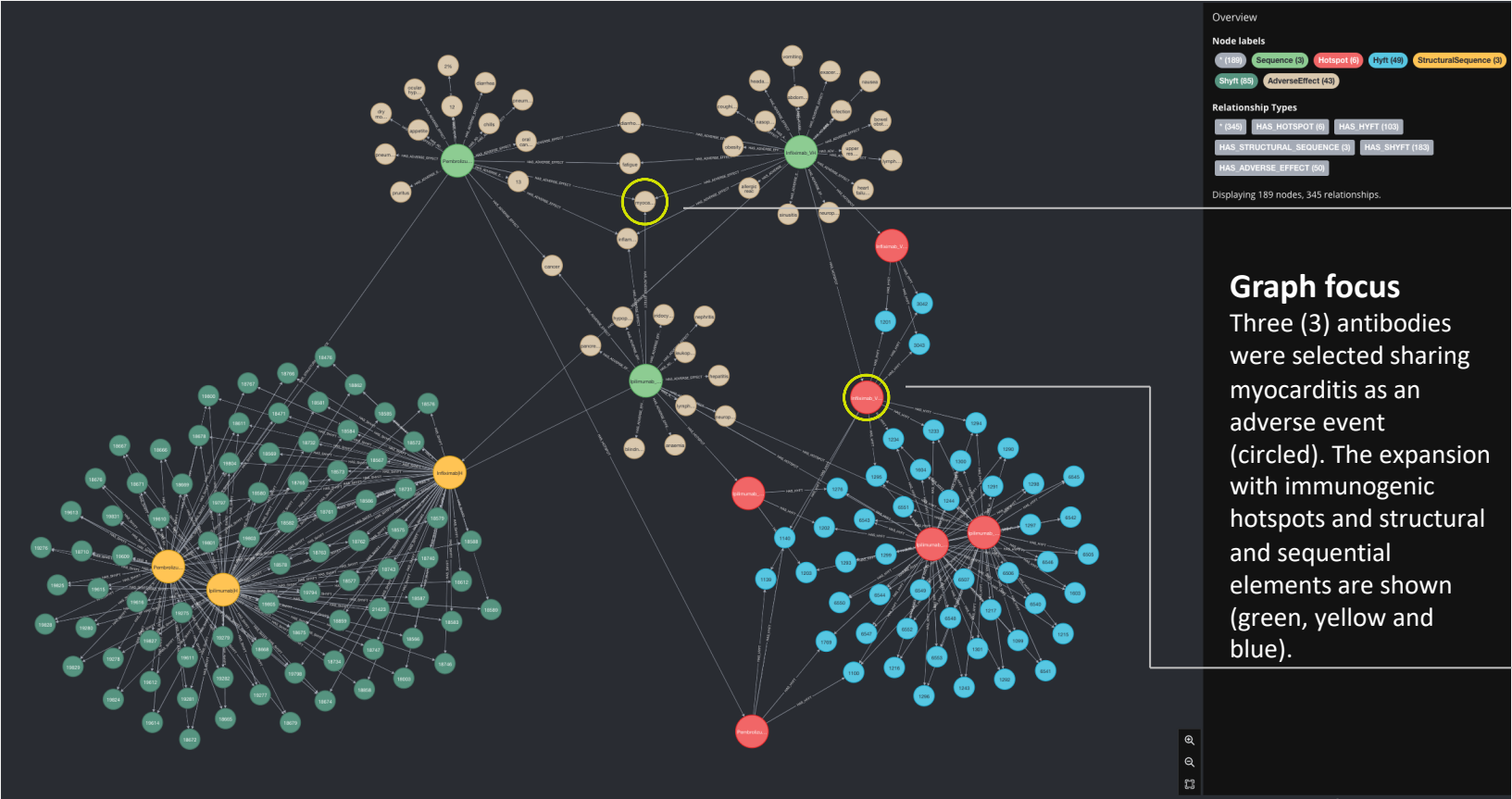
All information that is displayed can be traced back to the original source it came from.

## Relation first approach:

By providing an integrated view, the focus is on detecting biologically and functionally relevant relations to understand systems biology and biological complexity.

# 2. A layered view into insight foundations

Select the items relevant for your query and start exploring the interconnected world of sequence-structure-text



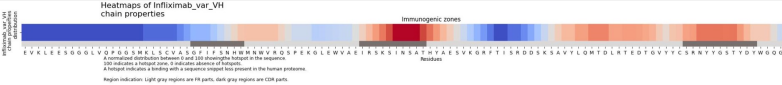
## Text-based insight

The myocarditis node is a higher-level symptom representation of all Pubmed abstracts containing findings on myocarditis. This node can be further expanded to the exact sentences mentioning myocarditis. The Pubmed ID is indicated to find the original abstract and paper.

PMID	Title	Sentence
PMID:31439303	Case Series of Ventricular Tachycardia and Myocarditis From Programmed Cell-Death Protein-1 Inhibitor Treated With Infiximab.	Case Series of Ventricular Tachycardia and Myocarditis From Programmed Cell-Death Protein-1 Inhibitor Treated With Infiximab.
PMID:21674722	Myocarditis associated with infiximab: a case report and review of the literature.	Myocarditis associated with infiximab: a case report and review of the literature.

## Subsequence-based insight

This node represents immunogenicity hotspot data of the heavy chain of Infiximab obtained via the LENS<sup>ai</sup> *in silico* immunogenicity screening: hotspots represent a higher risk for immunogenicity and are indicated in red



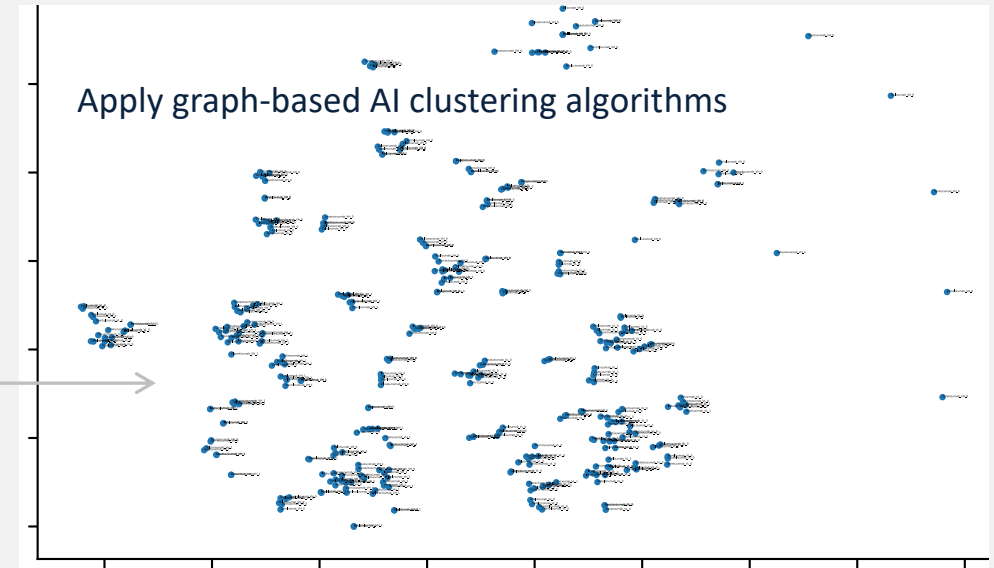
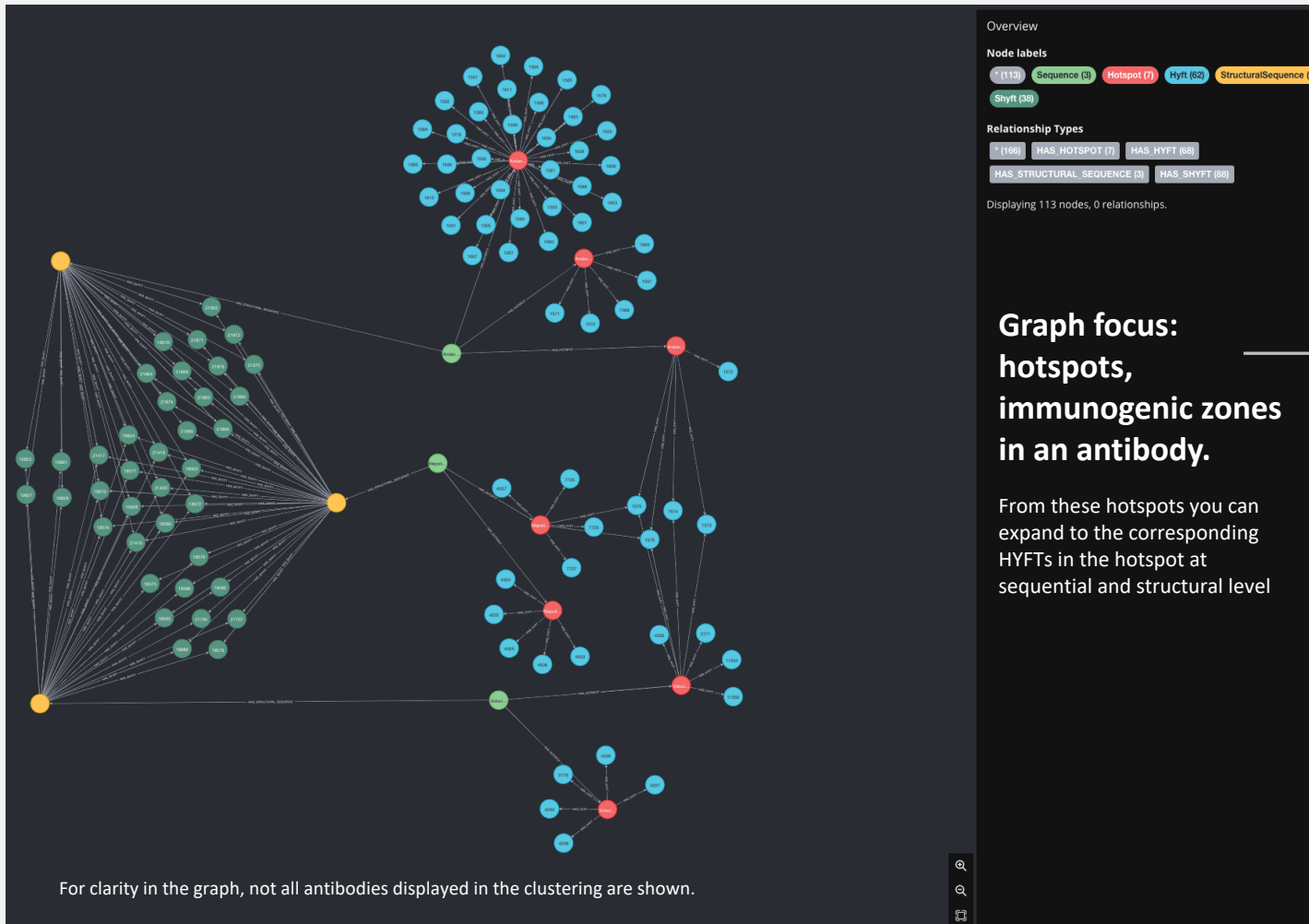
## Structural-based insight

Integrated overall into insight and embedded in SHYFT and structural sequence



# 3. Access deeper analysis through additional AI algorithms

Create predictions and in-depth various subanalysis



## Examples:

Predictive modeling  
Generative algorithms

From the graph a clustering is performed, the sequential and the structural dimensions related to the immunogenic hotspots of the antibodies are combined in one feature to detect groups that share syntactical and structural 'closeness'. This can be used to do high-throughput screening in early-stage discovery and improve antibody characteristics. Demonstrating value through accelerating the quality and quantity of leads.

LENS<sup>ai</sup> Integrated Intelligence Technology powered by HYFTs

# Empowering actionable data with integrated intelligence

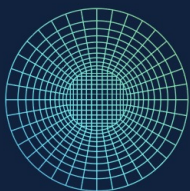
Discover the vast biotherapeutic horizon — from detailed data to expansive insight

- Data integration at subsequence level
- One seamless framework
- Infinitely scalable insights, supported by AI algorithms

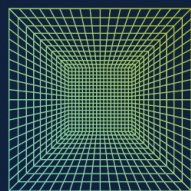
## Revolutionary data silo integration and optimization

Public and proprietary databases

Unstructured data



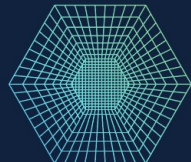
Structured data



Sequence data



Protein structure data

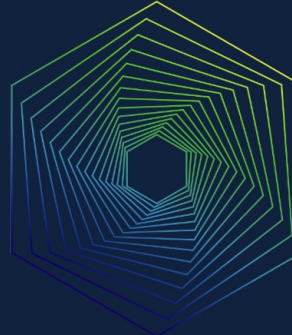


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## Unparalleled LENS<sup>ai</sup> technology

Analyze | Integrate | Learn | Generate

Sequence | Structure | Text

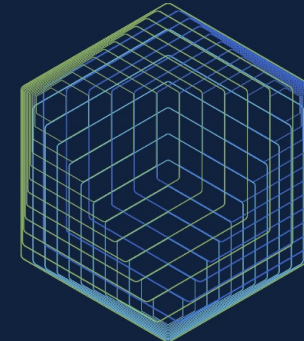


Powered by HYFT Technology

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## Powerful real-time infinite scalable data insight

Program design | Target identification | Lead discovery  
Biosimilars | Immunogenicity





We look forward to connecting on  
how LENS<sup>ai</sup> can be game-changing  
for your discovery.

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Powering the HUB of Biotherapeutic Intelligence