knowing⁰¹ Receives Public Funding to Advance Context-Enriched Drug Target Identification

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Munich-based startup knowing⁰¹ GmbH has successfully secured public funding from Bayern Innovativ's Bavarian funding program for technology-oriented startups (BayTOU) to advance research and development (R&D) of its artificial intelligence (AI)-based Software as a Service (SaaS) platform in the field of biotechnology. The funding will enable knowing⁰¹ to conduct the R&D needed to develop a **flexible context-scoring functionality to support drug target identification.** This work will address the challenge of automatically comparing highly variable molecular data, so-called Multiomics data, used for drug target identification. The novel solution helps reduce the risk of selecting drug targets that lack disease-modifying relevance.

Rethinking the drug discovery process at the intersection of DeepTech, Biotech and SaaS

knowing⁰¹ is uniquely positioned at the crossroads of DeepTech, Biotech and SaaS. By combining advanced AI with the power of biomedical data, the company is transforming how researchers unlock insights from complex datasets. This integrated approach helps biotech and pharmaceutical companies make smarter decisions, reducing the costs and risks of drug discovery in ways traditional methods cannot match.

knowing⁰¹'s proprietary <u>AI-powered Multiomics</u> <u>platform</u> allows researchers to extract insights from existing datasets in a scalable, *in silico*-first approach. Multiomics refers to the integration of various biological data types, such as genomics, proteomics and transcriptomics, to provide a comprehensive view of biological processes. By breaking down traditional technology-driven data silos of Multiomics data, the platform empowers scientists to start smart, leveraging all relevant data to drive better research outcomes with fewer errors.

Target identification is no longer limited by data quantity, but by data (re-)usability

Biotechs generate vast amounts of in-house data: disease-specific screens, genome-wide profiles, even patient-derived omics data. This results in an extensive catalog of possible drug targets. Despite this wealth of information, scientists still struggle to decide which hits are relevant for a given patient (sub)group.

The root problem is **fragmentation**. Relevant data is available in dozens of formats – RNA-seq, CRISPR screens, proteomics, metabolomics – collected from human samples, mouse models and cell lines. Public repositories–often filled by academia with even more data–hold numerous molecular clues. However, this data is of mixed quality, has inconsistent metadata and lacks common identifiers. Bringing everything together into a **complete, comparable and FAIR** view remains a largely manual and error-prone task.

Because integration is hard, teams default to the datasets they are most familiar with, leaving valuable external evidence untapped.

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Context-rich, in silico-first target-identification

Graph modelling and graph mining are just the first step – but not the last. For our MultiomicsAl technology, we have built a living knowledge graph that connects public and proprietary Multiomics data, phenotypes, model annotations and clinical evaluations. Fast graph mining pipelines uncover hidden gene-pathway-phenotype links.

The real breakthrough is leveraging this power for scientists who think in biology, not code. In an easyto-use workspace, users can load files, track their appearance in the graph, and answer the question 'Which druggable nodes are unique to my patient (sub)group?' in a few days.

Research grant boosts development of flexible data collection for all therapy areas

"Today only 5 to 20% of biomedical data is used in early target identification. We're unlocking the remaining 80 to 95%. When all evidence is available in one place, scientists can stop writing ad-hoc scripts and start choosing the right targets," adds Dr Nikola Müller, Founder and CEO of knowing⁰¹.

Our newly awarded research grant will fund the next leap towards radical flexibility. Each disease domain needs its own blend of genomic, clinical and literature evidence, and teams must upload these assets in bulk while maintaining context and structure. The grant will fund R&D to integrate this flexibility into the platform and release it as a production feature in 2026.

"The grant lets us stress-test storage engines, graph query layers, and data models that capture heterogeneous omics in a comparable way," says Flo Bittner, CTO of knowing⁰¹. "Once the research takes hold, we'll fold the best blocks straight into the software so users can add new data from day one, without requiring custom services."

Bottom line: We are turning fragmented evidence into a single, navigable map so teams can move from interesting hits to validated, high-impact targets – entirely *in silico* and entirely inside the platform. All analyses happen in an *in silico*-first manner: every hypothesis is stress-tested digitally before anyone touches a pipette.

About knowing01 GmbH

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knowing⁰¹ is a Biotech AI SaaS company specializing in unlocking the full potential of biomedical data to transform early-phase drug discovery. Founded in 2020, the company uses its proprietary Multiomics software platform to enable researchers to extract insights from complex datasets. knowing⁰¹'s mission is to redesign the drug development process by reducing the risks and costs associated with earlystage research. For more information, visit knowing01.com.

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