

Leveraging your research data using TenWise's KMAP & KMINE

TenWise offers text mining solutions by providing access to its KMAP platform.

Our **KMAP platform** captures validated scientific knowledge about human genes, micro-organisms, metabolites, pathways, phenotypes, diseases, drug compounds and research workflows, in over 200 million biological relations.

"TenWise use intelligent, innovative (bio)informatics techniques, mining data to uncover hidden relationships and networks in disease areas, their expertise providing new insight in pharma research, presented in intuitive, comprehensive reports"

BioAxis Research, customer for research in role of Brown fat in metabolic disorders and obesity

"We use KMAP for several applications both internally and externally. For example, to collect information regarding selected proteins to support our customers or for prioritization of new protein targets."

Olink Proteomics, CRO in the proteomics field

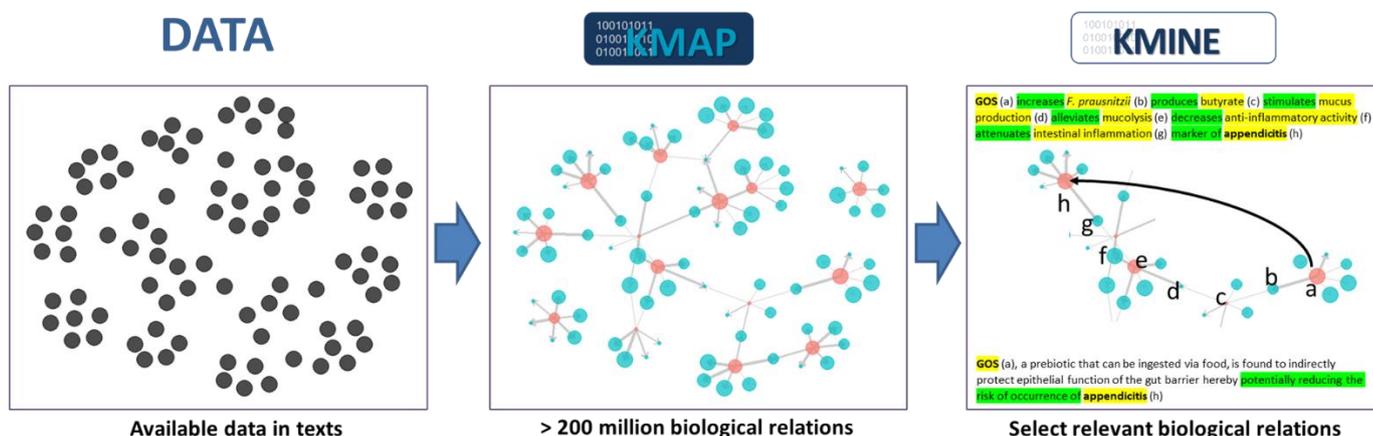
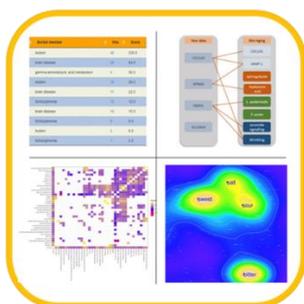


Figure: KMAP captures scientific knowledge in over 200 million biological relations and KMINE uncovers hidden relations

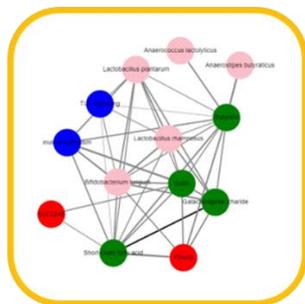
Our **KMINE products** offer access to the KMAP platform. These products are designed specifically for research teams and data engineers to assist in: **✓ discovery** **✓ drug repurposing** **✓ literature scoping** **✓ clinical validation**.



Direct access to KMAP



Web interface for interactive discovery

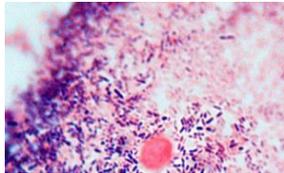


Dedicated literature reports



Scoping reviews

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Clinical Validation: predicting new relations with KMINE for Bacterial Vaginosis & vaginal microbiome

We used:



Clinical outcomes of a paper by Ceccarani *et al.* (2019) entitled: 'Diversity of vaginal microbiome and metabolome during genital infections' show how the vaginal microbiome shifts from healthy control group to Bacterial Vaginosis patients.

We compared the clinical outcomes of these microbiome shifts on a genus level to the results on species level obtained by KMINE text mining. **KMINE Literature Explorer** looked at both abstract level and sentence level in available literature. It uncovered not only relations, but also the possible modes of actions of the found species in Bacterial Vaginosis. For the main players *Gardnerella vaginalis*, *Atopobium vaginae* and *Prevotella bivia* these are shown below.

Genus from paper	Species from KMAP	# KMAP facts	Examples
<i>Gardnerella</i>	<i>vaginalis</i>	77	<ul style="list-style-type: none"> - <i>Gardnerella vaginalis</i>, the bacterial species most frequently isolated from women with bacterial vaginosis (BV), produces a cholesterol-dependent cytolysin (CDC), <i>vaginolysin</i> (VLY). - Biofilm-producing <i>Gardnerella vaginalis</i> are likely to play an important role in initiating the structured polymicrobial biofilm that is a hallmark of bacterial vaginosis. - FISH enabled us to show the presence of a polymicrobial biofilm in bacterial vaginosis, in which <i>Atopobium vaginae</i> is part of a <i>Gardnerella vaginalis</i>-dominated biofilm.
<i>Atopobium</i>	<i>vaginae</i>	53	<ul style="list-style-type: none"> - <i>Atopobium vaginae</i>, a fastidious, anaerobic, Gram-positive cocci-shaped bacterium that generates large quantities of lactic acid, is associated with bacterial vaginosis (BV). - New molecular techniques have increased our understanding of the numerous bacteria associated with bacterial vaginosis, and a biofilm containing mostly <i>Gardnerella</i> and <i>Atopobium vaginae</i>, which can persist after treatment has been described.
<i>Prevotella</i>	<i>bivia</i>	16	<ul style="list-style-type: none"> - <i>Prevotella bivia</i>, prevalent bacteria in the disturbed microbiota of bacterial vaginosis, induced strong upregulation of seven selected PIC-associated genes.

Conclusions: KMINE is able to **predict** with high accuracy the species and its possible **modes of actions** that are clinically associated with Bacterial Vaginosis whereas sequencing often only reveals the genus level information.

Want to know how to access KMAP? Call us or request a demonstration or quote:



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