

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

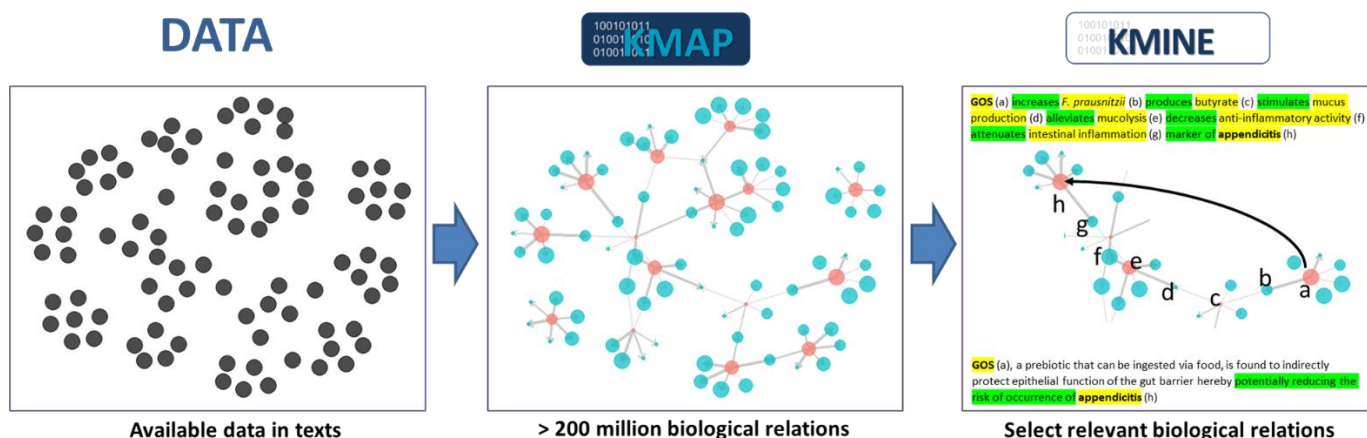
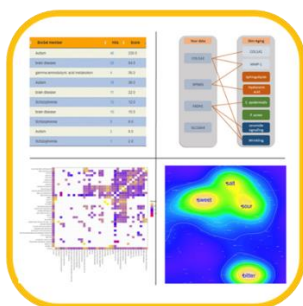


Figure: KMAP captures scientific knowledge in over 200 million biological relations and KMINE uncovers hidden relations

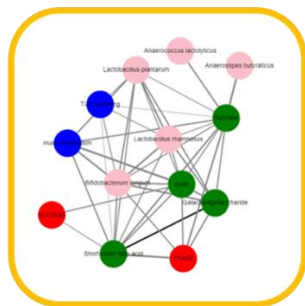
Our **KMINE products** offer access to the KMAP platform. These products are designed specifically for research teams and data engineers to assist in: **✓ discovery** **✓ drug repurposing** **✓ literature scoping** **✓ clinical validation**.



Direct access to KMAP



Web interface for interactive discovery



Dedicated literature reports



Scoping reviews

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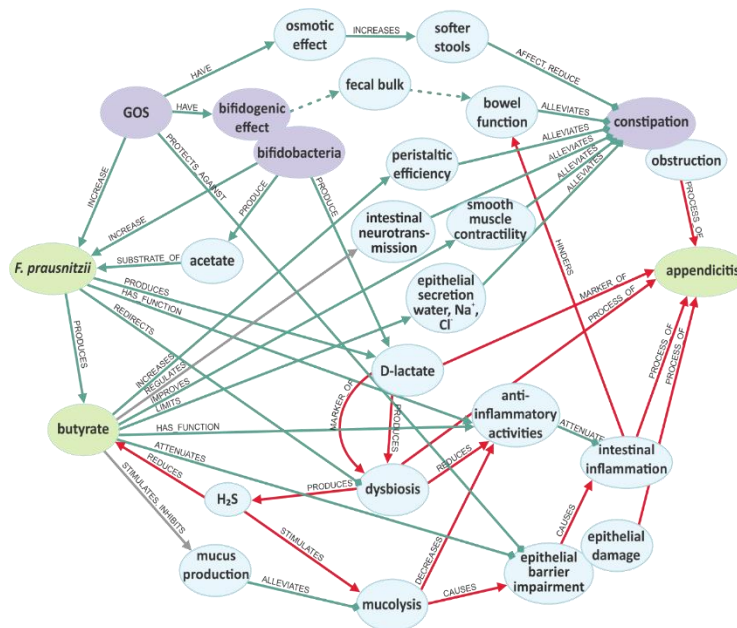


Discovery: Revealing new leads for the impact of galacto-oligosaccharides on gut health benefits

We used:



Co-occurrence text-mining - which is the core of our **KMINE REST-API** - has revealed that a large number of commensals such as *F. prausnitzii* found in the gut have a connection with *Bifidobacterium* species and with gut health effects. Word frequency analysis provided more insight into the functional nature of these relationships. Combined co-occurrence search results pointed to putative novel health benefits indirectly linked to *bifidobacteria* and the prebiotic GOS. The use of text mining has yielded the belowmentioned knowledge map that – in turn – has assisted researchers in finding novel leads regarding potential beneficial effects of GOS and *bifidobacteria*. These found effects are the increase of *F. prausnitzii* species in the gut microbiome, that consequently improve **protection of epithelial function and epithelial barrier impairment**, that are known markers for **appendicitis**.



Picture: Expert-generated knowledge maps with consolidated knowledge (from: Sijbers, Nauta, Schoenmaker and Alkema, 2020. Beneficial Microbes)

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



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