

Datasheet

Enhancing semantic search and discovery

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PAXIP1 Potentiates the Combination of WEE1 Inhibitor AZD1775 and Platinum Agents in Lung Cancer. The DNA damage response (DDR) involves a complex network of signaling events mediated by modular protein domains such as the BRCA1 C-terminal (BRCT) domain. Thus, proteins that interact with BRCT domains and are a part of the DDR constitute potential targets for sensitization to DNA-damaging chemotherapy agents. We performed a pharmacologic screen to evaluate 17 kinases, identified in a BRCT-mediated interaction network as targets to enhance platinum-based chemotherapy in lung cancer.

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As-You-Type Results

Summary

PAXIP1 Potentiates the Combination of WEE1 Inhibitor AZD1775 and Platinum Agents in Lung Cancer. The DNA damage response (DDR) involves a complex network of signaling events mediated by modular protein domains such as the BRCA1 C-terminal (BRCT) domain. Thus, proteins that interact with BRCT domains and are a part of the DDR constitute potential targets for sensitization to DNA-damaging chemotherapy agents. We performed a pharmacologic screen to evaluate 17 kinases, identified in a BRCT-mediated interaction network as targets to enhance platinum-based chemotherapy in lung cancer. Inhibition of mitotic kinase WEE1 was found to have the most effective response in combination with platinum compounds in lung cancer cell lines. In the BRCT-mediated interaction network, WEE1 was found in complex with PAXIP1, a protein containing six BRCT domains involved in transcription and in the cellular response to DNA damage. We show that PAXIP1 BRCT domains regulate WEE1-mediated phosphorylation of CDK1. Furthermore, ectopic expression of PAXIP1 promotes enhanced caspase-3-mediated apoptosis in cells treated with WEE1 inhibitor AZD1775 (formerly, MK-1775) and cisplatin compared with cells treated with AZD1775 alone. Cell lines and patient-derived xenograft models expressing both PAXIP1 and WEE1 exhibited synergistic effects of AZD1775 and cisplatin. In summary, PAXIP1 is involved in sensitizing lung cancer cells to the WEE1 inhibitor AZD1775 in combination with platinum-based treatment. We propose that WEE1 and PAXIP1 levels may be used as mechanism-based biomarkers of response when WEE1 inhibitor AZD1775 is combined with DNA-damaging agents.

- ◆ **ULTRA-FAST:** indexes at up to 1 million words per second
- ◆ **SMART:** detects ambiguity in natural language, supports multiple in/output formats
- ◆ **SCALABLE & FLEXIBLE:** powerful API that embeds into your workflow







Scan fast, tag right

We developed TERMite (TERM Identification Tagging and Extraction), a named entity recognition (NER) tool that rapidly scans and semantically annotates raw text (up to 1 million words per second) with entities from over 50 biopharma and biomedical topics. The entities are drawn from VOCabs, which is SciBite's flagship collection of manually curated vocabularies with >20 million synonyms, specifically tuned for NER text analytics. Since VOCabs are based on public ontologies, such as gene ontology, tagging entities with TERMite will map your data to those ontologies, align data to public standards, and improve data interoperability.

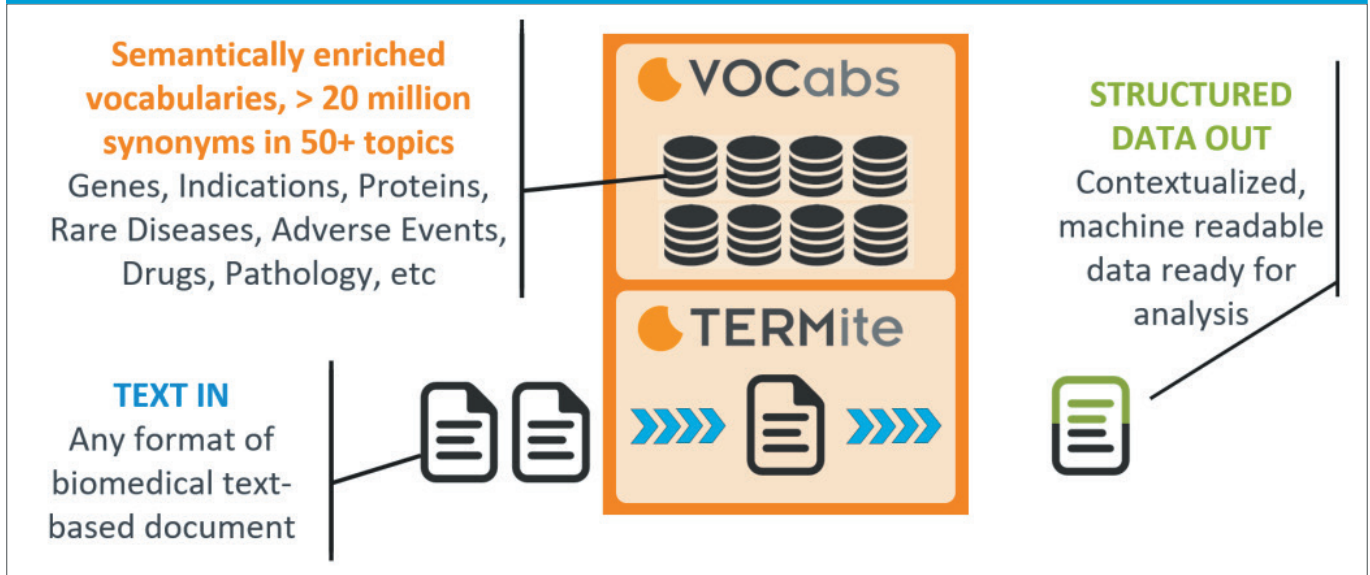
Text, text, and more text

In biomedical science and healthcare, text remains the most common medium for recording and sharing information. In the digital age, the ease of contributing text has led to an explosion of content that tends to be less structured than traditional formats (e.g. Medline articles, patent documents). Scientists nowadays need better tools to not only narrow down the search space, but also recognise and extract nuggets of key information from text for spotting hidden trends, hypothesis generation, and business intelligence. Frustratingly, many existing tools have a steep learning curve or aren't tuned for analyzing biological text. How can SciBite help?

Text can come from many disparate sources

 electronic lab books	 social media posts	 doctors' notes	 RSS feeds
 spreadsheets of free-text survey responses	 clinical trial records	 comments in patients' forums	 internal databases

A typical TERMite workflow



Understands nuances

Tagging the correct terms is only the first step. TERMite has built in relevance detection, distinguishing between terms that are “throwaway mentions” and those that really matter to your subject of interest.

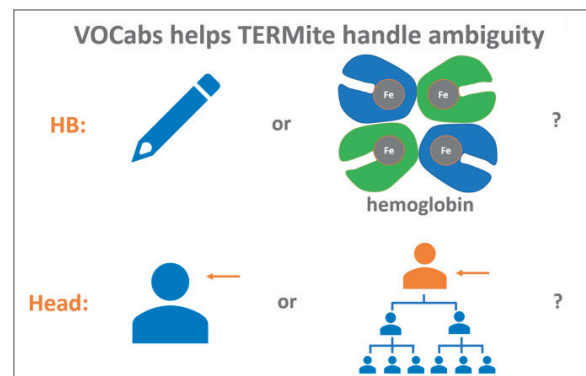
Powerful API for any use case

TERMite is our core platform from which we deliver additional capabilities for specific use cases. Developed in Java, the hassle-free set-up typically takes only a few minutes. As a Software as a Service (SaaS) solution, deployment of TERMite has never been simpler. Users benefit from the latest features through seamless product upgrades, as well as with expanded infrastructure support. You will have the freedom to run one-off analyses in the user interface, or embed TERMite into your analysis workflow to harness its full potential.

Popular use cases include:

- Mine the entire Medline database for gene-phenotype-disease correlations
- Analyse grants to discover new trends
- Scan internal documents to find hidden target-drug-indication relationships for drug repurposing

The possibilities are endless. What’s yours?



About SciBite

SciBite’s data-first, semantic analytics software is for those who want to innovate and get more from their data. At SciBite we believe data fuels discovery and we are leading the way with our pioneering infrastructure that combines the latest in machine learning with an ontology-led approach to unlock the value of scientific content. Supporting the world’s leading scientific organisations with use-cases from discovery through to development, SciBite’s suite of fast, flexible, deployable API technologies empower our customers, making it a critical component in scientific, data-led strategies. Contact us to find out how we can help you get more from your data.

To learn how SciBite can unlock the value of your data, speak to one of our experts today or email us at contact@scibite.com

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