

Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

SciBite

RRID:SCR_003952

Type: Tool

Proper Citation

SciBite (RRID:SCR_003952)

Resource Information

URL: <http://scibite.com/>

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Description: An informatics service focusing on competitor intelligence and text-mining within the life sciences. It mines a diverse array of scientific content to look for mentions of targets, indications, companies, drugs and technologies of interest to those involved in human health and drug discovery. A free newsletter service is provided to allow everyone to explore the therapeutic landscape and stay informed and a range of professional products and services are offered for those who need more in-depth analysis of the therapeutic landscape. Its text-mining engine can be configured to a variety of different use cases and performs with very high throughput. SciBite has a number of big-pharma and scientific publishers as current customers. SciBITES is free on the website but for extended functionality, including a data mining API and access to internal or commercial documents, you may wish to consider an installation of the SciBITES server software within your organization.

Abbreviations: SciBite

Synonyms: SciBite Limited

Resource Type: commercial organization

Keywords: text-mining, biomedical, drug discovery, pharmaceutical, data mining, biotechnology, drug, newsletter, semantics, ontology, termite, text-mining software

Availability: Free, Subscription, API access, License

Resource Name: SciBite

Resource ID: SCR_003952

Alternate IDs: nlx_158349

Record Creation Time: 20220129T080221+0000

Record Last Update: 20260905T132511+0000

Ratings and Alerts

No rating or validation information has been found for SciBite.

No alerts have been found for SciBite.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Perfetto L, et al. (2021) A Resource for the Network Representation of Cell Perturbations Caused by SARS-CoV-2 Infection. Genes, 12(3).

Ferrero E, et al. (2017) In silico prediction of novel therapeutic targets using gene-disease association data. Journal of translational medicine, 15(1), 182.