

Resource Summary Report

Generated by SPARC SAWG on Aug 9, 2026

SWEET-DB

RRID:SCR_005324

Type: Tool

Proper Citation

SWEET-DB (RRID:SCR_005324)

Resource Information

URL: <http://www.glycosciences.de/modeling/sweet2/>

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Description: Program that rapidly converts the primary sequence of a complex carbohydrate, as defined by standard nomenclature, directly into a reliable 3D molecular model by linking together preconstructed 3D molecular templates of monosaccharides in the manner specified by the sequence and then optimizing the 3D structure using the MM3 force field. The user interaction is supported by an input spreadsheet consisting of a grid of sugar symbol and connection type cells. Several ways to visualize and to output the generated structures and related information are implemented.

Abbreviations: SWEET, SWEET2

Synonyms: SWEET II, Sweet-2

Resource Type: production service resource, web service, software resource, data access protocol, data analysis service, analysis service resource, service resource

Defining Citation: [PMID:10498779](#)

Keywords: carbohydrate, saccharide, 3d model, sequence, oligosaccharide, polysaccharide, 3d spatial image, carbohydrate sequence, modeling, carbohydrate modeling

Resource Name: SWEET-DB

Resource ID: SCR_005324

Alternate IDs: nif-0000-03520

Old URLs: <http://www.dkfz-heidelberg.de/spec2/sweetdb/>,
<http://www.glycosciences.de/sweetdb/>

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260808T185837+0000

Ratings and Alerts

No rating or validation information has been found for SWEET-DB.

No alerts have been found for SWEET-DB.

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 [SPARC SAWG](#) .

L??tteke T, et al. (2012) The use of glycoinformatics in glycochemistry. Beilstein journal of organic chemistry, 8, 915.

Mazola Y, et al. (2011) Integrating bioinformatics tools to handle glycosylation. PLoS computational biology, 7(12), e1002285.