

Resource Summary Report

Generated by SPARC SAWG on Sep 18, 2026

Heparome

RRID:SCR_008615

Type: Tool

Proper Citation

Heparome (RRID:SCR_008615)

Resource Information

URL: <http://eep.tamu.edu/heparome/>

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Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on July 17, 2013. A database which contains the information of heparin-binding proteins of E. coli K-12 MG1655 cells. Heparin affinity columns were applied to enrich and fractionate proteins. Identification of proteins was done via the collaboration with David Russell's lab. Because heparin is negatively charged sulfated glucosaminoglycan, polyamion binding proteins, which contain nucleic acid-binding proteins, are expected to bind to heparin columns. Study of the expression pattern of heparin-binding proteins will help to study the nucleic acid-binding proteins, most of which are related to regulation. Moreover, heparin affinity columns will also erich low abundance proteins. Heparome database is constructed using MySQL. Website interface is built using HTML and PHP. Queries between MySQL database and website interface are executed using PHP. Besides including information of identified proteins, such as swiss accession number, gene name, molecular weight, isoelectric point, condon adaptation index (CAI), functional classification, et. al. , it also includes information of experiments, such as sample preparation, heparin-HPLC chromatography, SDS-PAGE gel separation and MALDI-MS.

Synonyms: Heparome

Resource Type: data or information resource, database

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Heparome

Resource ID: SCR_008615

Alternate IDs: nif-0000-31966

Record Creation Time: 20220129T080248+0000

Record Last Update: 20260912T200200+0000

Ratings and Alerts

No rating or validation information has been found for Heparome.

No alerts have been found for Heparome.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.