

Resource Summary Report

Generated by T1D on Aug 1, 2026

Loom

RRID:SCR_028253

Type: Tool

Proper Citation

Loom (RRID:SCR_028253)

Resource Information

URL: <https://linnarssonlab.org/loompy/format/index.html>

Proper Citation: Loom (RRID:SCR_028253)

Description: Loom is an efficient HDF5-based file format for storing large, high-dimensional single-cell genomics datasets, including data, metadata, and clustering results. Loom file format is designed to efficiently hold large omics datasets. Typically, such data takes the form of a large matrix of numbers, along with metadata for the rows and columns. Loom files (.loom) are created in the HDF5 file format, which supports an internal collection of numerical multidimensional datasets. HDF5 is supported by many computer languages, including Python, R, MATLAB, Mathematica, C, C++, Java, and Ruby.

Synonyms: , .loom, Loom File Format

Resource Type: narrative resource, data or information resource, standard specification

Keywords: HDF5-based file format, hold large omics datasets, large matrix of numbers, metadata for rows and columns,

Availability: Free, Freely available,

Resource Name: Loom

Resource ID: SCR_028253

Record Creation Time: 20260404T065920+0000

Record Last Update: 20260801T043000+0000

Ratings and Alerts

No rating or validation information has been found for Loom.

No alerts have been found for Loom.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.