

# Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 17, 2026

## Sno/scaRNAbase

RRID:SCR\_007938

Type: Tool

### Proper Citation

Sno/scaRNAbase (RRID:SCR\_007938)

### Resource Information

**URL:** <https://omictools.com/sno-scarabase-tool>

**Proper Citation:** Sno/scaRNAbase (RRID:SCR\_007938)

**Description:** A curated database for small nucleolar RNAs and small cajal body-specific RNAs. It presents sno/scaRNA-associated genetic and functional data and provides access to several other database sources via web-accessible search interfaces. Consisting of 1979 sno/scaRNA records obtained from 85 organisms, sno/scaRNAbase is a combination of systematic literature curation and annotation effort. small nucleolar RNA, small cajal body-specific RNA

**Synonyms:** Sno/scaRNAbase

**Resource Type:** data or information resource, database

**Keywords:** scarba, small cajal body-specific rna, small nucleolar rna, snorna

**Resource Name:** Sno/scaRNAbase

**Resource ID:** SCR\_007938

**Alternate IDs:** nif-0000-03475

**Old URLs:** <http://bioinfo.fudan.edu.cn/snoRNAbase.nsf>

**Record Creation Time:** 20220129T080244+0000

**Record Last Update:** 20260912T200156+0000

### Ratings and Alerts

No rating or validation information has been found for Sno/scaRNAbase.

No alerts have been found for Sno/scaRNAbase.

## Data and Source Information

**Source:** [SciCrunch Registry](#)

---

## Usage and Citation Metrics

We found 4 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [SPARC SAWG](#) .

Deschamps-Francoeur G, et al. (2014) Identification of discrete classes of small nucleolar RNA featuring different ends and RNA binding protein dependency. Nucleic acids research, 42(15), 10073.

Chorev M, et al. (2013) Computational identification of functional introns: high positional conservation of introns that harbor RNA genes. Nucleic acids research, 41(11), 5604.

Motsch N, et al. (2012) MicroRNA profiling of Epstein-Barr virus-associated NK/T-cell lymphomas by deep sequencing. PloS one, 7(8), e42193.

Scott MS, et al. (2012) Human box C/D snoRNA processing conservation across multiple cell types. Nucleic acids research, 40(8), 3676.