## **Resource Summary Report**

Generated by FDI Lab - SciCrunch.org on May 22, 2025

# NextGen Sequence Databases

RRID:SCR\_002152 Type: Tool

#### **Proper Citation**

NextGen Sequence Databases (RRID:SCR\_002152)

#### **Resource Information**

URL: http://mpss.danforthcenter.org/

Proper Citation: NextGen Sequence Databases (RRID:SCR\_002152)

**Description:** Informational portal that aggregates information about databases for next gen sequencing.

Synonyms: NextGen

Resource Type: portal, data or information resource, topical portal

Defining Citation: PMID:16381968

Keywords: next gen sequencing, data aggregation website

Funding:

Availability: Freely available, Acknowledgement requested

Resource Name: NextGen Sequence Databases

Resource ID: SCR\_002152

Alternate IDs: nif-0000-20944

Old URLs: http://mpss.dbi.udel.edu/

Record Creation Time: 20220129T080211+0000

Record Last Update: 20250522T060006+0000

### **Ratings and Alerts**

No rating or validation information has been found for NextGen Sequence Databases.

No alerts have been found for NextGen Sequence Databases.

#### Data and Source Information

Source: SciCrunch Registry

#### **Usage and Citation Metrics**

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Wong GY, et al. (2022) TRUEE; a bioinformatic pipeline to define the functional microRNA targetome of Arabidopsis. The Plant journal : for cell and molecular biology, 110(5), 1476.

Nething DB, et al. (2021) Posttranscriptional regulation of cellulose synthase genes by small RNAs derived from cellulose synthase antisense transcripts. Plant direct, 5(9), e347.

Li M, et al. (2021) An Atlas of Genomic Resources for Studying Rosaceae Fruits and Ornamentals. Frontiers in plant science, 12, 644881.

Teng C, et al. (2020) Dicer-like 5 deficiency confers temperature-sensitive male sterility in maize. Nature communications, 11(1), 2912.

Yu D, et al. (2018) Tracking microRNA Processing Signals by Degradome Sequencing Data Analysis. Frontiers in genetics, 9, 546.