

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 7, 2026

## CUSHAW

RRID:SCR\_005479

Type: Tool

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### Proper Citation

CUSHAW (RRID:SCR\_005479)

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### Resource Information

**URL:** <http://cushaw2.sourceforge.net/homepage.htm#latest>

**Proper Citation:** CUSHAW (RRID:SCR\_005479)

**Description:** Software package for next-generation sequencing read alignment that is fast and parallel gapped read alignment to large genomes, such as the human genome.

**Abbreviations:** CUSHAW

**Synonyms:** CUSHAW2, CUSHAW3

**Resource Type:** software resource

**Defining Citation:** [PMID:22576173](#), [PMID:24466273](#)

**Keywords:** next-generation sequencing, read alignment, genome, alignment

**Resource Name:** CUSHAW

**Resource ID:** SCR\_005479

**Alternate IDs:** OMICS\_00658

**Record Creation Time:** 20220129T080230+0000

**Record Last Update:** 20260905T132536+0000

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### Ratings and Alerts

No rating or validation information has been found for CUSHAW.

No alerts have been found for CUSHAW.

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### Data and Source Information

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

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [PRECISE-TBI](#) .

Schelkunov MI, et al. (2021) Genomic comparison of non-photosynthetic plants from the family Balanophoraceae with their photosynthetic relatives. PeerJ, 9, e12106.

Nath N, et al. (2020) Genome-Wide DNA Alterations in X-Irradiated Human Gingiva Fibroblasts. International journal of molecular sciences, 21(16).