

# Resource Summary Report

Generated by PRECISE-TBI on Sep 7, 2026

## Clonotator

RRID:SCR\_016730

Type: Tool

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### Proper Citation

Clonotator (RRID:SCR\_016730)

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### Resource Information

**URL:** <http://ec2-52-91-98-53.compute-1.amazonaws.com/run/>

**Proper Citation:** Clonotator (RRID:SCR\_016730)

**Description:** Web based platform that integrates several bioinformatics tools for screening and annotation of cDNA construct sequences. Translates the nucleotide sequence of the construct into an amino acid sequence, aligns the predicted sequence to a reference database of protein sequences and identifies the best protein and isoform match, annotates any variants present in the construct, and incorporates disease-associated mutations and transcriptomic data.

**Resource Type:** alignment software, data access protocol, data analysis software, data processing software, image analysis software, sequence analysis software, software application, software resource, web service

**Keywords:** screening, annotation, cDNA, sequence, amino acid, align, reference, database, protein, disease, mutation, transcriptomic, data

**Availability:** Free, Freely available, Registration required

**Resource Name:** Clonotator

**Resource ID:** SCR\_016730

**Alternate URLs:** <https://willseylab.com/clonotator/>

**Record Creation Time:** 20220129T080332+0000

**Record Last Update:** 20260905T132813+0000

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### Ratings and Alerts

No rating or validation information has been found for Clonotator.

No alerts have been found for Clonotator.

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## Data and Source Information

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

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.