

Resource Summary Report

Generated by SPARC SAWG on Jul 31, 2026

Clonotator

RRID:SCR_016730

Type: Tool

Proper Citation

Clonotator (RRID:SCR_016730)

Resource Information

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

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

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: 20260731T043003+0000

Ratings and Alerts

No rating or validation information has been found for Clonotator.

No alerts have been found for Clonotator.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.