

Resource Summary Report

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AutoCSA (Automatic Comparative Sequence Analysis)

RRID:SCR_010616

Type: Tool

Proper Citation

AutoCSA (Automatic Comparative Sequence Analysis) (RRID:SCR_010616)

Resource Information

URL: <http://www.sanger.ac.uk/genetics/CGP/Software/AutoCSA/>

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Description: AutoCSA (Automatic Comparative Sequence Analysis) is a mutation detection program designed to detect small mutations (1-50 bases) in sequence traces. The software is capable of detecting both homozygous and heterozygous base substitutions, as well as small insertions and deletions, to a high sensitivity. It has specifically been written with high throughput environments in mind, so it is easy to automate the analysis of large amounts of data with little manual intervention. AutoCSA is written in java and will run under java 1.4 or later versions which must be downloaded and installed on your computer. It should be emphasised that AutoCSA uses the raw sequence channels from the trace files generated by the ABI sequencers (.ab1 file extension). Traces which have been processed and the raw channels removed are not suitable for use with the software. The software has been tested successfully under Linux, MS windows XP, and Mac OS X 10.

Synonyms: AutoCSA, Automatic Comparative Sequence Analysis

Resource Type: software resource, data access protocol, application programming interface

Resource Name: AutoCSA (Automatic Comparative Sequence Analysis)

Resource ID: SCR_010616

Alternate IDs: nlx_53830

Record Creation Time: 20220129T080259+0000

Record Last Update: 20260801T191019+0000

Ratings and Alerts

No rating or validation information has been found for AutoCSA (Automatic Comparative Sequence Analysis).

No alerts have been found for AutoCSA (Automatic Comparative Sequence Analysis).

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.