

Ridom TraceEdit

Version 1.1



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1. Introduction

Ridom TraceEdit is a cross-platform graphical DNA trace viewer and editor. TraceEdit displays the chromatogram files from Applied Biosystems automated sequencers and files in the Staden SCF format. Incorrect base calls can be edited and saved. TraceEdit is designed to operate on Windows, MacOS X and UNIX platforms.

DNA sequencing has been the standard against which other types of DNA testing is compared. Major advances in DNA sequencing include the development of automated sequencers, discovery of fluorescent terminator chemistry, and cycle sequencing. These developments have made sequencing easier to perform and therefore more widely used. Currently, sequencing is used to identify microbial drug resistance mutations, cancer predisposition, somatic mutations, and genetic diseases. With the sequencing of the human genome and the “new era of molecular medicine”, one can only expect the use of DNA sequencing to increase. Therefore, an increasing number of people need to check the evidence for individual DNA sequences by inspecting the chromatograms (more commonly known as trace files) from which the base calls were deduced. Trace files are stored in proprietary formats, such as those of ABI, or public formats such as SCF.

Ridom TraceEdit can read ABI and SCF trace files and displays their contents. The program can be used to locate and delete the extent of low quality data at both ends of the sequence (trimming by Ns or low base quality values if available). It also enables the user to edit the base calls and to save them in SCF file format. A typical display from TraceEdit is shown in Figure 1. It includes the name and additional information of the sequence being inspected, the menu bar, the file list pane with tool bar, and the trace editor pane with tool bar. In the file list pane a trace file can be chosen to be displayed in the editor pane. The trace editor pane shows the trace data, the quality values (if available), the original sequence, the edited sequence, and the base positions. The extent of poor quality data at the left of the reading is denoted by gray shading. A separate text window (not shown) is used to display the textual data contained in the file.

The trace data can be scrolled using the scrollbar beneath the trace editor pane. The trace can be magnified in horizontal and vertical directions. The original sequence and the quality values (different formats are available) can either be switched on or off. It is possible to open several traces at once and shortcuts allow for quick navigation between traces. TraceEdit produces PDF files of the traces or sends them directly to the printer. Incorrect base calls selected using the mouse can be changed or deleted accordingly. Holding down the Backspace or Delete keys will rapidly delete successive bases, backwards for Backspace and forwards for Delete. To insert a base, the user must click between the bases with the right mouse-button. Once a base is selected, it is possible to scroll through the sequence using the left and right keyboard button (for further shortcuts it is referred to the Quick Reference section). The user can define, store, and search for nucleotide patterns that may include regular expressions. The edited sequence can be copied to the clipboard or exported to a file. Alternatively, a NCBI BLAST search may be initiated with the edited sequence directly from TraceEdit. Sequences from the NCBI nucleotide database can be directly imported into the software by stating the database accession numbers. The software behavior may be user defined in several aspects by the preferences menu option.

TraceEdit includes a feedback dialog to provide the user with a convenient way of sending messages such as feature requests and bug reports directly to the developers. Finally, a download option for online-updates is integrated into the software.

2. Features

- Operate on Windows, Mac OS X, and Linux operating systems
- View ABI and SCF chromatogram files
- Open at once several chromatogram files or whole directories
- Sort file list by different predefined options
- Navigate file list by keyboard shortcuts
- Scale the trace peak size vertically and horizontally
- Scroll a trace to a desired position
- Select bases from the trace
- Search for sequences using regular expressions
- Display or hide original base calls
- Display or hide quality values, if included in the chromatogram file
- Display as text other chromatogram information contained in the file
- Display as text the DNA sequence of your chromatogram
- Display the reverse complement of a trace
- Mark or unmark bases of interest (low quality, ambiguities)
- Import sequences from NCBI nucleotide database by accession numbers
- Print a trace
- Produce a PDF of a trace
- Copy, paste, and edit sequences
- Use contextual menus to copy, paste, and edit
- Trim sequence ends by Ns or low base quality values
- Save traces in SCF format
- Export base calls as a FASTA sequence
- Initiate a BLAST search from edited sequence
- Communicate directly from within the software with the developers for bug reports and feature requests
- Update the software automatically online

3. Installing Ridom TraceEdit

System Requirements

- An installed Java Runtime Environment 1.5 or higher is required to run Ridom TraceEdit. Java is freely available from www.java.com
- An installed PDF Viewer (e.g., Adobe Reader, www.adobe.com) is needed for viewing the manual and to use the “Print to PDF” feature
- The MS Windows version was tested on NT4.0, 2000 and XP with Java 1.5
- The MacOS X version was tested on 10.4 with Java 1.5
- The Linux version was tested with Java 1.5

Supported File Formats

Readable Formats

- SCF (v2.0, 3.0, 3.1) from ALF, Li-Cor, Visible Genetics OpenGene, Beckman CEQ 2000XL and CEQ 8000, and other sequencers; SCF with qualities from Phred and Ridom Tracer; ABIF from Applied Biosystems sequencers
- Import of consensus and chromatograms from RSX files (Ridom TraceEditPro file format)
- GenBank files
- FASTA; plain text files

Writable Formats

- SCF 3.0: An open binary file format for chromatogram sequences. In addition to the standard SCF, Ridom TraceEdit writes the original base-calls in a SCF-conform user block with the magic number 0x6f726263.
- FASTA: A text file format for base sequences. A sequence block consists of a comment line headed by “>” and several data lines with sequence bases.


Installing Instructions

- Download from www.ridom.de the newest version of Ridom TraceEdit
- Double click the downloaded file and follow the on-screen instructions (please remember, you have to install Java first before you are able to install Ridom TraceEdit)
- Ridom TraceEdit can now be started by clicking the software's icon (in the installed directory, on the desktop or in the *Start* Menu)

Updating the Software

A download option for online-updates is integrated into the software (*Help* menu).

Ridom TraceEdit Help


Use the  button in the *Help* menu to view this PDF-document (the document includes a Quick Reference with menu, tool bar functions and keyboard shortcuts).

4. Getting Started

Keyboard Shortcuts

Frequent occurring actions can be conveniently invoked by keyboard shortcuts (**Mac OS X**: use \wedge instead of Ctrl, to pop-up right-mouse-button menus under Mac OS X with a single button mouse, press Ctrl and the single mouse button). All menu commands can also be invoked (e.g., if no mouse is available) by using the Alt key in combination with a character as indicated by underscore in the menu (e.g., for the command “Open...” press Alt+F, P).

Main Window

Use drag and drop, the  button or the *Open...* function in the *File* menu to open a sequence file.

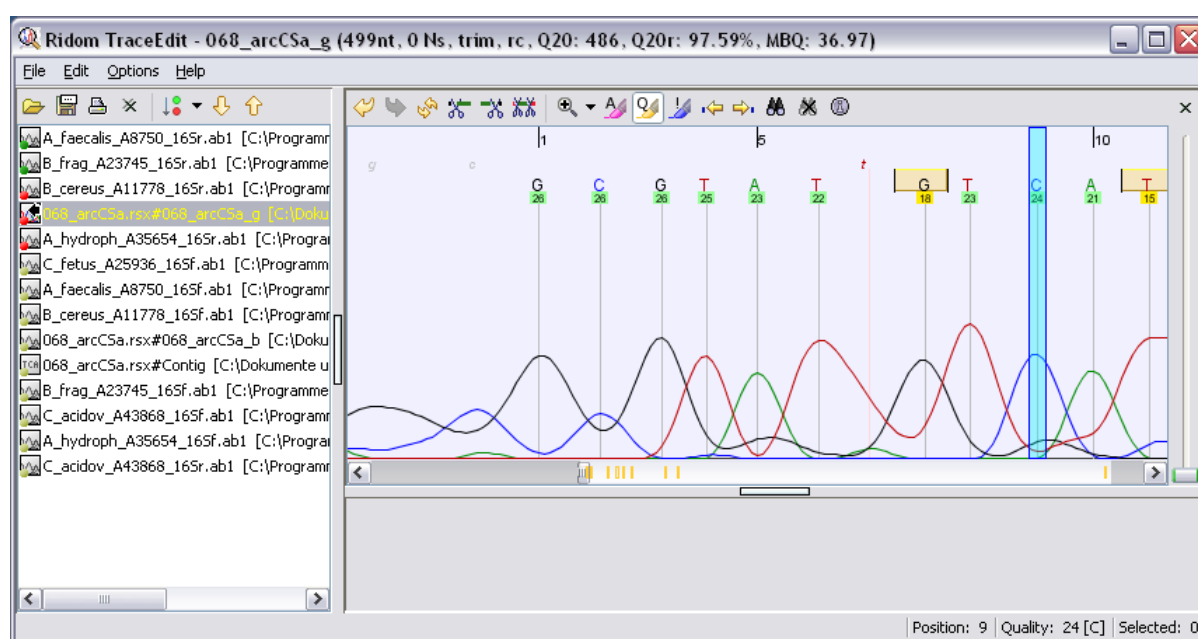




Fig. 1: Screen shot of Ridom TraceEdit (see text for details)

The main window (Figure 1) contains a list of sequence files on the left (the **file list pane** with tool bar), and the editor on the right (the **editor pane** with its own tool bar) shows the currently opened sequence. The icon left of the files shows the sequence type (text or chromatogram). The bullets in the lower left corner of the icon represent the status of the sequence (●yellow = opened, ●red = opened and edited, ●green = saved). If the sequence was reverse complemented, the icon contains an arrow (↔) in the upper right corner.


Double-click on a file in the file list pane to open its sequence in the editor pane. Click on the *Position* label in the **status bar**, to jump to a specific base number.

Use the *File* menu function  *Add Files/Directories...* to scan a whole directory subtree and to add all sequence files that are found to the list.

Info Window

Use the  button in the editor tool bar to display textual data contained in the sequence file. The opening window contains textual data about the particular sequencing experiment such as its chemistry, machine type and operating conditions etc. In addition are the sequence length, the number of ambiguities, the Q20, the Q20 ratio and the MBQ from the edited sequence shown. The Q20 defines the number of bases with a quality of ≥ 20 (the Q20ratio gives the ratio of Q20 to the total number of bases and the MBQ gives the mean base quality).

Find Dialog

Use the  *Find...* function in the *Edit* menu to search for strings in the sequence. The appearing Find dialog (Figure 2) offers two search modes:

- **Find Pattern** can be used to quickly search for a nucleotide pattern. The pattern may include regular expressions (see below). - By default, entered ambiguities are resolved during the search, i.e. an 'N' matches to bases 'A', 'C', 'G', 'T' or 'N'. If you want that an ambiguity matches exclusively only to its own letter (i.e. 'N' matches only 'N'), uncheck the *Resolve ambiguities* box.
- **Find Predefined Pattern** can be used to manage a list of often used search patterns. The pattern may also include regular expressions (see below). Ambiguities are always resolved (use the *OR* option to combine different patterns).

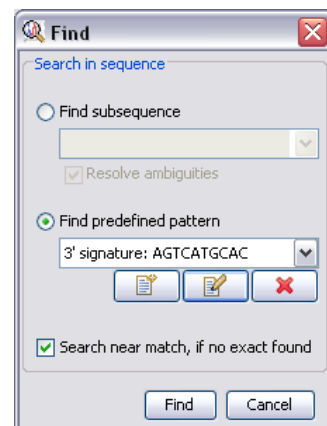


Fig.2: Find Dialog (see text for details)

Search Near Match can be enabled, to perform an alignment to find the nearest match, if an exact match was not found. All found matching positions are highlighted in the editor.

Regular Expressions

The sequence search supports the following regular expressions:

- **?** matches the preceding expression or the null string
(e.g: "AC?G" - matches "AG", and "ACG")
- ***** matches the null string or any number of repetitions of the preceding expression
(e.g: "AC*G" - matches "AG", "ACG", "ACCG", "ACCCG", and so on)
- **+** matches one or more repetitions of the preceding expression
(e.g: "AC+G" - matches "ACG", "ACCG", "ACCCG", "ACCCCG", and so on)
- **{m}** matches exactly *m* repetitions of the preceding expression
(e.g: "AC{3}G" - matches "ACCCG")
- **{m,n}** matches between *m* and *n* repetitions of the preceding expression, inclusive
(e.g: "AC{2,4}G" - matches "ACCG", "ACCCG", and "ACCCCG")
- **{m, }** matches *m* or more repetitions of the preceding expression
(e.g: "AC{2,}G" - matches "ACCG", "ACCCG", "ACCCCG", and so on)
- **a|b** matches whatever the expression *a* would match, or whatever the expression *b* would match
(e.g: "ACG|CAA" - matches "ACG", and "CAA")
- **(abc)** can be used for grouping expressions in combination with the operators above
(e.g: "A(CAT)?G" - matches "AG" and "ACATG")

Ambiguities are resolved by default, 'X' is treated like the ambiguity 'N'. Space characters are ignored.

NCBI Nucleotide Blast Search

Starts a NCBI BLAST search with the currently opened DNA sequence. The query page of the NCBI GenBank server is opened in your default WWW browser with the sequence already pasted into the form.

Import Sequence from NCBI Nucleotide DB

This menu option can be used to import sequences from the NCBI nucleotide database. These sequences are imported with associated parameter templates, that means sequences can be immediately cropped. The sequences are stored as assemblies and the associated report will contain the whole NCBI entry. To address the sequences the NCBI accession number must be stated. It is possible to address several sequences at once and to import the sequences in a batch process (e.g., AY688029-AY688031; AY688035 will result in the import of the sequences AY688029, AY688030, AY688031, and AY688035).

Send Bug Report

Ridom TraceEdit includes a feedback dialog to provide the user with a convenient way of sending messages directly to the developers such as features requests and bug reports. This dialog can be opened in the *Help* menu.

If an internal error occurs, this dialog window opens automatically. The report already contains the internal description of the error that occurred together with some system information (Ridom TraceEdit version, OS and Java version). If the error occurred after a specific user transaction it would be of help to us in solving the problem, if a description of the circumstances leading to the problem is given in the comment field. Inserting the software's error log in this field is achieved by clicking the right mouse-key and choosing the corresponding menu entry.

5. Configuration


Use the function *Preferences...* in the *Options* menu to open the configuration window with the following four tabs:

Editor Tab

Configures the display style of the sequence editor.

<i>Default base editing quality</i>	Defines the default quality that will be used when a base is substituted or inserted
<i>Default quality, if no qual. available</i>	Defines a default quality for FASTA sequences
<i>Show qualities as numbers</i>	Quality values will be displayed in a box below the base
<i>Show qualities as bars</i>	Quality are displayed through the length of a bar below the base
<i>Use gray (gradient) colors</i>	The quality value is visualized through the gray shading of the box/bar, ascending from light gray to dark gray
<i>Use threshold colors</i>	<p>The quality value is visualized by the defined threshold colors.</p> <p>The thresholds can be edited in the colored slider below:</p> <ul style="list-style-type: none"> • drag the thresholds with the left mouse button • double-click to change the color • right-click to add or remove thresholds
<i>Show base call center lines</i>	Show/hide the vertical line on a base-call position
<i>Show base qualities</i>	Show/hide the qualities of the bases (if available)
<i>Show original bases</i>	Show/hide the original bases above the edited ones

Trimming Tab

Ridom TraceEdit can detect unreliable 5' and/or 3' ends (by Ns or low base quality values) when opening a sequence. These regions are marked by writing the bases in gray color. Use the Auto-trim button  in the sequence editor, to cut off these unreliable regions.

Dialogs Tab

This tab contains an option to disable the confirmation dialog when exiting or closing unsaved chromatograms. In addition, it can be defined here whether the assembly icons of RSX files should be shown in the file open dialog (RSX assembly files are created by TraceEditPro).

Updates Tab








By default the search for software updates during program start is enabled in this tab. If a proxy server is necessary to access the Internet, the parameters can be configured here.

6. Quick Reference
















Keyboard Shortcuts

Frequent occurring actions can be conveniently invoked by keyboard shortcuts (**Mac OS X**: use ^ instead of Ctrl, to pop-up right-mouse-button menus under Mac OS X with a single button mouse, press Ctrl and the single mouse button). All menu commands can also be invoked (e.g., if no mouse is available) by using the Alt key in combination with a character as indicated by underscore in the menu (e.g., for the command “Open...” press Alt+F, P).

File List Functions

















Icon	Shortcut	Description
	Ctrl+O	Opens sequence files (SCF, ABI, FASTA, GenBank or plain text)
	Ctrl+S	Saves the opened sequence to a file (SCF or FASTA format)
	Ctrl+P	Prints the opened sequence chromatogram
	Ctrl+F8	Closes files that are currently selected in the list
		Sorts the files in the list by edit state, name or file path
	F10	Opens the previous file in the list
	F9	Opens the next file in the list
	F8	Closes the currently opened file
	Tab	Toggles the focus between the file list and the sequence editor

Sequence Editor Functions

Icon	Shortcut	Description
	Ctrl+Z	Undoes the last editing step(s)
	Ctrl+Shift+Z	Redoes the last editing step(s)
		Resets to original base-calls
	Ctrl+Alt+Home	Deletes all bases left to the selected base
	Ctrl+Alt+End	Deletes all bases right to the selected base
	Ctrl+T	Automatically trims the sequence by cutting off the unreliable 5'/3' regions that are marked by gray colored base characters
		Zooms in/out chromatograms
	Ctrl+Shift+A	Marks/Unmarks ambiguity bases in the consensus
	Ctrl+Shift+Q	Marks/Unmarks low quality bases in the consensus
	!	Marks/Unmarks current position in the consensus
	Ctrl+Left	Moves the cursor to the next ambiguity (low quality base) on the left
	Ctrl+Right	Moves the cursor to the next ambiguity (low quality base) on the right
	Ctrl+F	Searches a pattern in the consensus
		Removes found pattern marks
	Ctrl+I	Shows the sequence textual comments
	Left / Right	Moves the base-cursor one base left / right
	Home / End	Moves the base-cursor to first base / last base
	Shift+Left / Shift+Right	Moves the base-cursor one block left / right
	Ctrl+G	Goes to a base by specifying its base number in the status bar
	Tab	Toggles the focus between the file list and the sequence editor

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Menu Functions

Menu Item	Icon	Shortcut	Description
File			
Open...		Ctrl+O	Opens sequence files (SCF, ABI, FASTA, GenBank, RSX, or plain text)
Add Files/Directories...			Adds new sequence files to the file list. If a directory was selected, the whole subtree is scanned for sequence files and all sequence files are added to the list
New Sequence from Clipboard			Reads sequence data from clipboard
Save As...		Ctrl+S	Saves the opened sequence to a file (SCF or FASTA format)
Export...		Ctrl+E	Exports the opened sequence to a file (FASTA format)
Print...		Ctrl+P	Prints the opened sequence chromatogram
Print to PDF...			Prints the opened sequence chromatogram to a PDF file
Close...		Ctrl+F8	Closes all files that are currently selected in the list
Close Selected Files		Ctrl+Alt+F8	Closes all files in the list
Exit		Ctrl+Q	The preferred way to exit the program
Edit			
Find...		Ctrl+F	Searches for a pattern in the sequence (accepts ambiguities and regular expressions). The found matches are highlighted in the editor.
Remove Find Marks			Removes all highlighted search result marks
Refresh Auto-trim Marks			Refreshes the gray trim markings (e.g., after resetting the sequence to original base-calls)
Remove Auto-trim Marks			Removes the gray trim markings
Substitute Base...		A,C,G,T and R,Y,K,M,S,W,B ,D,H,V,N	Substitutes the selected base
Delete Base		Delete Backspace	Deletes the selected base (holding down the Backspace or Delete keys will rapidly delete successive bases, backwards for Backspace and forwards for Delete)
Insert Base...		Insert	Inserts a new base left to the selected base
Trim Left		Ctrl+Alt+Home	Deletes all bases left to the selected base
Trim Right		Ctrl+Alt+End	Deletes all bases right to the selected base
Cut by Auto-trim		Ctrl+T	Automatically trims the sequence by cutting off the unreliable 5'/3' regions that are marked by gray colored base characters
Copy Sequence to Clipboard			Copies the currently opened sequence to clipboard
Reverse Complement		Ctrl+R	Reverses and complements the sequence and the chromatogram
Options			
NCBI Blast Search		Ctrl+B	Performs a similarity search at the NCBI's Blast site with the edited sequence (requires an Internet connection and an installed WWW browser)
Import Sequence from NCBI Nucleotide DB...			Imports sequence(s) from the NCBI database via accession number(s)
Preferences...			Configures the TraceEdit parameters (editor, trimming, dialogs, updates)
Help			
TraceEdit Help		F1	Opens the program manual PDF in an external viewer (e.g., Adobe Reader)
Ridom Home Page			Opens the Ridom home page with the default WWW browser
Ridom TraceEditPro			Opens the web page of TraceEditPro, a commercial sequence assembling and editing software
Software Update			Makes available two sub-menus:  <i>Online Update</i> : searches for available software updates at the Ridom web server and <i>Import Update File...</i> : imports a software update file that was manually downloaded from the Ridom web server
Send Bug Report...			Sends a bug report or a request of new feature
About...			Opens the Ridom TraceEdit version info (including a system overview)

7.IUPAC Codes

<i>Symbol</i>	<i>Meaning</i>	<i>Origin of designation</i>
G	G	Guanine
A	A	Adenine
T	T	Thymine
C	C	Cytosine
R	G or A	puRine
Y	T or C	pYrimidine
M	A or C	aMino
K	G or T	Keto
S	G or C	Strong interaction (3 H bonds)
W	A or T	Weak interaction (2 H bonds)
H	A or C or T	not-G, H follows G in the alphabet
B	G or T or C	not-A, B follows A
V	G or C or A	not-T (not-U), V follows U
D	G or A or T	not-C, D follows C
N	G or A or T or C	aNy

8. Ridom TraceEdit Frequently Asked Questions (FAQ)

My chromatogram file format is not yet supported by Ridom TraceEdit!

This is possible. However, we always try to enhance the software's capabilities. Therefore, please send us a few sample files and tell us from which sequencing machine this files were derived and which collecting software was used. We will then try to incorporate an import filter with the next software update.

When I start Ridom TraceEdit, my firewall software tells me that the software tries to connect to the Internet!

Well, you are right. However, it is not our software but the Java virtual machine that tries to connect to the Internet to look for updates. We declare herewith that Ridom TraceEdit never tries to connect automatically to the Internet and that we by no means ever spy Ridom TraceEdit users. Of course, if you perform a BLAST search or search for software updates during program start (if enabled in the *Preferences* menu), Ridom TraceEdit connects to the Internet.

Why is Ridom TraceEdit for free available?

We are a bioinformatics company and we have to earn money to survive. Therefore, we produce also commercial software. However, we regard Ridom TraceEdit as a sort of marketing instrument and we hope that we can convince you with this free software that we are able to produce other quality software too (e.g., our sequence assembling editor TraceEdit**Pro**).

9. Ridom TraceEdit Version History

Ridom TraceEdit version 1.0 was released in February 2004.

Ridom TraceEdit version 1.1 was released in August 2005, with the following major improvements:

- support for automatic trimming,
- support for GenBank files and direct sequence import from NCBI, and
- extended support for SCF files.

10. End User Licence Contract for Ridom TraceEdit

Permission is granted to anyone to use this software FREELY for any purpose, subject to the following restrictions:

I. General

- a) This End User Licence Contract (EULC) forms a legally binding contract between you, the licensee, and Ridom GmbH, the licensor for the **Ridom TraceEdit** software and related media, materials and documentation (the software product).
- b) If you do not agree to these conditions, you are not entitled to use the software.
- c) The person who concludes this EULC assures and makes warranty that he is entitled to declare a legally binding contract on behalf of his employer as the licensee.
- d) The software product is licensed not given away.

II. Copyright

- a) The software product distributed by Ridom GmbH is protected both by copyright laws and international copyright treaties, and also by other laws and agreements concerning intellectual property.
- b) Ownership and copyright of the software product (including but not restricted to images, photographs, animations, video, audio, text and applets which are included in the software product), the accompanying printed material and each copy of the software product are the property of Ridom GmbH. All rights and intellectual property rights in and to content which can be accessed with the aid of this software product are the property of the respective owners of the content, and may be protected by applicable intellectual property rights laws and other laws and agreements on intellectual property. This EULC does not grant the licensee the right to use such content.

III. Scope of Licence

- a) The licensee is entitled to install the software product, the demonstration-version or an earlier version on several computers, workstations, portable PCs or another digital electronic device.
- b) The software product is licensed as a unitary product. The licensee is not entitled to separate its components for use.
- c) The licensee is not entitled to reverse develop, to decompile or to disassemble the software product. No changes to the existing source code, neither any re-use of parts of it are permitted.
- d) The licensee is not entitled to resell the software product or in any other way to transfer the software product for a counter-value. The licensee is not entitled to rent the software product, to lease it or to sell it.
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- f) Ridom GmbH reserves all rights not expressly granted. The individual provisions of this licence agreement can only be changed by Ridom GmbH. The written form is required for this, without any exception.

IV. Warranty and assurances

- a) This software is provided 'as-is', without any express or implied warranty. In no event will the Ridom GmbH be held liable for any damages (e.g., hardware damages, loss of data) or miscalculations arising from the use of this software.
- b) The software product is supplied in accordance with the current development status. Ridom GmbH draws attention to the fact that it is not possible in the current state of technology to create computer software such that it works without errors in all applications and combinations. The subject of this contract is therefore only software which is in principle usable in the sense of the program descriptions and user manual.
- c) Statements contained in brochures, advertisements and similar documents represent only descriptions, and do not contain any assurance of properties or guarantees.

V. Limitation of liability

- a) The licensee bears the responsibility for the selection and for the consequences of use of the software product, together with the results thereby intended or achieved.

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- b) Liability for damages of any kind (included without restriction are damages from loss of profit, loss of business information or from any other financial loss) which arises as a result of the use of this product or of the inability to use this product is expressly excluded.
- c) For damage or loss which involve death or physical injury, Ridom GmbH is in no case liable for aggravated compensation for damages or penalty compensation for damages, for any specific indirect, coincidental damage or loss or consequential loss or damage arising therefrom (this applies particularly, but not exclusively, for loss of use, loss of data, loss of profit and for loss of savings and business). This applies regardless of the basis of the claim or grievance.
- d) Ridom GmbH is not responsible for and makes no warranty for the product running without interruption or without error.

VI. Place of judgement and applicable law

- a) Place of fulfilment for all obligations arising from the contract relationship is, for both contract partners, Würzburg, the base of Ridom GmbH. This applies even if the residence of the customer is unknown or is outside Germany.

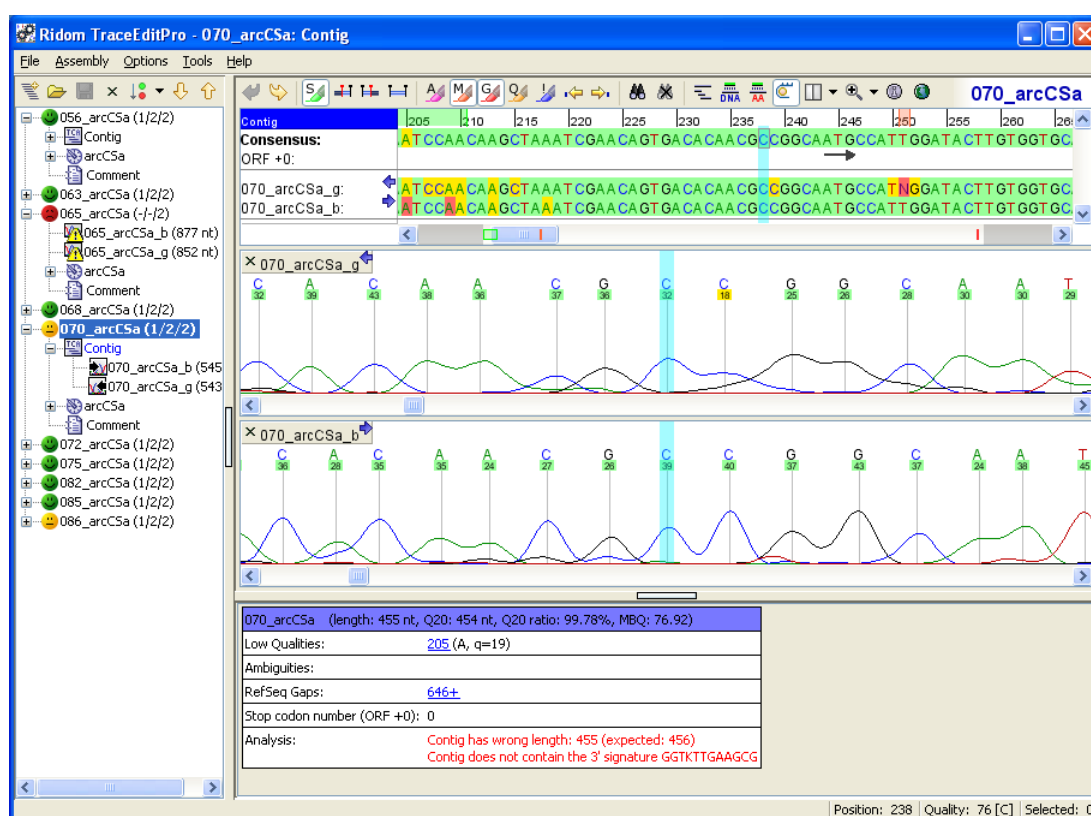
VII. Final provisions

- a) Should any provision of this EULC be or become ineffective or contestable for any reason, its content is not otherwise disturbed thereby. Rather, it is to be performed in accordance with the intent.
- b) Instead of the ineffective or contestable provision, an appropriate regulation is to apply which, as far as legally permissible, comes as close as possible to that which the parties who concluded the contract intended or would have intended in accordance with the sense and purpose of this contract if they had considered the point when concluding this contract. The same applies in the event of a lacuna in this contract. This also applies even if the ineffectiveness of a provision rests in any way on a measure of the performance and the time (period or date) prescribed in the contract. A legally permissible measure of the performance or time (date or period) which comes as close as possible to that which was intended shall then be deemed to be agreed.

Ridom TraceEdit, license version 1.1

11. Ridom TraceEdit^{Pro} Features

- DNA sequence assembling software for small and medium sized **(re)sequencing projects** (reads ABI-, SCF- chromatograms and GenBank & FASTA files)
- Flat learning curve by **simple but powerful** user interface
- **Quality values** for each base pair and consensus sequence
- **(Semi)automated analysis** of DNA sequence data allows for faster and more accurate results
- **Data visualization** allows for focusing on relevant data only
- Multiple **frame protein translation** with smart translation of ambiguous but non degenerated codons
- Easy linkage for querying to **Internet** and local reference sequence libraries
- Easy creation of local **reference sequence libraries**
- Designed for pathogen (sub)typing, allele identification and sequence confirmation



Interested?
 Download a demo version,
 request further information
 or ask for an offer
<http://www.ridom.de>