

JU SeqWorkbench Alpha User Guide — English Draft

Other Language: 한국어 | English

This document describes the currently implemented alpha behavior in reproducible steps for first-time testers. It uses the current English UI labels wherever practical.

1. JU SeqWorkbench Alpha overview

JU SeqWorkbench Alpha is a local desktop application focused on **Sanger/FASTA/MSA sequence review, editing, grouping, and site- or region-centered visualization**.

This application is not:

- an NGS mapper;
- a variant-calling pipeline;
- a genome assembler; or
- a clinical diagnostic system.

Recheck alpha results against representative data and keep backups of important originals.

2. Supported workflow and scope

1. Open FASTA/TXT or Sanger AB1/ABI files, or import them into the current viewer.
2. Review Sequence IDs and current working sequences, and edit only what is needed.
3. If necessary, align the sequences with a separately installed MAFFT or Clustal Omega executable.
4. Run Point Visualization, Region Visualization, ID/Name-based Grouping, AA Marker Classification, or Similarity-based Clustering.
5. Export Results Tables, figures, or FASTA files, or save the working state as a `.dvproj` project.

Depending on the operation, output may appear in a new viewer, a Results Table, a PNG/JPEG/SVG/PDF figure, a CSV or FASTA file, or a project file. Phylogenetic tree and Annotation layer are listed as planned features in Help and cannot be run from the current Analysis menu.

3. Main window layout

1. Use the top menu to access File, Edit, View, Alignment, Analysis, Web Resources, and Help.
2. Use the toolbar to control View/Edit , OVR/INS , InsV , ColType , DupV , ID , coordinate spacing, Dot , and Residue Colors.
3. Select rows in the Sequence ID panel on the left.
4. Review positions and characters in the Coordinate Ruler and Sequence Panel on the right.

Sequence Management (Planned) is visible but disabled. Hide or restore the ID panel through View > Show ID Panel or the toolbar ID control. Residue Colors can slow down large alignments.

Choose English or 한국어 under Help > Language . The choice is stored in local QSettings and, as the notice explains, requires an application restart before it applies throughout the UI.

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Main Viewer Layout



Core Areas

Menu: file, view, analysis, and help functions

Tool bar: edit state and quick actions

ID panel: strain / sequence ID selection

Seq panel: nucleotide or amino-acid sequence display

Key Toggles

View/Edit, INS/OVR, Dot, Residue Colors, Coordinates, ID panel visibility, and Clear all highlights directly affect screen behavior and editing targets.

Tip: Features outside the current alpha scope should be disabled or marked as Planned to reduce user confusion.

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4. Creating and opening projects

1. Open an empty workspace with File > New or Ctrl+N .
2. Open an existing project with File > Open Project... .
3. If the same project is already open, choose whether to activate the existing window, open an independent copy, or cancel.
4. An independent project copy cannot save directly to the original path; use Save Project As... .

The default project extension is `.dvproj`. The application can also open `.dvproj.json` and legacy `.json` files with a valid project signature. A normal sequence `Open` creates a separate viewer, while `Import` adds records to the current viewer.

5. Importing FASTA and sequence data

1. To view data in a new window, select `File > Open` or press `Ctrl+O`.
2. To add data to the current workspace, select `File > Import...` or press `Ctrl+I`.
3. Paste clipboard FASTA as new records with `Ctrl+Alt+V`.
4. If the application reports adjusted duplicate IDs, review the new suffixes.

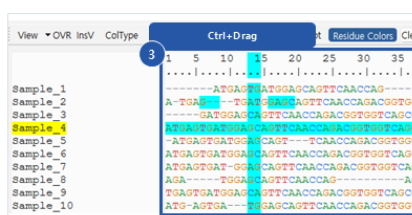
FASTA, plain-sequence TXT, and AB1/ABI are included in the supported paths. A one-line FASTA-like entry must distinguish the ID and sequence, for example `>Sample_1 SEQUENCE`. If the raw sequence type is ambiguous, the application may ask whether it should be treated as NT or AA.

6. Reviewing and editing sequences

1. Switch the toolbar to `Edit` mode.
2. Click the Sequence Panel to place the cursor, or drag to select a range.
3. Press `Insert` to switch between `INS` (Insert mode) and `OVR` (Overwrite mode).
4. Use character input, `Delete / Backspace`, `Ctrl+X`, and `Ctrl+V`.
5. Review the result with `Ctrl+Z / Ctrl+Y`.

A normal drag replaces the previous Sequence Panel highlight. Holding `Ctrl` while dragging adds another highlight layer.

Highlight and Selection Interactions



Basic Behavior

Drag sequence area: horizontal highlight

Drag ruler: column highlight

Ctrl+Drag: accumulated highlight

*Clear all highlights: remove all highlights

Alpha Limitations

Some drag selections may extend beyond the intended strain/row boundary. When multiple highlights exist, paste targets the most recently active highlight.

The ID panel and sequence panel use different selection models, so blank-area clicks, selection clearing, and right-click menus may not behave identically.

Characters that are invalid for the current row's NT, RNA, or AA type are blocked. When highlights exist, **Delete** removes actual sequence data from the most recent highlight, and **Ctrl+Delete** removes data from all active highlights. To remove only the visual highlighting, use **Clear All Highlights**.

To edit one sequence in a separate window, right-click its ID and select **Open Sequence in Editor...**. This modeless window can be switched freely with its parent viewer through **Alt+Tab**. **Apply** creates one undoable change in the parent.

7. Editing Sequence IDs

1. Select exactly one row in the ID panel.
2. Put either an ID copied with **Copy ID** or suitable plain text from an external application on the clipboard.
3. Keep focus in the ID panel and press **Ctrl+V**, or use the rename command in its context menu.
4. Check for **_2**, **_3**, or similar suffixes added to duplicate names.

The main ID-panel context-menu commands behave as follows.

- **Copy ID**: copies the selected ID name. With multiple selected rows, it copies the selected IDs.
- **Copy Sequence**: copies only the current working sequence of exactly one strain, without a header. This clipboard payload is not valid for renaming an ID.

- **Copy as FASTA** : copies IDs and sequences as FASTA. Multiple selected rows remain separate FASTA records.
- **Open Sequence in Editor...** : opens the selected single strain in a separate modeless editor.
- **Paste ID / Rename ID from Clipboard** : renames one ID from **Copy ID** data or suitable plain text. Data produced by **Copy Sequence** is not applied as an ID.
- **Delete Strain...** / **Delete Selected Strains...** : deletes the selected strains. The operation supports **Ctrl+Z** / **Ctrl+Y** undo and redo.
- **Move Sequence...** : with exactly one strain selected, start the command and click a destination ID to move the source immediately above it. Press **Esc** to cancel a pending move. The move supports **Ctrl+Z** / **Ctrl+Y**.
- **Move to Bottom** : moves the selected single strain to the end of the list and supports **Ctrl+Z** / **Ctrl+Y**.

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ID Panel Interactions

Basic Behavior

Open a dedicated editor for a single sequence, or copy and paste its ID and sequence data.

To reorder a sequence, select the move option and then click a different sequence ID. The selected sequence will be moved directly above the sequence you clicked.

Single-Sequence Editing

Edit the sequence ID or modify the nucleotide sequence directly.

Display options for nucleotide data can be configured in the **Editor** settings.

Copying and Pasting Sequences

Copy ID: Copies the sequence ID.

Copy Sequence: Copies only the nucleotide sequence data. (*Single sequence only.*)

Copy as FASTA: Copies both the sequence ID and nucleotide data in FASTA format.

Since the ID panel and the sequence panel use different selection models, behaviors such as clicking in the margin, deselecting, and right-click menu actions may differ.

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Clipboard rename does not run when multiple IDs or no ID are selected. With multiple selection, ID/FASTA copying and selected-strain deletion are available, but **Copy Sequence** does not run and directs the user to **Copy as FASTA**. Editor opening, ID rename, and movement follow the single-row policy. **Ctrl+Alt+V** in the ID panel retains its existing Paste as New Sequence meaning rather than renaming an ID.

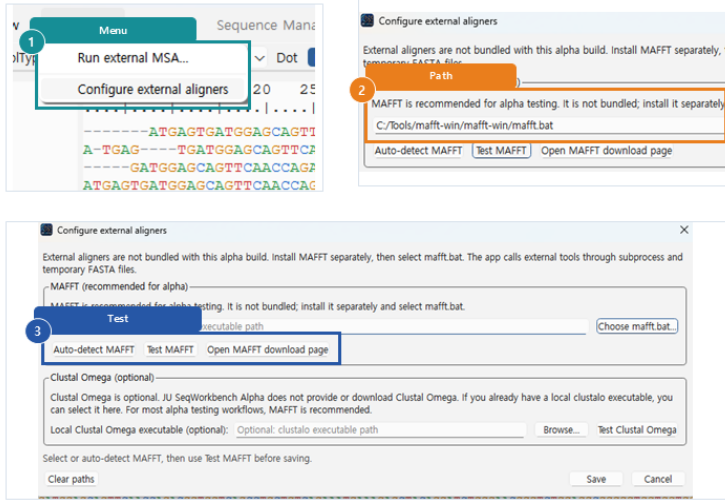
8. External alignment setup

1. Install MAFFT or Clustal Omega separately from the application.
2. Open **Alignment > Configure external aligners**.
3. Select a local executable, or leave its path empty.
4. Save the settings and close the configuration window.

The executables are not included with or automatically downloaded by JU SeqWorkbench. A path selected by the local user is stored in the existing QSettings. If the path is empty, the application checks `PATH` for `mafft` or `clustalo` when an alignment is run. The test controls in the settings window check the selected local executable with a temporary FASTA.

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External MSA Tool Setup



Setup Flow

Alignment > Configure external aligners

Select the MAFFT or Clustal Omega executable path

Use Test to confirm the executable works

*The path is saved as a local user setting

Distribution Policy

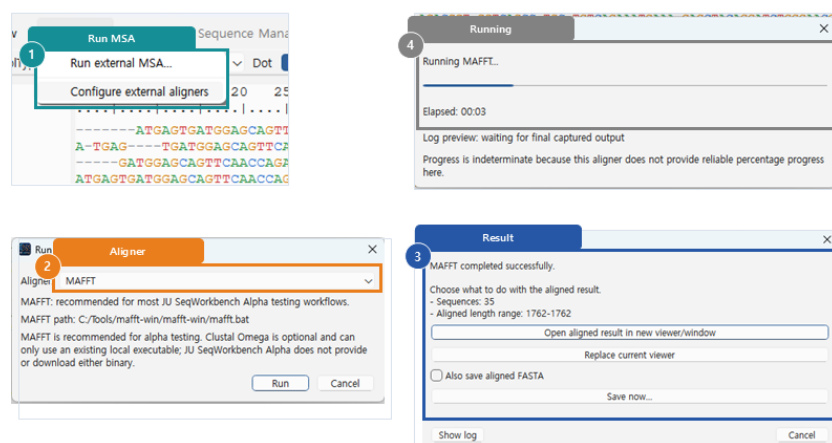
The alpha distribution does not include MAFFT or Clustal Omega binaries. Users connect separately installed local executables.

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9. Running MAFFT or supported aligners

1. Confirm that the current workspace contains at least two sequences to align.
2. Select **Alignment > Run external MSA...**
3. Choose MAFFT or Clustal Omega.
4. Review the progress window and any error or log output.
5. On success, choose whether to open a new viewer, replace the current viewer, save the aligned FASTA, or discard the result.

Running MSA and Applying Results



Result Handling

After running MSA, review the output in a separate result window. You can choose whether to replace the current viewer or open the result in a new viewer.

Note

Project files (.dproj) are not aligned directly. The app creates a temporary FASTA from the current viewer working sequences and passes it to the external tool.

The application creates a temporary FASTA, runs the external process, and reads the aligned FASTA. Replacing the current viewer is recorded in edit history and clears highlights. After failure, a temporary directory may be retained for diagnostics; its path and command are available in the log.

10. NT, AA, DNA, and RNA transformations

1. Select the ID rows to transform. With no selection, all rows are targeted.
2. Use **Ctrl+D** / **AA View** , **Ctrl+W** / **DNA View** , or **Ctrl+E** / **RNA View** .
3. Check the transformed, restored, and skipped counts in the status bar.
4. Use **Ctrl+Z** if the operation needs to be undone.

AA view translates NT source data in frame 0. DNA view returns to the retained NT working state and does not arbitrarily reverse-translate AA-only records. RNA view switches the **T/U** display. Transformations clear Sequence Panel and column highlights; RNA transformation also clears ID selection.

The shortcuts for reverse, complement, and reverse complement are **Ctrl+Alt+R** , **Ctrl+Alt+C** , and **Ctrl+Alt+X** . With no selected range or ID row, they apply to all sequences.

11. Point Visualization

1. Under **Analysis > Visualization**, choose AA, NT, or Codon Point Visualization.
2. Enter 1-based positions, for example **10,25,50**.
3. Choose a reference sequence and filters, and set the required include/exclude options.
4. Click **Run**.
5. Review the Visualization, Counts, Detail, and Warnings tabs.

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Point Visualization: Setup

Analysis Sequence Management (Planned) Web Resources

Visualization > Point Visualization (AA)
Clustering / Classification > Point Visualization (NT)
Point Visualization (Codon)
Region Visualization

Input Panel

Set Preset, Unit, Position, Stop codon handling, Filter, and Reference. Coordinate meaning changes depending on AA, NT, or Codon mode.

Output Panel

For the same set of positions, switch among logo plots, mutation maps, entropy, major allele frequency, composition bars, and other output types.

Input & Options

1. Preset: (AA) example_set1 Save Overwrite selected preset Delete

Unit: AA

Positions: 101,164,170,324,370,386,413,426,435,440,476

Stop codon handling: Truncate at first stop

☐ Include reference sequence
☐ Create per-strain detail table
☒ Trim length to a multiple of 3

Filter: (Header filter (subsetting))
(Automatic selection)

Reference: ☐ Convert viewer display to the analysis basis (link/highlight)

Run

Run / Run again Close

Output taps

2. Visualization Counts Detail Warnings

Visualization: Logo plot

3. Bits (information) Include

Press Run to generate results.

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Point Visualization provides logo plots, heatmaps, binary and categorical mutation maps, entropy, major allele frequency, excluded counts, variant bars, and composition stacked bars for selected positions.

Point Visualization: Figure Adjustment

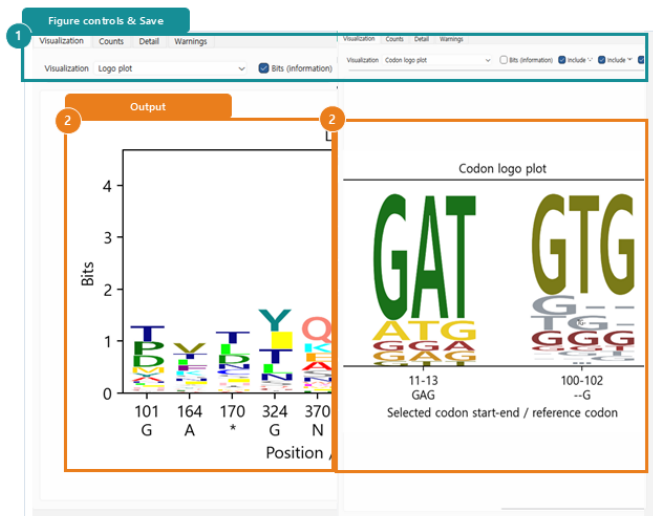


Figure Options

Adjust the title, axis labels, ticks, scale, text size, font, and style, then redraw using Rerender.

Visualization area

Multiple visualization modes are available, including Logo Plot. The rendering style may vary depending on the selected visualization mode and sequence unit (NT, AA, or codon). For example, a codon logo plot displays each codon as a three-character token.

Save

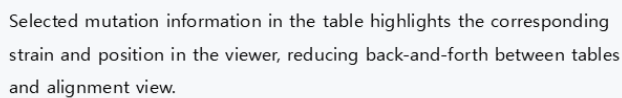
Use Save figure to export PNG/JPG images. For papers or reports, add numbering and captions later in PowerPoint or other layout tools.

Selecting a row in Counts or Detail highlights the corresponding parent-viewer positions and sequence rows when the sequence units are compatible. Results can be exported with the CSV and figure save controls.

Presets are stored in the user's settings location. The current distribution has no dataset-specific marker positions as defaults.

12. Codon logoplot

1. Choose **Logo plot** in AA or NT Point Visualization, or **Codon logo plot** in Codon Point Visualization.
2. Adjust the gap, stop, unknown, and bits/frequency options.
3. Choose the font, size, axis visibility, and publication style.
4. Render again and save the figure.



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13. Region Visualization

1. Open **Analysis > Visualization > Region Visualization**.
2. Enter one or more start-end ranges.
3. Choose the reference sequence and profile or summary options.
4. Run the analysis and review the figure and region metrics table.
5. Save output with **Export CSV** or **Save figure**.

Region Visualization: Regions and Figures



Region Definition

Define multiple regions using presets or manual input. Layout options include Panel and Concatenate modes.

Metric

Calculate region-centered metrics such as entropy, gap/unknown rate, non-reference rate, mutation map, and strain-wise profiles.

Performance Note

Lazy rendering is not yet implemented. Rendering may be slower with many sequences or color display enabled. Turning off Residue Colors can improve responsiveness.

Region Visualization covers variation by range, entropy, profiles, and burden summaries. Figure output supports PNG/JPEG and SVG/PDF paths. The window is currently English-first, and clicking a result cell or figure point does not highlight the parent viewer.

Region Visualization: Metrics Table

The screenshot shows the 'Metrics table' view. It has a 'Controls' panel at the top with options for 'table view' (Entropy), 'Sort column' (position), 'Direction' (ascending), and 'Scope' (within each region). Below the controls is a table with 7 columns: region_label, unit, position, entropy, observed_tokens, token_summary, valid_count, and excluded_count. The table lists metrics for various regions (A, B, C, D) and positions. The table is sorted by position in ascending order. The 'valid_count' and 'excluded_count' columns show the number of valid and excluded tokens for each region and position.

region_label	unit	position	entropy	observed_tokens	token_summary	valid_count	excluded_count
Region A	aa	10	2.5299789188029957	A.G.L.P.Q.R.T.V.W	A:1; G:14; L:1; P:2; Q:2; R:4; T:2; V:7; W:1	34	1
Region A	aa	11	2.5327195351219203	C.D.G.P.R.S.T.V.W	C:1; D:2; G:13; P:1; R:3; S:3; T:1; V:5; W:1	30	5
Region A	aa	12	2.5308006218550014	A.C.G.L.Q.S.T.V.W	A:1; C:1; G:3; L:2; Q:13; S:6; T:1; V:1; W:3	31	4
Region A	aa	13	2.6652399286796387	A.C.G.L.M.P.Q.R.S.V	A:1; C:1; G:2; L:7; M:1; P:13; Q:2; R:1; S:3; V:2	33	2
Region A	aa	14	2.70768021233142	A.C.G.K.L.Q.R.S.V.W	A:14; C:2; G:1; K:2; L:5; Q:2; R:2; S:4; V:1; W:1	34	1
Region A	aa	15	2.8501169519558163	A.C.E.L.N.P.Q.R.S.V.W	A:1; C:5; E:3; L:1; N:1; P:2; Q:1; R:1; S:7; V:11; W:1	34	1
Region A	aa	16	2.9220024616785656	A.C.E.K.L.M.N.Q.R.S	A:3; C:4; E:7; K:2; L:2; M:2; N:1; Q:1; R:10; S:2	34	1
Region A	aa	17	3.154559938249354	C.E.I.K.M.N.Q.R.S.T.V	C:2; E:1; I:2; K:4; M:5; N:8; Q:4; R:1; S:3; T:1; V:2	33	2
Region A	aa	18	2.496877994577654	A.C.D.E.K.L.M.Q.R.Y	A:1; C:2; D:1; E:13; K:10; L:1; M:1; Q:1; R:3; Y:1	34	1
Region A	aa	19	3.0130059710789405	A.C.E.K.L.M.N.Q.R.S.T	A:1; C:1; E:5; K:4; L:3; M:2; N:2; Q:1; R:10; S:2; T:1	32	3
Region A	aa	20	3.0520121205143798	A.E.G.I.K.L.Q.R.S.T.Y	A:9; E:4; G:2; I:1; K:5; L:5; Q:2; R:1; S:1; T:1; Y:2	33	2
Region A	aa	21	3.048794940693985	A.D.E.G.K.L.Q.R.S.T.W.Y	A:1; D:1; E:1; G:1; K:2; L:2; Q:5; R:5; S:2; T:10; W:1; Y:1	32	3
Region A	aa	22	3.124226763509437	A.D.E.I.J.K.L.Q.R.S.T.Y	A:3; D:4; E:1; G:10; I:3; K:1; L:2; Q:2; R:1; S:2; T:1; Y:1	31	4
Region A	aa	23	3.136324711025711	D.G.I.K.L.N.Q.R.S.T.W.Y	D:2; G:3; I:1; K:1; L:5; N:1; Q:1; R:2; S:10; T:4; W:3; Y:1	34	1
Region A	aa	24	2.468090781663233	D.E.G.I.L.N.S.T.W.Y	D:1; E:4; G:18; I:1; L:2; N:1; S:2; T:2; V:1; W:1; Y:1	34	1
Region A	aa	25	2.9357417972482365	A.E.G.L.N.R.S.T.W.Y	A:1; E:1; G:6; L:1; N:9; R:3; S:5; T:4; W:3; Y:1	34	1
Region A	aa	26	2.147805873542275	E.G.I.L.N.R.S.T.V	E:1; G:20; I:1; L:2; N:1; R:3; S:1; T:2; V:3	34	1

Table View

Show metrics table opens computed results as tables, including all-region views, per-region tabs, and long-form detail views.

Sorting and Search

Use Table view, Sort column, Direction, Scope, and Search options to narrow down the rows you need.

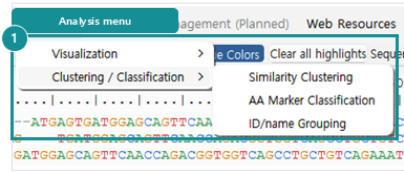
Export

Use CSV Export to save the current table. For very large detail tables, the preview and full export range may differ.

14. ID/Name-based Grouping

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Grouping and Classification Overview



Similarity Clustering

Groups strains by NT or AA sequence similarity and generates result tables and grouped FASTA outputs.

AA Marker Classification

Defines groups using combinations of conditions at specific AA positions. Example: position 10 = A, position 25 = G.

ID/name Grouping

Classifies sequences based on keywords in the sequence ID or description. Examples: Group_A, Year_2024.

Common Behavior

After successful classification, the setup window closes and the result table is brought forward. If validation or runtime errors occur, the setup window remains open for correction.

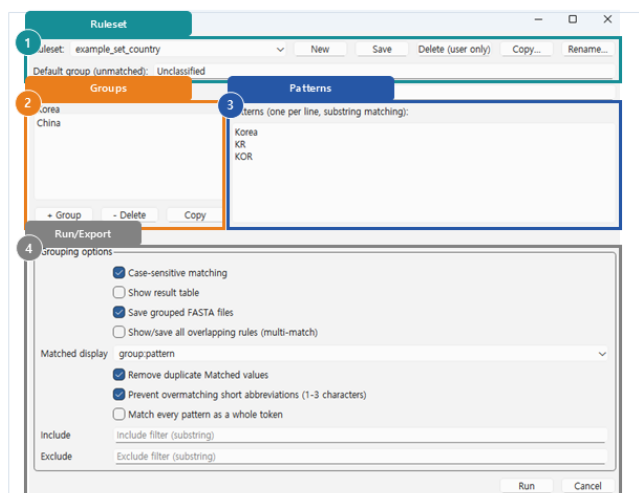
Each classification feature uses the current viewer working state and can export grouped FASTA files when needed.

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1. Open **Analysis > Clustering / Classification > ID/name Grouping**.
2. Create a ruleset with **New**, then add group rules.
3. Enter a neutral group name such as **Group_A** and one ID pattern per line.
4. Review case sensitivity, boundary matching, multiple-match, and display-format options, then save.
5. Choose whether to show the Results Table and save grouped FASTA, then run the grouping.

The application compares each current Sequence ID/name string with the rule patterns to form groups. On success, the configuration window closes and the Results Table is brought forward after the completion message. On validation or runtime failure, the window remains open. Normal row selection in this Results Table is not linked to parent-viewer highlighting.

ID/name Grouping

**Keyword-based Grouping**

Assign groups using words or patterns contained in the ID or description. Enter one pattern per line.

Matching Options

Choose case sensitivity, conservative boundary matching, first/all match behavior, and matched-display style.

Export

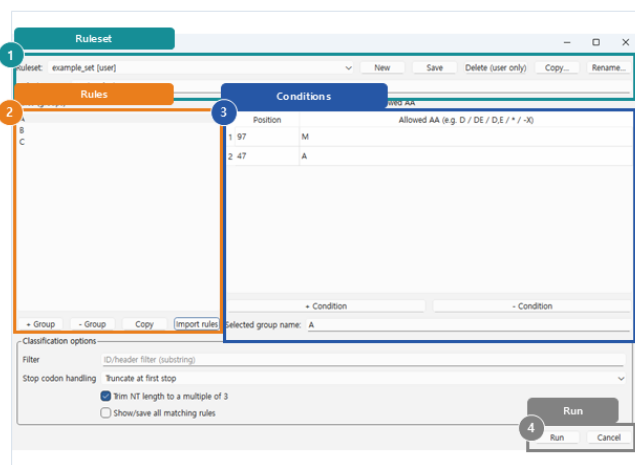
Supports classification result tables and grouped FASTA export. AA-only records are written to separate *_aa_only FASTA files.

15. AA Marker Classification

1. Open **Analysis > Clustering / Classification > AA Marker Classification**.
2. Because there is no built-in default ruleset, create a user ruleset with **New**.
3. Add groups and conditions, then enter a 1-based Position and Allowed AA values.
4. Save the ruleset and choose stop handling, multiple-match, Results Table, and grouped-FASTA options.
5. Click **Run** and review the output.

Position accepts digits only and then undergoes the existing range validation. Allowed AA is normalized to uppercase and accepts only supported characters. Incomplete or invalid editor buffers are not stored in the model. When moving to another rule, the application warns that unapplied values were discarded and displays the clicked rule. A completely blank new condition can be discarded without a warning.

AA Marker Classification

**Ruleset**

A saved set of marker rules. User-defined rulesets can be saved, copied, and deleted.

Rules and Conditions

Each rule represents one group. Multiple conditions define allowed characters at specific AA positions.

Input Validation

Position accepts digits only. Allowed AA accepts valid amino-acid characters only. Incomplete conditions are not applied.

On success, the configuration window closes and the Results Table is brought forward after the message. On failure, the window remains open. User rules continue to use the existing `typing_rulesets.json` storage format.

16. Similarity-based Clustering

1. Open `Analysis > Clustering / Classification > Similarity Clustering`.
2. Choose NT or AA comparison mode and a clustering threshold.
3. Set gap and ambiguity handling, full-sequence or manual range, and heatmap, dendrogram, and variation-range-table options.
4. Run it for the selected ID rows, or for all current sequences when no rows are selected.
5. Review the Results Table and any optional figure, FASTA, or result bundle.

At least two sequences are required. If lengths differ, the application asks you to check the alignment. A manual range uses 1-based coordinates in the current comparison mode. On success, the configuration window closes and the Results Table comes forward; on failure, it remains open. A Results Table row highlights cluster members, while a variation-range row highlights members and, where possible, the column range in the parent viewer.

Similarity Clustering

Comparison settings

Comparison mode: ☒ NT (nucleotide sequence) ☐ AA (amino-acid sequence)

Cluster threshold: 99.0%

Comparison scope: Full sequence 100-500

Range is applied to the current comparison mode coordinates.

☐ Include gaps (-) in comparison (- vs - counts as a match)

NT ambiguity handling (N/R/I/*): Ignore X/*

AA ambiguity handling (N/*): Ignore X/*

Result display

☒ Show variation range summary table and highlight on click

☐ Show similarity heatmap

☐ Reorder heatmap by cluster order

☐ Show dendrogram (average linkage)

☒ Auto-switch display mode when needed

Export

☐ Save cluster FASTA files

☐ Export result bundle to a folder (CSV/FASTA, etc.)

☐ Save similarity matrix CSV (large-output cautions)

Run

3 **Run** Cancel

Options

Choose NT/AA mode, similarity threshold, gap/unknown handling, and comparison range.

Results

Review cluster summaries, pairwise similarity, differing regions, heatmaps, and FASTA bundle export options.

Result table			Cluster Outliers Summary (percentage) - cluster 1		
	cluster	representative	mean_within_similarity%	mean_outlier_similarity%	ref_outlier
0	1	Sample_1	99.142	99.325	0
1	2	Sample_9	99.485	99.485	0
2	3	Sample_1	100.0	100.0	0
3	4	Sample_2	100.0	100.0	1
4	5	Sample_3	100.0	100.0	1
5	6	Sample_4	100.0	100.0	1
6	7	Sample_5	100.0	100.0	1
7	8	Sample_7	100.0	100.0	1
8	9	Sample_8	100.0	100.0	1
9	10	Sample_10	100.0	100.0	1
10	11	Sample_11	100.0	100.0	1
11	12	Sample_12	100.0	100.0	1
12	13	Sample_14	100.0	100.0	1
13	14	Sample_17	100.0	100.0	1
14	15	Sample_18	100.0	100.0	1
15	16	Sample_19	100.0	100.0	1
16	17	Sample_20	100.0	100.0	1

17. Results Tables and viewer highlighting

1. Select a row in Point Visualization Counts/Detail or a Similarity Results Table.
2. Check the highlighted ID rows and positions in the parent viewer.
3. If a display-mode mismatch message appears, compare the analysis mode with the current NT/AA display.
4. Use **Clear All Highlights** when the linked result should be cleared.

Not every Results Table is linked to its parent viewer. The confirmed links are Point Visualization and Similarity Results Tables. Normal row selection in Region Visualization, AA Marker Classification, and ID/Name-based Grouping tables does not provide the same linkage. **Ctrl+C** in a table copies selected cells, including headers, as TSV text.

18. AB1 chromatogram workflow

1. Use `File > Open` to open AB1/ABI as a new document.
2. To add it to the current viewer, select AB1 under `File > Import...`
3. Choose whether to show the trace window and whether to use original or reverse-complement orientation.
4. Review the trace, basecalled sequence, quality summary, and warnings.

5. Adjust the start/end trim range and import in the required orientation.

The application reads the basecalls already stored in the AB1 file and does not perform new basecalling. The trace window provides positional scrolling, previous/next navigation, zoom, and original/reverse-complement display. Duplicate IDs are adjusted when multiple AB1 files are imported.

User Guide · Alpha

Sanger AB1 Chromatogram Workflow

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Import options

- New Ctrl+N
- Open Ctrl+O
- Import... Ctrl+I
- Convert
- Open Project...
- Save Project Ctrl+S
- Save Project As... Ctrl+Shift+S
- Export sequences...

2

Orientation

☒ Show trace window

Import orientation: Original orientation

OK Cancel

Trace Preview

Open AB1/ABI files to inspect chromatograms, basecalled sequences, and quality summaries.

3

Trace

111_2_11815443_047.ab1 | Sample: 111_2 | Sequence length: 1157 | Quality: N/A

Per-base quality values were not found.

Orientation: Original orientation

Base position: 1 30 60 90 120 150 180 210 240 270 300

CHNNNNCGAGTTTGAAGTCGCGCTCGAGGCGATTANGTTTGAGAGCAGCTCTGTTTGGGCGTCATGCCCTGCGTCATCTTAGCCATCCATCTACTC

Signal

Sequence/Trim

Base position: 1-100 / 1157

Trim start: 1 Trim end: 1157

Basecalled sequence - Original orientation (trimmed length: 1157)

CHNNNNCGAGTTTGAAGTCGCGCTCGAGGCGATTANGTTTGAGAGCAGCTCTGTTTGGGCGTCATGCCCTGCGTCATCTTAGCCATCCATCTACTC

Close

Import

Select Original or Reverse complement orientation, adjust the trim range if needed, and import the sequence into the viewer.

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19. Exporting tables and figures

1. Export main sequences as FASTA, a CSV sequence table, or TXT through **File > Export sequences...**
2. Use a Results Table's CSV export button or its context-menu/copy commands.
3. Use the save controls in Point, Region, or Similarity figures.
4. When grouped FASTA output is enabled for grouping or classification, confirm the destination and overwrite choice.

Project save and data export are separate operations. **Ctrl+S** saves the project; it does not overwrite the source FASTA. AA-only records may be separated into AA FASTA and are not arbitrarily converted to NT. A Duplicate Viewer blocks project and viewer-level sequence-data exports.

20. Saving and reopening projects

1. Use `Ctrl+S` or `File > Save Project` .
2. Choose a path for the first save or for an independent project copy.
3. After ending the session, reopen it with `Open Project...` .
4. Check sequence order, current working state, and display settings.

Projects preserve original/current NT and AA working states and related viewer state. Undo/Redo history is not saved in the project, so a reopened session starts with new history. Keep a separate backup of project files during alpha testing.

21. Troubleshooting

1. If startup is slow, confirm that the startup screen appears first and wait for the first main-window event.
2. If an aligner executable error appears, check the configured path and `PATH` .
3. If Similarity or Point highlighting is not visible, align the NT/AA comparison mode with the current display type.
4. If FASTA paste is rejected in the Sequence Panel, use `Ctrl+Alt+V` .
5. To copy multiple records, use `Copy as FASTA` , not `Copy Sequence` .
6. The main `Ctrl+F` not performing a search is a known alpha limitation.
7. During large analyses, respond to the preflight notice, wait for the working indicator, and confirm that result generation has completed.

A configuration window that reports an error remains open so that its values can be corrected and run again. In an external MSA failure window, use `Show log` to inspect the command, output, and temporary path.

22. Known limitations

In summary, current limitations include separately installed external aligners, no cross-session Undo restoration, large-data performance, limited advanced AB1 functions, no main-viewer Find implementation, some English-first UI, and limited Results Table linkage. See `known_limitations_en.md` for the exact list.

23. Reporting feedback and bugs

1. Check the current alpha version under `Help > Version Information`.
2. Record the input type used for reproduction—FASTA, AB1, or project—along with sequence count and approximate length.
3. Record the click sequence, expected result, actual result, and any error message.
4. If possible, reproduce with neutral examples such as `Sample_1`, `Sample_2`, and positions `10`, `25`, `50`, with personal or sensitive sequences removed.
5. Report through the current Issues or Discussions path shown under `Help > User Guide`.

Before attaching a project or real sequence, confirm that the data may be shared publicly. Redact local executable paths and user-profile paths from reports.