

# Package ‘ggaligner’

May 8, 2026

**Title** Visualizing Sequence Alignment by Generating Publication-Ready Plots

**Version** 0.1

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**Description** Providing publication-ready graphs for Multiple sequence alignment. Moreover, it provides a unique solution for visualizing the multiple sequence alignment without the need to do the alignment in each run which is a big limitation in other available packages.

**License** GPL-3

**Encoding** UTF-8

**RoxygenNote** 7.1.2

**Imports** ggplot2, ggmsa, reshape2

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2023-06-14 16:22:05 UTC

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ggaligner                      *Visualize the alignment object from msa package*

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## Description

Generating a plot for msa object of DNA or Protein sequence

**Usage**

```
ggaligner(alignment, start=1, end=10, color="Clustal", font="helvetica", label_font = 12)
```

**Arguments**

alignment	alignment object returned from msa package
start	start position of the desired alignment region
end	end position of the desired alignment region
color	color scheme to use ex: Clustal, Chemistry_AA, Shapely_AA
font	font family to use ex: helvetica, TimesNewRoman
label_font	font size of sequence names

**Value**

An enhanced plot for the alignment using ggplot2 and ggmsa packages

**Author(s)**

Mohamed Soudy <Mohmedsoudy2009@gmail.com>

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Seqtochar

*Convert string to a character vector*

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**Description**

convert string that can be DNA or protein sequence to a character vector

**Usage**

```
Seqtochar(x)
```

**Arguments**

x	a sequence of DNA or Protein
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**Value**

this function is mainly used by ggaligner function to convert the input sequence to character vector

**Author(s)**

Mohamed Soudy <Mohmedsoudy2009@gmail.com>

**Examples**

```
Seqtochar("ATGACATAAT")
```

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