

# Package: helixvis (via r-universe)

September 2, 2024

**Type** Package

**Title** Visualize Alpha-Helical Peptide Sequences

**Version** 1.0.1

**Description** Create publication-quality, 2-dimensional visualizations of alpha-helical peptide sequences. Specifically, allows the user to programmatically generate helical wheels and wenxiang diagrams to provide a bird's eye, top-down view of alpha-helical oligopeptides. See Wadhwa RR, et al. (2018) <[doi:10.21105/joss.01008](https://doi.org/10.21105/joss.01008)> for more information.

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**Depends** R (>= 2.10)

**Imports** ggplot2 (>= 3.0.0), ggforce (>= 0.1.3), rlang (>= 0.2.2)

**URL** <https://github.com/rrrlw/helixvis>

**BugReports** <https://github.com/rrrlw/helixvis/issues>

**Suggests** knitr, rmarkdown, covr, testthat

**RoxygenNote** 6.1.0

**VignetteBuilder** knitr

**Repository** <https://rrrlw.r-universe.dev>

**RemoteUrl** <https://github.com/rrrlw/helixvis>

**RemoteRef** HEAD

**RemoteSha** 67cccf45b6c8143c8e2c13a8b4887a7fac850914

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draw_wenxiang	<i>Create Wenxiang diagrams to visualize alpha helical sequences.</i>
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**Description**

This function visualizes alpha-helical peptides as Wenxiang diagrams. Sequences between 2 and 18 (inclusive) characters can be visualized. The residue closest to the center represents the amino acid at the N-terminus (first in ‘sequence’).

**Usage**

```
draw_wenxiang(sequence, col = c("grey", "yellow", "blue", "red"),
  labels = FALSE, label.col = "black", fixed = TRUE,
  legend = FALSE)
```

**Arguments**

sequence	character vector containing amino acid sequence from N-terminus to C-terminus
col	colors for each amino acid type in the following order: nonpolar residues, polar residues, basic residues, acidic residues
labels	logical value; if TRUE, one-letter residue codes are overlaid on the residue circles
label.col	character value for color of labels added if ‘labels = TRUE’
fixed	if TRUE (default), ensures that residues will be circles (not ellipses) even if graphics device is rectangular
legend	if TRUE, adds legend to plot

**Examples**

```
draw_wenxiang("GIGAVLKVLTTGLPALIS")
draw_wenxiang("QQRKRKIWSILAPLGTTL")
```

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draw_wheel	<i>Create helical wheels to visualize alpha helical sequences.</i>
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**Description**

This function visualizes alpha-helical peptides as helical wheels. Sequences between 2 and 18 (inclusive) characters can be visualized. The residue in the upper half of the wheel lying at the horizontal center representing the amino acid at the N-terminus (first in ‘sequence’).

**Usage**

```
draw_wheel(sequence, col = c("grey", "yellow", "blue", "red"),
  labels = FALSE, label.col = "black", fixed = TRUE,
  legend = FALSE)
```

**Arguments**

sequence	character vector containing amino acid sequence from N-terminus to C-terminus
col	colors for each amino acid type in the following order: nonpolar residues, polar residues, basic residues, acidic residues
labels	logical value; if TRUE, one-letter residue codes are overlaid on the residue circles
label.col	character value for color of labels added if 'labels = TRUE'
fixed	if TRUE (default), ensures that residues will be circles (not ellipses) even if graphics device is rectangular
legend	if TRUE, adds legend to plot

**Examples**

```
draw_wheel("GIGAVLKVLTTGLPALIS")
draw_wheel("QQRKRKIWSILAPLGTTL")
```

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helixvis

*Quick and easy visualization of alpha-helical sequences.*


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**Description**

The helixvis package allows visualization of alpha-helical peptide sequences in the form of helical wheels. Although online servers currently exist that do this, all currently require entering sequences and storing images individually. None known to us are completely open-source. This package allows users to create visualizations for entire databases of amino acid sequences without need for manual input.

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sample\_seq

*Amino acid sequences of 5 antimicrobial peptides*


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**Description**

A dataset containing the name and residue sequence of five antimicrobial peptides from the Antimicrobial Peptide Database (APD3).

**Usage**

```
sample_seq
```

**Format**

A data frame with 5 rows and 2 variables:

**Name** antimicrobial peptide name

**Seq** antimicrobial residue sequence

**Details**

See Wang et al. (2016) <doi:10.1093/nar/gkv1278> for more information.

**Source**

<http://aps.unmc.edu/AP/>

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