

# Package: mSigPlot (via r-universe)

May 15, 2026

**Title** Plotting Mutational Signatures and Mutational Spectra

**Version** 2.0.41

**Description** Plotting functions for mutational signatures and mutational spectra, including single base substitutions (SBS), doublet base substitutions (DBS), and small insertions and deletions (indels). Generates plots similar to those used previously in Alexandrov et al. (2020)<[doi:10.1038/s41586-020-1943-3](https://doi.org/10.1038/s41586-020-1943-3)> and Rozen et al. (2026)<[doi:10.5281/zenodo.18451842](https://doi.org/10.5281/zenodo.18451842)>.

**License** GPL (>= 3)

**URL** <https://steverozen.github.io/mSigPlot/>,  
<https://github.com/steverozen/mSigPlot>

**BugReports** <https://github.com/steverozen/mSigPlot/issues>

**Imports** Cairo, dplyr, ggplot2, ggrepel, gridExtra, patchwork, scales

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## Description

Plot functions for SBS, DBS, and indel mutational signature catalogs as bar charts. Most functions return ggplot2 objects; plot\_SBS288 returns a patchwork object.

## Usage

```
plot_DBS144(
  catalog,
  plot_title = NULL,
  show_axis_text_x = TRUE,
  show_axis_text_y = TRUE,
  show_axis_title_x = TRUE,
  show_axis_title_y = TRUE,
  ylim = NULL,
  base_size = 11,
  plot_title_cex = 1,
  title_outside_plot = FALSE,
  axis_text_x_cex = 0.5,
  axis_title_x_cex = 0.8,
  axis_title_y_cex = 0.8,
  axis_text_y_cex = 0.7,
  grid = FALSE
)

plot_DBS144_pdf(catalog, filename, ...)

plot_DBS78(
  catalog,
  plot_title = NULL,
```

```
    grid = FALSE,
    upper = TRUE,
    show_axis_text_x = TRUE,
    show_axis_text_y = TRUE,
    show_axis_title_x = FALSE,
    show_axis_title_y = TRUE,
    ylim = NULL,
    base_size = 11,
    plot_title_cex = 1,
    title_outside_plot = FALSE,
    count_label_cex = 0.9,
    class_label_cex = 0.8,
    axis_text_x_cex = 0.5,
    axis_title_x_cex = 0.8,
    axis_title_y_cex = 0.8,
    axis_text_y_cex = 0.7,
    show_counts = NULL,
    num_peak_labels = 0,
    peak_label_cex = 0.7
)

plot_DBS78_pdf(catalog, filename, ...)

plot_ID166(
  catalog,
  plot_title = NULL,
  grid = FALSE,
  upper = TRUE,
  show_axis_text_x = TRUE,
  show_axis_text_y = TRUE,
  show_axis_title_x = FALSE,
  show_axis_title_y = TRUE,
  ylim = NULL,
  base_size = 11,
  plot_title_cex = 1,
  title_outside_plot = FALSE,
  title_x = 0.4,
  count_label_cex = 0.9,
  block_label_cex = 0.65,
  class_label_cex = 0.8,
  axis_text_x_cex = 0.5,
  bottom_label_cex = 0.65,
  axis_title_x_cex = 0.8,
  axis_title_y_cex = 0.8,
  axis_text_y_cex = 0.7,
  show_counts = NULL,
  num_peak_labels = 0,
  peak_label_cex = 0.7
```

```
)  
  
plot_ID166_pdf(catalog, filename, ...)  
  
plot_ID476(  
  catalog,  
  plot_title = NULL,  
  base_size = 11,  
  plot_title_cex = 1,  
  title_outside_plot = FALSE,  
  title_x = 0.4,  
  count_label_cex = 0.9,  
  class_label_cex = 0.8,  
  axis_text_x_cex = 0.5,  
  axis_title_x_cex = 0.8,  
  axis_title_y_cex = 0.8,  
  axis_text_y_cex = 0.7,  
  show_axis_text_x = TRUE,  
  show_axis_text_y = TRUE,  
  show_axis_title_x = TRUE,  
  show_axis_title_y = TRUE,  
  show_counts = NULL,  
  num_peak_labels = 4,  
  peak_label_cex = 0.7,  
  label_threshold_denominator = 7,  
  vline_labels = c(),  
  simplify_labels = FALSE,  
  plot_complex = FALSE,  
  grid = FALSE  
)  
  
plot_ID476_pdf(catalog, filename, ...)  
  
plot_ID476_right(  
  catalog,  
  plot_title = NULL,  
  base_size = 11,  
  plot_title_cex = 1,  
  title_outside_plot = FALSE,  
  title_x = 0.4,  
  count_label_cex = 0.9,  
  class_label_cex = 0.8,  
  axis_text_x_cex = 0.5,  
  axis_title_x_cex = 0.8,  
  axis_title_y_cex = 0.8,  
  axis_text_y_cex = 0.7,  
  show_axis_text_x = TRUE,  
  show_axis_text_y = TRUE,
```

```
    show_axis_title_x = TRUE,  
    show_axis_title_y = TRUE,  
    show_counts = NULL,  
    num_peak_labels = 3,  
    peak_label_cex = 0.7,  
    label_threshold_denominator = 7,  
    vline_labels = c(),  
    simplify_labels = TRUE,  
    plot_complex = FALSE,  
    grid = FALSE  
  )  
  
plot_ID476_right_pdf(catalog, filename, ...)
```

```
plot_ID83(  
  catalog,  
  plot_title = NULL,  
  grid = FALSE,  
  upper = TRUE,  
  show_axis_text_x = TRUE,  
  show_axis_text_y = TRUE,  
  show_axis_title_x = TRUE,  
  show_axis_title_y = TRUE,  
  ylim = NULL,  
  base_size = 11,  
  plot_title_cex = 1,  
  title_outside_plot = FALSE,  
  title_x = 0.4,  
  count_label_cex = 0.9,  
  block_label_cex = 0.65,  
  class_label_cex = 0.8,  
  axis_text_x_cex = 0.5,  
  bottom_label_cex = 0.65,  
  axis_title_x_cex = 0.8,  
  axis_title_y_cex = 0.8,  
  axis_text_y_cex = 0.7,  
  show_counts = NULL,  
  num_peak_labels = 0,  
  peak_label_cex = 0.7  
)  
  
plot_ID83_pdf(catalog, filename, ...)
```

```
plot_ID89(  
  catalog,  
  plot_title = NULL,  
  upper = TRUE,  
  show_axis_text_x = TRUE,
```

```
    show_axis_text_y = TRUE,
    show_axis_title_x = TRUE,
    show_axis_title_y = TRUE,
    ylim = NULL,
    base_size = 11,
    plot_title_cex = 1,
    title_outside_plot = FALSE,
    title_x = 0.4,
    count_label_cex = 0.9,
    block_label_cex = 0.65,
    class_label_cex = 0.8,
    axis_text_x_cex = 0.5,
    axis_title_x_cex = 0.8,
    axis_title_y_cex = 0.8,
    axis_text_y_cex = 0.7,
    show_counts = NULL,
    plot_complex = FALSE,
    num_peak_labels = 0,
    peak_label_cex = 0.7,
    grid = FALSE
)

plot_ID89_pdf(catalog, filename, ...)

plot_SBS12(
  catalog,
  plot_title = NULL,
  abundance = NULL,
  show_axis_text_x = TRUE,
  show_axis_text_y = TRUE,
  show_axis_title_x = FALSE,
  show_axis_title_y = TRUE,
  ylim = NULL,
  base_size = 11,
  plot_title_cex = 1,
  title_outside_plot = FALSE,
  axis_text_x_cex = 0.5,
  axis_title_x_cex = 0.8,
  axis_title_y_cex = 0.8,
  axis_text_y_cex = 0.7,
  grid = FALSE
)

plot_SBS12_pdf(catalog, filename, ...)

plot_SBS192(
  catalog,
  plot_title = NULL,
```

```
    grid = FALSE,
    upper = TRUE,
    show_axis_text_x = TRUE,
    show_axis_text_y = TRUE,
    show_axis_title_x = FALSE,
    show_axis_title_y = TRUE,
    ylim = NULL,
    base_size = 11,
    plot_title_cex = 1,
    title_outside_plot = FALSE,
    title_x = 0,
    count_label_cex = 0.9,
    class_label_cex = 0.8,
    axis_text_x_cex = 0.5,
    axis_title_x_cex = 0.8,
    axis_title_y_cex = 0.8,
    axis_text_y_cex = 0.7,
    show_counts = NULL,
    num_peak_labels = 0,
    peak_label_cex = 0.7
)

plot_SBS192_pdf(catalog, filename, ...)

plot_SBS288(
  catalog,
  plot_title = NULL,
  plot_title_cex = 1,
  title_outside_plot = FALSE,
  ...
)

plot_SBS288_pdf(catalog, filename, ...)

plot_SBS96(
  catalog,
  plot_title = NULL,
  grid = FALSE,
  upper = TRUE,
  show_axis_text_x = TRUE,
  show_axis_text_y = TRUE,
  show_axis_title_x = FALSE,
  show_axis_title_y = TRUE,
  ylim = NULL,
  base_size = 11,
  plot_title_cex = 1,
  title_outside_plot = FALSE,
  title_x = 0,
```

```

count_label_cex = 0.9,
class_label_cex = 0.8,
axis_text_x_cex = 0.5,
axis_title_x_cex = 0.8,
axis_title_y_cex = 0.8,
axis_text_y_cex = 0.7,
show_counts = NULL,
num_peak_labels = 0,
peak_label_cex = 0.7
)

plot_SBS96_pdf(catalog, filename, ...)

```

### Arguments

catalog	Numeric vector, single-column data.frame, matrix, tibble, or data.table. If there are row names (or for a vector, names), they will be checked against <code>catalog_row_order()</code> . SBS functions also accept "stapled" row names (e.g. A[C>A]A for SBS96, T:A[C>A]A for SBS288), which are automatically converted to compact format before validation.
plot_title	Character. Title displayed above the plot.
show_axis_text_x	Logical. If FALSE, hide x-axis tick labels.
show_axis_text_y	Logical. If FALSE, hide y-axis tick labels.
show_axis_title_x	Logical. If FALSE, hide the x-axis title.
show_axis_title_y	Logical. If FALSE, hide the y-axis title.
ylim	Optional y-axis limits. Either NULL (auto) or a length-2 numeric vector <code>c(ymin, ymax)</code> , following <code>ggplot2</code> 's <code>scale_y_continuous(limits = ...)</code> convention. A scalar is rejected with an error.
base_size	Numeric. Base font size in points.
plot_title_cex	Numeric. Multiplier for the plot title size.
title_outside_plot	Logical. If FALSE, the title is drawn inside the plot panel as an annotation (the <code>plot_ID83</code> style). If TRUE, the title is drawn above the panel via <code>ggtitle()</code> . For <code>plot_SBS288</code> , TRUE places the overall title above the 3-panel composite via <code>patchwork::plot_annotation()</code> ; FALSE prepends the title to each strand label ("Template", "Non-template", "Not-transcribed").
axis_text_x_cex	Numeric. Multiplier for x-axis labels.
axis_title_x_cex	Numeric. Multiplier for x-axis title size.
axis_title_y_cex	Numeric. Multiplier for the y-axis title size.

axis_text_y_cex	Numeric. Multiplier for the y-axis tick label size.
grid	Logical, draw horizontal grid lines at seq(0, ymax, ymax/4) over the data region. Available in all bar-plot functions except plot_SBS288 (which forwards grid to its three plot_SBS96 panels via ...).
filename	Character. Path to the output PDF file (_pdf functions only).
...	Additional arguments passed to plot_SBS96() (plot_SBS288 only).
upper	Logical, draw colored class rectangles and labels above bars (not available in plot_DBS144, plot_SBS12, plot_SBS288).
count_label_cex	Numeric. Multiplier for per-class count labels (not available in plot_DBS144, plot_SBS12).
class_label_cex	Numeric. Multiplier for major class labels.
show_counts	Logical or NULL. If TRUE, always display per-class count labels. If FALSE, never display them. If NULL, display them only when the catalog contains counts (sum > 1.1). Not available in plot_DBS144, plot_SBS12, plot_SBS288.
num_peak_labels	Integer. Number of top peaks to label (0 = none). Not available in plot_DBS144, plot_SBS12, plot_SBS288.
peak_label_cex	Numeric. Size multiplier for peak labels.
title_x	Numeric fraction in [0, 1] giving the horizontal position of the inside-panel title, as a fraction of the plot's bar range (0 = left edge, 1 = right edge). Ignored when title_outside_plot = TRUE. Default is 0 (far left) for SBS plots and 0.4 (a bit left of center) for ID plots, where the far-left corner often collides with ggrepel peak labels. Only available in plot_SBS96, plot_SBS192, plot_ID83, plot_ID89, plot_ID166, plot_ID476, plot_ID476_right.
block_label_cex	Numeric. Multiplier for colored category block labels (indel plots only).
bottom_label_cex	Numeric. Multiplier for bottom category description labels (indel plots only).
label_threshold_denominator	Numeric. Peaks below max/label_threshold_denominator are not labeled (plot_ID476, plot_ID476_right only).
vline_labels	Character vector. IndelType labels at which to draw vertical reference lines (plot_ID476, plot_ID476_right only).
simplify_labels	Logical. Simplify peak labels by removing the indel type prefix (plot_ID476, plot_ID476_right only).
plot_complex	Logical. Include Complex indel channels (plot_ID89, plot_ID476, plot_ID476_right only).
abundance	Numeric vector of per-class abundances for strand bias testing (plot_SBS12 only).

## Details

Functions in this family:

- `plot_SBS96`, `plot_SBS192`: SBS trinucleotide context
- `plot_DBS78`: DBS dinucleotide substitutions
- `plot_DBS144`: DBS with transcription strand
- `plot_SBS12`: SBS strand bias summary (collapses 192 to 12 bars)
- `plot_SBS288`: SBS with three-strand context
- `plot_ID166`: Indel genic/intergenic (166 channels)
- `plot_ID83`: Indel COSMIC classification (83 channels)
- `plot_ID89`: Indel Koh classification (89 channels)
- `plot_ID476`, `plot_ID476_right`: Indel with flanking context (476 channels)

Each has a corresponding `_pdf()` variant for multi-sample PDF export.

## Value

Plot functions return a `ggplot2` object (or a patchwork object for `plot_SBS288`), or `NULL` with a warning if the catalog is invalid (wrong size or row names). PDF functions return `NULL` invisibly (called for side effect of creating a PDF file), or stop with an error if the catalog is invalid.

## Examples

```
set.seed(1)
sig <- runif(144)
sig <- sig / sum(sig)
names(sig) <- catalog_row_order()$DBS144
plot_DBS144(sig, plot_title = "Example DBS144 signature")
```

```
set.seed(1)
sig <- runif(78)
sig <- sig / sum(sig)
names(sig) <- catalog_row_order()$DBS78
plot_DBS78(sig, plot_title = "Example DBS78 signature")
```

```
set.seed(1)
sig <- runif(166)
sig <- sig / sum(sig)
names(sig) <- catalog_row_order()$ID166
plot_ID166(sig, plot_title = "Example ID166 signature")
```

```
set.seed(1)
sig <- runif(476)
sig <- sig / sum(sig)
names(sig) <- catalog_row_order()$ID476
plot_ID476(sig, plot_title = "Example ID476")
```

```
set.seed(1)
sig <- runif(476)
sig <- sig / sum(sig)
names(sig) <- catalog_row_order()$ID476
plot_ID476_right(sig, plot_title = "Example ID476 right panel")
```

```
set.seed(1)
sig <- runif(83)
sig <- sig / sum(sig)
names(sig) <- catalog_row_order()$ID
plot_ID83(sig, plot_title = "Example ID83")
```

```
set.seed(1)
sig <- runif(89)
sig <- sig / sum(sig)
names(sig) <- catalog_row_order()$ID89
plot_ID89(sig, plot_title = "Example ID89")
```

```
set.seed(1)
sig <- runif(192)
sig <- sig / sum(sig)
names(sig) <- catalog_row_order()$SBS192
plot_SBS12(sig, plot_title = "Example SBS12 strand bias")
```

```
set.seed(1)
sig <- runif(192)
sig <- sig / sum(sig)
names(sig) <- catalog_row_order()$SBS192
plot_SBS192(sig, plot_title = "Example SBS192 signature")
```

```
set.seed(1)
sig <- runif(288)
names(sig) <- catalog_row_order()$SBS288
plot_SBS288(sig, plot_title = "Example SBS288")
```

```
# Plot a random SBS96 signature (proportions summing to 1)
set.seed(1)
sig <- runif(96)
sig <- sig / sum(sig)
names(sig) <- catalog_row_order()$SBS96
plot_SBS96(sig, plot_title = "Example SBS96 signature")
```

**Description**

Returns a named list containing the canonical row ordering for each catalog type. These are used for validation and ordering of mutation catalogs.

**Usage**

```
catalog_row_order()
```

**Details**

Row names use a compact 4-letter format for SBS types: e.g. ACAA encodes the trinucleotide context as <5' base><ref><3' base><alt>. SBS288 row names add a strand prefix: T:ACAA (transcribed), U:ACAA (untranscribed), N:ACAA (non-transcribed).

**Value**

A named list with elements: SBS96, SBS192, SBS288, SBS1536, DBS78, DBS136, DBS144, ID (83-category COSMIC indels), ID166, ID89, ID476.

**Examples**

```
cro <- catalog_row_order()
head(cro$SBS96)
length(cro$DBS78)
```

---

heatmap\_plots

*plot\_DBS136, plot\_DBS136\_pdf, plot\_SBS1536, plot\_SBS1536\_pdf*

---

**Description**

Plot functions for SBS and DBS mutational signature catalogs as heatmaps. Plot functions return patchwork objects (composites of ggplot2 panels).

**Usage**

```
plot_DBS136(
  catalog,
  plot_title = NULL,
  base_size = 11,
  plot_title_cex = 1.2,
  axis_text_cex = 0.8,
  strip_text_cex = 1,
  show_axis_text_x = TRUE,
  show_axis_text_y = TRUE,
  show_axis_title_x = TRUE,
  show_axis_title_y = TRUE
)
```

```
plot_DBS136_pdf(catalog, filename, ...)
```

```
plot_SBS1536(
  catalog,
  plot_title = NULL,
  base_size = 11,
  plot_title_cex = 1.2,
  axis_text_cex = 0.8,
  strip_text_cex = 1,
  show_axis_text_x = TRUE,
  show_axis_text_y = TRUE,
  show_axis_title_x = TRUE,
  show_axis_title_y = TRUE
)
```

```
plot_SBS1536_pdf(catalog, filename, ...)
```

### Arguments

catalog	Numeric vector, single-column data.frame, matrix, tibble, or data.table. If there are row names (or for a vector, names), they will be checked against <code>catalog_row_order()</code> .
plot_title	Character. Title displayed above the plot.
base_size	Numeric. Base font size in points.
plot_title_cex	Numeric. Multiplier for the plot title size.
axis_text_cex	Numeric. Multiplier for axis label size.
strip_text_cex	Numeric. Multiplier for panel/facet label size.
show_axis_text_x	Logical. If FALSE, hide x-axis base labels.
show_axis_text_y	Logical. If FALSE, hide y-axis base labels.
show_axis_title_x	Logical. If FALSE, hide the x-axis description.
show_axis_title_y	Logical. If FALSE, hide the y-axis description.
filename	Character. Path to the output PDF file ( <code>_pdf</code> functions only).
...	Additional arguments passed to the underlying plot function ( <code>_pdf</code> variants only).

### Details

Functions in this family:

- `plot_SBS1536`: SBS pentanucleotide context (1536 channels)
- `plot_DBS136`: DBS heatmap (136 channels, 10 4x4 panels)

Each has a corresponding `_pdf()` variant for multi-sample PDF export.

**Value**

Plot functions return a patchwork object (a composite of ggplot2 panels), or NULL with a warning if the catalog is invalid (wrong size or row names). Note: adding ggplot2 layers with + (e.g. + ggtitle()) applies only to the last sub-plot, not the composite; use `patchwork::plot_annotation()` for titles/captions on the whole composition. PDF functions return NULL invisibly (called for side effect of creating a PDF file), or stop with an error if the catalog is invalid.

**Examples**

```
set.seed(1)
sig <- runif(136)
sig <- sig / sum(sig)
names(sig) <- catalog_row_order()$DBS136
plot_DBS136(sig, plot_title = "Example DBS136")
```

```
set.seed(1)
sig <- runif(1536)
sig <- sig / sum(sig)
names(sig) <- catalog_row_order()$SBS1536
plot_SBS1536(sig, plot_title = "Example SBS1536")
```

---

id89\_figlabels

*Derive ID89 figure-axis labels from canonical IndelType strings*


---

**Description**

Rewrites the canonical ID89 channel names from `catalog_row_order()$ID89` into the compact tick-label style used on the x-axis of `plot_ID89()`.

**Usage**

```
id89_figlabels(indel_types)
```

**Arguments**

`indel_types` Character vector of ID89 IndelType strings, typically `catalog_row_order()$ID89`.

**Details**

Single-base channels (matching Del(C), Del(T), Ins(C), Ins(T)): the Del(.)/Ins(. ) wrapper and the :R prefix are dropped, and any open-ended repeat range (N, ) is rewritten as (N+).

Multi-base channels (longer Del/Ins/MH rows): leading Del(/Ins( is rewritten to L(, a leading open-ended length (N, ) is space-padded to (N, ), a trailing R(N, ) becomes R(N+), a trailing M(N, ) is space-padded to M(N, ), and all colons are removed.

The "Complex" channel is returned unchanged.

**Value**

A character vector of the same length as `indel_types`, giving the figure-label form of each channel name.

**Examples**

```
id89_figlabels(c(
  "[Del(C):R1]A",
  "Del(C):R(6,)",
  "Del(2,4):R1",
  "Del(2,):U(1,2):R(5,)",
  "Del(6,):M(4,)",
  "Complex"
))
```

---

plot\_guess

*plot\_guess, plot\_guess\_pdf*

---

**Description**

Automatically select the appropriate plotting function based on the number of rows in the catalog.

**Usage**

```
plot_guess(catalog, ...)
```

```
plot_guess_pdf(catalog, filename, ...)
```

**Arguments**

`catalog` Numeric vector, single-column data.frame, matrix, tibble, or data.table. The number of rows (or length) determines which plotting function is used:

- 1536 rows: calls `plot_SBS1536()`
- 476 rows: calls `plot_ID476()`
- 288 rows: calls `plot_SBS288()`
- 192 rows: calls `plot_SBS192()`
- 166 rows: calls `plot_ID166()`
- 144 rows: calls `plot_DBS144()`
- 136 rows: calls `plot_DBS136()`
- 96 rows: calls `plot_SBS96()`
- 89 rows: calls `plot_ID89()`
- 83 rows: calls `plot_ID83()`
- 78 rows: calls `plot_DBS78()`

The column names of `catalog` are used as plot titles.

`...` Additional arguments passed to the underlying plotting function.

`filename` Character. Path to the output PDF file (`plot_guess_pdf` only).

## Details

`plot_guess()` plots a single sample. `plot_guess_pdf()` creates a multi-page PDF file containing plots for multiple samples, arranged with 5 samples per page (except heatmap types: 1 per page). Uses Cairo for high-quality PDF rendering.

## Value

`plot_guess()` returns a plot object. The exact class depends on the dispatched function: most return a ggplot object; SBS288, DBS136, and SBS1536 return patchwork objects. Note: adding ggplot2 layers with `+` to a patchwork object (e.g. `+ ggtitle()`) applies only to the last sub-plot, not the composite; use `patchwork::plot_annotation()` instead. `plot_guess_pdf()` returns NULL invisibly (called for side effect of creating a PDF file).

## See Also

[plot\\_SBS96\(\)](#), [plot\\_SBS192\(\)](#), [plot\\_SBS288\(\)](#), [plot\\_SBS1536\(\)](#), [plot\\_DBS78\(\)](#), [plot\\_DBS136\(\)](#), [plot\\_DBS144\(\)](#), [plot\\_ID166\(\)](#), [plot\\_ID476\(\)](#), [plot\\_ID89\(\)](#), [plot\\_ID83\(\)](#)

## Examples

```
# Auto-detect a 96-channel catalog and dispatch to plot_SBS96
set.seed(1)
sig <- runif(96)
sig <- sig / sum(sig)
names(sig) <- catalog_row_order()$SBS96
plot_guess(sig, plot_title = "Auto-detected SBS96")

sig <- matrix(runif(96 * 3), nrow = 96)
rownames(sig) <- catalog_row_order()$SBS96
colnames(sig) <- paste0("Sig", 1:3)
plot_guess_pdf(sig, filename = tempfile(fileext = ".pdf"))
```

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