Package 'cosmicsig'

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Title Repository of Mutational Signatures Data from COSMIC (the Catalogue Of Somatic Mutations In Cancer)

Version 1.0.0

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Description Contains mutational signatures data from the COSMIC (the Catalogue Of Somatic Mutations In Cancer) website <https://cancer.sanger.ac.uk/signatures/>.

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URL https://github.com/Rozen-Lab/cosmicsig

BugReports https://github.com/Rozen-Lab/cosmicsig/issues

Language en-US

Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.2

Depends R (>= 3.5)

Suggests ICAMS

R topics documented:

COSMIC_v3.2	*Mutational signatures data from COSMIC, the Catalogue Of Somatic Mutations In Cancer, (v3.2 - March 2021)*

Description

Mutational signatures data from COSMIC, the Catalogue Of Somatic Mutations In Cancer, (v3.2 - March 2021)

Usage

```
COSMIC_v3.2
```

Format

A list with two elements, `signature` and `etiology`.

- `signature` is a list with one element:
  - genome: A list with the elements:
    * SBS96: Strand-agnostic single-base substitutions in trinucleotide context.
    * SBS192: Transcriptionally stranded single-base substitutions in trinucleotide context.
    * DBS78: Strand-agnostic doublet-base substitutions.
    * ID: Strand-agnostic indels.
- `etiology` is a list with elements:
  - SBS96
  - SBS192
  - DBS78
  - ID

  Each element in `etiology` is a single column matrix with rownames being the signature IDs and values being a short character string description of the proposed etiology.

  In general use `get_etiology`, which handles new signatures without elements in `etiology`.

Remark

The signatures are all from Human GRCh37 reference genome.

Note

SBS10c, SBS10d, SBS91, SBS92, SBS93, SBS94 (total 6) new SBS signatures were added in COSMIC v3.2. See the news from COSMIC release for more details `https://cosmic-blog.sanger.ac.uk/cosmic-mutational-signatures-release-v3-2/`

Source

Files downloaded from `https://cancer.sanger.ac.uk/signatures/downloads/`, 2021 Sep and saved in `data-raw/COSMIC_v3.2/data/`.
Populated by `data-raw/COSMIC_v3.2/code/generate_COSMIC_v3.2_data.R`.

Examples

```
SBS96_sigs <- COSMIC_v3.2$signature$genome$SBS96
```

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etiology	*List of mutational signature's proposed etiology summarized from COSMIC, the Catalogue Of Somatic Mutations In Cancer (v3.2 - March 2021)*

Description

List of mutational signature's proposed etiology summarized from COSMIC, the Catalogue Of Somatic Mutations In Cancer (v3.2 - March 2021)

Usage

```
etiology
```

Format

A list with the elements:

- SBS96
- SBS192
- DBS78
- ID

Each list element is a single column matrix with rownames being the signature IDs and values being a short character string description of the proposed etiology.

In general use [get_etiology](#), which handles new signatures without elements in `etiology`.

Examples

```
SBS96_etiology <- etiology$SBS96
```

SBS96_ID_to_SBS192_ID	*Translate SBS96 signature IDs to SBS192 signature IDs by adding "-E" if necessary*

Description

Translate SBS96 signature IDs to SBS192 signature IDs by adding "-E" if necessary

Usage

```
SBS96_ID_to_SBS192_ID(sig_ids)
```

Arguments

sig_ids	Character vector of SBS96 signature IDs.

Value

Character vector of corresponding SBS192 signature IDs; some have "-E" (for exome) post-pended.

Examples

```
SBS96_ids <- c("SBS1", "SBS23", "SBS25")
SBS192_ids <- SBS96_ID_to_SBS192_ID(SBS96_ids)
```

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signature	*Mutational signatures data from COSMIC, the Catalogue Of Somatic Mutations In Cancer (v3.2 - March 2021)*

Description

Mutational signatures data from COSMIC, the Catalogue Of Somatic Mutations In Cancer (v3.2 - March 2021)

Usage

```
signature
```

Format

A list with a single element, genome, which is a list containing:

SBS96 Strand-agnostic single-base substitutions in trinucleotide context.

SBS192 Transcriptionally stranded single-base substitutions in trinucleotide context.

DBS78 Strand-agnostic doublet-base substitutions.

ID Strand-agnostic indels.

Remark

The signatures are all from Human GRCh37 reference genome. See CatalogRowOrder for the classification of mutation types.

Note

SBS10c, SBS10d, SBS91, SBS92, SBS93, SBS94 (total 6) new SBS signatures were added in COSMIC v3.2. See the news from COSMIC release for more details `https://cosmic-blog.sanger.ac.uk/cosmic-mutational-signatures-release-v3-2/`

Source

Files downloaded from `https://cancer.sanger.ac.uk/signatures/downloads/`, 2021 Sep and saved in `data-raw/COSMIC_v3.2/data/`.
Populated by `data-raw/COSMIC_v3.2/code/generate_COSMIC_v3.2_genome_sigs.R`.

Examples

```
SBS96_sigs <- signature$genome$SBS96
```

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