

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>

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

This is a data package with 2 main package variables: `signature` and `etiology`.

Details

There are also several functions for handling COSMIC signatures:

- `get_etiology`
- `SBS96_ID_to_SBS192_ID`

Source

COSMIC mutational signatures data were downloaded from <https://cancer.sanger.ac.uk/signatures/downloads/>.

COSMIC_v3.0	<i>Mutational signatures data from COSMIC, the Catalogue Of Somatic Mutations In Cancer, (v3.0 - May 2019)</i>
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Description

Mutational signatures data from COSMIC, the Catalogue Of Somatic Mutations In Cancer, (v3.0 - May 2019)

Usage

COSMIC_v3.0

Format

A list with one element signature.

- 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.

Remark

The signatures are all from Human GRCh37 reference genome.

Source

Files downloaded from <https://cancer.sanger.ac.uk/signatures/downloads/>, 2021 Oct and saved in data-raw/COSMIC_v3.0/data/.
Populated by data-raw/COSMIC_v3.0/code/generate_COSMIC_v3.0_genome_sigs.R.

Examples

```
COSMIC_v3.0_SBS96.sigs <- COSMIC_v3.0$signature$genome$SBS96
```

COSMIC_v3.1	<i>Mutational signatures data from COSMIC, the Catalogue Of Somatic Mutations In Cancer, (v3.1 - June 2020)</i>
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Description

Mutational signatures data from COSMIC, the Catalogue Of Somatic Mutations In Cancer, (v3.1 - June 2020)

Usage

```
COSMIC_v3.1
```

Format

A list with one element signature.

- 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.

Remark

The signatures are all from Human GRCh37 reference genome.

Source

Files downloaded from <https://cancer.sanger.ac.uk/signatures/downloads/>, 2021 Oct and saved in data-raw/COSMIC_v3.1/data/.
Populated by data-raw/COSMIC_v3.1/code/generate_COSMIC_v3.1_genome_sigs.R.

Examples

```
COSMIC_v3.1_SBS96.sigs <- COSMIC_v3.1$signature$genome$SBS96
```

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 Oct and saved in data-raw/COSMIC_v3.2/data/.

Populated by data-raw/COSMIC_v3.2/code/generate_COSMIC_v3.2_data.R.

Examples

```
COSMIC_v3.2_SBS96_sigs <- COSMIC_v3.2$signature$genome$SBS96
```

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

get_etiology	<i>Get the proposed etiology of COSMIC signature</i>
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Description

Get the proposed etiology of COSMIC signature

Usage

```
get_etiology(mutation_type, sig_id, cosmic_version = "3.2")
```

Arguments

`mutation_type` Character string, one of "SBS96", "SBS192", "DBS78", "ID".

`sig_id` Character vector with signature ids, e.g. `c("SBS3", "SBS5")`.

`cosmic_version` COSMIC signature version.

Value

A character vector of the same length as `sig_id`, each element of which is the etiology of the corresponding signature, if known, or else the empty string.

Examples

```
get_etiology(mutation_type = "ID", sig_id = c("ID1", "foo", "ID3"))
```

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)
```

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