Package ‘curatedMetagenomicData’

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Type Package

Title Curated Metagenomic Data of the Human Microbiome

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Description The curatedMetagenomicData package provides taxonomic, functional, and gene marker abundance for samples collected from different bodysites.

License Artistic-2.0

Encoding UTF-8

Depends R (>= 3.3.0), dplyr (>= 0.5.0), phyloseq (>= 1.18.0), Biobase (>= 2.34.0), ExperimentHub (>= 1.0.0), AnnotationHub (>= 2.6.0), magrittr

Imports BiocInstaller, utils, tidyr

Suggests devtools, roxygen2, testthat, covr, knitr, rmarkdown, BiocCheck, BiocStyle, BiocInstaller, BiocParallel, readr, RISmed

VignetteBuilder knitr

biocViews Homo_sapiens_Data, ReproducibleResearch, MicrobiomeData

RoxygenNote 5.0.1

NeedsCompilation no

R topics documented:

`curatedMetagenomicData` *Curated Metagenomic Data of the Human Microbiome*

Description

The curatedMetagenomicData package provides taxonomic, functional, and gene marker abundance for samples collected from different bodysites. It provides data from aproximately 3000 human microbiome samples that has been highly processed, refined, and curated such that analysis that might otherwise require a computing cluster can be done on an ordianary laptop.

`ExpressionSet2phyloseq` *Convert an ExpressionSet object to a phyloseq object*

Description

Convert an ExpressionSet object to a phyloseq object

Usage

```
ExpressionSet2phyloseq(eset, simplify = TRUE, relab = TRUE)
```

Arguments

`eset`	An eset object
`simplify`	if TRUE the most detailed clade name is used
`relab`	if FALSE, values are multiplied by read depth to approximate counts, if TRUE (default) values kept as relative abundances between 0 and 100%.

Value

A phyloseq object

Examples

```
LomanNJ_2013_Mi.metaphlan_bugs_list.stool() %>%
ExpressionSet2phyloseq()
```

`HMP_2012.genefamilies_relab` *Relabeled genefamilies data from the HMP_2012 dataset*

Description

Relabeled genefamilies data from the HMP_2012 dataset

Datasets

HMP_2012.genefamilies_relab.anterior_nares: An ExpressionSet with 93 samples and 1,964,481 features specific to the anterior_nares bodysite

HMP_2012.genefamilies_relab.buccal_mucosa: An ExpressionSet with 119 samples and 1,964,481 features specific to the buccal_mucosa bodysite

HMP_2012.genefamilies_relab.hard_palate: An ExpressionSet with 1 sample and 1,964,481 features specific to the hard_palate bodysite

HMP_2012.genefamilies_relab.keratinized_gingiva: An ExpressionSet with 6 samples and 1,964,481 features specific to the keratinized_gingiva bodysite

HMP_2012.genefamilies_relab.l_retroauricular_crease: An ExpressionSet with 9 samples and 1,964,481 features specific to the l_retroauricular_crease bodysite

HMP_2012.genefamilies_relab.mid_vagina: An ExpressionSet with 2 samples and 1,964,481 features specific to the mid_vagina bodysite

HMP_2012.genefamilies_relab.palatine_tonsils: An ExpressionSet with 6 samples and 1,964,481 features specific to the palatine_tonsils bodysite

HMP_2012.genefamilies_relab.posterior_fornix: An ExpressionSet with 62 samples and 1,964,481 features specific to the posterior_fornix bodysite

HMP_2012.genefamilies_relab.r_retroauricular_crease: An ExpressionSet with 18 samples and 1,964,481 features specific to the r_retroauricular_crease bodysite

HMP_2012.genefamilies_relab.saliva: An ExpressionSet with 5 samples and 1,964,481 features specific to the saliva bodysite

HMP_2012.genefamilies_relab.stool: An ExpressionSet with 147 samples and 1,964,481 features specific to the stool bodysite

HMP_2012.genefamilies_relab.subgingival_plaque: An ExpressionSet with 7 samples and 1,964,481 features specific to the subgingival_plaque bodysite

HMP_2012.genefamilies_relab.supragingival_plaque: An ExpressionSet with 128 samples and 1,964,481 features specific to the supragingival_plaque bodysite

HMP_2012.genefamilies_relab.throat: An ExpressionSet with 7 samples and 1,964,481 features specific to the throat bodysite

HMP_2012.genefamilies_relab.tongue_dorsum: An ExpressionSet with 136 samples and 1,964,481 features specific to the tongue_dorsum bodysite

HMP_2012.genefamilies_relab.vaginal_introitus: An ExpressionSet with 3 samples and 1,964,481 features specific to the vaginal_introitus bodysite

Source

Department of Psychology, Abdul Haq Campus, Federal Urdu University for Arts, Science and Technology, Karachi, Pakistan. shahiq_psy@yahoo.com

See Also

`HMP_2012.marker_abundance`, `HMP_2012.marker_presence`, `HMP_2012.metaphlan_bugs_list`, `HMP_2012.pathabundance_relab`, `HMP_2012.pathcoverage`

Examples

```
HMP_2012.genefamilies_relab.anterior_nares()
```

`HMP_2012.marker_abundance`

Marker abundance data from the HMP_2012 dataset

Description

Marker abundance data from the HMP_2012 dataset

Datasets

HMP_2012.marker_abundance.anterior_nares: An ExpressionSet with 93 samples and 162,108 features specific to the anterior_nares bodysite

HMP_2012.marker_abundance.buccal_mucosa: An ExpressionSet with 119 samples and 162,108 features specific to the buccal_mucosa bodysite

HMP_2012.marker_abundance.hard_palate: An ExpressionSet with 1 sample and 162,108 features specific to the hard_palate bodysite

HMP_2012.marker_abundance.keratinized_gingiva: An ExpressionSet with 6 samples and 162,108 features specific to the keratinized_gingiva bodysite

HMP_2012.marker_abundance.l_retroauricular_crease: An ExpressionSet with 9 samples and 162,108 features specific to the l_retroauricular_crease bodysite

HMP_2012.marker_abundance.mid_vagina: An ExpressionSet with 2 samples and 162,108 features specific to the mid_vagina bodysite

HMP_2012.marker_abundance.palatine_tonsils: An ExpressionSet with 6 samples and 162,108 features specific to the palatine_tonsils bodysite

HMP_2012.marker_abundance.posterior_fornix: An ExpressionSet with 62 samples and 162,108 features specific to the posterior_fornix bodysite

HMP_2012.marker_abundance.r_retroauricular_crease: An ExpressionSet with 18 samples and 162,108 features specific to the r_retroauricular_crease bodysite

HMP_2012.marker_abundance.saliva: An ExpressionSet with 5 samples and 162,108 features specific to the saliva bodysite

HMP_2012.marker_abundance.stool: An ExpressionSet with 147 samples and 162,108 features specific to the stool bodysite

HMP_2012.marker_abundance.subgingival_plaque: An ExpressionSet with 7 samples and 162,108 features specific to the subgingival_plaque bodysite

HMP_2012.marker_abundance.supragingival_plaque: An ExpressionSet with 128 samples and 162,108 features specific to the supragingival_plaque bodysite

HMP_2012.marker_abundance.throat: An ExpressionSet with 7 samples and 162,108 features specific to the throat bodysite

HMP_2012.marker_abundance.tongue_dorsum: An ExpressionSet with 136 samples and 162,108 features specific to the tongue_dorsum bodysite

HMP_2012.marker_abundance.vaginal_introitus: An ExpressionSet with 3 samples and 162,108 features specific to the vaginal_introitus bodysite

Source

Department of Psychology, Abdul Haq Campus, Federal Urdu University for Arts, Science and Technology, Karachi, Pakistan. shahiq_psy@yahoo.com

See Also

`HMP_2012.genefamilies_relab`, `HMP_2012.marker_presence`, `HMP_2012.metaphlan_bugs_list`, `HMP_2012.pathabundance_relab`, `HMP_2012.pathcoverage`

Examples

```
HMP_2012.marker_abundance.anterior_nares()
```

`HMP_2012.marker_presence`

Marker presence data from the HMP_2012 dataset

Description

Marker presence data from the HMP_2012 dataset

Datasets

HMP_2012.marker_presence.anterior_nares: An ExpressionSet with 93 samples and 158,646 features specific to the anterior_nares bodysite

HMP_2012.marker_presence.buccal_mucosa: An ExpressionSet with 119 samples and 158,646 features specific to the buccal_mucosa bodysite

HMP_2012.marker_presence.hard_palate: An ExpressionSet with 1 sample and 158,646 features specific to the hard_palate bodysite

HMP_2012.marker_presence.keratinized_gingiva: An ExpressionSet with 6 samples and 158,646 features specific to the keratinized_gingiva bodysite

HMP_2012.marker_presence.l_retroauricular_crease: An ExpressionSet with 9 samples and 158,646 features specific to the l_retroauricular_crease bodysite

HMP_2012.marker_presence.mid_vagina: An ExpressionSet with 2 samples and 158,646 features specific to the mid_vagina bodysite

HMP_2012.marker_presence.palatine_tonsils: An ExpressionSet with 6 samples and 158,646 features specific to the palatine_tonsils bodysite

HMP_2012.marker_presence.posterior_fornix: An ExpressionSet with 62 samples and 158,646 features specific to the posterior_fornix bodysite

HMP_2012.marker_presence.r_retroauricular_crease: An ExpressionSet with 18 samples and 158,646 features specific to the r_retroauricular_crease bodysite

HMP_2012.marker_presence.saliva: An ExpressionSet with 5 samples and 158,646 features specific to the saliva bodysite

HMP_2012.marker_presence.stool: An ExpressionSet with 147 samples and 158,646 features specific to the stool bodysite

HMP_2012.marker_presence.subgingival_plaque: An ExpressionSet with 7 samples and 158,646 features specific to the subgingival_plaque bodysite

HMP_2012.marker_presence.supragingival_plaque: An ExpressionSet with 128 samples and 158,646 features specific to the supragingival_plaque bodysite

HMP_2012.marker_presence.throat: An ExpressionSet with 7 samples and 158,646 features specific to the throat bodysite

HMP_2012.marker_presence.tongue_dorsum: An ExpressionSet with 136 samples and 158,646 features specific to the tongue_dorsum bodysite

HMP_2012.marker_presence.vaginal_introitus: An ExpressionSet with 3 samples and 158,646 features specific to the vaginal_introitus bodysite

Source

Department of Psychology, Abdul Haq Campus, Federal Urdu University for Arts, Science and Technology, Karachi, Pakistan. shahiq_psy@yahoo.com

See Also

`HMP_2012.genefamilies_relab`, `HMP_2012.marker_abundance`, `HMP_2012.metaphlan_bugs_list`, `HMP_2012.pathabundance_relab`, `HMP_2012.pathcoverage`

Examples

```
HMP_2012.marker_presence.anterior_nares()
```

`HMP_2012.metaphlan_bugs_list` *Taxonomic abundance data from the HMP_2012 dataset*

Description

Taxonomic abundance data from the HMP_2012 dataset

Datasets

HMP_2012.metaphlan_bugs_list.anterior_nares: An ExpressionSet with 93 samples and 1,988 features specific to the anterior_nares bodysite

HMP_2012.metaphlan_bugs_list.buccal_mucosa: An ExpressionSet with 119 samples and 1,988 features specific to the buccal_mucosa bodysite

HMP_2012.metaphlan_bugs_list.hard_palate: An ExpressionSet with 1 sample and 1,988 features specific to the hard_palate bodysite

HMP_2012.metaphlan_bugs_list.keratinized_gingiva: An ExpressionSet with 6 samples and 1,988 features specific to the keratinized_gingiva bodysite

HMP_2012.metaphlan_bugs_list.l_retroauricular_crease: An ExpressionSet with 9 samples and 1,988 features specific to the l_retroauricular_crease bodysite

HMP_2012.metaphlan_bugs_list.mid_vagina: An ExpressionSet with 2 samples and 1,988 features specific to the mid_vagina bodysite

HMP_2012.metaphlan_bugs_list.palatine_tonsils: An ExpressionSet with 6 samples and 1,988 features specific to the palatine_tonsils bodysite

HMP_2012.metaphlan_bugs_list.posterior_fornix: An ExpressionSet with 62 samples and 1,988 features specific to the posterior_fornix bodysite

HMP_2012.metaphlan_bugs_list.r_retroauricular_crease: An ExpressionSet with 18 samples and 1,988 features specific to the r_retroauricular_crease bodysite

HMP_2012.metaphlan_bugs_list.saliva: An ExpressionSet with 5 samples and 1,988 features specific to the saliva bodysite

HMP_2012.metaphlan_bugs_list.stool: An ExpressionSet with 147 samples and 1,988 features specific to the stool bodysite

HMP_2012.metaphlan_bugs_list.subgingival_plaque: An ExpressionSet with 7 samples and 1,988 features specific to the subgingival_plaque bodysite

HMP_2012.metaphlan_bugs_list.supragingival_plaque: An ExpressionSet with 128 samples and 1,988 features specific to the supragingival_plaque bodysite

HMP_2012.metaphlan_bugs_list.throat: An ExpressionSet with 7 samples and 1,988 features specific to the throat bodysite

HMP_2012.metaphlan_bugs_list.tongue_dorsum: An ExpressionSet with 136 samples and 1,988 features specific to the tongue_dorsum bodysite

HMP_2012.metaphlan_bugs_list.vaginal_introitus: An ExpressionSet with 3 samples and 1,988 features specific to the vaginal_introitus bodysite

Source

Department of Psychology, Abdul Haq Campus, Federal Urdu University for Arts, Science and Technology, Karachi, Pakistan. shahiq_psy@yahoo.com

See Also

`HMP_2012.genefamilies_relab`, `HMP_2012.marker_abundance`, `HMP_2012.marker_presence`, `HMP_2012.pathabundance_relab`, `HMP_2012.pathcoverage`

Examples

```
HMP_2012.metaphlan_bugs_list.anterior_nares()
```

`HMP_2012.pathabundance_relab` *Relabeled pathabundance data from the HMP_2012 dataset*

Description

Relabeled pathabundance data from the HMP_2012 dataset

Datasets

HMP_2012.pathabundance_relab.anterior_nares: An ExpressionSet with 93 samples and 23,271 features specific to the anterior_nares bodysite

HMP_2012.pathabundance_relab.buccal_mucosa: An ExpressionSet with 119 samples and 23,271 features specific to the buccal_mucosa bodysite

HMP_2012.pathabundance_relab.hard_palate: An ExpressionSet with 1 sample and 23,271 features specific to the hard_palate bodysite

HMP_2012.pathabundance_relab.keratinized_gingiva: An ExpressionSet with 6 samples and 23,271 features specific to the keratinized_gingiva bodysite

HMP_2012.pathabundance_relab.l_retroauricular_crease: An ExpressionSet with 9 samples and 23,271 features specific to the l_retroauricular_crease bodysite

HMP_2012.pathabundance_relab.mid_vagina: An ExpressionSet with 2 samples and 23,271 features specific to the mid_vagina bodysite

HMP_2012.pathabundance_relab.palatine_tonsils: An ExpressionSet with 6 samples and 23,271 features specific to the palatine_tonsils bodysite

HMP_2012.pathabundance_relab.posterior_fornix: An ExpressionSet with 62 samples and 23,271 features specific to the posterior_fornix bodysite

HMP_2012.pathabundance_relab.r_retroauricular_crease: An ExpressionSet with 18 samples and 23,271 features specific to the r_retroauricular_crease bodysite

HMP_2012.pathabundance_relab.saliva: An ExpressionSet with 5 samples and 23,271 features specific to the saliva bodysite

HMP_2012.pathabundance_relab.stool: An ExpressionSet with 147 samples and 23,271 features specific to the stool bodysite

HMP_2012.pathabundance_relab.subgingival_plaque: An ExpressionSet with 7 samples and 23,271 features specific to the subgingival_plaque bodysite

HMP_2012.pathabundance_relab.supragingival_plaque: An ExpressionSet with 128 samples and 23,271 features specific to the supragingival_plaque bodysite

HMP_2012.pathabundance_relab.throat: An ExpressionSet with 7 samples and 23,271 features specific to the throat bodysite

HMP_2012.pathabundance_relab.tongue_dorsum: An ExpressionSet with 136 samples and 23,271 features specific to the tongue_dorsum bodysite

HMP_2012.pathabundance_relab.vaginal_introitus: An ExpressionSet with 3 samples and 23,271 features specific to the vaginal_introitus bodysite

Source

Department of Psychology, Abdul Haq Campus, Federal Urdu University for Arts, Science and Technology, Karachi, Pakistan. shahiq_psy@yahoo.com

See Also

`HMP_2012.genefamilies_relab`, `HMP_2012.marker_abundance`, `HMP_2012.marker_presence`, `HMP_2012.metaphlan_bugs_list`, `HMP_2012.pathcoverage`

Examples

```
HMP_2012.pathabundance_relab.anterior_nares()
```

`HMP_2012.pathcoverage` *Pathcoverage data from the HMP_2012 dataset*

Description

Pathcoverage data from the HMP_2012 dataset

Datasets

HMP_2012.pathcoverage.anterior_nares: An ExpressionSet with 93 samples and 23,271 features specific to the anterior_nares bodysite

HMP_2012.pathcoverage.buccal_mucosa: An ExpressionSet with 119 samples and 23,271 features specific to the buccal_mucosa bodysite

HMP_2012.pathcoverage.hard_palate: An ExpressionSet with 1 sample and 23,271 features specific to the hard_palate bodysite

HMP_2012.pathcoverage.keratinized_gingiva: An ExpressionSet with 6 samples and 23,271 features specific to the keratinized_gingiva bodysite

HMP_2012.pathcoverage.l_retroauricular_crease: An ExpressionSet with 9 samples and 23,271 features specific to the l_retroauricular_crease bodysite

HMP_2012.pathcoverage.mid_vagina: An ExpressionSet with 2 samples and 23,271 features specific to the mid_vagina bodysite

HMP_2012.pathcoverage.palatine_tonsils: An ExpressionSet with 6 samples and 23,271 features specific to the palatine_tonsils bodysite

HMP_2012.pathcoverage.posterior_fornix: An ExpressionSet with 62 samples and 23,271 features specific to the posterior_fornix bodysite

HMP_2012.pathcoverage.r_retroauricular_crease: An ExpressionSet with 18 samples and 23,271 features specific to the r_retroauricular_crease bodysite

HMP_2012.pathcoverage.saliva: An ExpressionSet with 5 samples and 23,271 features specific to the saliva bodysite

HMP_2012.pathcoverage.stool: An ExpressionSet with 147 samples and 23,271 features specific to the stool bodysite

HMP_2012.pathcoverage.subgingival_plaque: An ExpressionSet with 7 samples and 23,271 features specific to the subgingival_plaque bodysite

HMP_2012.pathcoverage.supragingival_plaque: An ExpressionSet with 128 samples and 23,271 features specific to the supragingival_plaque bodysite

HMP_2012.pathcoverage.throat: An ExpressionSet with 7 samples and 23,271 features specific to the throat bodysite

HMP_2012.pathcoverage.tongue_dorsum: An ExpressionSet with 136 samples and 23,271 features specific to the tongue_dorsum bodysite

HMP_2012.pathcoverage.vaginal_introitus: An ExpressionSet with 3 samples and 23,271 features specific to the vaginal_introitus bodysite

Source

Department of Psychology, Abdul Haq Campus, Federal Urdu University for Arts, Science and Technology, Karachi, Pakistan. shahiq_psy@yahoo.com

See Also

`HMP_2012.genefamilies_relab`, `HMP_2012.marker_abundance`, `HMP_2012.marker_presence`, `HMP_2012.metaphlan_bugs_list`, `HMP_2012.pathabundance_relab`

Examples

```
HMP_2012.pathcoverage.anterior_nares()
```

`KarlssonFH_2013.genefamilies_relab` *Relabeled genefamilies data from the KarlssonFH_2013 dataset*

Description

Relabeled genefamilies data from the KarlssonFH_2013 dataset

Datasets

KarlssonFH_2013.genefamilies_relab.stool: An ExpressionSet with 145 samples and 1,415,610 features specific to the stool bodysite

Source

Department of Chemical and Biological Engineering, Chalmers University of Technology, SE-412 96 Gothenburg, Sweden.

See Also

`KarlssonFH_2013.marker_abundance`, `KarlssonFH_2013.marker_presence`, `KarlssonFH_2013.metaphlan_bugs_`
`KarlssonFH_2013.pathabundance_relab`, `KarlssonFH_2013.pathcoverage`

Examples

```
KarlssonFH_2013.genefamilies_relab.stool()
```

`KarlssonFH_2013.marker_abundance`

Marker abundance data from the KarlssonFH_2013 dataset

Description

Marker abundance data from the KarlssonFH_2013 dataset

Datasets

KarlssonFH_2013.marker_abundance.stool: An ExpressionSet with 145 samples and 101,168 features specific to the stool bodysite

Source

Department of Chemical and Biological Engineering, Chalmers University of Technology, SE-412 96 Gothenburg, Sweden.

See Also

`KarlssonFH_2013.genefamilies_relab`, `KarlssonFH_2013.marker_presence`, `KarlssonFH_2013.metaphlan_bug`
`KarlssonFH_2013.pathabundance_relab`, `KarlssonFH_2013.pathcoverage`

Examples

```
KarlssonFH_2013.marker_abundance.stool()
```

`KarlssonFH_2013.marker_presence`

Marker presence data from the KarlssonFH_2013 dataset

Description

Marker presence data from the KarlssonFH_2013 dataset

Datasets

KarlssonFH_2013.marker_presence.stool: An ExpressionSet with 145 samples and 95,322 features specific to the stool bodysite

Source

Department of Chemical and Biological Engineering, Chalmers University of Technology, SE-412 96 Gothenburg, Sweden.

See Also

`KarlssonFH_2013.genefamilies_relab`, `KarlssonFH_2013.marker_abundance`, `KarlssonFH_2013.metaphlan_bu`
`KarlssonFH_2013.pathabundance_relab`, `KarlssonFH_2013.pathcoverage`

Examples

```
KarlssonFH_2013.marker_presence.stool()
```

KarlssonFH_2013.metaphlan_bugs_list

Taxonomic abundance data from the KarlssonFH_2013 dataset

Description

Taxonomic abundance data from the KarlssonFH_2013 dataset

Datasets

KarlssonFH_2013.metaphlan_bugs_list.stool: An ExpressionSet with 145 samples and 1,140 features specific to the stool bodysite

Source

Department of Chemical and Biological Engineering, Chalmers University of Technology, SE-412 96 Gothenburg, Sweden.

See Also

`KarlssonFH_2013.genefamilies_relab`, `KarlssonFH_2013.marker_abundance`, `KarlssonFH_2013.marker_prese`
`KarlssonFH_2013.pathabundance_relab`, `KarlssonFH_2013.pathcoverage`

Examples

```
KarlssonFH_2013.metaphlan_bugs_list.stool()
```

KarlssonFH_2013.pathabundance_relab

Relabeled pathabundance data from the KarlssonFH_2013 dataset

Description

Relabeled pathabundance data from the KarlssonFH_2013 dataset

Datasets

KarlssonFH_2013.pathabundance_relab.stool: An ExpressionSet with 145 samples and 13,392 features specific to the stool bodysite

Source

Department of Chemical and Biological Engineering, Chalmers University of Technology, SE-412 96 Gothenburg, Sweden.

See Also

KarlssonFH_2013.genefamilies_relab, KarlssonFH_2013.marker_abundance, KarlssonFH_2013.marker_prese
KarlssonFH_2013.metaphlan_bugs_list, KarlssonFH_2013.pathcoverage

Examples

```
KarlssonFH_2013.pathabundance_relab.stool()
```

KarlssonFH_2013.pathcoverage

Pathcoverage data from the KarlssonFH_2013 dataset

Description

Pathcoverage data from the KarlssonFH_2013 dataset

Datasets

KarlssonFH_2013.pathcoverage.stool: An ExpressionSet with 145 samples and 13,392 features specific to the stool bodysite

Source

Department of Chemical and Biological Engineering, Chalmers University of Technology, SE-412 96 Gothenburg, Sweden.

See Also

KarlssonFH_2013.genefamilies_relab, KarlssonFH_2013.marker_abundance, KarlssonFH_2013.marker_prese
KarlssonFH_2013.metaphlan_bugs_list, KarlssonFH_2013.pathabundance_relab

Examples

```
KarlssonFH_2013.pathcoverage.stool()
```

LeChatelierE_2013.genefamilies_relab

Relabeled genefamilies data from the LeChatelierE_2013 dataset

Description

Relabeled genefamilies data from the LeChatelierE_2013 dataset

Datasets

LeChatelierE_2013.genefamilies_relab.stool: An ExpressionSet with 292 samples and 1,519,376 features specific to the stool bodysite

Source

INRA, Institut National de la Recherche Agronomique, US1367 Metagenopolis, 78350 Jouy en Josas, France.

See Also

`LeChatelierE_2013.marker_abundance`, `LeChatelierE_2013.marker_presence`, `LeChatelierE_2013.metaphlan`
`LeChatelierE_2013.pathabundance_relab`, `LeChatelierE_2013.pathcoverage`

Examples

```
LeChatelierE_2013.genefamilies_relab.stool()
```

`LeChatelierE_2013.marker_abundance`

Marker abundance data from the LeChatelierE_2013 dataset

Description

Marker abundance data from the LeChatelierE_2013 dataset

Datasets

LeChatelierE_2013.marker_abundance.stool: An ExpressionSet with 292 samples and 130,621 features specific to the stool bodysite

Source

INRA, Institut National de la Recherche Agronomique, US1367 Metagenopolis, 78350 Jouy en Josas, France.

See Also

`LeChatelierE_2013.genefamilies_relab`, `LeChatelierE_2013.marker_presence`, `LeChatelierE_2013.metaphl`
`LeChatelierE_2013.pathabundance_relab`, `LeChatelierE_2013.pathcoverage`

Examples

```
LeChatelierE_2013.marker_abundance.stool()
```

`LeChatelierE_2013.marker_presence` *Marker presence data from the LeChatelierE_2013 dataset*

Description

Marker presence data from the LeChatelierE_2013 dataset

Datasets

LeChatelierE_2013.marker_presence.stool: An ExpressionSet with 292 samples and 117,258 features specific to the stool bodysite

Source

INRA, Institut National de la Recherche Agronomique, US1367 Metagenopolis, 78350 Jouy en Josas, France.

See Also

`LeChatelierE_2013.genefamilies_relab`, `LeChatelierE_2013.marker_abundance`, `LeChatelierE_2013.metaph`
`LeChatelierE_2013.pathabundance_relab`, `LeChatelierE_2013.pathcoverage`

Examples

```
LeChatelierE_2013.marker_presence.stool()
```

`LeChatelierE_2013.metaphlan_bugs_list` *Taxonomic abundance data from the LeChatelierE_2013 dataset*

Description

Taxonomic abundance data from the LeChatelierE_2013 dataset

Datasets

LeChatelierE_2013.metaphlan_bugs_list.stool: An ExpressionSet with 292 samples and 1,542 features specific to the stool bodysite

Source

INRA, Institut National de la Recherche Agronomique, US1367 Metagenopolis, 78350 Jouy en Josas, France.

See Also

`LeChatelierE_2013.genefamilies_relab`, `LeChatelierE_2013.marker_abundance`, `LeChatelierE_2013.marker`
`LeChatelierE_2013.pathabundance_relab`, `LeChatelierE_2013.pathcoverage`

Examples

```
LeChatelierE_2013.metaphlan_bugs_list.stool()
```

`LeChatelierE_2013.pathabundance_relab`

Relabeled pathabundance data from the LeChatelierE_2013 dataset

---

Description

Relabeled pathabundance data from the LeChatelierE_2013 dataset

Datasets

LeChatelierE_2013.pathabundance_relab.stool: An ExpressionSet with 292 samples and 13,504 features specific to the stool bodysite

Source

INRA, Institut National de la Recherche Agronomique, US1367 Metagenopolis, 78350 Jouy en Josas, France.

See Also

`LeChatelierE_2013.genefamilies_relab`, `LeChatelierE_2013.marker_abundance`, `LeChatelierE_2013.marker`
`LeChatelierE_2013.metaphlan_bugs_list`, `LeChatelierE_2013.pathcoverage`

Examples

```
LeChatelierE_2013.pathabundance_relab.stool()
```

`LeChatelierE_2013.pathcoverage`

Pathcoverage data from the LeChatelierE_2013 dataset

Description

Pathcoverage data from the LeChatelierE_2013 dataset

Datasets

LeChatelierE_2013.pathcoverage.stool: An ExpressionSet with 292 samples and 13,504 features specific to the stool bodysite

Source

INRA, Institut National de la Recherche Agronomique, US1367 Metagenopolis, 78350 Jouy en Josas, France.

See Also

`LeChatelierE_2013.genefamilies_relab`, `LeChatelierE_2013.marker_abundance`, `LeChatelierE_2013.marker`
`LeChatelierE_2013.metaphlan_bugs_list`, `LeChatelierE_2013.pathabundance_relab`

Examples

```
LeChatelierE_2013.pathcoverage.stool()
```

`LomanNJ_2013_Hi.genefamilies_relab`
Relabeled genefamilies data from the LomanNJ_2013_Hi dataset

Description

Relabeled genefamilies data from the LomanNJ_2013_Hi dataset

Datasets

LomanNJ_2013_Hi.genefamilies_relab.stool: An ExpressionSet with 44 samples and 718,320 features specific to the stool bodysite

Source

Institute of Microbiology and Infection, University of Birmingham, Birmingham, England.

See Also

`LomanNJ_2013_Hi.marker_abundance`, `LomanNJ_2013_Hi.marker_presence`, `LomanNJ_2013_Hi.metaphlan_bugs_`
`LomanNJ_2013_Hi.pathabundance_relab`, `LomanNJ_2013_Hi.pathcoverage`

Examples

```
LomanNJ_2013_Hi.genefamilies_relab.stool()
```

`LomanNJ_2013_Hi.marker_abundance`
Marker abundance data from the LomanNJ_2013_Hi dataset

Description

Marker abundance data from the LomanNJ_2013_Hi dataset

Datasets

LomanNJ_2013_Hi.marker_abundance.stool: An ExpressionSet with 44 samples and 56,689 features specific to the stool bodysite

Source

Institute of Microbiology and Infection, University of Birmingham, Birmingham, England.

See Also

`LomanNJ_2013_Hi.genefamilies_relab`, `LomanNJ_2013_Hi.marker_presence`, `LomanNJ_2013_Hi.metaphlan_bug`
`LomanNJ_2013_Hi.pathabundance_relab`, `LomanNJ_2013_Hi.pathcoverage`

Examples

```
LomanNJ_2013_Hi.marker_abundance.stool()
```

`LomanNJ_2013_Hi.marker_presence`

Marker presence data from the LomanNJ_2013_Hi dataset

Description

Marker presence data from the LomanNJ_2013_Hi dataset

Datasets

LomanNJ_2013_Hi.marker_presence.stool: An ExpressionSet with 44 samples and 53,443 features specific to the stool bodysite

Source

Institute of Microbiology and Infection, University of Birmingham, Birmingham, England.

See Also

`LomanNJ_2013_Hi.genefamilies_relab`, `LomanNJ_2013_Hi.marker_abundance`, `LomanNJ_2013_Hi.metaphlan_bu`
`LomanNJ_2013_Hi.pathabundance_relab`, `LomanNJ_2013_Hi.pathcoverage`

Examples

```
LomanNJ_2013_Hi.marker_presence.stool()
```

`LomanNJ_2013_Hi.metaphlan_bugs_list`
Taxonomic abundance data from the LomanNJ_2013_Hi dataset

Description

Taxonomic abundance data from the LomanNJ_2013_Hi dataset

Datasets

LomanNJ_2013_Hi.metaphlan_bugs_list.stool: An ExpressionSet with 44 samples and 736 features specific to the stool bodysite

Source

Institute of Microbiology and Infection, University of Birmingham, Birmingham, England.

See Also

`LomanNJ_2013_Hi.genefamilies_relab`, `LomanNJ_2013_Hi.marker_abundance`, `LomanNJ_2013_Hi.marker_prese`
`LomanNJ_2013_Hi.pathabundance_relab`, `LomanNJ_2013_Hi.pathcoverage`

Examples

```
LomanNJ_2013_Hi.metaphlan_bugs_list.stool()
```

`LomanNJ_2013_Hi.pathabundance_relab`
Relabeled pathabundance data from the LomanNJ_2013_Hi dataset

---

Description

Relabeled pathabundance data from the LomanNJ_2013_Hi dataset

Datasets

LomanNJ_2013_Hi.pathabundance_relab.stool: An ExpressionSet with 44 samples and 8,716 features specific to the stool bodysite

Source

Institute of Microbiology and Infection, University of Birmingham, Birmingham, England.

See Also

`LomanNJ_2013_Hi.genefamilies_relab`, `LomanNJ_2013_Hi.marker_abundance`, `LomanNJ_2013_Hi.marker_prese`
`LomanNJ_2013_Hi.metaphlan_bugs_list`, `LomanNJ_2013_Hi.pathcoverage`

Examples

```
LomanNJ_2013_Hi.pathabundance_relab.stool()
```

`LomanNJ_2013_Hi.pathcoverage` *Pathcoverage data from the LomanNJ_2013_Hi dataset*

Description

Pathcoverage data from the LomanNJ_2013_Hi dataset

Datasets

LomanNJ_2013_Hi.pathcoverage.stool: An ExpressionSet with 44 samples and 8,716 features specific to the stool bodysite

Source

Institute of Microbiology and Infection, University of Birmingham, Birmingham, England.

See Also

`LomanNJ_2013_Hi.genefamilies_relab`, `LomanNJ_2013_Hi.marker_abundance`, `LomanNJ_2013_Hi.marker_prese`
`LomanNJ_2013_Hi.metaphlan_bugs_list`, `LomanNJ_2013_Hi.pathabundance_relab`

Examples

```
LomanNJ_2013_Hi.pathcoverage.stool()
```

`LomanNJ_2013_Mi.genefamilies_relab` *Relabeled genefamilies data from the LomanNJ_2013_Mi dataset*

Description

Relabeled genefamilies data from the LomanNJ_2013_Mi dataset

Datasets

LomanNJ_2013_Mi.genefamilies_relab.stool: An ExpressionSet with 9 samples and 337,637 features specific to the stool bodysite

Source

Institute of Microbiology and Infection, University of Birmingham, Birmingham, England.

See Also

`LomanNJ_2013_Mi.marker_abundance`, `LomanNJ_2013_Mi.marker_presence`, `LomanNJ_2013_Mi.metaphlan_bugs_`
`LomanNJ_2013_Mi.pathabundance_relab`, `LomanNJ_2013_Mi.pathcoverage`

Examples

```
LomanNJ_2013_Mi.genefamilies_relab.stool()
```

`LomanNJ_2013_Mi.marker_abundance`

Marker abundance data from the LomanNJ_2013_Mi dataset

Description

Marker abundance data from the LomanNJ_2013_Mi dataset

Datasets

LomanNJ_2013_Mi.marker_abundance.stool: An ExpressionSet with 9 samples and 24,228 features specific to the stool bodysite

Source

Institute of Microbiology and Infection, University of Birmingham, Birmingham, England.

See Also

`LomanNJ_2013_Mi.genefamilies_relab`, `LomanNJ_2013_Mi.marker_presence`, `LomanNJ_2013_Mi.metaphlan_bug`
`LomanNJ_2013_Mi.pathabundance_relab`, `LomanNJ_2013_Mi.pathcoverage`

Examples

```
LomanNJ_2013_Mi.marker_abundance.stool()
```

`LomanNJ_2013_Mi.marker_presence`

Marker presence data from the LomanNJ_2013_Mi dataset

Description

Marker presence data from the LomanNJ_2013_Mi dataset

Datasets

LomanNJ_2013_Mi.marker_presence.stool: An ExpressionSet with 9 samples and 22,710 features specific to the stool bodysite

Source

Institute of Microbiology and Infection, University of Birmingham, Birmingham, England.

See Also

`LomanNJ_2013_Mi.genefamilies_relab`, `LomanNJ_2013_Mi.marker_abundance`, `LomanNJ_2013_Mi.metaphlan_bu`
`LomanNJ_2013_Mi.pathabundance_relab`, `LomanNJ_2013_Mi.pathcoverage`

Examples

```
LomanNJ_2013_Mi.marker_presence.stool()
```

`LomanNJ_2013_Mi.metaphlan_bugs_list` *Taxonomic abundance data from the LomanNJ_2013_Mi dataset*

Description

Taxonomic abundance data from the LomanNJ_2013_Mi dataset

Datasets

LomanNJ_2013_Mi.metaphlan_bugs_list.stool: An ExpressionSet with 9 samples and 399 features specific to the stool bodysite

Source

Institute of Microbiology and Infection, University of Birmingham, Birmingham, England.

See Also

`LomanNJ_2013_Mi.genefamilies_relab`, `LomanNJ_2013_Mi.marker_abundance`, `LomanNJ_2013_Mi.marker_prese`
`LomanNJ_2013_Mi.pathabundance_relab`, `LomanNJ_2013_Mi.pathcoverage`

Examples

```
LomanNJ_2013_Mi.metaphlan_bugs_list.stool()
```

`LomanNJ_2013_Mi.pathabundance_relab` *Relabeled pathabundance data from the LomanNJ_2013_Mi dataset*

Description

Relabeled pathabundance data from the LomanNJ_2013_Mi dataset

Datasets

LomanNJ_2013_Mi.pathabundance_relab.stool: An ExpressionSet with 9 samples and 4,606 features specific to the stool bodysite

Source

Institute of Microbiology and Infection, University of Birmingham, Birmingham, England.

See Also

`LomanNJ_2013_Mi.genefamilies_relab`, `LomanNJ_2013_Mi.marker_abundance`, `LomanNJ_2013_Mi.marker_prese`
`LomanNJ_2013_Mi.metaphlan_bugs_list`, `LomanNJ_2013_Mi.pathcoverage`

Examples

```
LomanNJ_2013_Mi.pathabundance_relab.stool()
```

`LomanNJ_2013_Mi.pathcoverage`

Pathcoverage data from the LomanNJ_2013_Mi dataset

Description

Pathcoverage data from the LomanNJ_2013_Mi dataset

Datasets

LomanNJ_2013_Mi.pathcoverage.stool: An ExpressionSet with 9 samples and 4,606 features specific to the stool bodysite

Source

Institute of Microbiology and Infection, University of Birmingham, Birmingham, England.

See Also

`LomanNJ_2013_Mi.genefamilies_relab`, `LomanNJ_2013_Mi.marker_abundance`, `LomanNJ_2013_Mi.marker_prese`
`LomanNJ_2013_Mi.metaphlan_bugs_list`, `LomanNJ_2013_Mi.pathabundance_relab`

Examples

```
LomanNJ_2013_Mi.pathcoverage.stool()
```

`NielsenHB_2014.genefamilies_relab`

Relabeled genefamilies data from the NielsenHB_2014 dataset

Description

Relabeled genefamilies data from the NielsenHB_2014 dataset

Datasets

NielsenHB_2014.genefamilies_relab.stool: An ExpressionSet with 396 samples and 1,730,384 features specific to the stool bodysite

Source

[1] Center for Biological Sequence Analysis, Technical University of Denmark, Kongens Lyngby, Denmark. [2] Novo Nordisk Foundation Center for Biosustainability, Technical University of Denmark, Kongens Lyngby, Denmark. [3].

See Also

`NielsenHB_2014.marker_abundance`, `NielsenHB_2014.marker_presence`, `NielsenHB_2014.metaphlan_bugs_lis`
`NielsenHB_2014.pathabundance_relab`, `NielsenHB_2014.pathcoverage`

Examples

```
NielsenHB_2014.genefamilies_relab.stool()
```

`NielsenHB_2014.marker_abundance`

Marker abundance data from the NielsenHB_2014 dataset

Description

Marker abundance data from the NielsenHB_2014 dataset

Datasets

NielsenHB_2014.marker_abundance.stool: An ExpressionSet with 396 samples and 222,838 features specific to the stool bodysite

Source

[1] Center for Biological Sequence Analysis, Technical University of Denmark, Kongens Lyngby, Denmark. [2] Novo Nordisk Foundation Center for Biosustainability, Technical University of Denmark, Kongens Lyngby, Denmark. [3].

See Also

`NielsenHB_2014.genefamilies_relab`, `NielsenHB_2014.marker_presence`, `NielsenHB_2014.metaphlan_bugs_l`
`NielsenHB_2014.pathabundance_relab`, `NielsenHB_2014.pathcoverage`

Examples

```
NielsenHB_2014.marker_abundance.stool()
```

`NielsenHB_2014.marker_presence`

Marker presence data from the NielsenHB_2014 dataset

Description

Marker presence data from the NielsenHB_2014 dataset

Datasets

NielsenHB_2014.marker_presence.stool: An ExpressionSet with 396 samples and 188,447 features specific to the stool bodysite

Source

[1] Center for Biological Sequence Analysis, Technical University of Denmark, Kongens Lyngby, Denmark. [2] Novo Nordisk Foundation Center for Biosustainability, Technical University of Denmark, Kongens Lyngby, Denmark. [3].

See Also

NielsenHB_2014.genefamilies_relab, NielsenHB_2014.marker_abundance, NielsenHB_2014.metaphlan_bugs_
NielsenHB_2014.pathabundance_relab, NielsenHB_2014.pathcoverage

Examples

```
NielsenHB_2014.marker_presence.stool()
```

NielsenHB_2014.metaphlan_bugs_list

Taxonomic abundance data from the NielsenHB_2014 dataset

Description

Taxonomic abundance data from the NielsenHB_2014 dataset

Datasets

NielsenHB_2014.metaphlan_bugs_list.stool: An ExpressionSet with 396 samples and 1,939 features specific to the stool bodysite

Source

[1] Center for Biological Sequence Analysis, Technical University of Denmark, Kongens Lyngby, Denmark. [2] Novo Nordisk Foundation Center for Biosustainability, Technical University of Denmark, Kongens Lyngby, Denmark. [3].

See Also

NielsenHB_2014.genefamilies_relab, NielsenHB_2014.marker_abundance, NielsenHB_2014.marker_presence
NielsenHB_2014.pathabundance_relab, NielsenHB_2014.pathcoverage

Examples

```
NielsenHB_2014.metaphlan_bugs_list.stool()
```

NielsenHB_2014.pathabundance_relab

Relabeled pathabundance data from the NielsenHB_2014 dataset

Description

Relabeled pathabundance data from the NielsenHB_2014 dataset

Datasets

NielsenHB_2014.pathabundance_relab.stool: An ExpressionSet with 396 samples and 17,280 features specific to the stool bodysite

Source

[1] Center for Biological Sequence Analysis, Technical University of Denmark, Kongens Lyngby, Denmark. [2] Novo Nordisk Foundation Center for Biosustainability, Technical University of Denmark, Kongens Lyngby, Denmark. [3].

See Also

`NielsenHB_2014.genefamilies_relab`, `NielsenHB_2014.marker_abundance`, `NielsenHB_2014.marker_presence`
`NielsenHB_2014.metaphlan_bugs_list`, `NielsenHB_2014.pathcoverage`

Examples

```
NielsenHB_2014.pathabundance_relab.stool()
```

`NielsenHB_2014.pathcoverage`

Pathcoverage data from the NielsenHB_2014 dataset

Description

Pathcoverage data from the NielsenHB_2014 dataset

Datasets

NielsenHB_2014.pathcoverage.stool: An ExpressionSet with 396 samples and 17,280 features specific to the stool bodysite

Source

[1] Center for Biological Sequence Analysis, Technical University of Denmark, Kongens Lyngby, Denmark. [2] Novo Nordisk Foundation Center for Biosustainability, Technical University of Denmark, Kongens Lyngby, Denmark. [3].

See Also

`NielsenHB_2014.genefamilies_relab`, `NielsenHB_2014.marker_abundance`, `NielsenHB_2014.marker_presence`
`NielsenHB_2014.metaphlan_bugs_list`, `NielsenHB_2014.pathabundance_relab`

Examples

```
NielsenHB_2014.pathcoverage.stool()
```

`Obregon_TitoAJ_2015.genefamilies_relab`

Relabeled genefamilies data from the Obregon_TitoAJ_2015 dataset

---

Description

Relabeled genefamilies data from the Obregon_TitoAJ_2015 dataset

Datasets

Obregon_TitoAJ_2015.genefamilies_relab.stool: An ExpressionSet with 58 samples and 1,192,382 features specific to the stool bodysite

Source

[1] Department of Anthropology, University of Oklahoma, Dale Hall Tower, 521 Norman, Oklahoma 73019, USA [2] Universidad Cientifica del Sur, Lima 18, Peru [3] City of Hope, NCI-designated Comprehensive Cancer Center, Duarte, California 91010, USA.

See Also

`Obregon_TitoAJ_2015.marker_abundance`, `Obregon_TitoAJ_2015.marker_presence`, `Obregon_TitoAJ_2015.met`
`Obregon_TitoAJ_2015.pathabundance_relab`, `Obregon_TitoAJ_2015.pathcoverage`

Examples

```
Obregon_TitoAJ_2015.genefamilies_relab.stool()
```

`Obregon_TitoAJ_2015.marker_abundance`

Marker abundance data from the Obregon_TitoAJ_2015 dataset

Description

Marker abundance data from the Obregon_TitoAJ_2015 dataset

Datasets

Obregon_TitoAJ_2015.marker_abundance.stool: An ExpressionSet with 58 samples and 195,320 features specific to the stool bodysite

Source

[1] Department of Anthropology, University of Oklahoma, Dale Hall Tower, 521 Norman, Oklahoma 73019, USA [2] Universidad Cientifica del Sur, Lima 18, Peru [3] City of Hope, NCI-designated Comprehensive Cancer Center, Duarte, California 91010, USA.

See Also

`Obregon_TitoAJ_2015.genefamilies_relab`, `Obregon_TitoAJ_2015.marker_presence`, `Obregon_TitoAJ_2015.m`
`Obregon_TitoAJ_2015.pathabundance_relab`, `Obregon_TitoAJ_2015.pathcoverage`

Examples

```
Obregon_TitoAJ_2015.marker_abundance.stool()
```

`Obregon_TitoAJ_2015.marker_presence`

Marker presence data from the Obregon_TitoAJ_2015 dataset

Description

Marker presence data from the Obregon_TitoAJ_2015 dataset

Datasets

Obregon_TitoAJ_2015.marker_presence.stool: An ExpressionSet with 58 samples and 150,347 features specific to the stool bodysite

Source

[1] Department of Anthropology, University of Oklahoma, Dale Hall Tower, 521 Norman, Oklahoma 73019, USA [2] Universidad Cientifica del Sur, Lima 18, Peru [3] City of Hope, NCI-designated Comprehensive Cancer Center, Duarte, California 91010, USA.

See Also

`Obregon_TitoAJ_2015.genefamilies_relab`, `Obregon_TitoAJ_2015.marker_abundance`, `Obregon_TitoAJ_2015.`
`Obregon_TitoAJ_2015.pathabundance_relab`, `Obregon_TitoAJ_2015.pathcoverage`

Examples

```
Obregon_TitoAJ_2015.marker_presence.stool()
```

`Obregon_TitoAJ_2015.metaphlan_bugs_list`

Taxonomic abundance data from the Obregon_TitoAJ_2015 dataset

---

Description

Taxonomic abundance data from the Obregon_TitoAJ_2015 dataset

Datasets

Obregon_TitoAJ_2015.metaphlan_bugs_list.stool: An ExpressionSet with 58 samples and 1,548 features specific to the stool bodysite

Source

[1] Department of Anthropology, University of Oklahoma, Dale Hall Tower, 521 Norman, Oklahoma 73019, USA [2] Universidad Cientifica del Sur, Lima 18, Peru [3] City of Hope, NCI-designated Comprehensive Cancer Center, Duarte, California 91010, USA.

See Also

`Obregon_TitoAJ_2015.genefamilies_relab`, `Obregon_TitoAJ_2015.marker_abundance`, `Obregon_TitoAJ_2015.`
`Obregon_TitoAJ_2015.pathabundance_relab`, `Obregon_TitoAJ_2015.pathcoverage`

Examples

```
Obregon_TitoAJ_2015.metaphlan_bugs_list.stool()
```

`Obregon_TitoAJ_2015.pathabundance_relab`
Relabeled pathabundance data from the Obregon_TitoAJ_2015 dataset

Description

Relabeled pathabundance data from the Obregon_TitoAJ_2015 dataset

Datasets

Obregon_TitoAJ_2015.pathabundance_relab.stool: An ExpressionSet with 58 samples and 10,438 features specific to the stool bodysite

Source

[1] Department of Anthropology, University of Oklahoma, Dale Hall Tower, 521 Norman, Oklahoma 73019, USA [2] Universidad Cientifica del Sur, Lima 18, Peru [3] City of Hope, NCI-designated Comprehensive Cancer Center, Duarte, California 91010, USA.

See Also

`Obregon_TitoAJ_2015.genefamilies_relab`, `Obregon_TitoAJ_2015.marker_abundance`, `Obregon_TitoAJ_2015.`
`Obregon_TitoAJ_2015.metaphlan_bugs_list`, `Obregon_TitoAJ_2015.pathcoverage`

Examples

```
Obregon_TitoAJ_2015.pathabundance_relab.stool()
```

`Obregon_TitoAJ_2015.pathcoverage` *Pathcoverage data from the Obregon_TitoAJ_2015 dataset*

Description

Pathcoverage data from the Obregon_TitoAJ_2015 dataset

Datasets

Obregon_TitoAJ_2015.pathcoverage.stool: An ExpressionSet with 58 samples and 10,438 features specific to the stool bodysite

Source

[1] Department of Anthropology, University of Oklahoma, Dale Hall Tower, 521 Norman, Oklahoma 73019, USA [2] Universidad Cientifica del Sur, Lima 18, Peru [3] City of Hope, NCI-designated Comprehensive Cancer Center, Duarte, California 91010, USA.

See Also

`Obregon_TitoAJ_2015.genefamilies_relab`, `Obregon_TitoAJ_2015.marker_abundance`, `Obregon_TitoAJ_2015.`
`Obregon_TitoAJ_2015.metaphlan_bugs_list`, `Obregon_TitoAJ_2015.pathabundance_relab`

Examples

```
Obregon_TitoAJ_2015.pathcoverage.stool()
```

`OhJ_2014.genefamilies_relab` *Relabeled genefamilies data from the OhJ_2014 dataset*

Description

Relabeled genefamilies data from the OhJ_2014 dataset

Datasets

OhJ_2014.genefamilies_relab.skin: An ExpressionSet with 291 samples and 3,956,473 features specific to the skin bodysite

Source

Translational and Functional Genomics Branch, National Human Genome Research Institute, NIH, Bethesda, Maryland 20892, USA.

See Also

`OhJ_2014.marker_abundance`, `OhJ_2014.marker_presence`, `OhJ_2014.metaphlan_bugs_list`, `OhJ_2014.pathabundance_relab`, `OhJ_2014.pathcoverage`

Examples

```
OhJ_2014.genefamilies_relab.skin()
```

`OhJ_2014.marker_abundance`

Marker abundance data from the OhJ_2014 dataset

Description

Marker abundance data from the OhJ_2014 dataset

Datasets

OhJ_2014.marker_abundance.skin: An ExpressionSet with 291 samples and 202,658 features specific to the skin bodysite

Source

Translational and Functional Genomics Branch, National Human Genome Research Institute, NIH, Bethesda, Maryland 20892, USA.

See Also

`OhJ_2014.genefamilies_relab`, `OhJ_2014.marker_presence`, `OhJ_2014.metaphlan_bugs_list`, `OhJ_2014.pathabundance_relab`, `OhJ_2014.pathcoverage`

Examples

```
OhJ_2014.marker_abundance.skin()
```

`OhJ_2014.marker_presence`

Marker presence data from the OhJ_2014 dataset

Description

Marker presence data from the OhJ_2014 dataset

Datasets

OhJ_2014.marker_presence.skin: An ExpressionSet with 291 samples and 184,915 features specific to the skin bodysite

Source

Translational and Functional Genomics Branch, National Human Genome Research Institute, NIH, Bethesda, Maryland 20892, USA.

See Also

`OhJ_2014.genefamilies_relab`, `OhJ_2014.marker_abundance`, `OhJ_2014.metaphlan_bugs_list`, `OhJ_2014.pathabundance_relab`, `OhJ_2014.pathcoverage`

Examples

```
OhJ_2014.marker_presence.skin()
```

`OhJ_2014.metaphlan_bugs_list` *Taxonomic abundance data from the OhJ_2014 dataset*

Description

Taxonomic abundance data from the OhJ_2014 dataset

Datasets

OhJ_2014.metaphlan_bugs_list.skin: An ExpressionSet with 291 samples and 2,461 features specific to the skin bodysite

Source

Translational and Functional Genomics Branch, National Human Genome Research Institute, NIH, Bethesda, Maryland 20892, USA.

See Also

`OhJ_2014.genefamilies_relab`, `OhJ_2014.marker_abundance`, `OhJ_2014.marker_presence`, `OhJ_2014.pathabundance_relab`, `OhJ_2014.pathcoverage`

Examples

```
OhJ_2014.metaphlan_bugs_list.skin()
```

`OhJ_2014.pathabundance_relab` *Relabeled pathabundance data from the OhJ_2014 dataset*

Description

Relabeled pathabundance data from the OhJ_2014 dataset

Datasets

OhJ_2014.pathabundance_relab.skin: An ExpressionSet with 291 samples and 48,536 features specific to the skin bodysite

Source

Translational and Functional Genomics Branch, National Human Genome Research Institute, NIH, Bethesda, Maryland 20892, USA.

See Also

`OhJ_2014.genefamilies_relab`, `OhJ_2014.marker_abundance`, `OhJ_2014.marker_presence`, `OhJ_2014.metaphlan_bugs_list`, `OhJ_2014.pathcoverage`

Examples

```
OhJ_2014.pathabundance_relab.skin()
```

`OhJ_2014.pathcoverage` *Pathcoverage data from the OhJ_2014 dataset*

Description

Pathcoverage data from the OhJ_2014 dataset

Datasets

OhJ_2014.pathcoverage.skin: An ExpressionSet with 291 samples and 48,536 features specific to the skin bodysite

Source

Translational and Functional Genomics Branch, National Human Genome Research Institute, NIH, Bethesda, Maryland 20892, USA.

See Also

`OhJ_2014.genefamilies_relab`, `OhJ_2014.marker_abundance`, `OhJ_2014.marker_presence`, `OhJ_2014.metaphlan_bugs_list`, `OhJ_2014.pathabundance_relab`

Examples

```
OhJ_2014.pathcoverage.skin()
```

`QinJ_2012.genefamilies_relab`

Relabeled genefamilies data from the QinJ_2012 dataset

Description

Relabeled genefamilies data from the QinJ_2012 dataset

Datasets

QinJ_2012.genefamilies_relab.stool: An ExpressionSet with 363 samples and 1,690,774 features specific to the stool bodysite

Source

BGI-Shenzhen, Shenzhen 518083, China.

See Also

`QinJ_2012.marker_abundance`, `QinJ_2012.marker_presence`, `QinJ_2012.metaphlan_bugs_list`, `QinJ_2012.pathabundance_relab`, `QinJ_2012.pathcoverage`

Examples

```
QinJ_2012.genefamilies_relab.stool()
```

`QinJ_2012.marker_abundance`

Marker abundance data from the QinJ_2012 dataset

Description

Marker abundance data from the QinJ_2012 dataset

Datasets

QinJ_2012.marker_abundance.stool: An ExpressionSet with 363 samples and 132,934 features specific to the stool bodysite

Source

BGI-Shenzhen, Shenzhen 518083, China.

See Also

`QinJ_2012.genefamilies_relab`, `QinJ_2012.marker_presence`, `QinJ_2012.metaphlan_bugs_list`, `QinJ_2012.pathabundance_relab`, `QinJ_2012.pathcoverage`

Examples

```
QinJ_2012.marker_abundance.stool()
```

`QinJ_2012.marker_presence`

Marker presence data from the QinJ_2012 dataset

Description

Marker presence data from the QinJ_2012 dataset

Datasets

QinJ_2012.marker_presence.stool: An ExpressionSet with 363 samples and 125,127 features specific to the stool bodysite

Source

BGI-Shenzhen, Shenzhen 518083, China.

See Also

`QinJ_2012.genefamilies_relab`, `QinJ_2012.marker_abundance`, `QinJ_2012.metaphlan_bugs_list`, `QinJ_2012.pathabundance_relab`, `QinJ_2012.pathcoverage`

Examples

```
QinJ_2012.marker_presence.stool()
```

`QinJ_2012.metaphlan_bugs_list`

Taxonomic abundance data from the QinJ_2012 dataset

Description

Taxonomic abundance data from the QinJ_2012 dataset

Datasets

QinJ_2012.metaphlan_bugs_list.stool: An ExpressionSet with 363 samples and 1,588 features specific to the stool bodysite

Source

BGI-Shenzhen, Shenzhen 518083, China.

See Also

`QinJ_2012.genefamilies_relab`, `QinJ_2012.marker_abundance`, `QinJ_2012.marker_presence`, `QinJ_2012.pathabundance_relab`, `QinJ_2012.pathcoverage`

Examples

```
QinJ_2012.metaphlan_bugs_list.stool()
```

`QinJ_2012.pathabundance_relab`

Relabeled pathabundance data from the QinJ_2012 dataset

Description

Relabeled pathabundance data from the QinJ_2012 dataset

Datasets

QinJ_2012.pathabundance_relab.stool: An ExpressionSet with 363 samples and 18,478 features specific to the stool bodysite

Source

BGI-Shenzhen, Shenzhen 518083, China.

See Also

`QinJ_2012.genefamilies_relab`, `QinJ_2012.marker_abundance`, `QinJ_2012.marker_presence`, `QinJ_2012.metaphlan_bugs_list`, `QinJ_2012.pathcoverage`

Examples

```
QinJ_2012.pathabundance_relab.stool()
```

`QinJ_2012.pathcoverage`

Pathcoverage data from the QinJ_2012 dataset

Description

Pathcoverage data from the QinJ_2012 dataset

Datasets

QinJ_2012.pathcoverage.stool: An ExpressionSet with 363 samples and 18,478 features specific to the stool bodysite

Source

BGI-Shenzhen, Shenzhen 518083, China.

See Also

`QinJ_2012.genefamilies_relab`, `QinJ_2012.marker_abundance`, `QinJ_2012.marker_presence`, `QinJ_2012.metaphlan_bugs_list`, `QinJ_2012.pathabundance_relab`

Examples

```
QinJ_2012.pathcoverage.stool()
```

`QinN_2014.genefamilies_relab` *Relabeled genefamilies data from the QinN_2014 dataset*

Description

Relabeled genefamilies data from the QinN_2014 dataset

Datasets

QinN_2014.genefamilies_relab.stool: An ExpressionSet with 237 samples and 1,747,534 features specific to the stool bodysite

Source

[1] State Key Laboratory for Diagnosis and Treatment of Infectious Disease, The First Affiliated Hospital, College of Medicine, Zhejiang University, 310003 Hangzhou, China [2] Collaborative Innovation Center for Diagnosis and Treatment of Infectious Diseases, Zhejiang University, 310003 Hangzhou, China [3].

See Also

`QinN_2014.marker_abundance`, `QinN_2014.marker_presence`, `QinN_2014.metaphlan_bugs_list`, `QinN_2014.pathabundance_relab`, `QinN_2014.pathcoverage`

Examples

```
QinN_2014.genefamilies_relab.stool()
```

`QinN_2014.marker_abundance` *Marker abundance data from the QinN_2014 dataset*

Description

Marker abundance data from the QinN_2014 dataset

Datasets

QinN_2014.marker_abundance.stool: An ExpressionSet with 237 samples and 132,775 features specific to the stool bodysite

Source

[1] State Key Laboratory for Diagnosis and Treatment of Infectious Disease, The First Affiliated Hospital, College of Medicine, Zhejiang University, 310003 Hangzhou, China [2] Collaborative Innovation Center for Diagnosis and Treatment of Infectious Diseases, Zhejiang University, 310003 Hangzhou, China [3].

See Also

`QinN_2014.genefamilies_relab`, `QinN_2014.marker_presence`, `QinN_2014.metaphlan_bugs_list`, `QinN_2014.pathabundance_relab`, `QinN_2014.pathcoverage`

Examples

```
QinN_2014.marker_abundance.stool()
```

`QinN_2014.marker_presence` *Marker presence data from the QinN_2014 dataset*

Description

Marker presence data from the QinN_2014 dataset

Datasets

QinN_2014.marker_presence.stool: An ExpressionSet with 237 samples and 126,097 features specific to the stool bodysite

Source

[1] State Key Laboratory for Diagnosis and Treatment of Infectious Disease, The First Affiliated Hospital, College of Medicine, Zhejiang University, 310003 Hangzhou, China [2] Collaborative Innovation Center for Diagnosis and Treatment of Infectious Diseases, Zhejiang University, 310003 Hangzhou, China [3].

See Also

`QinN_2014.genefamilies_relab`, `QinN_2014.marker_abundance`, `QinN_2014.metaphlan_bugs_list`, `QinN_2014.pathabundance_relab`, `QinN_2014.pathcoverage`

Examples

```
QinN_2014.marker_presence.stool()
```

`QinN_2014.metaphlan_bugs_list` *Taxonomic abundance data from the QinN_2014 dataset*

Description

Taxonomic abundance data from the QinN_2014 dataset

Datasets

QinN_2014.metaphlan_bugs_list.stool: An ExpressionSet with 237 samples and 1,512 features specific to the stool bodysite

Source

[1] State Key Laboratory for Diagnosis and Treatment of Infectious Disease, The First Affiliated Hospital, College of Medicine, Zhejiang University, 310003 Hangzhou, China [2] Collaborative Innovation Center for Diagnosis and Treatment of Infectious Diseases, Zhejiang University, 310003 Hangzhou, China [3].

See Also

`QinN_2014.genefamilies_relab`, `QinN_2014.marker_abundance`, `QinN_2014.marker_presence`, `QinN_2014.pathabundance_relab`, `QinN_2014.pathcoverage`

Examples

```
QinN_2014.metaphlan_bugs_list.stool()
```

`QinN_2014.pathabundance_relab` *Relabeled pathabundance data from the QinN_2014 dataset*

Description

Relabeled pathabundance data from the QinN_2014 dataset

Datasets

QinN_2014.pathabundance_relab.stool: An ExpressionSet with 237 samples and 19,418 features specific to the stool bodysite

Source

[1] State Key Laboratory for Diagnosis and Treatment of Infectious Disease, The First Affiliated Hospital, College of Medicine, Zhejiang University, 310003 Hangzhou, China [2] Collaborative Innovation Center for Diagnosis and Treatment of Infectious Diseases, Zhejiang University, 310003 Hangzhou, China [3].

See Also

`QinN_2014.genefamilies_relab`, `QinN_2014.marker_abundance`, `QinN_2014.marker_presence`, `QinN_2014.metaphlan_bugs_list`, `QinN_2014.pathcoverage`

Examples

```
QinN_2014.pathabundance_relab.stool()
```

`QinN_2014.pathcoverage`

Pathcoverage data from the QinN_2014 dataset

Description

Pathcoverage data from the QinN_2014 dataset

Datasets

QinN_2014.pathcoverage.stool: An ExpressionSet with 237 samples and 19,418 features specific to the stool bodysite

Source

[1] State Key Laboratory for Diagnosis and Treatment of Infectious Disease, The First Affiliated Hospital, College of Medicine, Zhejiang University, 310003 Hangzhou, China [2] Collaborative Innovation Center for Diagnosis and Treatment of Infectious Diseases, Zhejiang University, 310003 Hangzhou, China [3].

See Also

`QinN_2014.genefamilies_relab`, `QinN_2014.marker_abundance`, `QinN_2014.marker_presence`, `QinN_2014.metaphlan_bugs_list`, `QinN_2014.pathabundance_relab`

Examples

```
QinN_2014.pathcoverage.stool()
```

`RampelliS_2015.genefamilies_relab`

Relabeled genefamilies data from the RampelliS_2015 dataset

Description

Relabeled genefamilies data from the RampelliS_2015 dataset

Datasets

RampelliS_2015.genefamilies_relab.stool: An ExpressionSet with 38 samples and 788,641 features specific to the stool bodysite

Source

Department of Pharmacy and Biotechnology, University of Bologna, Bologna 40126, Italy.

See Also

`RampelliS_2015.marker_abundance`, `RampelliS_2015.marker_presence`, `RampelliS_2015.metaphlan_bugs_lis`
`RampelliS_2015.pathabundance_relab`, `RampelliS_2015.pathcoverage`

Examples

```
RampelliS_2015.genefamilies_relab.stool()
```

`RampelliS_2015.marker_abundance`

Marker abundance data from the RampelliS_2015 dataset

Description

Marker abundance data from the RampelliS_2015 dataset

Datasets

RampelliS_2015.marker_abundance.stool: An ExpressionSet with 38 samples and 50,395 features specific to the stool bodysite

Source

Department of Pharmacy and Biotechnology, University of Bologna, Bologna 40126, Italy.

See Also

`RampelliS_2015.genefamilies_relab`, `RampelliS_2015.marker_presence`, `RampelliS_2015.metaphlan_bugs_l`
`RampelliS_2015.pathabundance_relab`, `RampelliS_2015.pathcoverage`

Examples

```
RampelliS_2015.marker_abundance.stool()
```

`RampelliS_2015.marker_presence`

Marker presence data from the RampelliS_2015 dataset

Description

Marker presence data from the RampelliS_2015 dataset

Datasets

RampelliS_2015.marker_presence.stool: An ExpressionSet with 38 samples and 47,456 features specific to the stool bodysite

Source

Department of Pharmacy and Biotechnology, University of Bologna, Bologna 40126, Italy.

See Also

`RampelliS_2015.genefamilies_relab`, `RampelliS_2015.marker_abundance`, `RampelliS_2015.metaphlan_bugs_`
`RampelliS_2015.pathabundance_relab`, `RampelliS_2015.pathcoverage`

Examples

```
RampelliS_2015.marker_presence.stool()
```

`RampelliS_2015.metaphlan_bugs_list`

Taxonomic abundance data from the RampelliS_2015 dataset

Description

Taxonomic abundance data from the RampelliS_2015 dataset

Datasets

RampelliS_2015.metaphlan_bugs_list.stool: An ExpressionSet with 38 samples and 727 features specific to the stool bodysite

Source

Department of Pharmacy and Biotechnology, University of Bologna, Bologna 40126, Italy.

See Also

`RampelliS_2015.genefamilies_relab`, `RampelliS_2015.marker_abundance`, `RampelliS_2015.marker_presence`
`RampelliS_2015.pathabundance_relab`, `RampelliS_2015.pathcoverage`

Examples

```
RampelliS_2015.metaphlan_bugs_list.stool()
```

`RampelliS_2015.pathabundance_relab`

Relabeled pathabundance data from the RampelliS_2015 dataset

Description

Relabeled pathabundance data from the RampelliS_2015 dataset

Datasets

RampelliS_2015.pathabundance_relab.stool: An ExpressionSet with 38 samples and 6,798 features specific to the stool bodysite

Source

Department of Pharmacy and Biotechnology, University of Bologna, Bologna 40126, Italy.

See Also

`RampelliS_2015.genefamilies_relab`, `RampelliS_2015.marker_abundance`, `RampelliS_2015.marker_presence`
`RampelliS_2015.metaphlan_bugs_list`, `RampelliS_2015.pathcoverage`

Examples

```
RampelliS_2015.pathabundance_relab.stool()
```

`RampelliS_2015.pathcoverage`

Pathcoverage data from the RampelliS_2015 dataset

Description

Pathcoverage data from the RampelliS_2015 dataset

Datasets

RampelliS_2015.pathcoverage.stool: An ExpressionSet with 38 samples and 6,798 features specific to the stool bodysite

Source

Department of Pharmacy and Biotechnology, University of Bologna, Bologna 40126, Italy.

See Also

`RampelliS_2015.genefamilies_relab`, `RampelliS_2015.marker_abundance`, `RampelliS_2015.marker_presence`
`RampelliS_2015.metaphlan_bugs_list`, `RampelliS_2015.pathabundance_relab`

Examples

```
RampelliS_2015.pathcoverage.stool()
```

`TettAJ_2016.genefamilies_relab` *Relabeled genefamilies data from the TettAJ_2016 dataset*

Description

Relabeled genefamilies data from the TettAJ_2016 dataset

Datasets

TettAJ_2016.genefamilies_relab.left_ear: An ExpressionSet with 22 samples and 1,183,854 features specific to the left_ear bodysite

TettAJ_2016.genefamilies_relab.left_elbow: An ExpressionSet with 26 samples and 1,183,854 features specific to the left_elbow bodysite

TettAJ_2016.genefamilies_relab.right_ear: An ExpressionSet with 26 samples and 1,183,854 features specific to the right_ear bodysite

TettAJ_2016.genefamilies_relab.right_elbow: An ExpressionSet with 23 samples and 1,183,854 features specific to the right_elbow bodysite

See Also

`TettAJ_2016.marker_abundance`, `TettAJ_2016.marker_presence`, `TettAJ_2016.metaphlan_bugs_list`, `TettAJ_2016.pathabundance_relab`, `TettAJ_2016.pathcoverage`

Examples

```
TettAJ_2016.genefamilies_relab.left_ear()
```

`TettAJ_2016.marker_abundance` *Marker abundance data from the TettAJ_2016 dataset*

Description

Marker abundance data from the TettAJ_2016 dataset

Datasets

TettAJ_2016.marker_abundance.left_ear: An ExpressionSet with 22 samples and 64,040 features specific to the left_ear bodysite

TettAJ_2016.marker_abundance.left_elbow: An ExpressionSet with 26 samples and 64,040 features specific to the left_elbow bodysite

TettAJ_2016.marker_abundance.right_ear: An ExpressionSet with 26 samples and 64,040 features specific to the right_ear bodysite

TettAJ_2016.marker_abundance.right_elbow: An ExpressionSet with 23 samples and 64,040 features specific to the right_elbow bodysite

See Also

TettAJ_2016.genefamilies_relab, TettAJ_2016.marker_presence, TettAJ_2016.metaphlan_bugs_list, TettAJ_2016.pathabundance_relab, TettAJ_2016.pathcoverage

Examples

```
TettAJ_2016.marker_abundance.left_ear()
```

TettAJ_2016.marker_presence

Marker presence data from the TettAJ_2016 dataset

Description

Marker presence data from the TettAJ_2016 dataset

Datasets

TettAJ_2016.marker_presence.left_ear: An ExpressionSet with 22 samples and 57,429 features specific to the left_ear bodysite

TettAJ_2016.marker_presence.left_elbow: An ExpressionSet with 26 samples and 57,429 features specific to the left_elbow bodysite

TettAJ_2016.marker_presence.right_ear: An ExpressionSet with 26 samples and 57,429 features specific to the right_ear bodysite

TettAJ_2016.marker_presence.right_elbow: An ExpressionSet with 23 samples and 57,429 features specific to the right_elbow bodysite

See Also

TettAJ_2016.genefamilies_relab, TettAJ_2016.marker_abundance, TettAJ_2016.metaphlan_bugs_list, TettAJ_2016.pathabundance_relab, TettAJ_2016.pathcoverage

Examples

```
TettAJ_2016.marker_presence.left_ear()
```

`TettAJ_2016.metaphlan_bugs_list`

Taxonomic abundance data from the TettAJ_2016 dataset

Description

Taxonomic abundance data from the TettAJ_2016 dataset

Datasets

TettAJ_2016.metaphlan_bugs_list.left_ear: An ExpressionSet with 22 samples and 1,004 features specific to the left_ear bodysite

TettAJ_2016.metaphlan_bugs_list.left_elbow: An ExpressionSet with 26 samples and 1,004 features specific to the left_elbow bodysite

TettAJ_2016.metaphlan_bugs_list.right_ear: An ExpressionSet with 26 samples and 1,004 features specific to the right_ear bodysite

TettAJ_2016.metaphlan_bugs_list.right_elbow: An ExpressionSet with 23 samples and 1,004 features specific to the right_elbow bodysite

See Also

`TettAJ_2016.genefamilies_relab`, `TettAJ_2016.marker_abundance`, `TettAJ_2016.marker_presence`, `TettAJ_2016.pathabundance_relab`, `TettAJ_2016.pathcoverage`

Examples

```
TettAJ_2016.metaphlan_bugs_list.left_ear()
```

`TettAJ_2016.pathabundance_relab`

Relabeled pathabundance data from the TettAJ_2016 dataset

Description

Relabeled pathabundance data from the TettAJ_2016 dataset

Datasets

TettAJ_2016.pathabundance_relab.left_ear: An ExpressionSet with 22 samples and 21,899 features specific to the left_ear bodysite

TettAJ_2016.pathabundance_relab.left_elbow: An ExpressionSet with 26 samples and 21,899 features specific to the left_elbow bodysite

TettAJ_2016.pathabundance_relab.right_ear: An ExpressionSet with 26 samples and 21,899 features specific to the right_ear bodysite

TettAJ_2016.pathabundance_relab.right_elbow: An ExpressionSet with 23 samples and 21,899 features specific to the right_elbow bodysite

See Also

`TettAJ_2016.genefamilies_relab`, `TettAJ_2016.marker_abundance`, `TettAJ_2016.marker_presence`, `TettAJ_2016.metaphlan_bugs_list`, `TettAJ_2016.pathcoverage`

Examples

```
TettAJ_2016.pathabundance_relab.left_ear()
```

`TettAJ_2016.pathcoverage` *Pathcoverage data from the TettAJ_2016 dataset*

Description

Pathcoverage data from the TettAJ_2016 dataset

Datasets

TettAJ_2016.pathcoverage.left_ear: An ExpressionSet with 22 samples and 21,899 features specific to the left_ear bodysite

TettAJ_2016.pathcoverage.left_elbow: An ExpressionSet with 26 samples and 21,899 features specific to the left_elbow bodysite

TettAJ_2016.pathcoverage.right_ear: An ExpressionSet with 26 samples and 21,899 features specific to the right_ear bodysite

TettAJ_2016.pathcoverage.right_elbow: An ExpressionSet with 23 samples and 21,899 features specific to the right_elbow bodysite

See Also

`TettAJ_2016.genefamilies_relab`, `TettAJ_2016.marker_abundance`, `TettAJ_2016.marker_presence`, `TettAJ_2016.metaphlan_bugs_list`, `TettAJ_2016.pathabundance_relab`

Examples

```
TettAJ_2016.pathcoverage.left_ear()
```

`ZellerG_2014.genefamilies_relab`

Relabeled genefamilies data from the ZellerG_2014 dataset

Description

Relabeled genefamilies data from the ZellerG_2014 dataset

Datasets

ZellerG_2014.genefamilies_relab.stool: An ExpressionSet with 156 samples and 1,796,274 features specific to the stool bodysite

Source

Structural and Computational Biology Unit, European Molecular Biology Laboratory, Heidelberg, Germany.

See Also

`ZellerG_2014.marker_abundance`, `ZellerG_2014.marker_presence`, `ZellerG_2014.metaphlan_bugs_list`, `ZellerG_2014.pathabundance_relab`, `ZellerG_2014.pathcoverage`

Examples

```
ZellerG_2014.genefamilies_relab.stool()
```

`ZellerG_2014.marker_abundance`

Marker abundance data from the ZellerG_2014 dataset

Description

Marker abundance data from the ZellerG_2014 dataset

Datasets

ZellerG_2014.marker_abundance.stool: An ExpressionSet with 156 samples and 130,272 features specific to the stool bodysite

Source

Structural and Computational Biology Unit, European Molecular Biology Laboratory, Heidelberg, Germany.

See Also

`ZellerG_2014.genefamilies_relab`, `ZellerG_2014.marker_presence`, `ZellerG_2014.metaphlan_bugs_list`, `ZellerG_2014.pathabundance_relab`, `ZellerG_2014.pathcoverage`

Examples

```
ZellerG_2014.marker_abundance.stool()
```

`ZellerG_2014.marker_presence`

Marker presence data from the ZellerG_2014 dataset

Description

Marker presence data from the ZellerG_2014 dataset

Datasets

ZellerG_2014.marker_presence.stool: An ExpressionSet with 156 samples and 126,622 features specific to the stool bodysite

Source

Structural and Computational Biology Unit, European Molecular Biology Laboratory, Heidelberg, Germany.

See Also

`ZellerG_2014.genefamilies_relab`, `ZellerG_2014.marker_abundance`, `ZellerG_2014.metaphlan_bugs_list`, `ZellerG_2014.pathabundance_relab`, `ZellerG_2014.pathcoverage`

Examples

```
ZellerG_2014.marker_presence.stool()
```

`ZellerG_2014.metaphlan_bugs_list`

Taxonomic abundance data from the ZellerG_2014 dataset

Description

Taxonomic abundance data from the ZellerG_2014 dataset

Datasets

ZellerG_2014.metaphlan_bugs_list.stool: An ExpressionSet with 156 samples and 1,505 features specific to the stool bodysite

Source

Structural and Computational Biology Unit, European Molecular Biology Laboratory, Heidelberg, Germany.

See Also

`ZellerG_2014.genefamilies_relab`, `ZellerG_2014.marker_abundance`, `ZellerG_2014.marker_presence`, `ZellerG_2014.pathabundance_relab`, `ZellerG_2014.pathcoverage`

Examples

```
ZellerG_2014.metaphlan_bugs_list.stool()
```

`ZellerG_2014.pathabundance_relab` *Relabeled pathabundance data from the ZellerG_2014 dataset*

Description

Relabeled pathabundance data from the ZellerG_2014 dataset

Datasets

ZellerG_2014.pathabundance_relab.stool: An ExpressionSet with 156 samples and 17,888 features specific to the stool bodysite

Source

Structural and Computational Biology Unit, European Molecular Biology Laboratory, Heidelberg, Germany.

See Also

`ZellerG_2014.genefamilies_relab`, `ZellerG_2014.marker_abundance`, `ZellerG_2014.marker_presence`, `ZellerG_2014.metaphlan_bugs_list`, `ZellerG_2014.pathcoverage`

Examples

```
ZellerG_2014.pathabundance_relab.stool()
```

`ZellerG_2014.pathcoverage` *Pathcoverage data from the ZellerG_2014 dataset*

Description

Pathcoverage data from the ZellerG_2014 dataset

Datasets

ZellerG_2014.pathcoverage.stool: An ExpressionSet with 156 samples and 17,888 features specific to the stool bodysite

Source

Structural and Computational Biology Unit, European Molecular Biology Laboratory, Heidelberg, Germany.

See Also

`ZellerG_2014.genefamilies_relab`, `ZellerG_2014.marker_abundance`, `ZellerG_2014.marker_presence`, `ZellerG_2014.metaphlan_bugs_list`, `ZellerG_2014.pathabundance_relab`

Examples

```
ZellerG_2014.pathcoverage.stool()
```

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