Package ‘antiProfilesData’

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License  Artistic-2.0
Title Normal colon and cancer preprocessed affy data for antiProfile
 building.
Description  Colon normal tissue and cancer samples used in Corrada Bravo, et
doi:10.1186/1471-2105-13-272. Measurements are z-scores obtained from the
GeneExpression Barcode in the ‘frma’ package
LazyData yes
Depends Biobase,
Suggests frma, GEOquery, GEOmetadb
biocViews  ExperimentData, MicroarrayData, Tissue, CancerData,
ColonCancerData
Collate 'antiProfilesData-package.r' 'apColonData.r'
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R topics documented:

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antiProfilesData-package

Curated dataset of normal and cancer samples on Affymetrix hgu133plus2 expression arrays.

Description


Author(s)

Hector Corrada Bravo

References


apColonData

Curated dataset of many colon normal and cancer samples on Affymetrix hgu133plus2 expression arrays.

Description


format

Data is an ExpressionSet object. The exprs slot contains gene expression barcode z-scores from frma preprocessed data. The phenoData slot contains a data frame with the following columns:

filename: The CEL filename in the Gene Expression Omnibus (GEO)
DB_ID: The GSM sample id in GEO
ExperimentID: The GSE experiment id in GEO
Tissue: Tissue type, obtained from the gene expression barcode annotation
SubType: Sample sub-type, obtained from the gene expression barcode annotation
ClinicalGroup: Clinical sample annotation, obtained from the gene expression barcode annotation
Status: Normal (0) or Cancer (1) indicator
Author(s)
Hector Corrada Bravo

References

See Also
ExpressionSet for the class definition, frma for the preprocessing method used, barcode for the function to obtain the z-score definition.

Examples
data(apColonData)
pData(apColonData)
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