

Package: Qindex.data (via r-universe)

August 23, 2024

Type Package

Title Data for Package 'Qindex'

Version 0.1.1

Date 2024-04-24

Description Example data used in package 'Qindex'.

LazyData true

LazyDataCompression xz

RoxygenNote 7.3.1

Encoding UTF-8

License GPL-2

Depends R (>= 4.3),

Language en-US

Suggests knitr

NeedsCompilation no

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Repository <https://tingtingzhan.r-universe.dev>

RemoteUrl <https://github.com/cran/Qindex.data>

RemoteRef HEAD

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Contents

Qindex.data-package	2
celldata	2

Index	4
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Qindex.data-package *Data for Package 'Qindex'*

Description

Example data used in package 'Qindex'.

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References

Selection of optimal quantile protein biomarkers based on cell-level immunohistochemistry data. Misung Yi, Tingting Zhan, Amy P. Peck, Jeffrey A. Hooke, Albert J. Kovatich, Craig D. Shriver, Hai Hu, Yunguang Sun, Hallgeir Rui and Inna Chervoneva. BMC Bioinformatics, 2023. [doi:10.1186/s12859023054088](#)

Quantile index biomarkers based on single-cell expression data. Misung Yi, Tingting Zhan, Amy P. Peck, Jeffrey A. Hooke, Albert J. Kovatich, Craig D. Shriver, Hai Hu, Yunguang Sun, Hallgeir Rui and Inna Chervoneva. Laboratory Investigation, 2023. [doi:10.1016/j.labinv.2023.100158](#)

celldata *Ki67 Data*

Description

Ki67 cell data containing 622 patients

Usage

Ki67

Format

PATIENT_ID [factor](#), unique patient identifier

tissueID [factor](#), TMA core identifier

RECURRENCE [integer](#), recurrence indicator, 1 = Recurred, 0 = not Recurred

RECFREESURV_MO [integer](#), recurrence-free survival time in months

Marker [double](#), cell signal intensity of the protein immunofloerscence signal

inner_x [integer](#), x -coordinate in the cell centroid in the TMA core

inner_y **integer**, *y*-coordinate in the cell centroid in the TMA core
AGE_AT_DX **integer**, age at diagnosis
Tstage **integer**, tumor stage
NodeSt **integer**, node stage, -1 = unknown, 0 = Node Negative, 1 = Node Positive
HRpos **integer**, indicator of hormone positive status (ER+ or PR+), 1 = positive, 0 = negative
HistologicalGrade **integer**, histology grade
Her2_path_qIF **integer**, Her2 status, 1 = positive, 0 = negative
RACE **character**, race, White, Black, Asian, Native Hawaiian or Other Pacific Islander, American Indian or Alaska Native, Unknown
RadjCHEMO **integer**, adjuvant chemo treatment, 0 = unknown, 1 = done, 2 = NOT done
RadjRAD **integer**, adjuvant radiation treatment, 0 = unknown, 1 = done, 2 = NOT done
HORM_4cat **integer**, hormone treatment, 0 = unknown, 1 = not indicated, 2 = done, 3 = recommended, but not done
MSI **double**, mean signal intensity (mean over all cells in the TMA core)

Index

* datasets

cellldata, [2](#)

cellldata, [2](#)

character, [3](#)

double, [2](#), [3](#)

factor, [2](#)

integer, [2](#), [3](#)

Ki67 (cellldata), [2](#)

Qindex.data (Qindex.data-package), [2](#)

Qindex.data-package, [2](#)