Package 'msProstate'

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Type Package

Title Protein Mass Spectra Dataset from a Prostate Cancer Study

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Depends R (>= 2.5.0), RSQLite

DependsSplus

Suggests msProcess

Description This package provides a dataset of protein mass spectra generated from patients with prostate cancer, benign prostatic hypertrophy, and normal controls.

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R topics documented:

`Prostate2000Peaks`   *Prostate Cancer 2000 Peaks*

Description

A data object of class `msSet`, consisting of 779 peaks detected in 652 spectra (326 spectra in duplicate) from 2000 to 40000 Da. The peak detection was performed by East Virginia Medical School. Please see the references for more details.

1

References

B.L. Adam, Y. Qu, J.W. Davis, M.D. Ward, M.A. Clements, L.H. Cazares, O.J. Semmes, P.F. Schellhammer, Y. Yasui, Z. Feng, and G.L. Wright, Jr., "Serum protein fingerprinting coupled with a pattern-matching algorithm distinguishes prostate cancer from benign prostate hyperplasia and healthy men," *Cancer Research*, **62**(13):3609–14, 2002.

Y. Qu, B.L. Adam, Y. Yasui, M.D. Ward, L.H. Cazares, P.F. Schellhammer, Z. Feng, O.J. Semmes, and G.L. Wright Jr., "Boosted decision tree analysis of surface-enhanced laser desorption/ionization mass spectral serum profiles discriminates prostate cancer from noncancer patients," *Clinical Chemistry*, **48**(10):1835–43, 2002.

See Also

Prostate2000Raw.

Examples

```
if (require("msProcess")) {
if (!exists("Prostate2000Peaks")) data("Prostate2000Peaks", package="msProstate")

## plot a few spectra
plot(Prostate2000Peaks, subset=1:16)

## image of a subset of spectra
image(Prostate2000Peaks)
}
```

Prostate2000Raw   *Prostate Cancer 2000 Raw Spectra*

Description

A data object of class msSet, consisting of 654 mass spectra (327 spectra in duplicate) from 2000 to 20000 Da, which were generated from patients with prostate cancer, benign prostatic hypertrophy, and normal controls. These spectra are already baseline corrected and normalized. Please see the references for more details.

References

B.L. Adam, Y. Qu, J.W. Davis, M.D. Ward, M.A. Clements, L.H. Cazares, O.J. Semmes, P.F. Schellhammer, Y. Yasui, Z. Feng, and G.L. Wright, Jr., "Serum protein fingerprinting coupled with a pattern-matching algorithm distinguishes prostate cancer from benign prostate hyperplasia and healthy men," *Cancer Research*, **62**(13):3609–14, 2002.

Y. Qu, B.L. Adam, Y. Yasui, M.D. Ward, L.H. Cazares, P.F. Schellhammer, Z. Feng, O.J. Semmes, and G.L. Wright Jr., "Boosted decision tree analysis of surface-enhanced laser desorption/ionization mass spectral serum profiles discriminates prostate cancer from noncancer patients," *Clinical Chemistry*, **48**(10):1835–43, 2002.

See Also

Prostate2000Peaks.

Examples

```
if (require("msProcess")) {
if (!exists("Prostate2000Raw")) data("Prostate2000Raw", package="msProstate")

## plot a few spectra
plot(Prostate2000Raw, subset=1:8)

## image of a subset of spectra
image(Prostate2000Raw, subset=1:64)
}
```

Index