

# Package ‘CardinalWorkflows’

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**Type** Package

**Title** Datasets and workflows for the Cardinal mass spectrometry imaging package

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**Description** Datasets and workflows for Cardinal: DESI and MALDI examples including pig fetus, cardinal painting, and human RCC.

**License** Artistic-2.0

**Depends** R (>= 2.10), Cardinal, methods

**Suggests** BiocStyle, knitr, rmarkdown

**VignetteBuilder** knitr

**biocViews** ExperimentData, MassSpectrometryData, ImagingMassSpectrometryData

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CardinalWorkflows-package

*Datasets and workflows for the Cardinal mass spectrometry imaging package*

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## Description

Datasets and workflows for Cardinal: MS imaging data examples including cardinal painting, pig fetus, and human RCC.

## Usage

```
# Load and return an example MSI dataset
exampleMSIData(name = c("cardinal", "pig206", "rcc"))
```

## Arguments

name                    The name of the dataset.

## Details

CardinalWorkflows provides datasets and example workflows of mass spectrometry imaging experiments using the Cardinal package for MS imaging analysis.

To view the example workflows, use `browseVignettes("CardinalWorkflows")`.

## Value

The dataset as an `MSImagingExperiment`.

## Author(s)

Kylie A. Bemis

## See Also

[cardinal](#), [pig206](#), [rcc](#)

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cardinal-data

*Cardinal Painting*

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### **Description**

DESI-imaging mass spectra collected from the oil painting of a cardinal. Should be loaded with `exampleMSIData()`.

### **Source**

Aston Labs (Livia S. Eberlin, Christina Ferreira, and R. Graham Cooks).

### **Examples**

```
cardinal <- exampleMSIData("cardinal")
cardinal
```

---

pig206-data

*Cross-Section of a Whole Pig Fetus*

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### **Description**

DESI-imaging mass spectra collected from the cross-section of a whole pig fetus. Should be loaded with `exampleMSIData()`.

### **Source**

Aston Labs (Livia S. Eberlin, Christina Ferreira, and R. Graham Cooks).

### **Examples**

```
pig206 <- exampleMSIData("pig206")
pig206
```

---

rcc-data

*Human Renal Cell Carcinoma*

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### **Description**

Eight matched pairs of human renal cell carcinoma (RCC) labeled as cancer or normal.

Data are DESI-imaging mass spectra with each matched pair as a separate sample on a separate slide.

Should be loaded with `exampleMSIData()`.

### **Source**

Aston Labs (Livia S. Eberlin and R. Graham Cooks).

### **References**

Dill, A. L., Eberlin, L. S., Zheng, C., Costa, A. B., Ifa, D. R., Cheng, L., et al. (2010). Multivariate statistical differentiation of renal cell carcinomas based on lipidomic analysis by ambient ionization imaging mass spectrometry. *Analytical and Bioanalytical Chemistry*, 298(7-8), 2969-2978.

Dill, A. L., Eberlin, L. S., Zheng, C., Costa, A. B., Ifa, D. R., Cheng, L., et al. (2010). Multivariate Statistical Identification of Human Bladder Carcinomas Using Ambient Ionization Imaging Mass Spectrometry. *Chemistry - a European Journal*, 17(10), 2897-2902.

### **Examples**

```
rcc <- exampleMSIData("rcc")  
rcc
```

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