

# Package ‘tinesath1cdf’

October 17, 2024

**Title** tinesath1cdf

**Version** 1.42.0

**Created** Monday August 7th 2006

**Author** Tine Casneuf

**Description** A package containing an environment representing the newcdf/tinesATH1.cdf.cdf file.

**Maintainer** Tine Casneuf <tine@ebi.ac.uk>

**License** Artistic-2.0

**biocViews** Arabidopsis\_thaliana\_Data, ChipOnChipData

**git\_url** <https://git.bioconductor.org/packages/tinesath1cdf>

**git\_branch** RELEASE\_3\_19

**git\_last\_commit** 656f351

**git\_last\_commit\_date** 2024-04-30

**Repository** Bioconductor 3.19

**Date/Publication** 2024-10-17

## Contents

i2xy . . . . .	1
tinesath1cdf . . . . .	2

<b>Index</b>	<b>3</b>
--------------	----------

---

i2xy	<i>Convert (x,y)-coordinates to single-number indices and back.</i>
------	---

---

## Description

Convert (x,y)-coordinates on the chip (and in the CEL file) to the single-number indices used in AffyBatch and CDF environment, and back.

**Usage**

```
i2xy(i)
xy2i(x,y)
```

**Arguments**

x	numeric. x-coordinate (from 1 to 712)
y	numeric. y-coordinate (from 1 to 712)
i	numeric. single-number index (from 1 to 506944)

**Details**

Type `i2xy` and `xy2i` at the R prompt to view the function definitions.

**Examples**

```
xy2i(5,5)
i      = 1:(712*712)
coord = i2xy(i)
j      = xy2i(coord[, "x"], coord[, "y"])
stopifnot(all(i==j))
range(coord[, "x"])
range(coord[, "y"])
```

---

tinesath1cdf

*environment containing the location probe set membership mapping*

---

**Description**

environment describing the CDF file

# Index

## \* datasets

i2xy, 1

tinesath1cdf, 2

i2xy, 1

tinesath1cdf, 2

xy2i (i2xy), 1