

# Package ‘transomics2cytoscape’

December 6, 2021

**Title** A tool set for 3D Trans-Omic network visualization with Cytoscape

**Version** 1.5.0

**Description** transomics2cytoscape generates a file for 3D transomics visualization by providing input that specifies the IDs of multiple KEGG pathway layers, their corresponding Z-axis heights, and an input that represents the edges between the pathway layers. The edges are used, for example, to describe the relationships between kinase on a pathway and enzyme on another pathway. This package automates creation of a transomics network as shown in the figure in Yugi.2014 (<https://doi.org/10.1016/j.celrep.2014.07.021>) using Cytoscape automation (<https://doi.org/10.1186/s13059-019-1758-4>).

**License** Artistic-2.0

**Imports** RCy3, KEGGREST, dplyr

**Suggests** testthat, roxygen2, knitr, BiocStyle, rmarkdown

**Encoding** UTF-8

**LazyData** true

**biocViews** Network, Software, Pathways, DataImport, KEGG

**VignetteBuilder** knitr

**SystemRequirements** Java 11, Cytoscape 3.8.2, Cy3D >= 1.1.3

**RoxygenNote** 7.1.1

**git\_url** <https://git.bioconductor.org/packages/transomics2cytoscape>

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create3Dnetwork	<i>Create 3D network view for transomics visualization.</i>
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### Description

Import multiple KEGG pathways and integrate the pathways into Cy3D renderer

### Usage

```
create3Dnetwork(networkDataDir, networkLayers, stylexml)
```

### Arguments

networkDataDir	Path of a directory to put the network files of the second column of networkLayers TSV.
networkLayers	Path of a TSV file with the 3 columns (layer index, the network file name in networkDataDir, Z-height of the network).
stylexml	Path of a XML file for Cytoscape style

### Value

A SUID of the 3D network.

### Author(s)

Kozo Nishida

### Examples

```
## Not run:
networkDataDir <- tempfile(); dir.create(networkDataDir)
networkLayers <- system.file("extdata", "yugi2014.tsv",
  package = "transomics2cytoscape")
stylexml <- system.file("extdata", "transomics.xml",
  package = "transomics2cytoscape")
suid <- create3Dnetwork(networkDataDir, networkLayers, stylexml)

## End(Not run)
```

---

createTransomicEdges *Create Trans-Omic edges between layers of the network.*

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**Description**

Create Trans-Omic edges between layers of the network

**Usage**

```
createTransomicEdges(suid, transomicEdges)
```

**Arguments**

suid	A SUID of Cytoscape network
transomicEdges	Path of a TSV file with the 9 columns (layer index of a source node, name or KEGG object ID that the source node should have, layer index of a target node, name or KEGG object ID that the target node should have, interaction type).

**Value**

A SUID of the 3D network.

**Author(s)**

Kozo Nishida

**Examples**

```
## Not run:  
transomicEdges <- system.file("extdata", "allosteric.tsv",  
  package = "transomics2cytoscape")  
createTransomicEdges(suid, transomicEdges)  
  
## End(Not run)
```

---

ec2reaction *Convert KEGG enzyme IDs to KEGG reaction IDs.*

---

**Description**

Convert KEGG enzyme IDs to KEGG reaction IDs

**Usage**

```
ec2reaction(tsvFilePath, columnIndex, outputFilename)
```

**Arguments**

tsvFilePath Path of a TSV file with the 9 columns (layer index of a source node, name or KEGG object ID that the source node should have, layer index of a target node, name or KEGG object ID that the target node should have, interaction type).

columnIndex The column number

outputFilename The output filename

**Value**

None

**Author(s)**

Kozo Nishida

**Examples**

```
## Not run:  
ec = system.file("extdata", "allosteric_ecnumber.tsv",  
  package = "transomics2cytoscape")  
ec2reaction(ec, 8, "allosteric.tsv")  
  
## End(Not run)
```

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installCyApps

*Install the Cytoscape Apps the transomics2cytoscape depends.*

---

**Description**

Install the Cytoscape Apps the transomics2cytoscape depends

**Usage**

```
installCyApps()
```

**Value**

None

**Author(s)**

Kozo Nishida

**Examples**

```
## Not run:  
installCyApps()  
  
## End(Not run)
```

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