

Package ‘HiCDataHumanIMR90’

June 6, 2023

Title Human IMR90 Fibroblast HiC data from Dixon et al. 2012

Description The HiC data from Human Fibroblast IMR90 cell line (HindIII restriction) was retrieved from the GEO website, accession number GSE35156 (<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE35156>). The raw reads were processed as explained in Dixon et al. (Nature 2012).

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Author Nicolas Servant

Maintainer Nicolas Servant <Nicolas.Servant@curie.fr>

Suggests HiTC

biocViews ExperimentData, Genome, Homo_sapiens_Data, GEO

License GPL-3

InstallableEverywhere yes

Depends R (>= 2.10)

git_url <https://git.bioconductor.org/packages/HiCDataHumanIMR90>

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R topics documented:

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Dixon2012_IMR90	<i>HiC data Human IMR90</i>
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Description

Human Fibroblast IMR90 Hi-C Data (Dixon et al.)

Usage

```
data(Dixon2012_IMR90)
```

Format

Contains one `HTClist` objects (`hic_imr90_40`) and one `GRanges` object (`tads_imr90`). The `hic_imr90_40` object contains all intra/interchromosomal contact maps. The `tads_imr90` object contains the intervals of topological domains.

Details

This HiC dataset published by Dixon et al ([GSE35156](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE35156)), contains all genome-wide contact maps.

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE35156>

References

Dixon JR, Selvaraj S, Yue F, Kim A et al. Topological domains in mammalian genomes identified by analysis of chromatin interactions. *Nature* 2012 Apr 11;485(7398):376-80.

Examples

```
data(Dixon2012_IMR90)
show(hic_imr90_40)
show(tads_imr90)
```

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* **datasets**

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