

# Package ‘HiCDataHumanIMR90’

April 11, 2019

**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).

**Version** 1.2.0

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**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>

**git\_branch** RELEASE\_3\_8

**git\_last\_commit** 823e9ad

**git\_last\_commit\_date** 2018-10-30

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## R topics documented:

Dixon2012_IMR90 . . . . .	2
<b>Index</b>	<b>3</b>

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Dixon2012\_IMR90

*HiC data Human IMR90*

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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)
```

# Index

## \*Topic **datasets**

Dixon2012\_IMR90, [2](#)

Dixon2012\_IMR90, [2](#)

hic\_imr90\_40 (Dixon2012\_IMR90), [2](#)

tads\_imr90 (Dixon2012\_IMR90), [2](#)