

# Package ‘HiCDataHumanIMR90’

April 23, 2026

**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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**Suggests** HiTC, BiocStyle

**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** devel

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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)
```

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## \* datasets

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