

# Package ‘ELMER.data’

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**Title** Data for the ELMER package

**Version** 2.21.0

**Author** Tiago Chedraoui Silva,  
Lijing Yao  
Simon Coetzee,  
Benjamin P. Berman

**Maintainer** Tiago Chedraoui Silva <tiagochst@gmail.com>

**Description** Supporting data for the ELMER package.

It includes:

- elmer.data.example.promoter: mae.promoter
- elmer.data.example: data
- EPIC.hg38.manifest
- EPIC.hg19.manifest
- hm450.hg38.manifest
- hm450.hg19.manifest
- hocomoco.table
- human.TF
- LUSC\_meth\_refined: Meth
- LUSC\_RNA\_refined: GeneExp
- Probes.motif.hg19.450K
- Probes.motif.hg19.EPIC
- Probes.motif.hg38.450K
- Probes.motif.hg38.EPIC
- TF.family
- TF.subfamily
- Human\_genes\_\_GRCh37\_p13
- Human\_genes\_\_GRCh38\_p12
- Human\_genes\_\_GRCh37\_p13\_\_tss
- Human\_genes\_\_GRCh38\_p12\_\_tss

**License** GPL-3

**LazyData** false

**Depends** R (>= 3.5.0)

**Imports** GenomicRanges

**Suggests** BiocStyle, knitr, dplyr, devtools, DT, rmarkdown

**biocViews** AssayDomainData, TechnologyData, OrganismData

**VignetteBuilder** knitr

**RoxygenNote** 6.1.1

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

**git\_branch** master

**git\_last\_commit** 1d376bc

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**Date/Publication** 2022-07-26

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### Description

ELMER is package using DNA methylation to identify enhancers, and correlates enhancer state with expression of nearby genes to identify one or more transcriptional targets. Transcription factor (TF) binding site analysis of enhancers is coupled with expression analysis of all TFs to infer upstream regulators. ELMER.data provide the necessary data for ELMER analysis:

- `Probes.motif`: motif occurrences within  $\pm 250$ bp of probe sites on HM450K/EPIC array aligned against hg19/hg38.
- DNA methylation platform manifest: from <http://zwdzwd.github.io/InfiniumAnnotation>
- `TF.family` TFs family from `TFClass`
- `TF.subfamily` TFs subfamily from `TFClass`

For more information how to create these objects please read the vignette of this package with the following command: `browseVignettes("ELMER.data")`

### See Also

[EPIC.hg19.manifest](#), [EPIC.hg38.manifest](#), [hm450.hg19.manifest](#), [hm450.hg38.manifest](#), [Probes.motif.hg19.450K](#), [Probes.motif.hg38.450K](#), [Probes.motif.hg38.EPIC](#), [Probes.motif.hg19.EPIC](#), [Human\\_genes\\_\\_GRCh37\\_p13\\_\\_tss](#), [Human\\_genes\\_\\_GRCh37\\_p13](#), [Human\\_genes\\_\\_GRCh38\\_p12](#), [Human\\_genes\\_\\_GRCh38\\_p12\\_\\_tss](#), `TF.subfamily`, `TF.family`, and `hocomoco.table`

### Examples

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# Please see the datasets
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