

Resource Summary Report

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Replication Domain

RRID:SCR_012941

Type: Tool

Proper Citation

Replication Domain (RRID:SCR_012941)

Resource Information

URL: <http://www.replicationdomain.org>

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Description: ReplicationDomain is an online database resource for storing, sharing and visualizing DNA replication timing and transcription data, as well as other numerical epigenetic data types. Data is typically obtained from DNA microarrays or DNA sequencing. Our site has a user registration system that allows registered users to upload their own data sets. While non-registered users may freely view and download public data sets, registered users may upload their own data sets and view them privately, share them with other registered users, or make published data sets publicly available. In addition we have implemented additional mechanisms that allow users to restrict sharing of data sets to a user designated group of registered users. Further details on the database usage are in the User Guide Page, while data set details are in the Documentation Page. Replication timing data were obtained by hybridizing early and late replication intermediates to Nimblegen oligonucleotide arrays, as described in Hiratani et al [PLoS Biology (2008) 6: e245]. Briefly, replication intermediates are prepared from cells that are first pulse-labeled with BrdU and then sorted into early and late stages of S-phase by flow cytometry, followed by anti-BrdU immunoprecipitation of the BrdU-substituted (nascent) replication intermediates that were synthesized either early or late during S-phase. After unbiased amplification of recovered DNA, the samples are differentially labeled with Cy3 and Cy5 and hybridized to Nimblegen CGH arrays containing one oligonucleotide probe every 5.8 kb across the mouse genome (Nimblegen, 2006-07-26_MM8_WG_CGH). Raw data from two independent biological replicates in which the early and late replicating DNA were labeled reciprocally with Cy3 and Cy 5 (dye switch) are loess-normalized and scaled to have the same median-absolute deviation using the limma package (R/Bioconductor) and then averaged. Finally, the data are smoothed with a weighted moving average (loess: local polynomial smoothing).

Synonyms: Replication Domain

Resource Type: data or information resource, database

Resource Name: Replication Domain

Resource ID: SCR_012941

Alternate IDs: nif-0000-31444

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260912T200208+0000

Ratings and Alerts

No rating or validation information has been found for Replication Domain.

No alerts have been found for Replication Domain.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Nie R, et al. (2025) Mitigating Cell Cycle Effects in Multi-Omics Data: Solutions and Analytical Frameworks. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(29), e05823.

Nishiyama A, et al. (2020) Two distinct modes of DNMT1 recruitment ensure stable maintenance DNA methylation. Nature communications, 11(1), 1222.

Schreiber J, et al. (2020) Avocado: a multi-scale deep tensor factorization method learns a latent representation of the human epigenome. Genome biology, 21(1), 81.

Chen Y, et al. (2019) Synchronized replication of genes encoding the same protein complex in fast-proliferating cells. Genome research, 29(12), 1929.

Rivera-Mulia JC, et al. (2019) Replication timing networks reveal a link between transcription regulatory circuits and replication timing control. Genome research, 29(9), 1415.

Rivera-Mulia JC, et al. (2018) Allele-specific control of replication timing and genome organization during development. Genome research, 28(6), 800.

Mukherjee K, et al. (2018) Counting motifs in dynamic networks. BMC systems biology, 12(Suppl 1), 6.

Yu S, et al. (2018) The long-range interaction map of ribosomal DNA arrays. PLoS genetics, 14(3), e1007258.

Tasan I, et al. (2018) CRISPR/Cas9-mediated knock-in of an optimized TetO repeat for live cell imaging of endogenous loci. *Nucleic acids research*, 46(17), e100.

Link V, et al. (2017) Male Mutation Bias Is the Main Force Shaping Chromosomal Substitution Rates in Monotreme Mammals. *Genome biology and evolution*, 9(9), 2198.

Hu X, et al. (2016) A novel method for discovering local spatial clusters of genomic regions with functional relationships from DNA contact maps. *Bioinformatics (Oxford, England)*, 32(12), i111.

Peng C, et al. (2015) Recent advances in the genome-wide study of DNA replication origins in yeast. *Frontiers in microbiology*, 6, 117.

Kuznetsova T, et al. (2015) Glucocorticoid receptor and nuclear factor kappa-b affect three-dimensional chromatin organization. *Genome biology*, 16, 264.

Rivera-Mulia JC, et al. (2015) Dynamic changes in replication timing and gene expression during lineage specification of human pluripotent stem cells. *Genome research*, 25(8), 1091.

Takebayashi S, et al. (2013) Murine esBAF chromatin remodeling complex subunits BAF250a and Brg1 are necessary to maintain and reprogram pluripotency-specific replication timing of select replication domains. *Epigenetics & chromatin*, 6(1), 42.

Chandra T, et al. (2012) Independence of repressive histone marks and chromatin compaction during senescent heterochromatic layer formation. *Molecular cell*, 47(2), 203.

Nellaker C, et al. (2012) The genomic landscape shaped by selection on transposable elements across 18 mouse strains. *Genome biology*, 13(6), R45.

Pope BD, et al. (2011) DNA replication timing is maintained genome-wide in primary human myoblasts independent of D4Z4 contraction in FSH muscular dystrophy. *PloS one*, 6(11), e27413.

Helmrich A, et al. (2011) Collisions between replication and transcription complexes cause common fragile site instability at the longest human genes. *Molecular cell*, 44(6), 966.

Weddington N, et al. (2008) ReplicationDomain: a visualization tool and comparative database for genome-wide replication timing data. *BMC bioinformatics*, 9, 530.