



PHi-D : 4Dゲノム状態の理解と可視化を支援するデータベース

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<https://phid.riken.jp/>

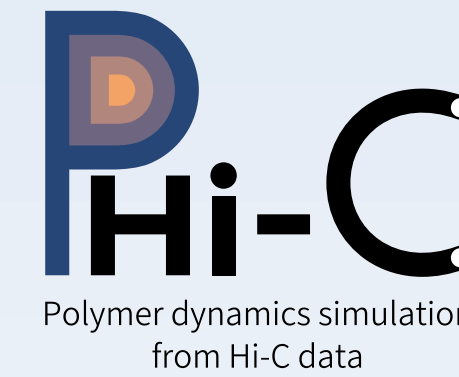
NEW RELEASE | 本日 正式版公開！

4D Nucleome Data Portal



入力データセット

- **1,082**個の.hicファイル
- 合計 **3 TB**
- 主にヒト・マウスの全染色体
- **50 kb**解像度



Polymer dynamics simulation
from Hi-C data

- 最適化アルゴリズムを高速化
- GPU実装で大規模化
- **2ヶ月**で計算完了



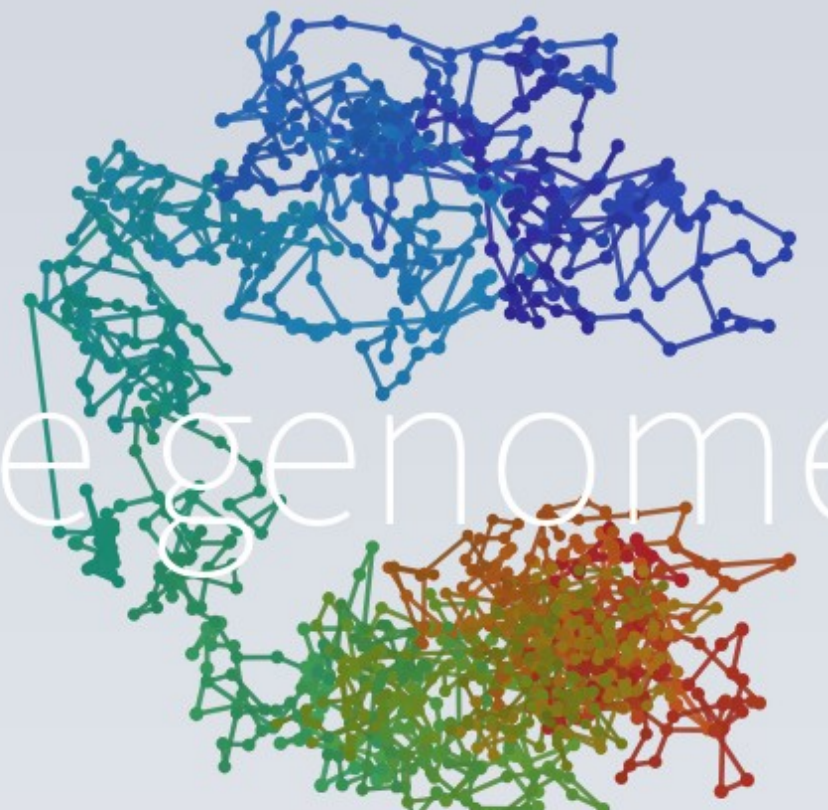
格納データセット

- コンタクトマップ
- 相互作用マップ
- MSDマップ
- Loss tangentマップ
- 合計 **5 TB**



PHi-C
Database

[Data](#) [About](#) [Compare \(Prototype\)](#)



See the genome in 4D.

drag to rotate

Human · chr11 · 4DNFILMGFDL

start  end

PHi-D shares and visualizes **PHi-C** data to explore the dynamic 3D organization and physical properties of the genome.

[Browse Database](#)

PHi-C = Polymer dynamics simulation from Hi-C data. It turns a Hi-C contact matrix into a polymer model, transforming the same dataset into maps of dynamic physical properties, such as mean-square displacement (MSD) and loss tangent, and into a dynamic 3D genome structure.

In **PHi-D**, these dynamic properties can be mapped directly onto 3D genome structures. PHi-D is designed to integrate genomic annotations and experimental tracks, bringing genome structure, dynamics, and genomic information together in a unified view.

This is a beta version. The official release is scheduled for October 2026.



PHi-D

[Data](#) [About](#) [Home](#) [Compare \(Prototype\)](#)

Data Directory

GRCh38

192627

CC-2551

CyT49

CyT49 differentiated to definitive endoderm

CyT49 differentiated to endoderm of foregut

dTAG-NIPBL hTERT-RPE-1 - clone D7

dTAG-RAD21 hTERT-RPE-1 - clone B1

dTAG-RAD21 hTERT-RPE-1 - clone B3

GM12878

4DNFIUEG1HD

chr1 0.956

chr2 0.996

chr3 0.999

chr4 0.999

chr5 0.957

chr6 0.999

chr7 0.997

chr8 0.999

chr9 0.999

chr10 0.992

chr11 0.727

chr12 0.995

chr13 0.999

chr14 0.999

chr15 0.994

chr16 0.995

chr17 0.999

chr18 0.999

chr19 0.999

chr20 0.999

chr21 0.864

chr22 0.998

chrX 0.996

4DNFISGQ46V

4DNFI31XAD26

4DNFIAHOU1R2

4DNFI3GMMSC

4DNFIHAT8TZ

4DNFIPAIX8BS

4DNFIW663ATT

4DNFIK4PKKZ

H1-hESC

H1-hESC (Tier 1)

H1-hESC differentiated to definitive endoderm

H9 with targeted integration of GFP-tag

H9 with targeted integration of GFP-tag

H9 with targeted integration of GFP-tag

HAP-1

HCT116 with Crispr generated mClover

HCT116 with Crispr generated mClover

heart left atrium

Metadata

Accession

4DNFIUEG1HD

Pearson r

0.9562

Chromosome

chr1

Contact Max

5.252e+0

Organism

Homo sapiens

Contact Mean

1.958e-3

Assembly

GRCh38

Source

4DN

Biosource

GM12878

Experiment

in situ Hi-C

Lab

4DN DCIC, HMS

Resolution

50 kb

Normalization

KR

Tolerance

0.9

Bins

4980 (400 removed)

Contact Map

MSD

Loss-tangent

3D Dynamics

Data

About

IGV

hg38

chr1:186,687,756-248,937,756

Q 62 mb

Select Tracks

Crosshairs

Center Line

Track Labels

190 mb

200 mb

210 mb

220 mb

230 mb

240 mb

Contact Map · Hi-C / PHi-C

Hi-C

PHi-C

MSD Map · locus × lag-time

Loss-tangent Map · locus × frequency

3D Dynamics · generated from lam / Q

3D Dynamics

Control

3D Dynamics

SIMULATION

Run

Refresh

Step (s)

1.0e-3

STRAND

Shape

Tube

Smooth

High

Width

COLOR

Color

Loss-tangent

Slice

50%

Fade

67%

SCENE

Depth

SSAO → screen-space ambient occlusion

Background

White

Spin

Recenter

LABELS

Labels

Interval (beads)

320

Hover

4DNFIUEG1HD · chr1 · GM12878 · GRCh38 · in situ Hi-C · res 50 kb · KR · tol 0.9 · 4980 (400 removed) bins · pearson 0.9562

Left Bottom Right

Explore

PHi-C Home

Tools for the physical interpretation of Hi-C data.

Explore observed and reconstructed Hi-C contact maps, dynamic 3D genome structures, and genome-wide physical dynamics.

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