

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

[Cinteny](#)

RRID:SCR_002147

Type: Tool

Proper Citation

Cinteny (RRID:SCR_002147)

Resource Information

URL: <http://cinteny.cchmc.org/>

Proper Citation: Cinteny (RRID:SCR_002147)

Description: Online database for finding and analyzing syntenic regions across multiple genomes and measuring the extent of genome rearrangement using reversal distance as a measure.

Synonyms: Cinteny Server for Synteny Identification and Analysis of Genome Rearrangement

Resource Type: software resource, data or information resource, web application, database

Defining Citation: [PMID:17343765](#)

Keywords: syntenic genes, genome rearrangement, online genome database

Funding: NIAID R21 AI055338;
NIAMS R01 AR050688

Availability: Free, Freely available

Resource Name: Cinteny

Resource ID: SCR_002147

Alternate IDs: OMICS_00931

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260801T190159+0000

Ratings and Alerts

No rating or validation information has been found for Cinteny.

No alerts have been found for Cinteny.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Nmezi B, et al. (2025) An oligodendrocyte silencer element underlies the pathogenic impact of lamin B1 structural variants. *Nature communications*, 16(1), 1373.

Gatticchi L, et al. (2020) Tm7sf2 Disruption Alters Radial Gene Positioning in Mouse Liver Leading to Metabolic Defects and Diabetes Characteristics. *Frontiers in cell and developmental biology*, 8, 592573.

Krishna KH, et al. (2018) Molecular evolution and functional divergence of eukaryotic translation initiation factor 2-alpha kinases. *PloS one*, 13(3), e0194335.

Iyer S, et al. (2018) A comparative bioinformatic analysis of C9orf72. *PeerJ*, 6, e4391.

Kirk IK, et al. (2017) The impact of the protein interactome on the syntenic structure of mammalian genomes. *PloS one*, 12(9), e0179112.

Sarda S, et al. (2017) Distal CpG islands can serve as alternative promoters to transcribe genes with silenced proximal promoters. *Genome research*, 27(4), 553.

Jayachandran P, et al. (2016) Microtubule-associated protein 1b is required for shaping the neural tube. *Neural development*, 11, 1.

Pavlopoulos GA, et al. (2015) Visualizing genome and systems biology: technologies, tools, implementation techniques and trends, past, present and future. *GigaScience*, 4, 38.

Manoli M, et al. (2014) nkx2.1 and nkx2.4 genes function partially redundant during development of the zebrafish hypothalamus, preoptic region, and pallidum. *Frontiers in neuroanatomy*, 8, 145.

Tiirikka T, et al. (2014) Clustering of gene ontology terms in genomes. *Gene*, 550(2), 155.

Gupta M, et al. (2013) Identification and expression analysis of zebrafish glypicans during embryonic development. *PloS one*, 8(11), e80824.

Sällman Almén M, et al. (2012) The dispanins: a novel gene family of ancient origin that contains 14 human members. *PloS one*, 7(2), e31961.

Lemay DG, et al. (2012) G-NEST: a gene neighborhood scoring tool to identify co-conserved, co-expressed genes. *BMC bioinformatics*, 13, 253.

Sandhu KS, et al. (2012) Large-scale functional organization of long-range chromatin interaction networks. *Cell reports*, 2(5), 1207.

Maddirevula S, et al. (2011) Nrdp1 governs differentiation of the melanocyte lineage via Erbb3b signaling in the zebrafish embryogenesis. *Biochemical and biophysical research communications*, 409(3), 454.

Guo FB, et al. (2010) Chromosome translocation and its consequence in the genome of *Burkholderia cenocepacia* AU-1054. *Biochemical and biophysical research communications*, 403(3-4), 375.

Sinha AU, et al. (2007) Cinteny: flexible analysis and visualization of synteny and genome rearrangements in multiple organisms. *BMC bioinformatics*, 8, 82.