

# Formation of DRIP coactivator complex

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06/05/2024

## Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

## Literature references

- Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*, 18, 142. [↗](#)
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
- Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res*, 46, D649-D655. [↗](#)
- Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology*, 14, e1005968. [↗](#)

Reactome database release: 88

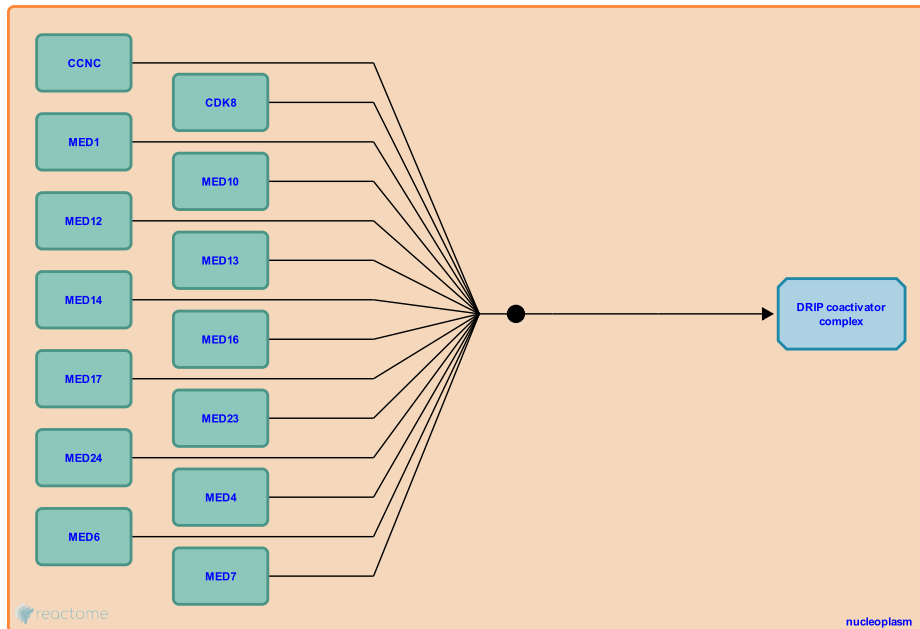
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## Formation of DRIP coactivator complex ↗

**Stable identifier:** R-HSA-212432

**Type:** binding

**Compartments:** nucleoplasm



### DRIP co-activator complex and assembly

The DRIP co-activator complex is a subset of 14 proteins from the set of at least 31 Mediator proteins that, in different combinations, form "Adapter" complexes. Adapter complexes bridge between the basal transcription factors (including Pol II) and tissue-specific transcription factors (TFs) bound to sites within upstream Proximal Promoter regions or distal Enhancer regions (reviewed in Maston, 2006 and Naar, 2001).

The DRIP complex was originally identified and named as a co-activator complex associated with the Vitamin D Receptor member of the nuclear receptor family of transcription factors (Rachez, 1998). It was later determined that all of the components of the DRIP complex were also in the TRAP complex, and the ARC complex.

The DRIP complex contains the following 14 proteins, which also are common to the ARC and TRAP complexes: MED1, MED4, MED6, MED7, MED10, MED12, MED13, MED14, MED16, MED17, MED23, MED24, CDK8, CycC.

All of the DRIP adapter complex components are present in the ARC adapter complex, but the ARC complex also has 4 additional components (Rachez, 1999). These ARC-specific components are now called: MED8, MED15, MED25, and MED 26 in the unified nomenclature scheme (Bourbon, 2004).

Similarly, all 14 of the DRIP adapter complex components are present in the TRAP adapter complex, but the TRAP complex also has 4 additional components (Bourbon, 2004), These TRAP-specific components are now called: MED20, MED27, MED30, and MED 31 in the unified nomenclature scheme.

In addition, these various transcription co-activator proteins identified in mammalian cells were found to be the orthologues or homologues of the Mediator complex identified in yeast, first identified by Kornberg and colleagues (Kelleher, 1990).

## Literature references

Suldan, Z., Freedman, LP., Chang, CP., Ward, J., Tempst, P., Rachez, C. et al. (1998). A novel protein complex that interacts with the vitamin D3 receptor in a ligand-dependent manner and enhances VDR transactivation in a cell-free system. *Genes Dev*, 12, 1787-800. ↗

Lemon, BD., Tjian, R., Näär, AM. (2001). Transcriptional coactivator complexes. *Annu Rev Biochem*, 70, 475-501. ↗

Bromleigh, V., Gamble, M., Suldan, Z., Lemon, BD., Freedman, LP., Tempst, P. et al. (1999). Ligand-dependent transcription activation by nuclear receptors requires the DRIP complex. *Nature*, 398, 824-8. [↗](#)

Maston, GA., Green, MR., Evans, SK. (2006). Transcriptional regulatory elements in the human genome. *Annu Rev Genomics Hum Genet*, 7, 29-59. [↗](#)

Kornberg, RD., Kelleher RJ, 3rd., Flanagan, PM. (1990). A novel mediator between activator proteins and the RNA polymerase II transcription apparatus. *Cell*, 61, 1209-15. [↗](#)

## **Editions**

2008-02-26

Reviewed

Freedman, LP.