Delayed Early (DE) Gene Expression

Caposio, P., Streblow, DN.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

03/05/2024

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. ↗

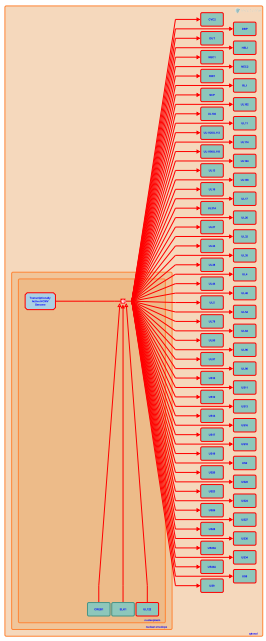
Delayed Early (DE) Gene Expression ↗

Stable identifier: R-HSA-9623096

Type: uncertain

Compartments: nucleoplasm

Diseases: disease by infectious agent



Following peak expression of major immediate early (MIE) regulatory proteins, the second class of early genes, delayed early (DE), become transcriptionally active independent of the host cell type. Although some DE gene products are produced in abundance from the start, most of the proteins and assorted miRNAs accumulate gradually. The DE period of viral replication continues until viral DNA synthesis initiates. DE genes are crucial for viral DNA synthesis and include several functions that become important later in infection for maturation and egress. Many DE genes have a substantial impact on replication when disrupted. DE gene products dispensable for replication in fibroblasts may contribute to modulation of the host cell and host animal response to infection. Several HCMV DE genes switch or add transcriptional start sites later in infection, which means that transcript levels represent the combined products of different kinetic classes of gene expression.

Literature references

Knipe, DM., Howley, PM. (2013). Chapter 62 - Cytomegaloviruses, Fields Virology. *Lippincott Williams & Wilkins*.

Editions

2019-10-18	Reviewed	Streblow, DN., Caposio, P.