

MERTK receptor binds ligands (Gas6 or

Protein S)

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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.

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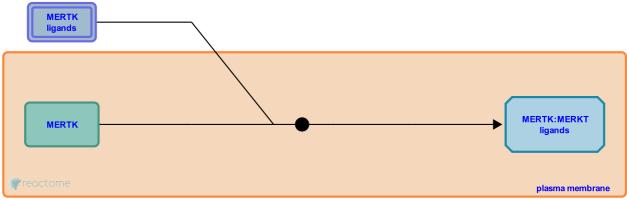
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Stable identifier: R-HSA-202710

Type: binding

Compartments: plasma membrane, extracellular region



MerTK appears to be required for ingestion of apoptotic cells by professional phagocytes such as monocytes/macrophages, retinal pigment epithelial cells and dendritic cells. Mer appears to be able to induce the cytoskeletal remodelling that is required for engulfment during phagocytosis. For instance, a deletion in the MERTK gene was identified as the underlying cause for retinal dystrophy which involves an impairment in the ingestion of shed photoreceptor cell fragments by retinal pigment epithelial cells.

The biological ligands for MerTK are two highly similar vitamin K-dependent proteins, Gas6 and protein S (PS), a negative regulator of blood coagulation. Both proteins are composed an N-terminal region containing multiple post-translationally modified gamma-carboxyglutamic acid residues (Gla). The Gla region possesses the ability to interact in a conformationally specific manner with negatively charged membrane phospholipids, which is thought to mediate the binding of both Gas6 and PS to apoptotic cells. In this way, they are thought to act as recognition bridges between apoptotic cells and the phagocyte cell that ingest them.

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Editions

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