Phosphorylated MAPKs translocate into the nucleus

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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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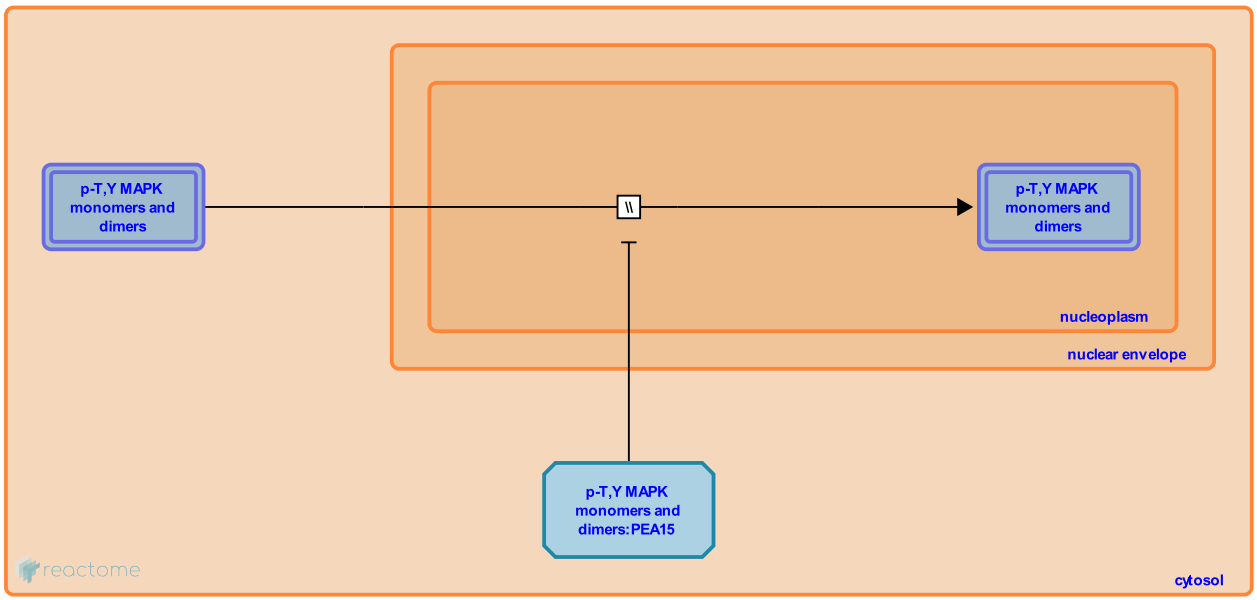

After phosphorylation by MAP2Ks, a proportion of activated MAPK translocates into the nucleus where it activates nuclear targets (reviewed in Roskoski, 2012b). MAPKs, which lack a nuclear localization signal (NLS), may 'piggyback' into the nucleus in complex with other nuclear-targeted proteins or may translocate by virtue of interaction with components of the nuclear pore complex (Brunet et al, 1999; Adachi et al, 1999; Matsubayashi et al, 2001; Whitehurst et al, 2002; Khokhlatchev et al, 1998; reviewed in Roskoski, 2012b). Although dimerization of MAPKs was thought to be critical for nuclear translocation, a number of studies have now challenged the physiological relevance of MAPK dimerization and this remains an area of uncertainty (Lenormand et al, 1993; Chen et al, 1992; Casar et al, 2008; Lidke et al, 2010; Burack and Shaw, 2005; reviewed in Casar et al, 2009; Roskoski, 2012b)

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