**Rule-based Modeling of VEGF Signaling**

VEGF (*Vascular Endothelial Growth Factor*) is a crucial regulator of angiogenesis, which has an important role in diseases such as cancer and arthritis. Although there are several published models of VEGF binding to its receptors, no models exist that consider events following receptor aggregation. Development of such models may provide comprehensive understanding of the pathway dynamics and assist in developing new anti-tumor drugs and other therapies. Because the number of possible phosphorylation states and signaling complexes can be very large, we develop our model using the BioNetGen software platform, in which objects and their components represent signaling molecules and their functional elements, and rules describe biochemical interactions. We are developing a model including VEGFR phosphorylation sites that couple directly to angiogenesis. The model extends published models for the ligand-induced aggregation of VEGF receptors and co-receptors with the addition of kinase activation, receptor phosphorylation, and recruitment of downstream effectors.