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*Cover:* Vascular endothelial growth factor VEGF (blue) and its soluble receptor sVEGFR1 (orange) are key molecules that regulate angiogenesis, the growth of new capillaries from pre-existent microvasculature. In our computational model of the systems biology of VEGF, a system of 61 ordinary differential equations describes the interactions between VEGF, sVEGFR1, and other VEGF receptors (VEGFR1, VEGFR2, neuropilin-1, matrix proteoglycans), as well as intercompartmental transport processes (vascular permeability, lymphatic drainage, plasma clearance). A selection of these molecular interactions and transport processes is illustrated in the middle row. Solutions to the mathematical equations allow the prediction of in vivo systemic distributions of VEGF—among body compartments (e.g., interstitial fluid in muscle tissue vs. plasma) and among its various molecular binding partners (e.g., free vs. sVEGFR1-bound vs. bound to endothelial cell surface receptors)—under varying conditions of protein expression rates (e.g., endogenous production rates of sVEGFR1 in the *x*- and *y*-axes of the 3-dimensional plots) and transport rates (e.g., +Ctrl vs. E1 vs. E2 vs. E3 in the 3-dimensional plots). For details, see Wu FT, Stefanini MO, Mac Gabhann F, Kontos CD, Annex BH, Popel AS. A computational kinetic model of VEGF trapping by soluble VEGF receptor-1: effects of transendothelial and lymphatic macromolecular transport. *Physiol Genomics* 38: 29–41, 2009 (first published April 7, 2009; doi:10.1152/physiolgenomics.00031.2009).

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