Structural characterization of capillary morphogenesis gene 2 inhibitors

Sara Soleimani^a, James D.Moody^b

^aBrigham Young University, 701. E. University Parkway, Provo, UT, 84602, <u>sara@chem.byu.edu</u>

^bBrigham Young University, 701. E. University Parkway, Provo, UT, 84602, <u>jdmoody@chem.byu.edu</u>

Capillary Morphogenesis Gene 2 (CMG2) plays a significant role in mediating angiogenesis. Competitive inhibition of CMG2 binding to its physiological ligands results in a substantial reduction of pathological angiogenesis versus the growth factors as observed in models of corneal neovascularization, endothelial tube formation, and endothelial cell migration.

CMG2 is one of the proteins which is produced in cases of cancer. CMG2 overexpression is associated with increased tumor grade and poor patient survival. Peptides and small molecules have been developed which bind with CMG2 to block its functionalities in cancers. The ability to block the functionality of CMG2 will hopefully be used to treat the cancer. Atomic-level structures of CMG2 bound to the peptides will give us more insights about their binding modes.

CMG2 will be purified by Affinity Chromatography and Size Exclusion Chromatography. Crystallization conditions are known and crystallization will be achieved using sitting drop Vapor diffusion. Then, the crystals will be inspected by X-Ray diffraction. The novelty of this research is to use structure-based drug design. Having pictures of CMG2 bound with peptides will allow us to modify the peptides to function better in blocking the CMG2 proteins.