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**The Structure of the Angiogenesis Inhibitor Angiostatin Bound to a Peptide from the Group A Streptococcal Surface Protein PAM.** S.E. Weaver<sup>1</sup>, J.H. Geiger<sup>2</sup>, <sup>1</sup>Dept. of Biochemistry & <sup>2</sup>Dept. of Chemistry, Michigan State Univ., East Lansing, MI 48824 USA.

The x-ray crystallographic structure of the angiogenesis inhibitor angiostatin containing plasminogen kringles 1-3 bound to VEK-30 an internal peptide from the group A streptococcal surface protein PAM was determined by molecular replacement and refined to 2.4 Å resolution to a R-factor of 21.8%. The space group is P6<sub>1</sub>22 and the cell dimensions are a=b=58Å and c=391Å with one molecule in the asymmetric unit. It is the first structure of angiostatin bound to a ligand and provides a model as to how angiostatin binds protein ligands involved in angiogenesis. The VEK-30 peptide contains a pseudo-lysine moiety where arginine and glutamate separated by almost one helical turn bind within the bipolar angiostatin kringle 2 domain lysine-binding site. The structure also reveals that plasminogen kringle domains are able to undergo significant structural rearrangement relative to one another. Dimerization between two molecules of angiostatin/VEK-30 related by crystallographic symmetry occurs and provides insight into the function of plasminogen during streptococcal infection.