Unruptured intracranial aneurysms occur in about 3% of the general population. Rupture of the intracranial aneurysm results with subarachnoid hemorrhage, which is a devastating type of stroke related to high mortality. Despite extensive research, factors predisposing to aneurysm rupture remain unclear. One of the aspects that might contribute to better assessment of aneurysm risk rupture is analysis of its hemodynamics. Current methods of computational modelling allow to analyze blood flow through aneurysm dome and calculate hemodynamic parameters that define patterns of flow alterations. However, definitive correlations between certain hemodynamic descriptors and risk of rupture have not been established. Previous researchers showed that endothelial cells might respond to changes in blood flow by regulating expression of genes and proteins. Therefore, analysis of protein expression in aneurysm dome might contribute to better understanding of biological processes that occur in its wall due to altered blood flow. The aim of the project is comprehensive analysis of aneurysm hemodynamic profile and determination of its influence on protein expression in aneurysm wall. We plan to include 81 patients with unruptured intracranial aneurysm, qualified to its surgical clipping. During the procedure, we will obtain tissue sample of aneurysm dome and two control samples of other arteries. Based on imaging data, we will perform Computational Fluid Dynamics analysis and define the hemodynamic profile of the aneurysm. For obtained samples we will perform analysis of protein expression in relation to control samples. Proteins differently expressed in aneurysm dome will then be compared between distinguished hemodynamic profiles. We will further determine biological processes which involve those proteins. Performed analysis will contribute to better understanding of molecular consequences of altered blood flow and might contribute to determination of the hemodynamics role in aneurysm rupture assessment.