Cleavage and breakdown of proteins (proteolysis) occurs through the hydrolysis of peptide bonds, which link amino acids together in these biopolymers. The reaction is carried out by a subclass of hydrolases referred to proteases. Proteolysis plays an essential role in all physiological processes but since the cleavage is irreversible, proteases needs to be tightly regulated at many levels, from gene expression to the protein maturation process. In multicellular eukaryotic organisms, control of proteolytic function is achieved by the production of specialized proteins, called protease inhibitors, which binds to proteases and blocks their activities. Interestingly, in prokaryotes, occurrence of protease inhibitors is rare and they are scattered among different bacterial species despite that each bacterium produces many different proteases. Moreover, we do not know what role the prokaryotic protease inhibitors have on cellular function of the organism. Therefore, we were excited to discover several protease inhibitors in *Tannerella forsythia* – a bacterium playing an important role in development of gum disease called periodontitis. These protease inhibitors, we referred to as LIPINs (***Li***poprotein ***P***rotease ***IN***hibitor***s***), lie adjacent to their target proteases in the genome of *T. forsythia*. Such arrangement suggests LIPINs have the function to control proteases secreted by this bacterium. In addition, it cannot be excluded that LIPINs will also inhibit human and other bacteria-derived proteases. This is likely because *T. forsythia* often resides within a multibacterial biofilm on the tooth surface together with other highly proteolytic bacteria. The microorganisms are also exposed to host proteases from the innate immune response. These LIPINs are unique and do not resemble any other known protease inhibitor at the amino acid sequence level. As a matter of fact, there seems to be no other proteins as LIPINs in living organisms. As a consequence, they are likely to have unique structure and mechanism of inhibition. Therefore, the general overarching objective of this project is to characterize the structure and function of LIPINs in the context of their housekeeping activity (regulation of proteolysis within the biofilm structure) and the potential of being novel virulence factors. This objective will be reached by: (***i***) determine the spectrum of proteases, both human and bacterial, which are inhibited by each LIPIN and then characterize kinetically the interaction. In this way, we will learn how fast each inhibitory complex is formed and how stable it is. In addition, obtained data will reveal the function of LIPINs beyond the inhibition of their target proteases in *T. forsythia.* (***ii***) Solving the 3D atomic structure of LIPINs alone and in inhibitory complexes by X-ray diffraction of obtained protein crystals. This study will reveal the structure of LIPINs and the molecular mechanism of inhibition. (***iii***) Assessment of the role of LIPINs in *T. forsythia* physiology and in the formation and maintenance of multibacterial biofim. To this end, we will generate *T. forsythia* strains depleted of up to three LIPIN genes alone or together with a co-transcribed protease and study bacterial viability and effects on multibacterial biofilm formation, biofilm structure and biofilm composition. Finally, we will also study the effect of different LIPIN mutants on pathogenicity of biofilm in a cell culture model. Together, the impact of this project will be structural and functional characterization of unique protease inhibitors with potentially novel mechanism of inhibition, the elucidation of the role of LIPINs in *T. forsythia* physiology and in formation of dysbiotic multibacterial biofilm. The latter will expand our knowledge on pathogenesis of periodontitis. Finally, taking into account that many proteases are targets for drug development, the obtained structural data can serve as excellent entry points for a hit-to-lead optimization process to develop therapeutic inhibitors.