Neutrophil extracellular traps (NETs) are a newly described mechanism of immune defense typical for neutrophils. NETs are multidimensional meshworks composed of chromatin, which is decorated with histones, proteolytic enzymes, antibacterial peptides and proteins of oxidative burst. The structure and biochemical composition of NETs enable efficient entrapment and rapid elimination of pathogens. The role of NETs in the regulation of immunological reactions remains still elusive. Among unravelled points is the role of NETs in the development of the inflammation. Despite their proinflammatory composition NETs does not entail a strong inflammatory reaction in naive immunological cells. Therefore, the overall objective of this project is identification of mechanisms that control the inflammatory potential of NETs. We hypothesize, that the control/restriction of NETs-inflammatory propensity is executed on the level of posttranslational modifications of proteins associated with DNA. To verify this contention we will determine the role of highly active enzymes identified in NETs (deiminases and proteases) on the inflammatory potential of NETs. Applying the global proteome analysis we will pinpoint the molecular targets for post-translational modifications in NETs. Finally, we will define the immunomodulatory role of modified proteins and their molecular mechanism of action. The results of the proposed basic research project will expend our knowledge about the role of NETs in the regulation of immune defence. Understanding the mechanisms of the immunomodulatory potential of NETs is also invaluable from the clinical point of view, not only in the context of infectious diseases, but also in case of aseptic systemic and autoimmune diseases.