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Prologue

The human genome comprises of more than 22.000 genes. These genes encode for proteins playing a role in many general or tissue-specific biological processes, but for many of them the function is not yet unraveled yet. A way to study all the different genes at once in a certain biological process is by genome-wide screening. By considering all genes in a pathway, new players can be identified that would otherwise not have been linked to the studied process. In this thesis, I describe a siRNA-based genome-wide screen used to identify new proteins involved in MHC class II antigen presentation, expression and transport. The data obtained from this screen not only led to the identification of proteins involved in the MHC class II pathway specifically, but we also identified a regulator of a more general process namely intracellular endosome localization. This shows the importance of genome-wide screening in the identification of new players and regulators of certain biological pathways which may be considered as new drug targets to cure diseases.