

## **Deciphering the protein interactome of SATB1 in T cells**

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Special AT-rich sequence-binding protein 1 (SATB1) is a nuclear matrix protein with a central role in high order chromatin organization and gene regulation. Elevated expression or/and mutation of SATB1 is associated with progression and poor prognosis in a plethora of malignancies. Although highly expressed in T cells, the molecular mechanism of SATB1 function in the thymus has been elusive. In this study, we sought to identify protein interaction partners of SATB1 using a co-immunoprecipitation approach coupled with state-of-the-art “bottom-up” proteomics and bioinformatics using primary murine thymocyte extracts. A comprehensive protein network map of SATB1 interactions in T cells was created showing, among others, that SATB1 interacts with several known transcription factors and kinases involved in thymic development and in the establishment of T cell tolerance. Moreover, several members of specific histone modification complexes involved in gene regulation were also found to co-precipitate with SATB1, suggesting an active role in the establishment/maintenance of T cell chromatin structure and gene regulation. Our results shed more light on the mechanism underlying the function of SATB1 in T cells and uncovered the role of other proteins in chromatin organization and gene regulation