

## Project abstract

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### PROJECT PROPOSAL

Lymphomas are the most common hematologic malignancies in adults. The last two decades have produced a myriad of novel targeted agents for lymphoma therapy. However, there are hardly any predictive biomarkers that could guide the usage of these drugs. Until now, all molecular lymphoma classifications have been based on the genetic profile of the malignant cell, but have not included comprehensive proteomic analyses. This could be one reason for their failure to predict treatment response.

In this project the clinician scientist will isolate proteomic information from the blood stream of patients with lymphoma treated in the Hematology/Oncology unit at University Hospital Mannheim. Bioinformatic investigations will be performed to discover lymphoma-associated proteomic signatures. Finally, molecular and biochemical methods will be used in our research laboratory to investigate these novel mechanisms and validate their potential as predictive biomarkers.

The aim of this translational project is the identification of novel candidate biomarkers and therapeutic targets in lymphoma.



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AND BACK

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