INNOVECTIS
Ein Unternehmen der Johann Wolfgang Goethe-Universität Frankfurt am Main

Service & Licensing Offer
Proteogenomic Platform for Early Detection of High-Risk DLBCL ("PG4-like DLBCL")

Benefits

- Precise identification of a clinically high-risk DLBCL subset beyond conventional cell-of-origin and genomic classification.
- Early prediction of reduced overall and progression-free survival and poor R-CHOP response based on combined tumor-intrinsic and tumor microenvironment features.
- Enables risk-adapted therapy decisions (R-CHOP vs. alternative/ intensified regimens) and provides a robust companion-diagnostic framework for targeted and immunotherapeutic trials in DLBCL.

Technology Stage

- Discovery cohort: 332 R-CHOP-treated DLBCL patients with matched mutation, transcriptome and proteome data; robust identification of PG4.
- Validation in independent cohorts (Cornell, NCI, BCC) confirms the adverse PG4 phenotype and predictive performance of the classifier.
- Sinlge-cell RNA/ATAC profiling in 43 cases assigns PG4-defining signals to malignant B cells and an exhausted CD8 T-cell compartment.

Patents

- PCT/EP2025/081300 "Method and Kit for Diagnosis, Prognosis, and/or Stratification of Diffuse Large B-Cell Lymphoma (DLBCL)", filed Oct. 29th 2025

Partnership Opportunities

- **Technologie as a service**
- **Technologie can be licensed**
- **Collaborations for further development welcome**

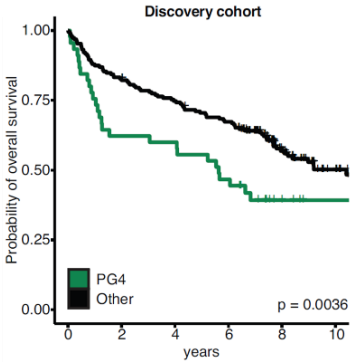
Summary

Scientists at Goethe University Frankfurt and DKFZ Heidelberg have developed a proteogenomic diagnostic platform that classifies diffuse large B-cell lymphoma (DLBCL) in seven different proteogenotypes (PG) reflecting specific pathophysiological features. Combining genomic, proteomic and microenvironmental features enables early risk stratification and supports personalized treatment decisions. Remarkably, PG4 was identified as a clinically aggressive, high-risk subset with poor outcome under standard R-CHOP therapy.

Technical Approach

From a patient sample (FFPE lymph node or other lymphoma tissue), the method determines whether at least two, preferably three or more defined features are present, using sequencing, proteomics and/or immunoassays.

A machine-learning classifier (XGBoost-based) integrates selected transcriptomic and proteomic markers to assign samples to PG4 versus other PG with high accuracy (PG4 vs. rest AUC ~0.9–0.95 in multiple cohorts).



PG4 is consistently associated with the worst overall survival (OS). OS estimate stratified for PG4 versus all other DLBCL PGs in DLBCL NOS (not otherwise specified) with R-CHOP treatment.

Market Need

- 30–40% of DLBCL patients are refractory or relapse after R-CHOP; about half of these failures cannot be explained by genomics alone.
- Current classifiers (ABC/GCB, genomic subtypes, IPI) do not reliably identify the highest-risk patients at diagnosis.

Applications of this technology

- Pre-treatment identification of high-risk ("PG4-like") DLBCL from FFPE tissue.
- Prognosis and prediction of poor R-CHOP response.
- Stratification into alternative or intensified regimens (e.g. CAR-T, bispecific antibodies, ViPOR-like combinations) and biomarker-guided clinical trials.

This technology can be accessed through flexible models — as a licensed solution or a dedicated service.

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