

fédérative de recherc





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## **INTRODUCTION**

Becker muscular dystrophy is a genetic disorder causing progressive muscle weakness in need of reliable plasma biomarkers for early diagnosis, monitoring, and treatment follow-up.

## **THE CHALLENGE: HIGH DYNAMIC RANGE**

99% of plasma proteome comes from the 22 most abundant proteins





An average of 657±95 PG IDs in neat plasma using EV-boost approach. An average of 3366 ±720 PG ID (Ca. 4x increase in number of proteins identified) using Proteograph assay.

CVs of 40-50% in neat and 30-50% in NP-enrich plasma.



The number of proteins ID correlated with contamination from plasma cells and coagulation factors.

## CHEMOKINES DETECTION IN PROTEOGRAPH ASSAY

The Proteograph assay enables the identification abundance of low proteins.

Notably, the detection of these proteins is independent of the number of proteins IDs and of the platelet contamination level.



**PROTEOGRAPH ASSAY** 

## SIGNIFICANTLY DIFFERENTIAL PROTEINS



			20-					
<ul> <li>✓ Library free mode</li> <li>✓ MBR Evboost<sup>*</sup></li> <li>✓ Human SwissProt DB 20K entries</li> </ul>	<ul> <li>✓ Library free mode</li> <li>✓ MBR</li> <li>✓ Human SwissProt DB 20K entries</li> </ul>	Data exploitation (months)	18 16 14 19		1: 1( [III/ bd	Classic plasma proteins	Tissue leakage	Cytok
DIRECT ANALYSIS OF UNDEPLETED (NEAT) PLASMA	IN-DEPTH ANALYSIS OF PL BY PROTEOGRAPH ASS	LASMA SAY	PROTEOGRAI	<ul> <li>BC</li> <li>BC</li> <li>BC2</li> <li>BC3</li> <li>BC_CTRL ◆ Imputed</li> </ul>	Concentration (log 10			
AIM : IDENTIFY BIOMARKERS OF	PROGNOSIS AND EARLY CARDI	ΟΡΑΤΗΥ	The ar damage	nalysis with NP-enriched sa at levels as low as 100pg/r	mples allov nL.	vs to detect clear mar	kers of mus	cle

CONCLUSION

Nanoparticle (NP)-based enrichment compresses the dynamic range of plasma and enhance proteome coverage without compromising quantification. The NP analysis allows to detect proteins of known low abundance, such as tissues leakage derived proteins and chemokines. This detection seems independent of the platelet contamination and the number of proteins identified.

Nanoparticle (NP)-based enrichment allowed to identify higher levels of pertinent markers currently under validation.

\* Neat plasma proteomics: getting the best out of the worst. I Metatla, K Roger et al. *Clin Proteom* 21, 22 (2024). PE Geyer et al., 2016 (<u>http://plasmaproteomeprofiling.com</u>)