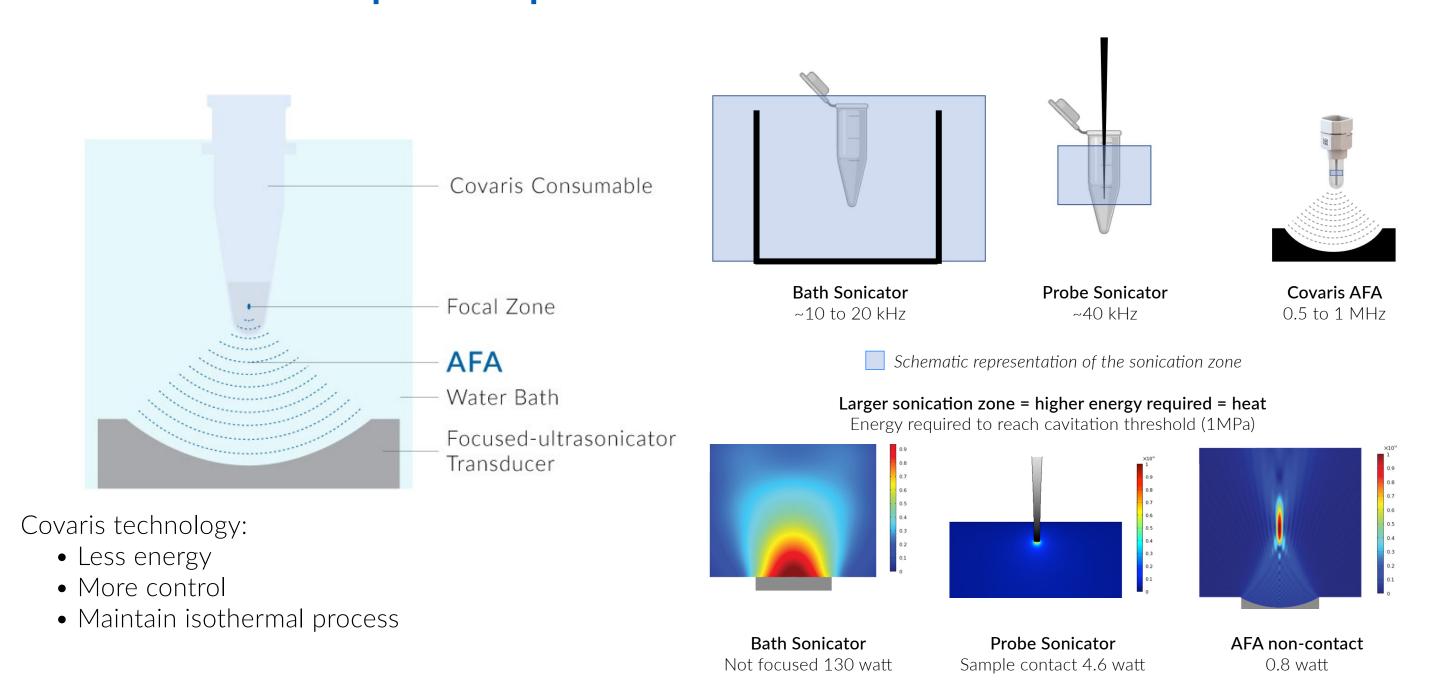
Standardized Sample Preparation Workflows for Clinical Proteomics

Nicolas Autret - Covaris Inc., Woburn, MA, USA



Adaptive Focused Acoustics® (AFA®) in Pre-analytical Sample Prep: Extraction with Precision



Key Takeaways

Covaris promotes robust, easy, and scalable sample preparation through:

- Standardized tissue/cell disruption
 - Improved consistency and reproducibility
 - Hands-free, automated
 - Processing in different formats, from single tube up to 96-well plate, with same sample-to-sample quality
- Fast, non-contact, easy, cold, and reproducible extraction for all soft and hard tissue samples*
 - Use your buffer of choice
 - Scale up from single tube to 96 well format and beyond
- Active deparaffinization and improved rehydration of FFPE tissue - Enables "fresh frozen like" protein extraction from FFPE samples, without any organic solvent
- *Includes non-mammalian samples like plants, yeast and bacteria

Standardized Protein Sample Preparation from Fresh Frozen Tissue

A. cryoPREP: Contact-free Tissue Pulverization

Liang et al., Methods Mol Biol., 2019 "optimal preservation of precious material, fast, enable multiOMICs"

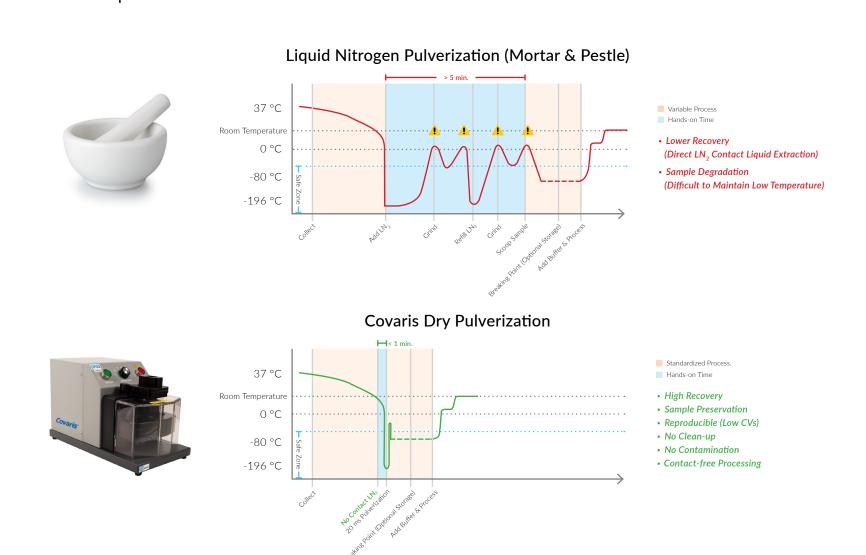
Tabb et al., Journal of proteome research, 2015 "high consitency, high quality, non-contact, improves extraction efficiency"

Schultz et al., Metabolites, 2019 "uncovers more biomolecules, cold, fast, reproducible"

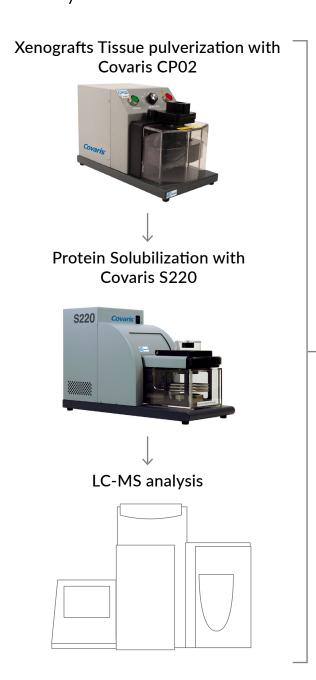
Wylezich et al., Scientific Reports, 2017

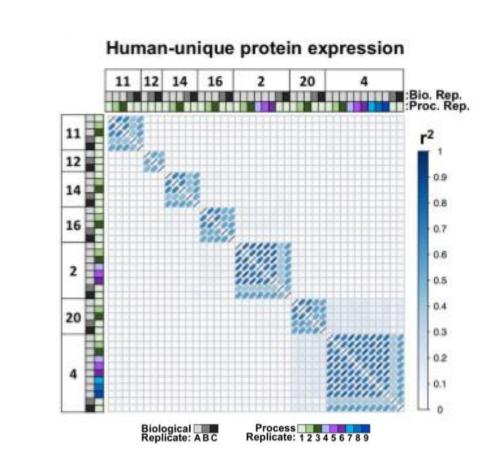
"highly reliable, most efficient method"

B. Optimal Biomolecule Preservation



C. cryoPREP Combined with AFA Enables High Reproducibility





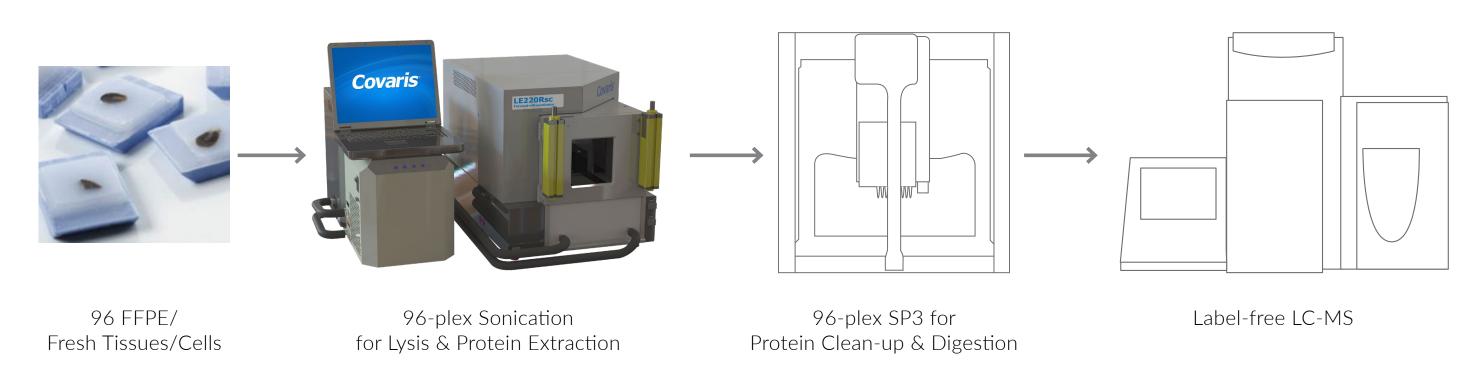
"Relative protein abundance in process replicates was highly correlated with an average R2 of 0.75 (fig. S3A), indicating high technical reproducibility in the proteomic workflow."

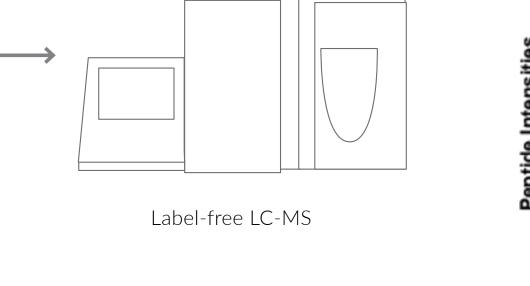
Wang et al., Sci Signal, 2017.

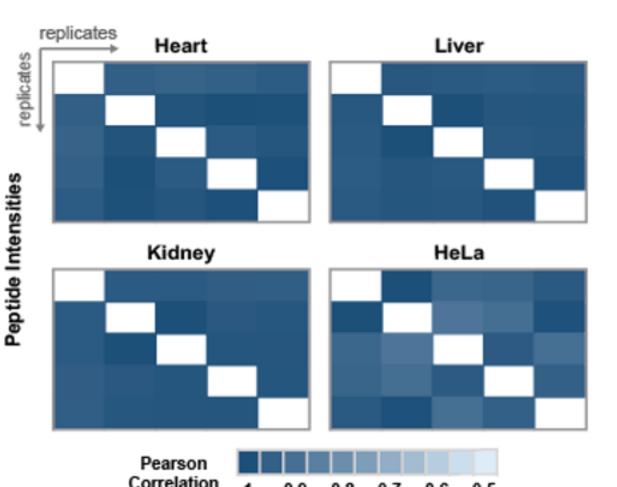
Improved Data Consistency with Automated Extraction from Low Input Samples

A. Hands-free, High-throughput Proteomics from FFPE* and Fresh Tissues or Cells

B. Automated Sample Preparation with SP3 for Low-input Clinical Proteomics





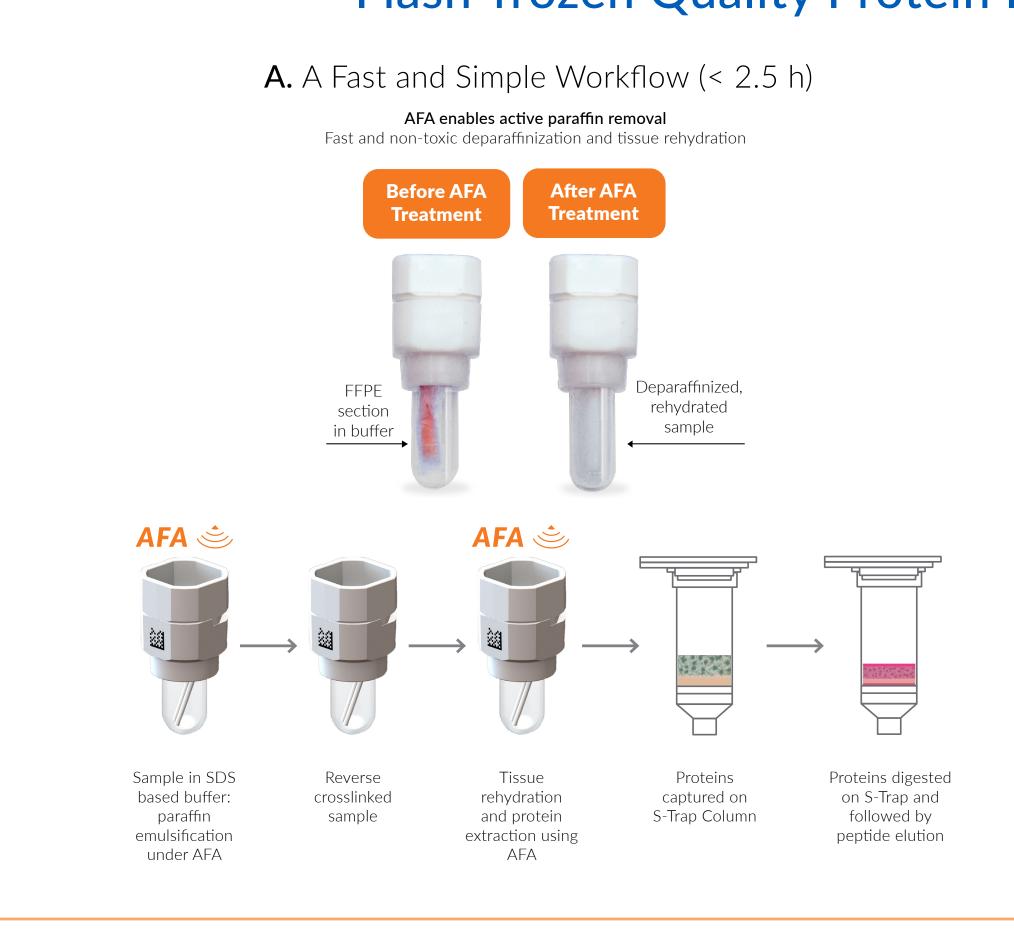


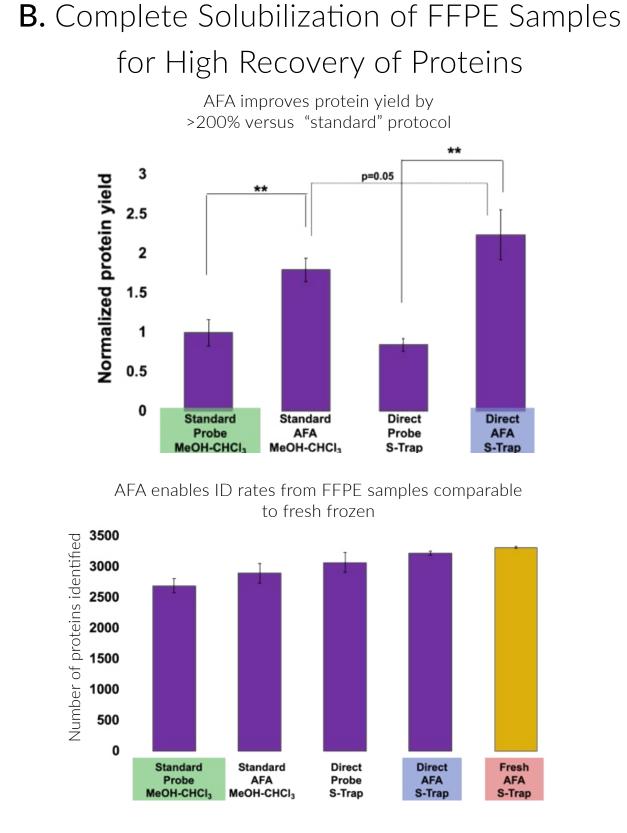
"multiplexed ultrasonication combined with autoSP3 constitutes a highly standardized pipeline that should contribute to the identification of biological or clinical determinants in cohorts of dozens or hundreds of samples"

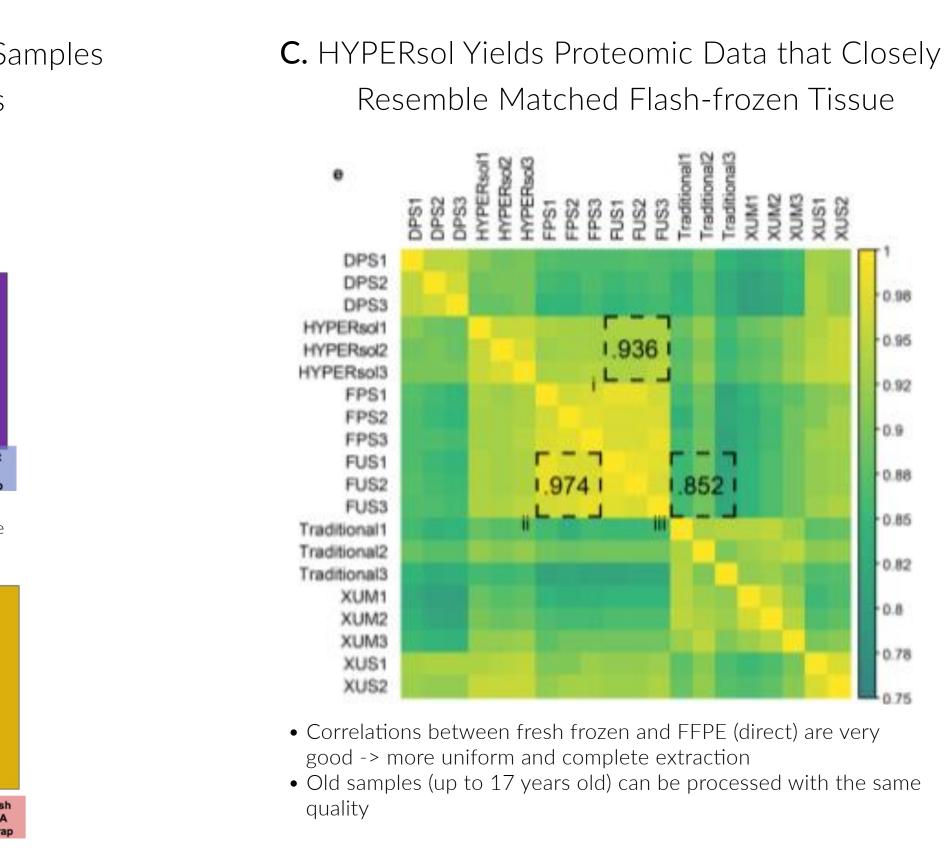
T Mueller, J Krijgsveld et al. Molecular Systems Biology 16:e9111 | 2020

*includes Laser Captured Microdissection (LCM) samples

Flash-frozen Quality Protein Extraction from Old Archived FFPE Samples with ProtiFi







Marchione, Wojcik et al. – J Prot Research 2020