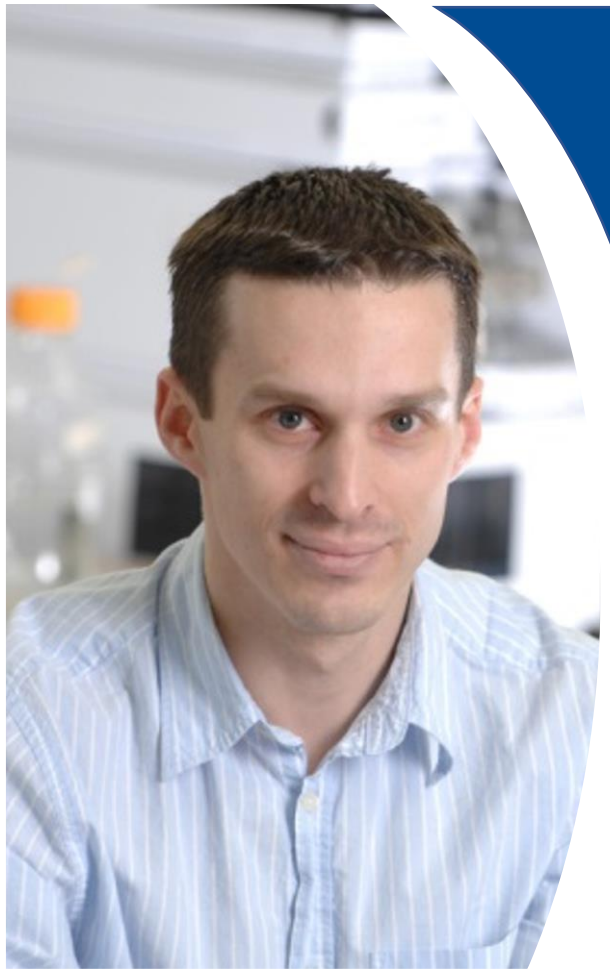
Streamlined SDS-based Workflows in the ProTrap XG for Top-down or Bottom-up Proteomics



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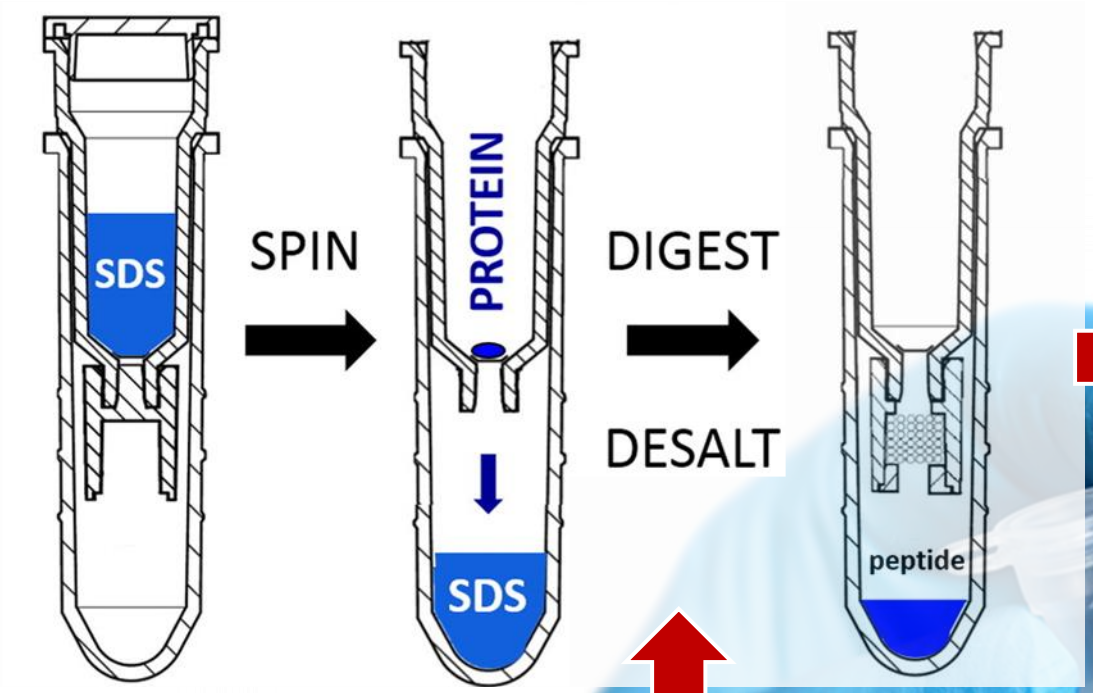
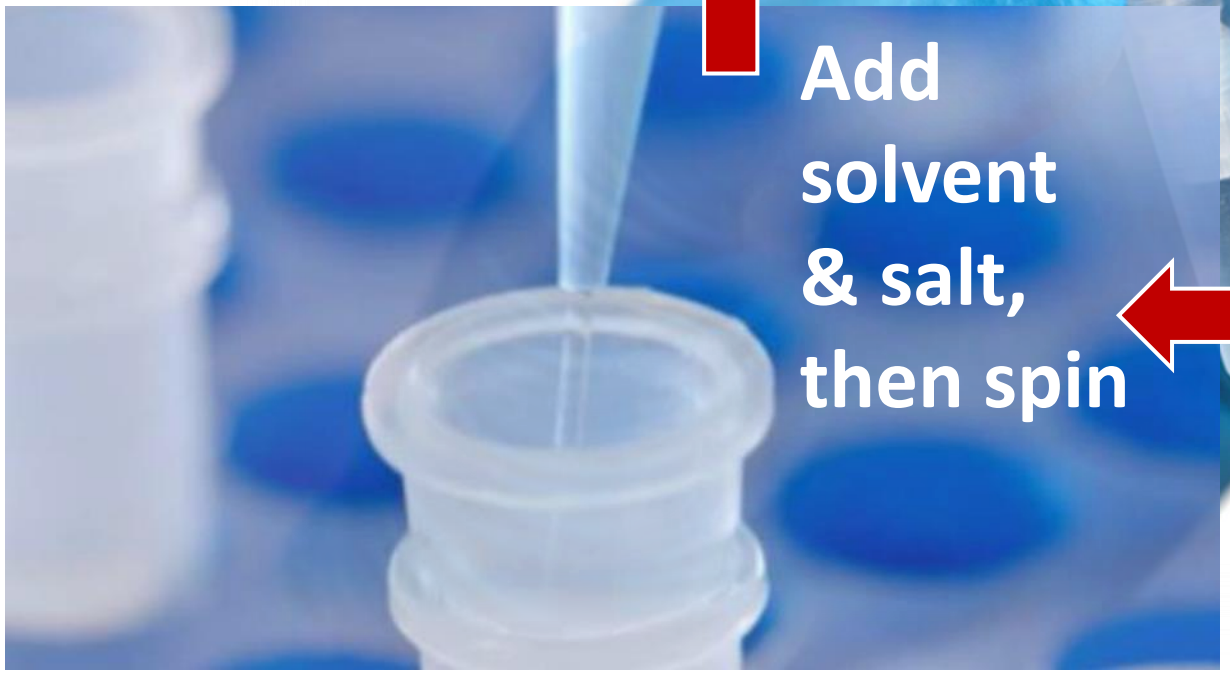
Better Tools.
Better Science.





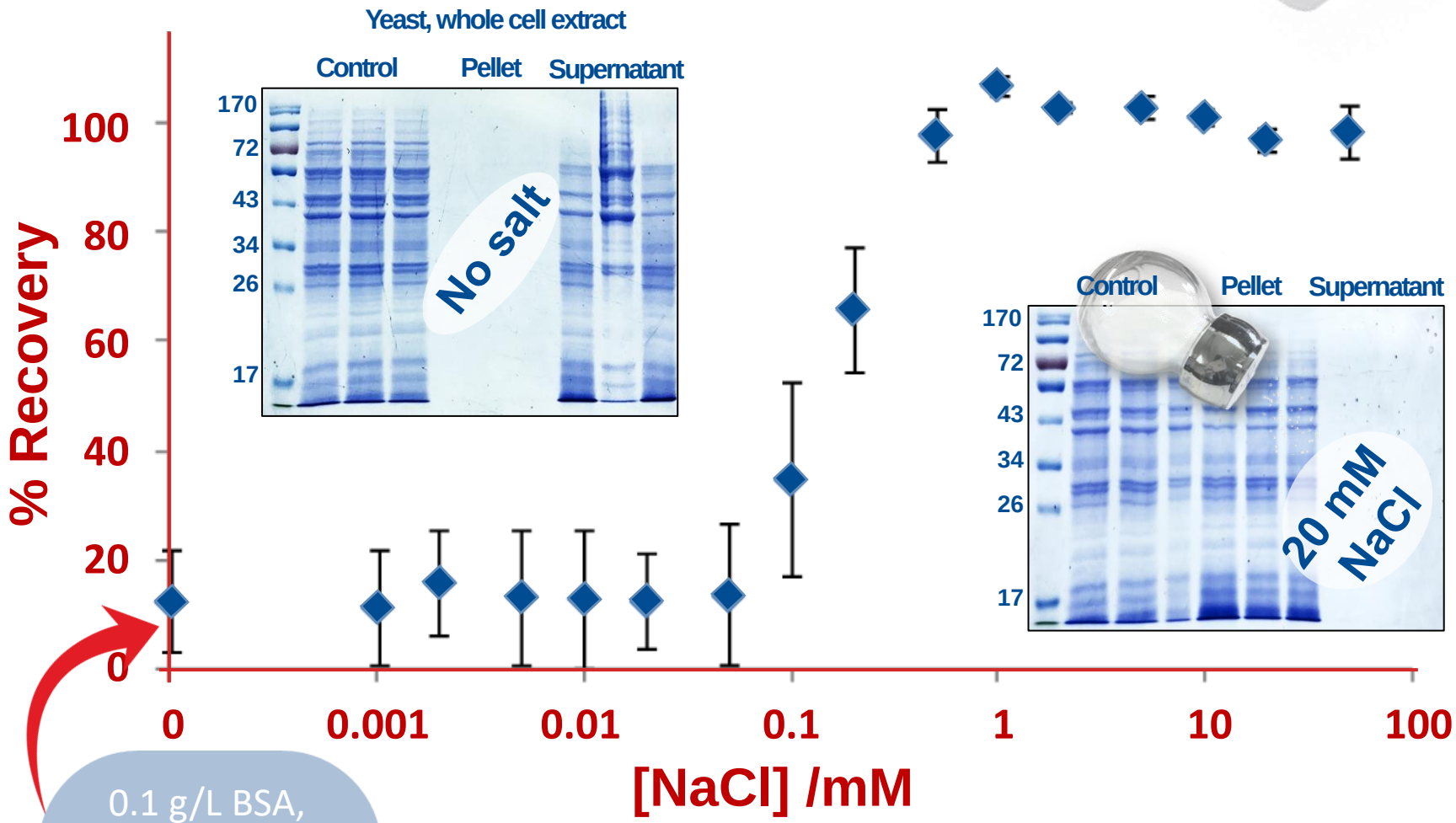
Add solvent & salt, then spin

What is the ProTrap XG ?

- A two-stage filter & extraction cartridge
- Facilitates protein cleanup by **precipitation**
- Provides high protein RECOVERY & PURITY

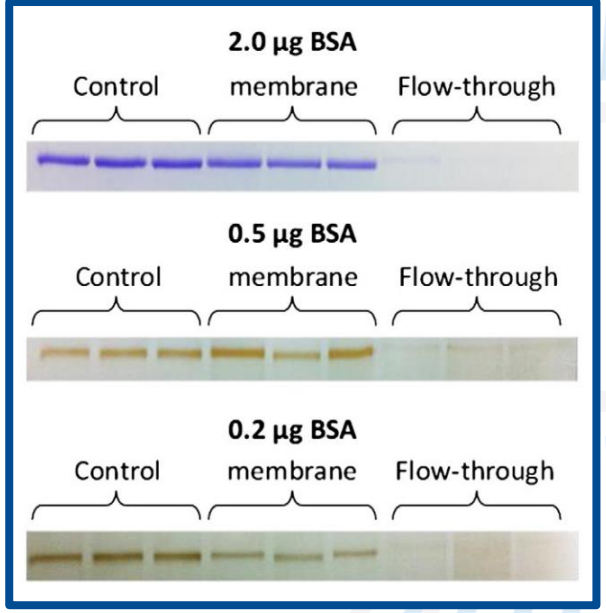
Crowell *et al.* (**2015**) *J Proteomics*, 118:140-50

Solvent precipitation requires SALT for maximal protein recovery



0.1 g/L BSA, with 80% acetone

High Protein Yields

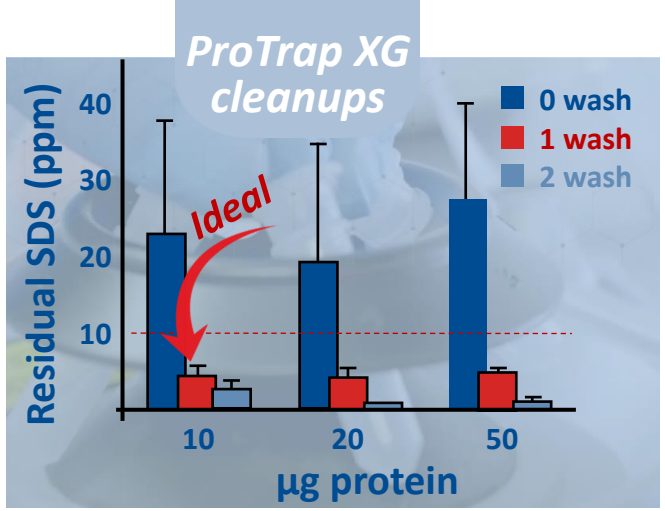


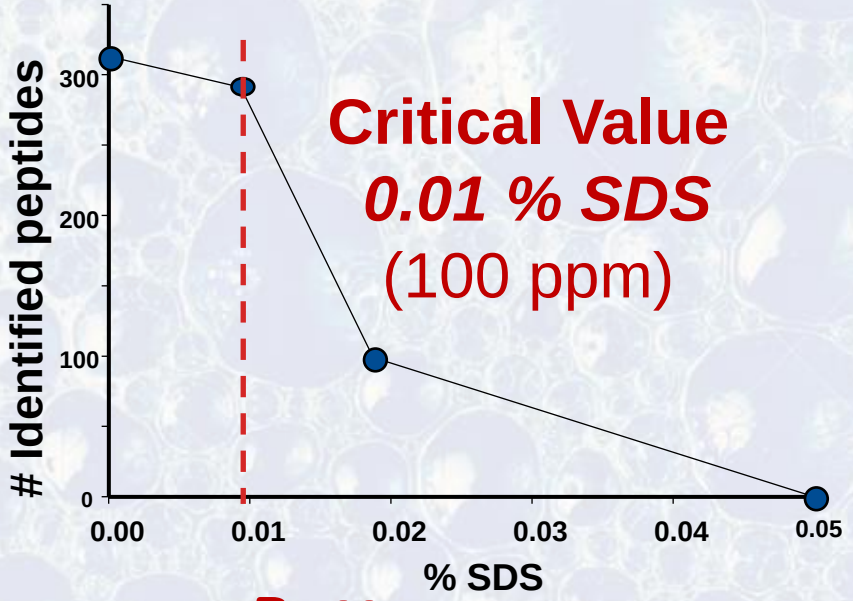
For optimal LC –MS/MS analysis,

Residual SDS

< 0.01% (bottom-up)

< 0.001% (top-down)

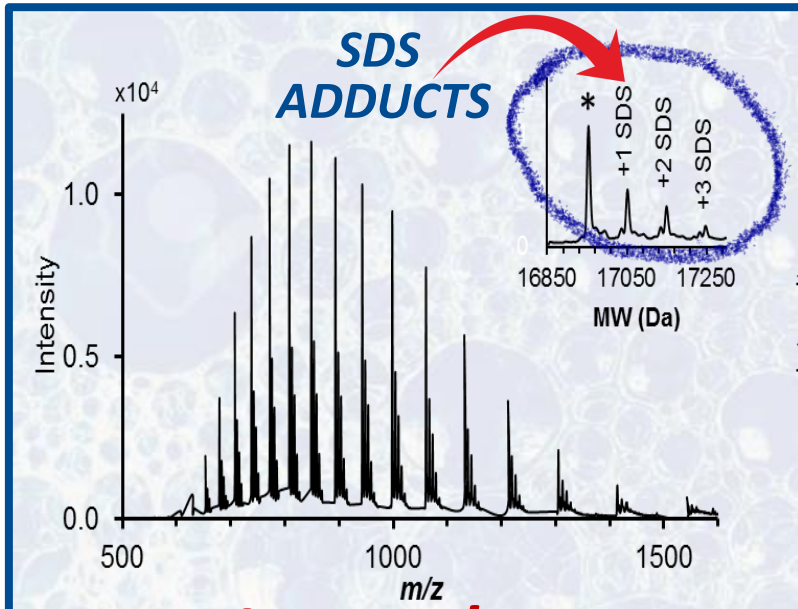




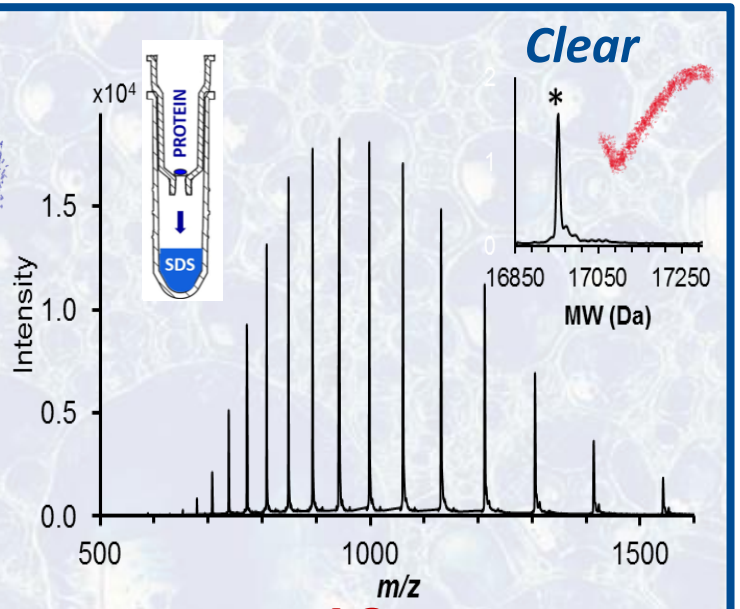
Critical Value
0.01 % SDS
(100 ppm)

Bottom-up Peptide ID

Yeast digest (+ SDS)



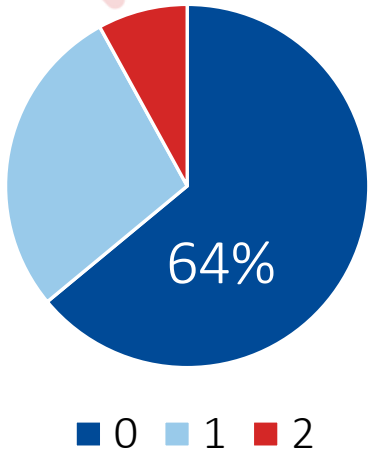
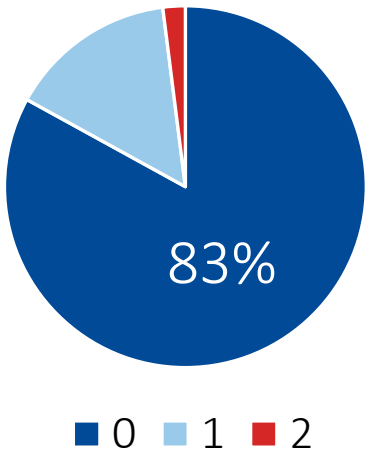
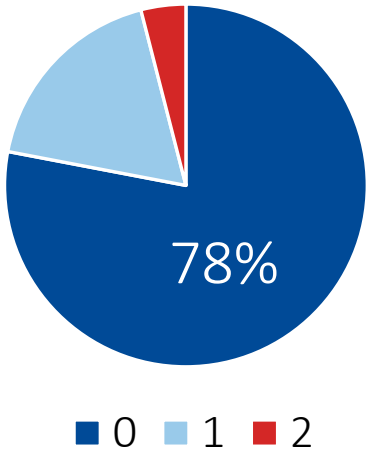
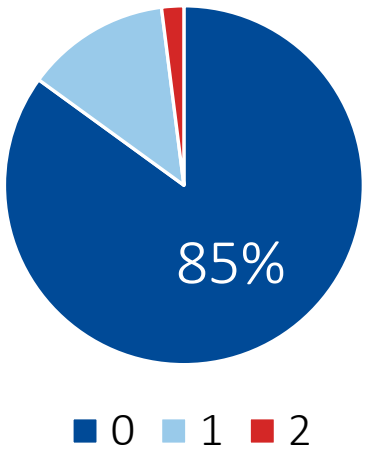
Incomplete SDS removal



<10 ppm Residual SDS

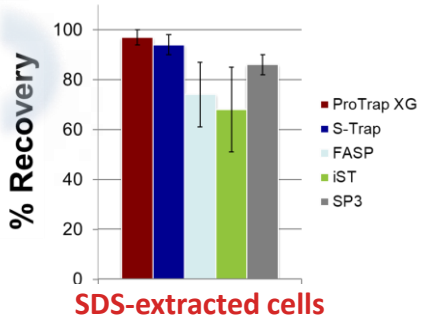
Intact myoglobin (+1% SDS)

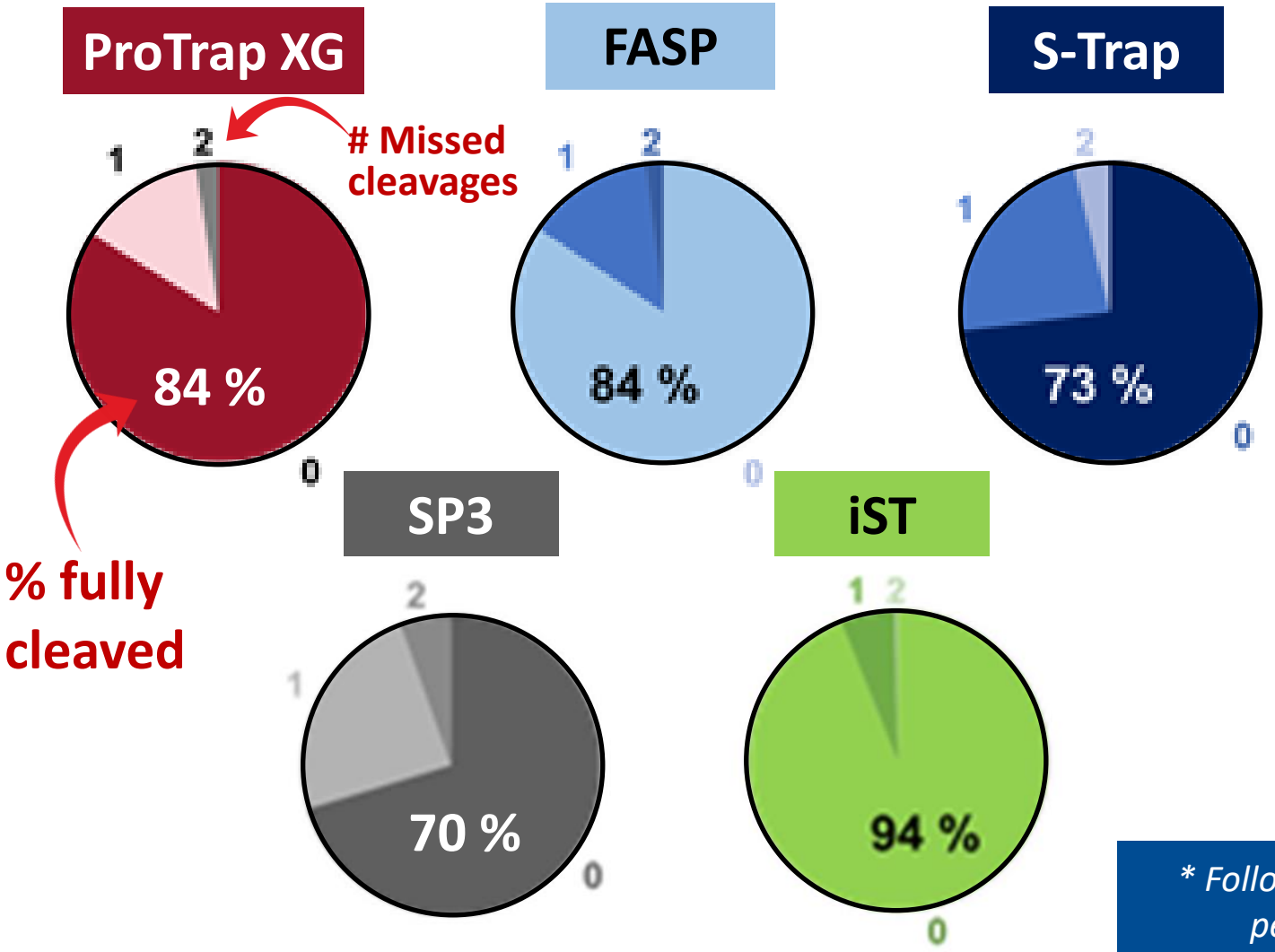
In-Solution Digestion: Cleavage efficiency

	Control	Mixed Enzyme	Elevated Temp	Overnight digest
	25:1 trypsin 37 °C 1 h	> 10:1 Lys C/trypsin 37 °C 1 h	25:1 trypsin 47 °C 1 h	25:1 trypsin 37 °C overnight
# Missed Cleavages				
# PSMs	940 ± 200	2050 ± 100	1720 ± 110	1850 ± 120

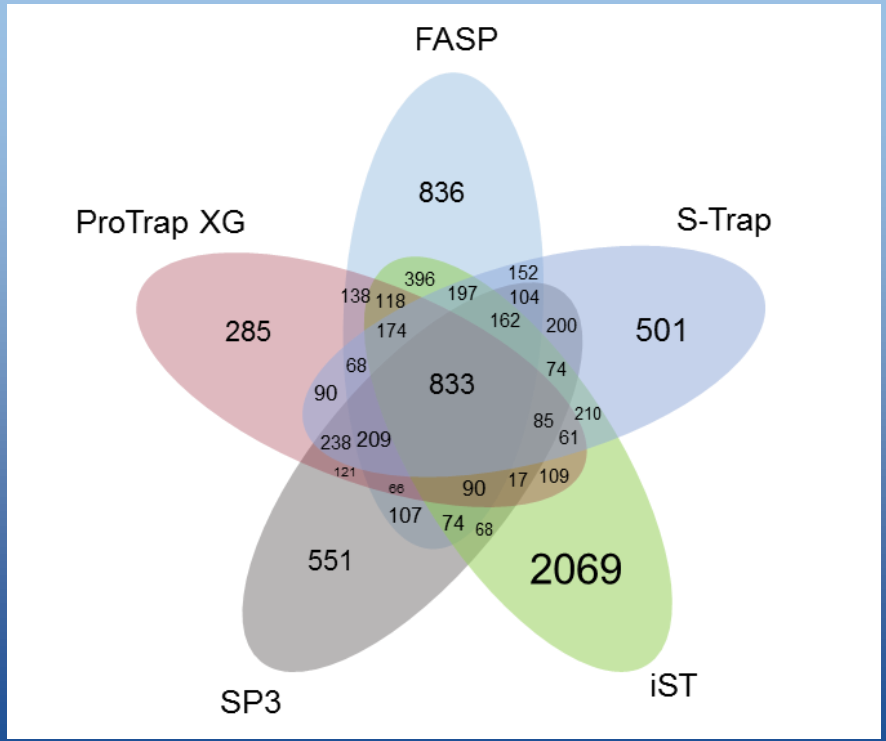
Trypsin digests within ProTrap XG

Provides favorable cleavage efficiency vs other devices





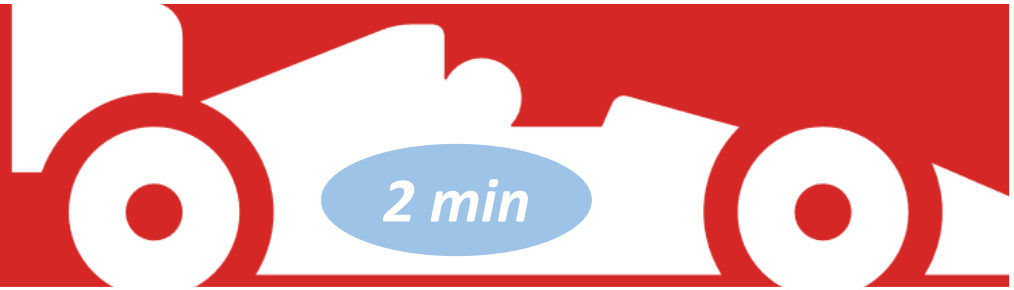
Peptide IDs from BUP LC MS/MS

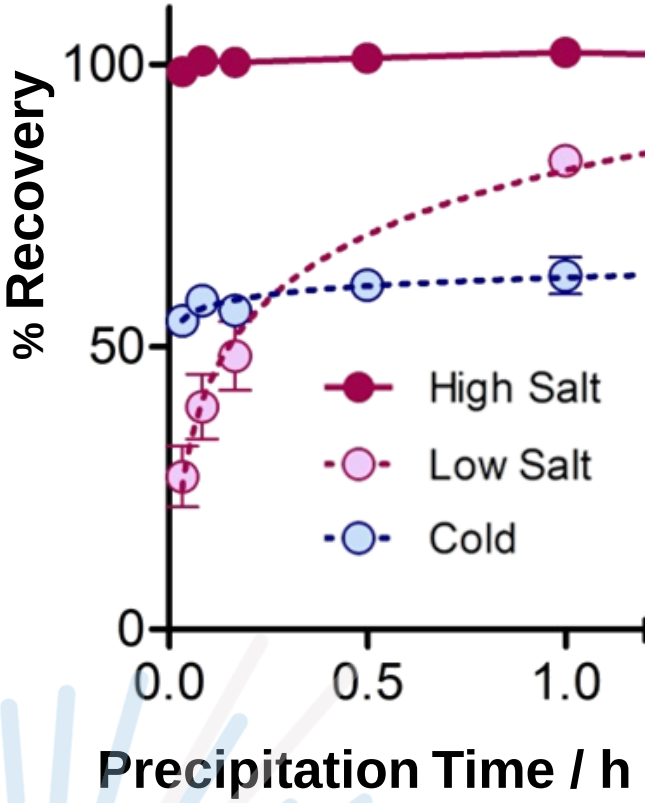


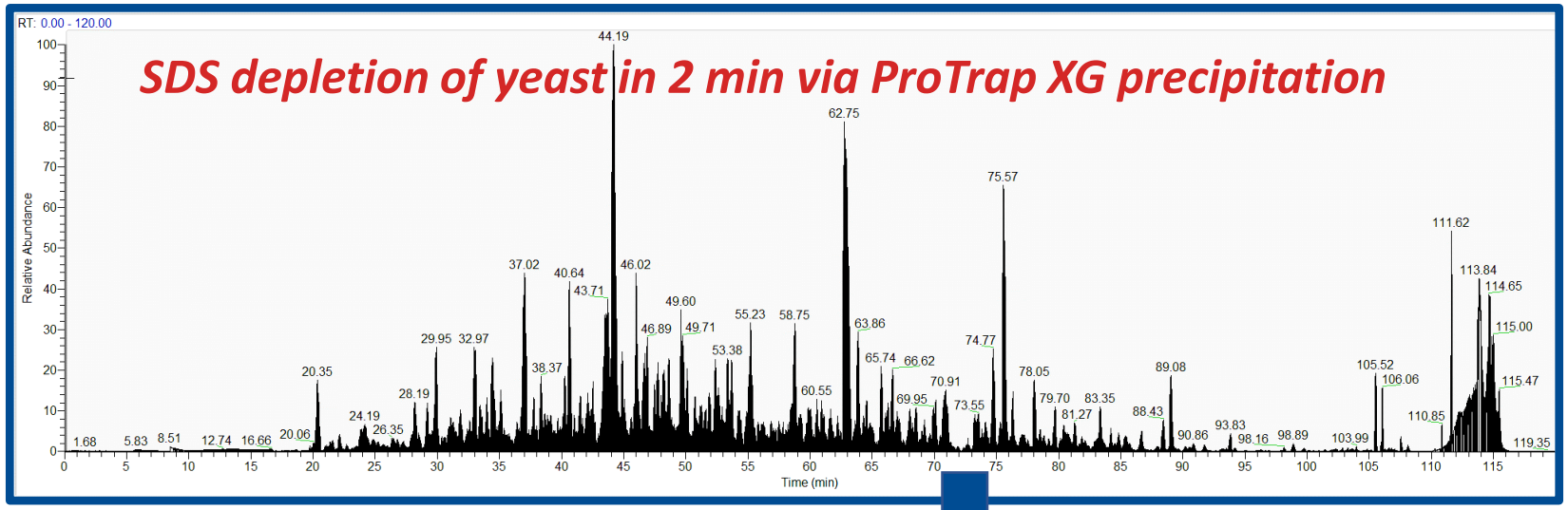
** Following respective user-guide digestion protocols. Number of peptides identified from whole yeast proteome extracts*

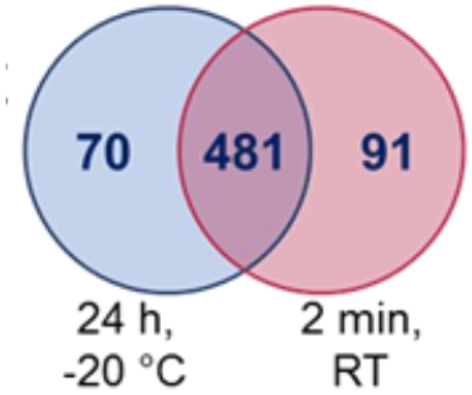
FASTER Sample Preparation

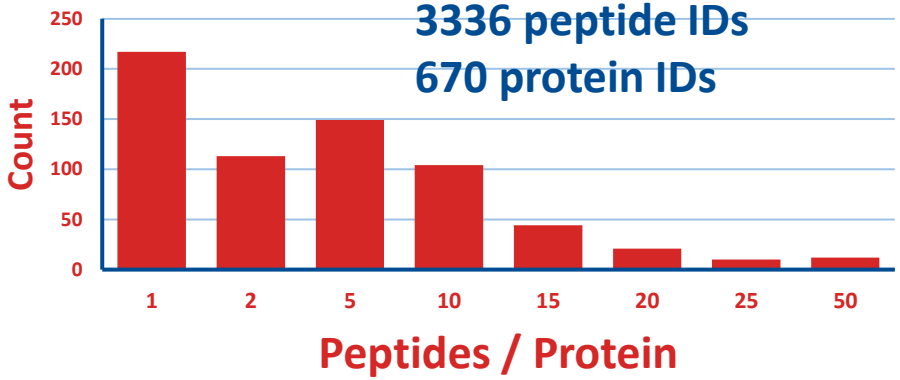
From RAPID acetone precipitation @ room temperature with 100 mM NaCl





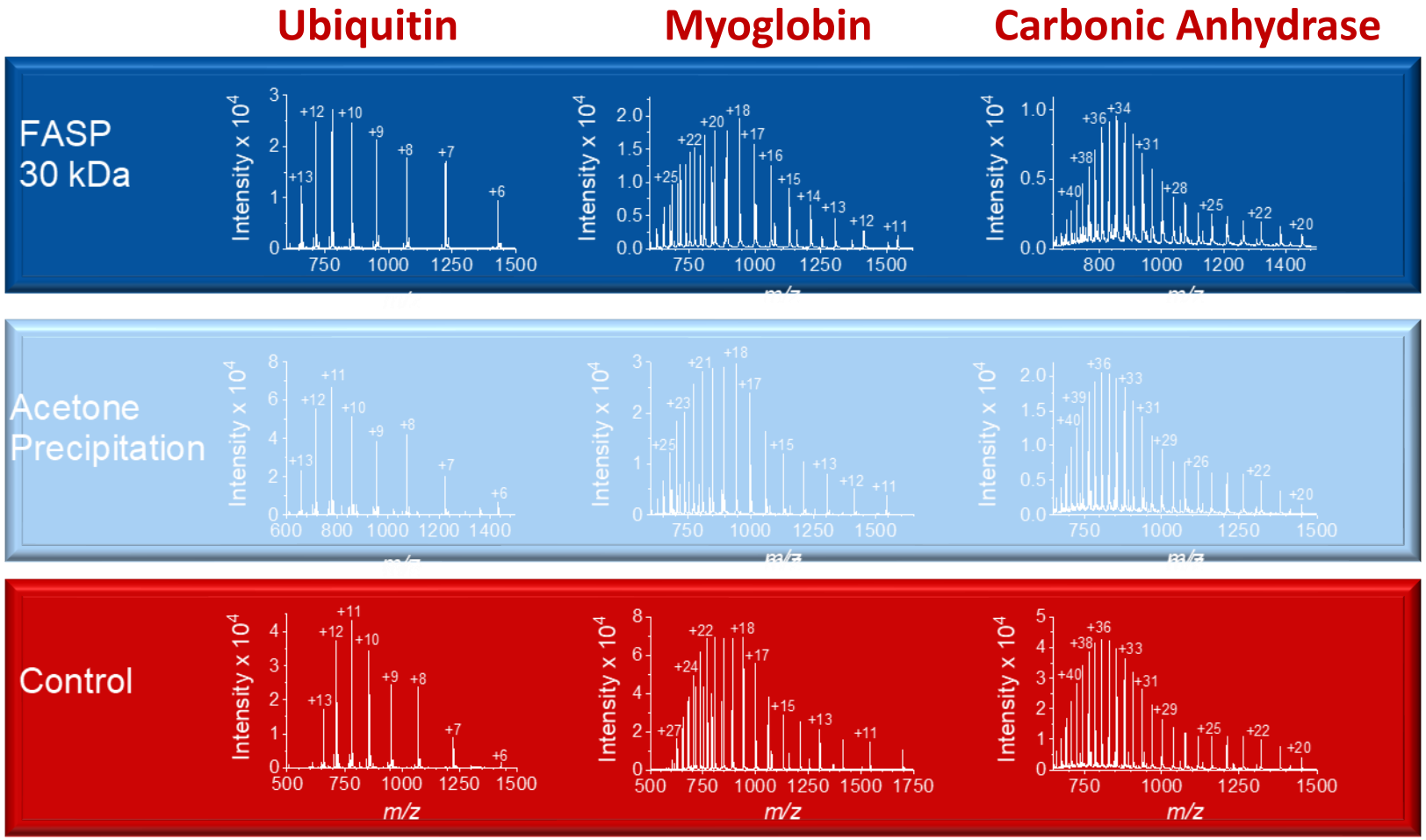






Resolubilize INTACT proteins in COLD formic acid

Cold (-20°C) 80% formic acid added to ProTrap XG following precipitation
Requires ~ 10 min to resolubilize intact proteins. Then dilute with water; LC/MS



Thank you for your interest in this work

References:

Crowell *et al* (2013), *Anal Chim Acta*, 796:48-54

Doucette *et al* (2014) *J Prot Research*, 13:6001-6012

Crowell *et al* (2015) *J Proteomics*, 118:140-50

Nickerson *et al* (2020) *J Prot Research*, 19:2035-2042

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