

Thermo Fisher S C I E N T I F I C

From analytical to nano-flow LC-MS: high robustness and sensitivity to answer complex biological questions

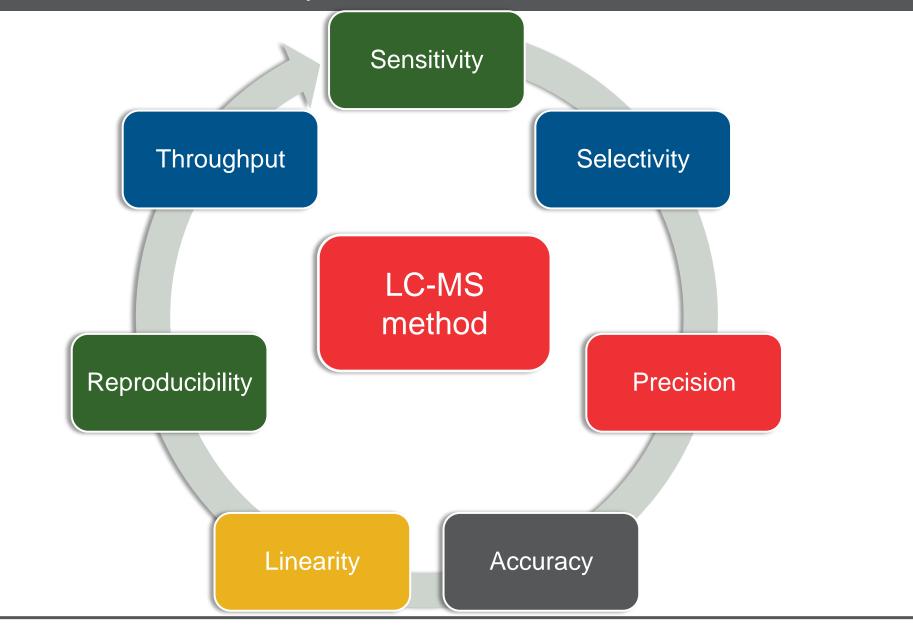
2017-03-26 Alexander Boychenko, Remco Swart

Content

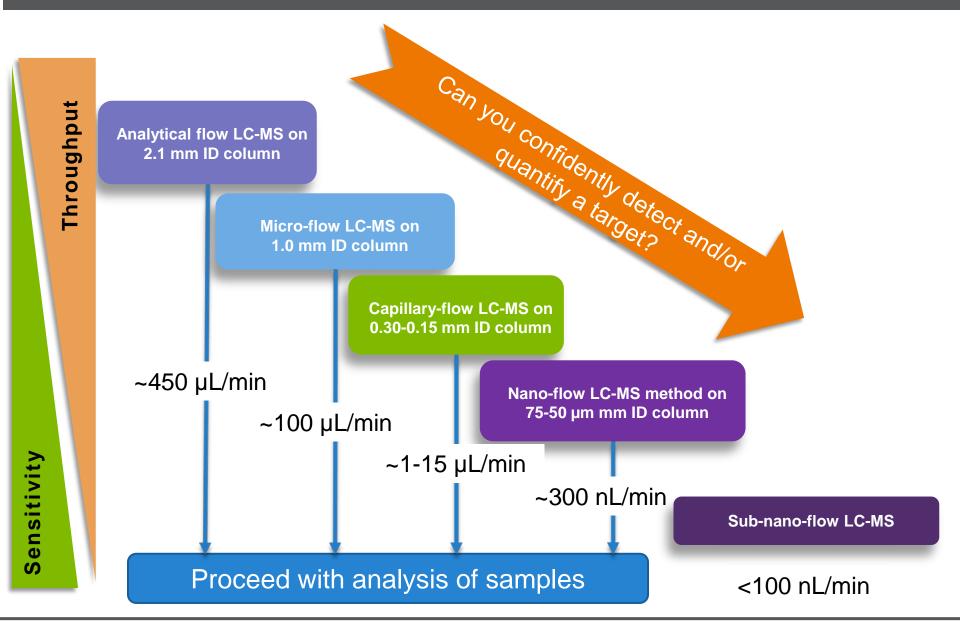
- LC-MS sensitivity gains and tailored method selection
- Capillary and micro-flow LC-MS: what to expect?
- Nano-flow LC-MS: the gold standard in proteomics
- Why chromatography is important for LC-MS proteomics
- Nano-flow and sub-nano flow rates



LC-MS method development



When do you need to downscale your chromatography?



LC-MS with ESI: flow rate and sensitivity gain

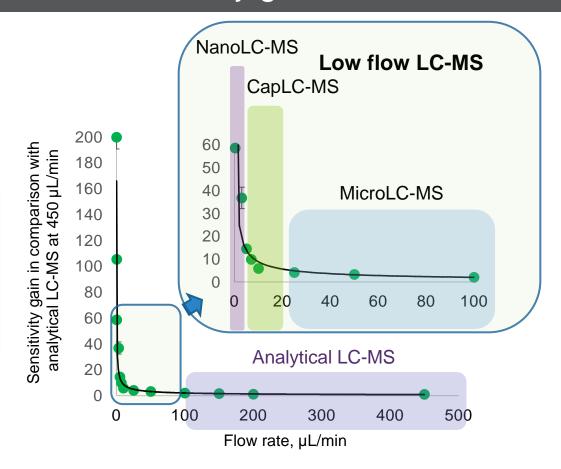
ESI-MS exhibits a mixed behavior of both concentration and mass-sensitive detectors

Sensitivity gains (experimental, relative to 2.1 mm ID)

microLC-MS: 2-4 capLC-MS: 4-50 nanoLC-MS: > 50 sub-nanoLC-MS: > 100

Reasons

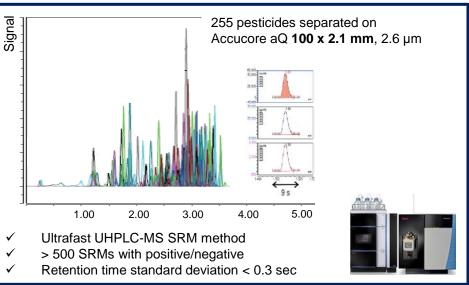
- Increase of analyte concentration with decrease of column ID
- Improved ionization efficiency

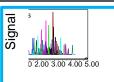


The sensitivity gains were measured as a relative peak area averaged for Cytochrome C tryptic peptides



From analytical to micro-flow LC-MS

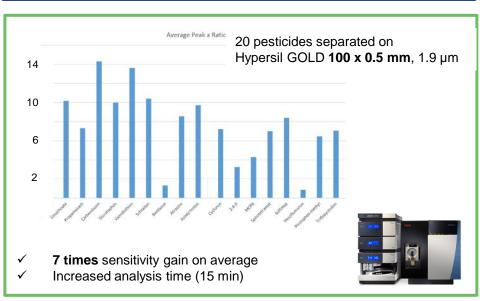


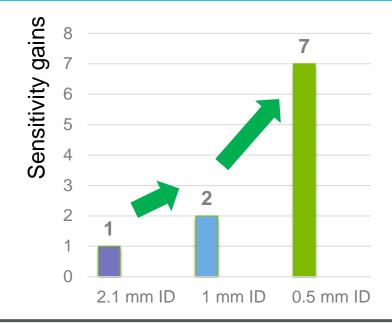


255 pesticides separated on Hypersil GOLD **100 x 1.0 mm**, 1.9 μm

✓ Same throughput and robustness as for 2.1 mm ID
 ✓ 2 times sensitivity gain on average



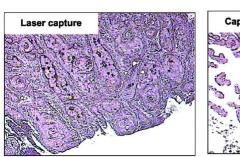


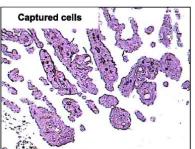




Why do we need nanoLC-MS?

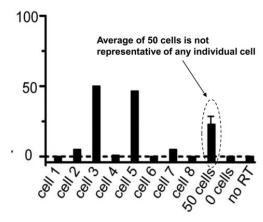
- Extremely low amount of sample (e.g. laser micro-disected cells, small animal bio-fluids)
- Tumor biopsies
- Low analyte concentration in a complex matrix (biomarkers)
- High sample complexity and wide dynamic range
- Single cell -omics





LMD captured cells

Patel et al. doi: 10.1158/1078-0432.CCR-07-1497

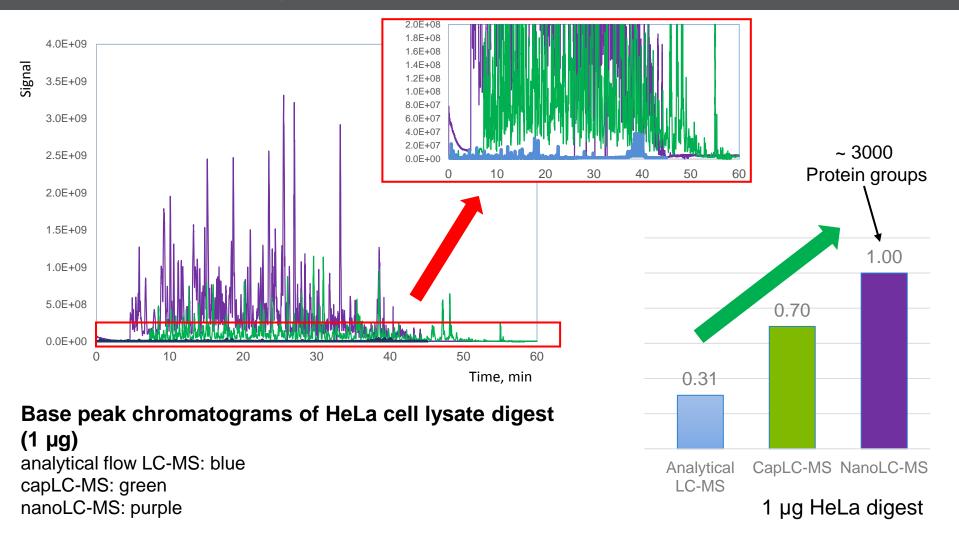


mRNA expression of GAPDH from individual Jurkat cells

Toriello et al. doi: 10.1073/pnas.0806355106



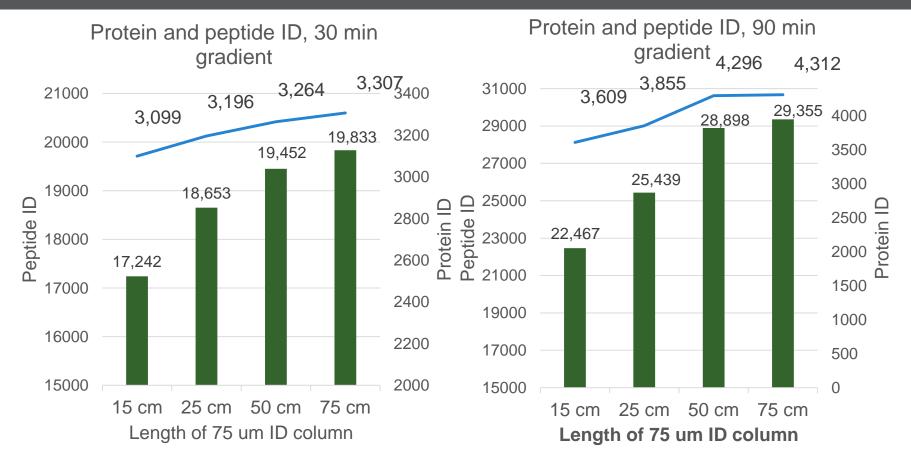
NanoLC-MS is a gold standard in proteomics



√ High LC-MS sensitivity is essential for deep proteomics



NanoLC-MS proteomics: the effect of column length

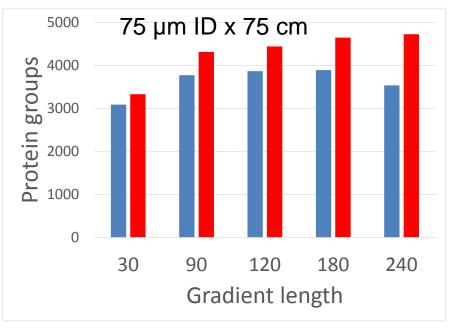


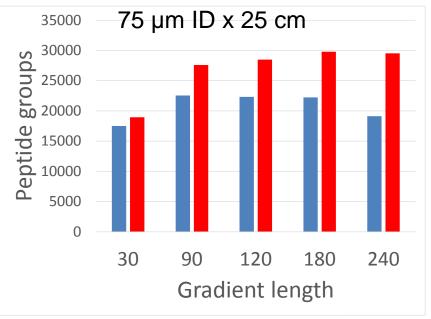
Protein ID: blue line Peptide ID: green bars

Deeper proteome coverage with longer columns

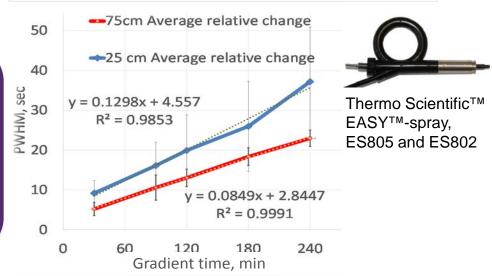


Why chromatography is important

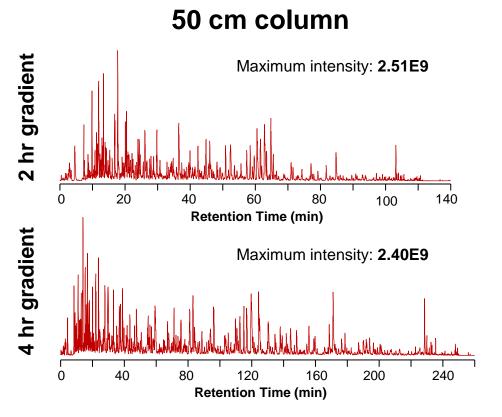




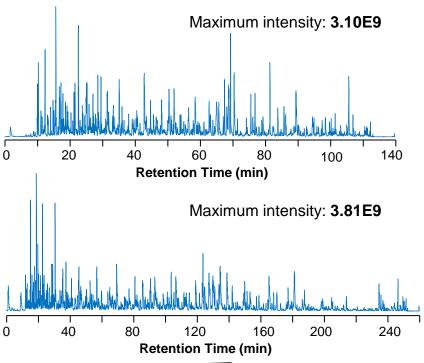
- Longer gradients give more peak capacity
- ✓ The peak width increases proportionally to the gradient time
- Longer columns should be used with long gradients



Increased protein identification rates with 75 cm columns



75 cm column



- Comparison of 75 cm and 50 cm EASY-Spray column
 - Sample: HeLa Digest (1 μg)
 - Gradient: 120 min or 240 min

Application Note AN639

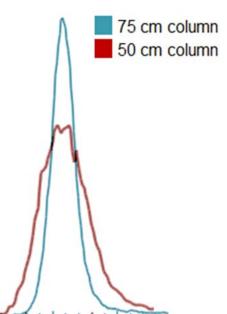


Thermo Scientific™ EASY-nLC™ 1200 system Thermo Scientific™
Orbitrap Fusion™
Lumos™ Tribrid™ MS

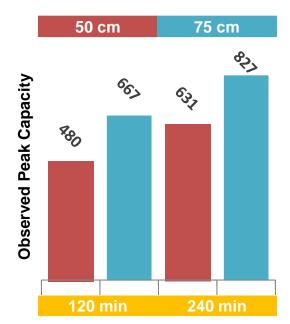


Increased protein identification rates with 75 cm columns

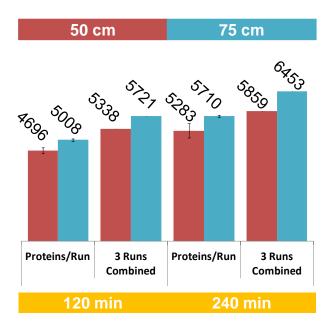




Peak Capacity



Identified Proteins



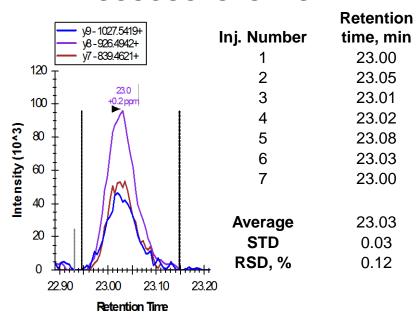
75 cm long columns give:

- Narrower peak width and higher peaks
- Higher peak capacity
- √ ~ 10% more protein identifications than 50 cm long column



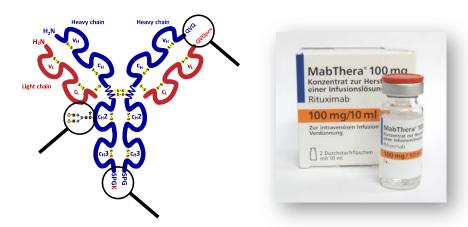
NanoLC HRAM MS targeted quantification

FSGSGSGTSYSLTISR



1:10⁴ rituximab to HeLa total protein amount in a sample

- 7 consecutive replicates
- 30 min gradient
- EASY-Spray 75 μm x 50 cm, 2 μm
- 4 sec peak width
- 30 min gradient



Multiplexed scheduled HRAM analysis of rituximab in human matrix

Heavy chain: 5 unique peptides Light chain: 3 unique peptides

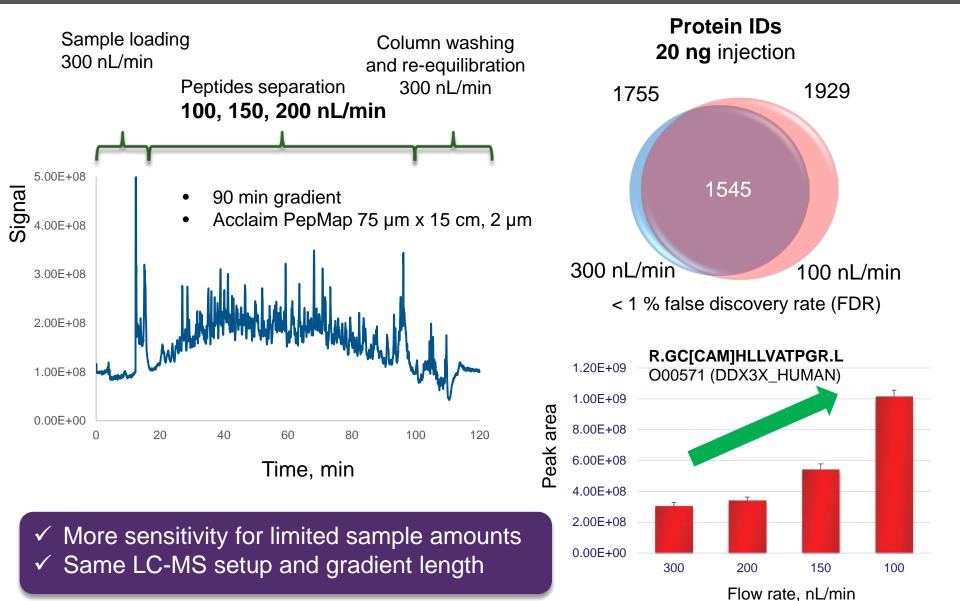


Thermo Scientific™ UltiMate™ 3000 RSLCnano system Thermo Scientific™ Q Exactive™ HF hybrid quadrupole-Orbitrap mass spectrometer

✓ LOD at amol level for PRM quantification in matrix

High RT reproducibility permits PRM scheduling

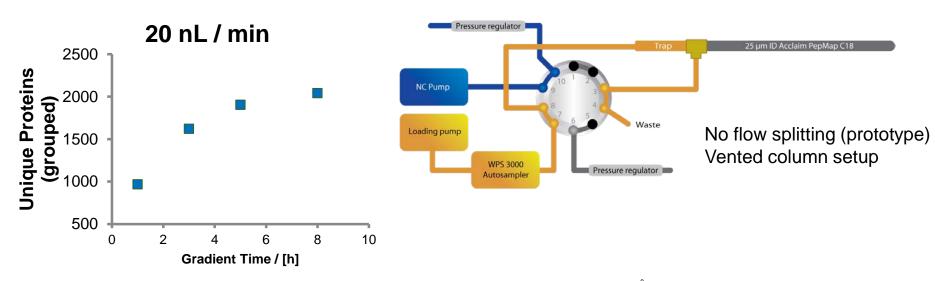
Enhanced sensitivity with low nano-flow rates





Ultralow-flow nanoLC (100-10 nL/min)

Protein IDs 10 ng injection



Analytical Column (prototype): 25 μm ID x 25 cm, Acclaim PepMap RSLC C18, 2 μm, 100 Å

Trap: 50 µm ID x 7 cm (2 cm packed), Acclaim PepMap C18, 3 µm, 100 Å

Emitter: 10 μ m ID, tip opening 5 μ m Connections: 10 μ m ID nanoViper

- Increased sensitivity in comparison with regular nanoLC-MS
- ✓ Good retention time precision, RSD < 0.2%

Development and performance evaluation of an ultralow-flow nanoliquid chromatography-tandem mass spectrometry set-up; Thomas Köcher et. al., Proteomics, 2014, 14, 1999–2007



Conclusions

- Downscaling LC separations results in significant increases in LC-MS sensitivity, permits the analysis of complex samples and facilitates very low level quantification
- The chromatographic scale adopted for an LC-MS method should be chosen according to the relative importance of sensitivity and throughput
- Nano LC-MS using long separation columns is now routine in proteomics
- Ready-to-use capillary connections, integrated plug-and-spray consumables and easy-to-operate LC systems have made nano LC-MS accessible to people with limited LC experience
- Extremely high sensitivity can be obtained using ultra-low nano flow rates.
 However, a great deal of expertise is required for such setups