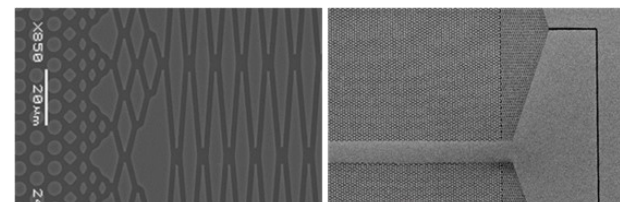


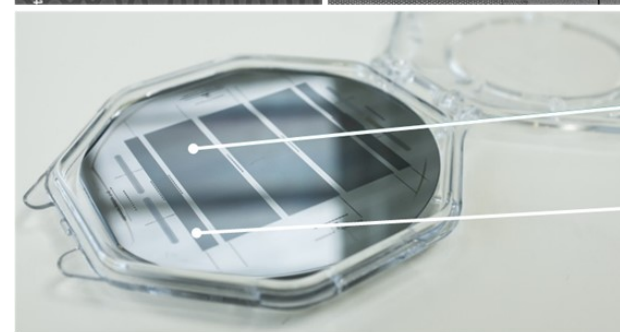
# $\mu$ PAC™ or micro Pillar Array Columns

The next step towards robustness, reproducibility and resolution in low flow LC-MS

# Enjoy the beauty of pillars

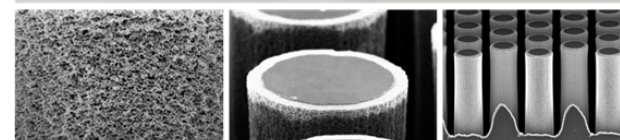


Flow distribution for perfect plug conservation in inlets and turns



200 cm  $\mu$ PAC™ column

50 cm  $\mu$ PAC™ column



Stationary Phase controlled by design





# μPAC™ Performance in deepest diving proteomics

## Article

## The proteome landscape of the kingdoms of life

<https://doi.org/10.1038/s41586-020-2402-x>

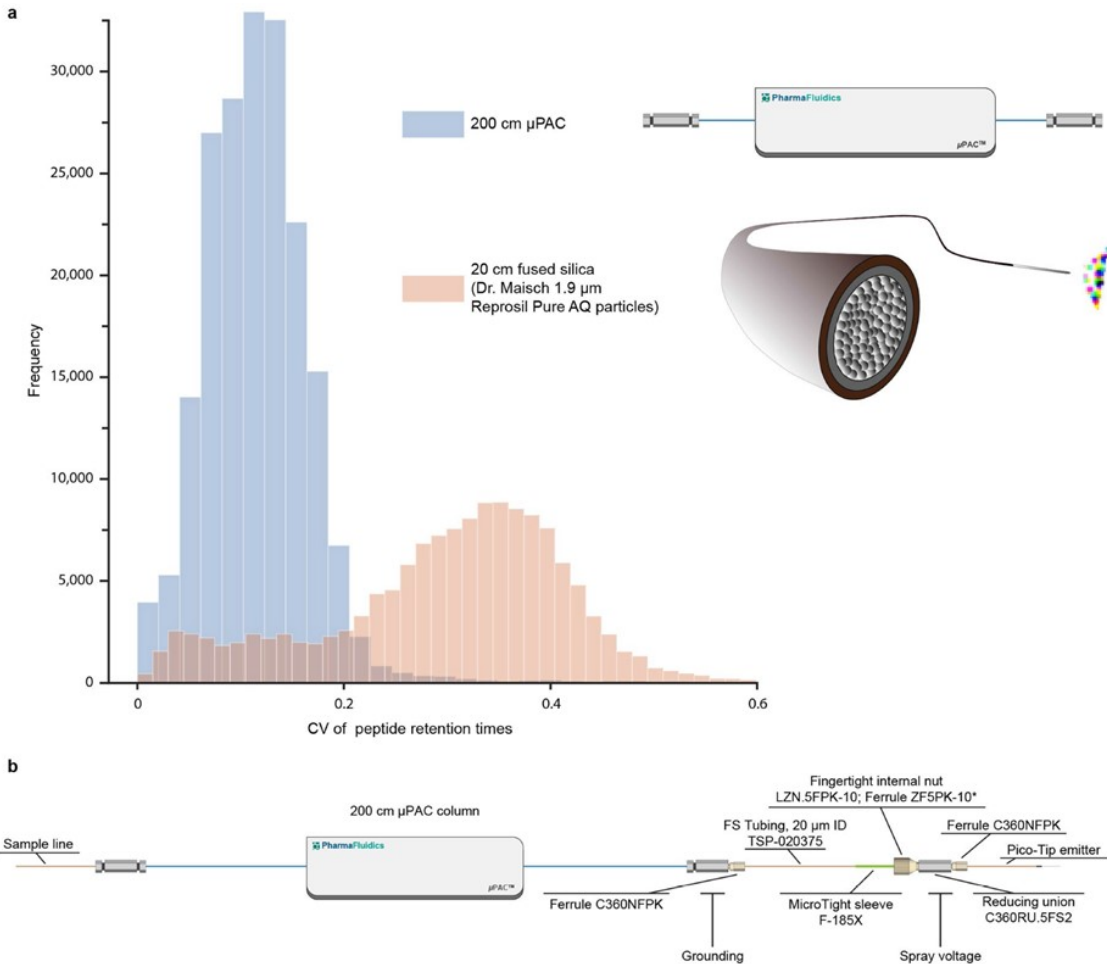
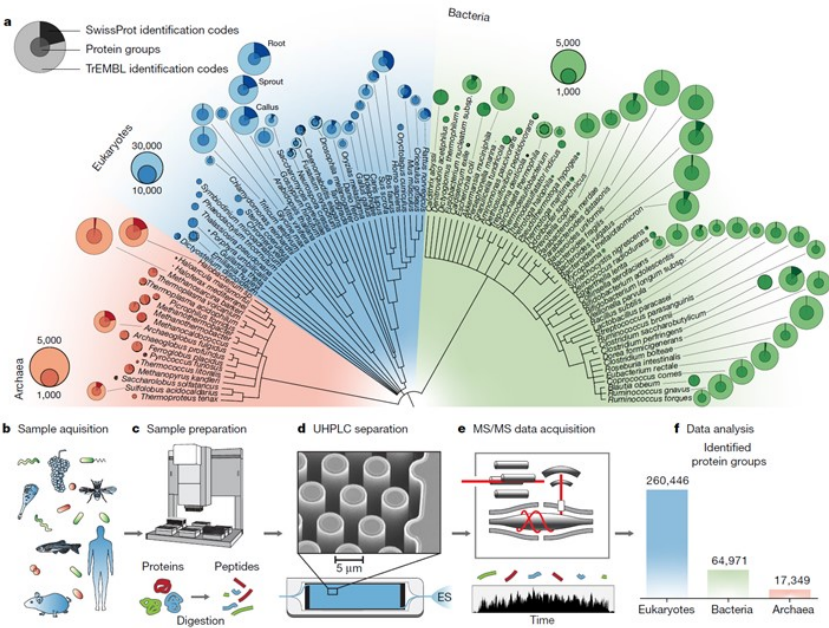
Received: 2 August 2019

Accepted: 27 April 2020

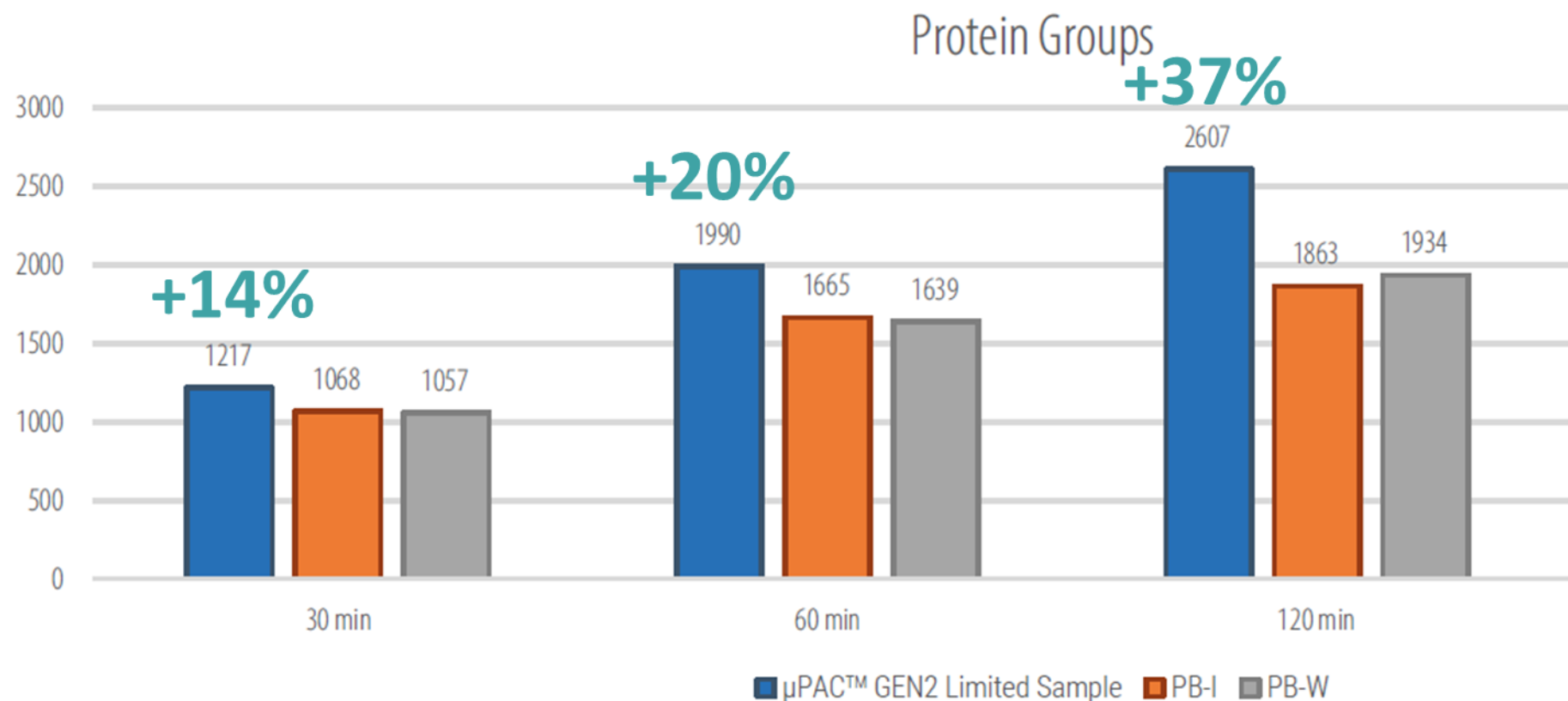
Published online: 17 June 2020

Check for updates

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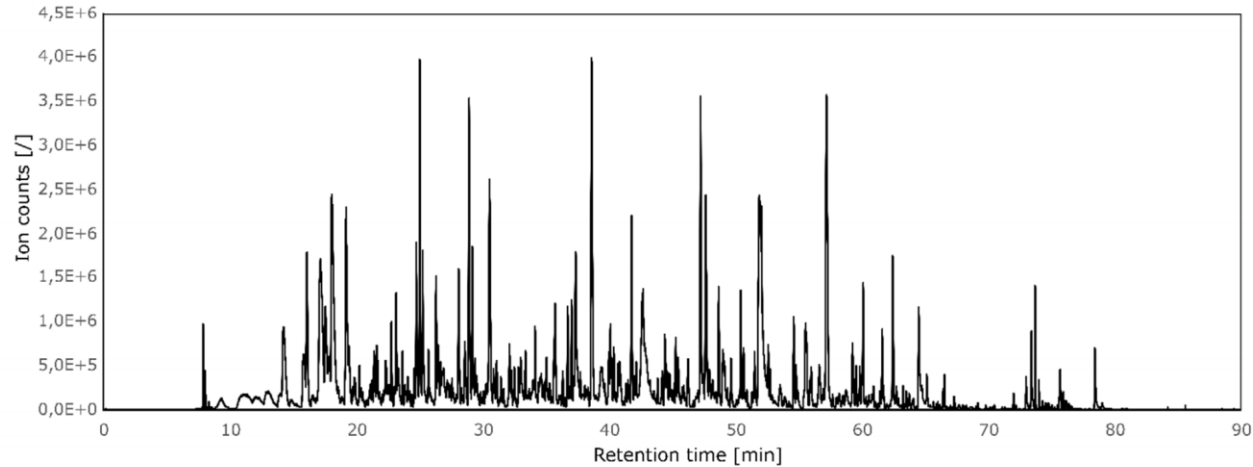
# Benchmarking 50 $\mu$ PAC™ GEN2 Limited Sample (10 ng)



50  $\mu$ PAC Limited Sample &  $\mu$ PAC Flex iON Connect

- Outstanding results against packed-bed emitter type (PB-I) and packed-bed (W) columns

# Pushing towards single cell sensitivity



MS basepeak chromatogram obtained for the separation of 250 pg HeLa tryptic digest using a 60 min non-linear gradient at 250 nL/min



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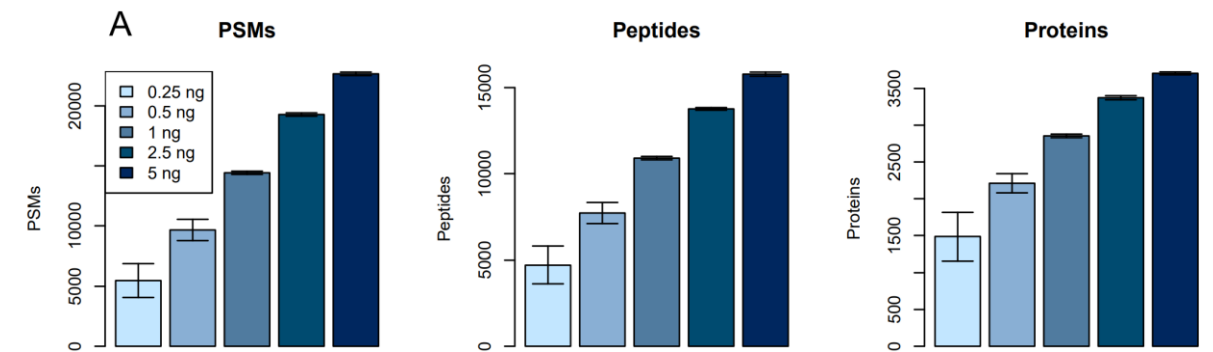
New Results

[Comment on this paper](#)

**Ultra-sensitive nanoLC-MS using second generation micro pillar array LC technology with Orbitrap Exploris 480 and FAIMS PRO to enable single cell proteomics**

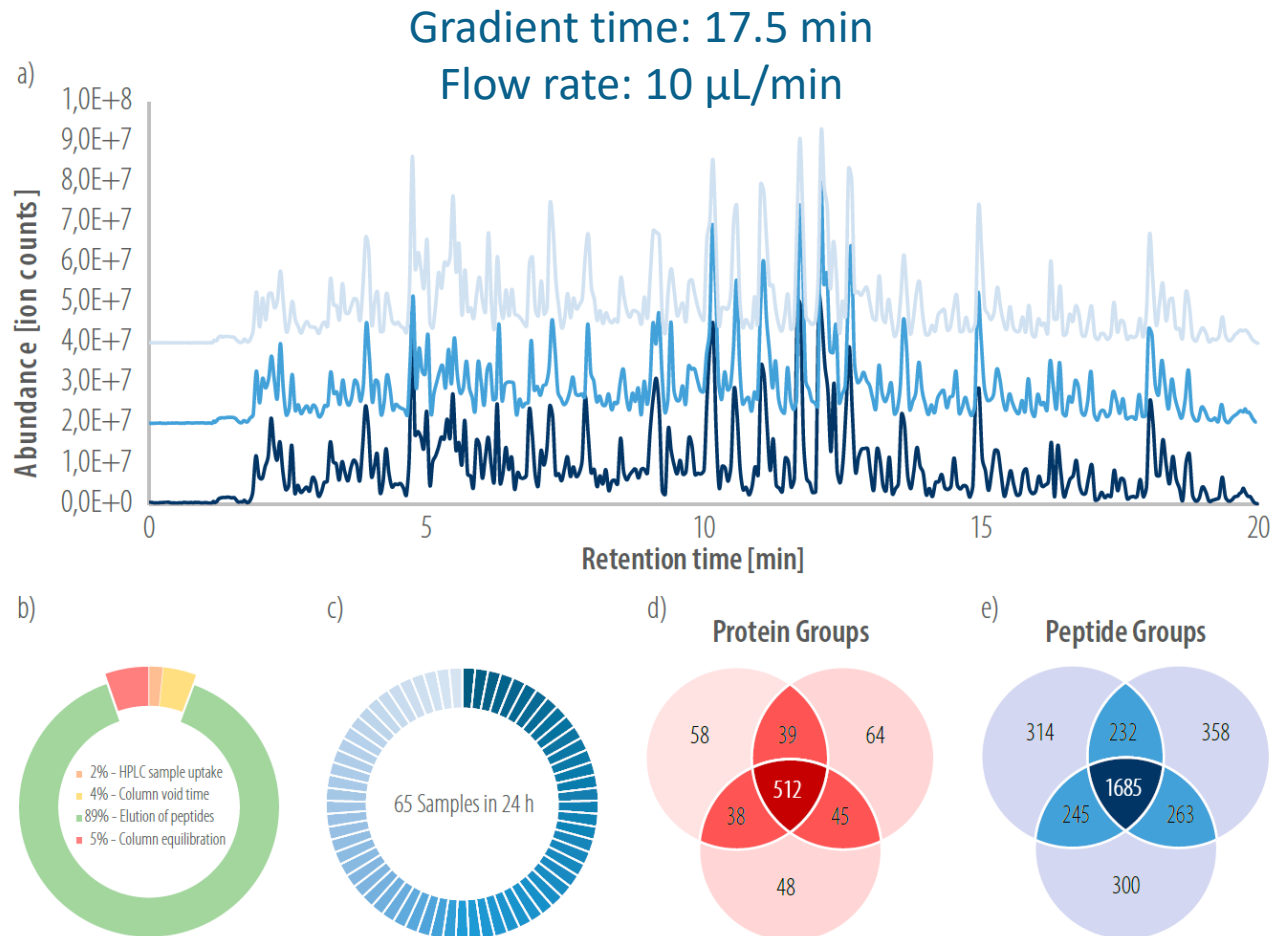
Karel Stejskal, Jeff Op de Beeck, Gerhard Dürnberger, Paul Jacobs, Karl Mechtler  
doi: <https://doi.org/10.1101/2021.02.10.430648>

This article is a preprint and has not been certified by peer review [what does this mean?]



PSM, peptide and protein identifications obtained for a dilution series of HeLa tryptic digest (5 to 0.25 ng injected)

# Increasing throughput with $\mu$ PAC™ capLC



# Small sample volumes in metabolomics/lipidomics

- Separations using 2.1 mm ID columns
- Small model organisms provide smaller sample volumes  $\geq 1 \mu\text{L}$
- Requiring more sensitivity in LC/MS



Zebrafish



E coli



C elegans

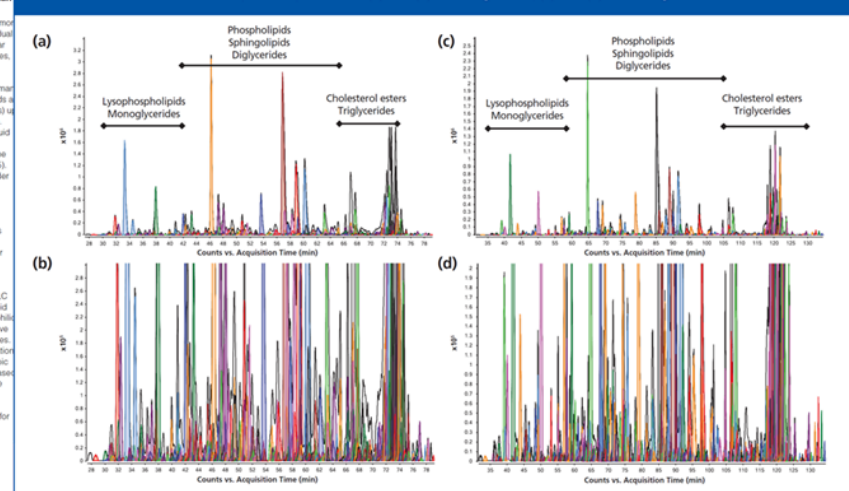
## Evaluation of Micro-Pillar Array Columns ( $\mu\text{PAC}$ ) Combined with High Resolution Mass Spectrometry for Lipidomics

Koen Sandra<sup>1</sup>, Jonathan Vandebussche<sup>1</sup>, Ruben Kindt<sup>1</sup>, Bo Claerebout<sup>2</sup>, Jeff Op de Beeck<sup>2</sup>, Wim De Maessche<sup>1,3</sup>, Gert Desmet<sup>1,3</sup>, and Pat Sandra<sup>1</sup>, <sup>1</sup>Research Institute for Chromatography (RiC) and Metaboly, Kortrijk, Belgium, <sup>2</sup>PharmaFluidics, Ghent, Belgium, <sup>3</sup>Vrije Universiteit Brussel, Brussels, Belgium

In the 21st century, numerous advances have been made in liquid chromatography (LC) column technology. The best known are columns packed with sub-2- $\mu\text{m}$  porous particles or sub-3- $\mu\text{m}$  superficially particles, and monolithic columns. Another very novel and original development is micro-pillar array columns ( $\mu\text{PAC}$ ).  $\mu\text{PAC}$ s are produced by a lithographic etching process to create a silicon chip. Although the performance in terms of efficiency for analysis of real complex samples has yet to be fully demonstrated, state-of-the-art  $\mu\text{PAC}$  columns coated with octadecyl are applicable to lipidomics. The performance is illustrated with the analysis of human

Lipidomics aims at the comprehensive and comparative analysis of lipids in biological samples and has the potential to impact on biomarker discovery, drug discovery and development, system knowledge, and other areas (1). In lipidomics, the researcher is confronted with a substantial complexity. To date, the LIPID MAPS Structure Database is populated with over 40,000 structures comprising fatty acids, glycerolipids, glycosphingolipids, sphingolipids, sterol lipids, prenol lipids, saccharolipids, and polyketides (2,3). The complexity of the lipidome arises through alterations in the nature of the head group (defining the lipid classes), the chain length of the individual aliphatic chains, the number, position, and stereochemistry of double bonds, hydroxyl groups and other functionalities in the individual aliphatic chains, and the nature of the covalent bond (ester, ether, vinyl ether) to the head group, to name just a few examples. It does not therefore come as a surprise that this also gives rise to various isomeric species. As well as describing the lipidome in terms of numbers, it is important to realize that the different lipid species possess diverse physicochemical properties. Lipids span a substantial polarity and molecular weight (MW) range, with the sterol esters and triacylglycerols being very apolar and neutral, the glycosphingolipids more polar and charged, and the individual fatty acids being of lower molecular weight. On top of these complexities, one is inevitably confronted with a substantial dynamic range within biological matrices. One mL of human plasma, for example, contains lipids at a low femtomole level (icosanoids) to micromole level (cholesterol) (4). In contemporary lipidomics, liquid chromatography (LC) combined with mass spectrometry (MS) is the principal enabling technology (1,5). The complexity of the sample under investigation evidently benefits from the use of highly efficient chromatographic separations, accurate mass, and tandem mass spectrometry. Various reports describe the combination of either reversed-phase, normal-phase, or hydrophilic interaction liquid chromatography (HILIC) with MS for lipidomics (1). Normal-phase LC and HILIC typically distinguish lipid species according to their hydrophilic functionalities and, as such, resolve lipids in their representative classes. In reversed-phase LC, the separation is mainly based on the hydrophobic properties of lipids, in essence based on the number of carbons and the degree of saturation. The use of reversed-phase LC substantially increases the separation window for

Figure 5: LC-MS compound chromatograms at different scaling (zoomed and unzoomed) obtained in the positive electrospray ionization mode for a human blood plasma lipid extract. (a) and (b) 60-min gradient, (c) and (d) 120-min gradient.





# User comments on robustness

Als antwoord op @UCDProteomics en @Thomas\_Beer

Have you seen PharmaFluidics now have a capillary flow column? I've been blown away by the micropillar chemistry in nano and it's run (in direct injection) for 6 months straight-absolutely no loss in performance. Expensive but only bought one 🔥

[Tweet vertalen](#)

11:05 p.m. · 9 mrt. 2020 · Twitter for iPhone

1 Retweeten · 1 Vind-ik-leuk

- **Brett Phinney** @UCDProteomics · 9 mrt.  
Als antwoord op @duncoafc en @Thomas\_Beer  
What flow rate were you running at? I tried one and I could not get it to work well. They have that really stupid half meter outlet tubing on the end. I'm think of trying it again and using a higher flow (1.5 ul/min) and a easyspray cap emitter  
1 1
- **Dunc Smith** /// @duncoafc · 9 mrt.  
280 nl/min routinely but also brilliant for ballistic gradients at 600nl/min for injection to injection in 30 mins with 20 min separation for higher throughput of simpler samples. Stunning and I think micro flow could be its real sweet spot  
1 1
- **Brett Phinney** @UCDProteomics · 9 mrt.  
Thanks ! What length are you using? It's so expensive I'd be frightened to do direct injection on it. I'm planning to demo it again soon. Maybe I'll have better luck  
1 1
- **Dunc Smith** /// @duncoafc · 9 mrt.  
50cm.....got a 2M in a drawer but not had the time to play yet. It hasn't missed a beat-really impressive and running at lower pressure is so much more chilled 🔥  
1 1



Dr. Goran Mitulović

Back in 2017, Goran Mitulović was one of the first to get his hands on the brand-new 200 cm  $\mu$ PAC™. As the head of the Proteomics Core Facility of the Medical University of Vienna, the potential of the new separation technology to improve his analytical services intrigued him. Recently, he has co-authored a paper detailing his first experiences with the column, optimizing the analytical workflow and benchmarking its performance. These initial results proved so good that  $\mu$ PAC™ has since been introduced as the state-of-the-art for all proteomics analyses at the Core Facility. We spoke to Dr. Mitulović about his work and his recent publication.

## The art of tinkering

The Proteomics Core Facility supports researchers and clinicians at the Medical University of Vienna with on-demand...

Interview\_Goran-Mitulović\_Towards-clinical-proteomics-applications.pdf

[pharmafluidics.com](https://pharmafluidics.com)

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Add a comment...



**Goran Mitulović** · 1st

Actively pursuing new challenge! Experienced analytical scientist (chromat...

6d...

Well, I am happy to say that a single 200-cm column has handled already more than 2000 injections and is still running without performance loss. Thanks [#Pharmafluidics](#).





**Join us in the meet & greet**