

Analysis of Biomacromolecules by LC-MS Utilizing Novel, Narrow-bore, Wide Pore Monolithic and Superficially Porous Stationary Phases

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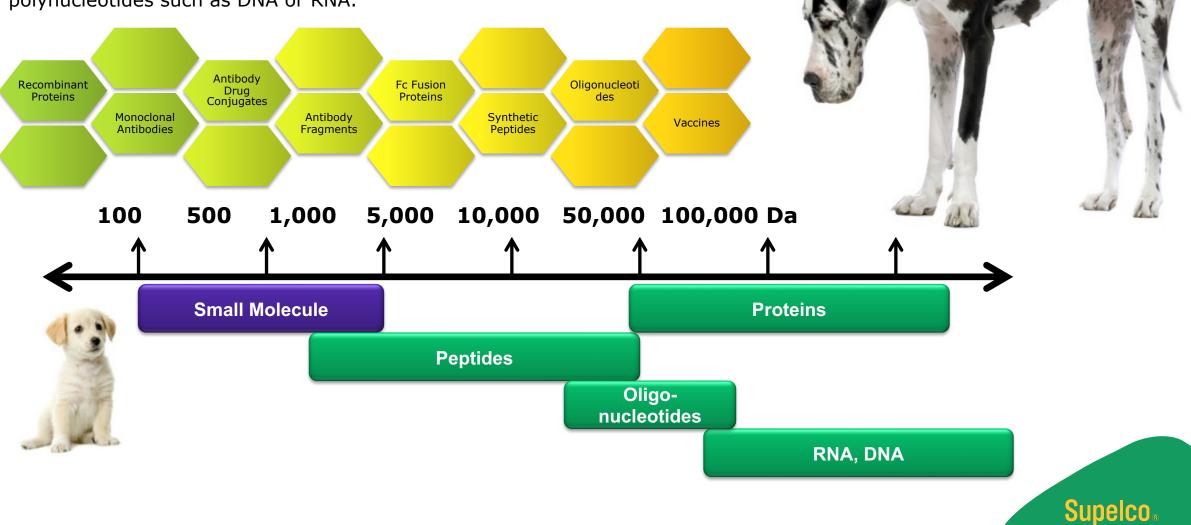
The life science business of Merck operates as MilliporeSigma in the U.S. and Canada.



Small molecules – Large molecules

Biomolecules are compounds created by living organisms.

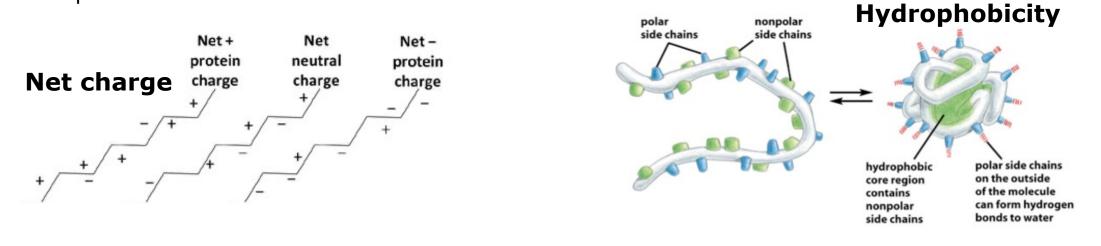
They can range in size from amino acids and small lipids to large polynucleotides such as DNA or RNA.

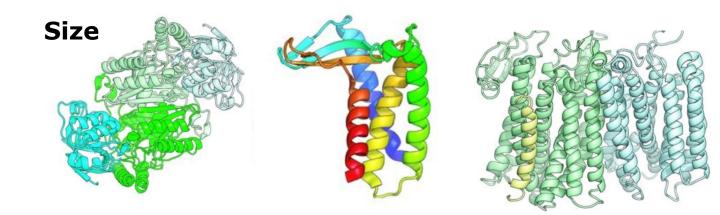


Chemical Properties of Proteins and peptides



Proteins and peptides consist of amino acids (20 naturally occuring) The composition determines:







Techniques used to separate & analyse proteins



SDS-PAGE (Sodium dodecyl polyacrylamide electrophoresis)

IEF (Isoelectric focusing)

CE (Capillary Electrophoresis)

Immunoassay/ELISA

 Monoclonal antibodies (MAbs) typically analysed using this but they could also be done as an intact protein by MALDI MS, or as a digest, using LC/MS/MS

Immunohistochemistry (IHC)

HPLC – various techniques



HPLC Separation Techniques for Proteins/Peptides



- **SEC** (Size Exclusion Chromatography)
- For proteins: GFC (gel filtration chromatography)
- Proteins separates according to their relative size

Ion exchange

Protein is displaced by salt concentration or pH changes from ionic surface

Reversed phase

- Simple adsorption and desorption, protein is displaced by organic solvent.
- Usually uses wide-pore silica (pore size 300 Å or larger) with C18, C8, C5/C4, CN

Affinity chromatography

• Protein is displaced by salt concentration or pH changes from specific adsorption

Hydrophobic interaction

• Separates by dispersion interactions, protein is displaced by water (decreasing salt concentration)

HILIC

• For highly proteins, but more often used in Glycan Analysis

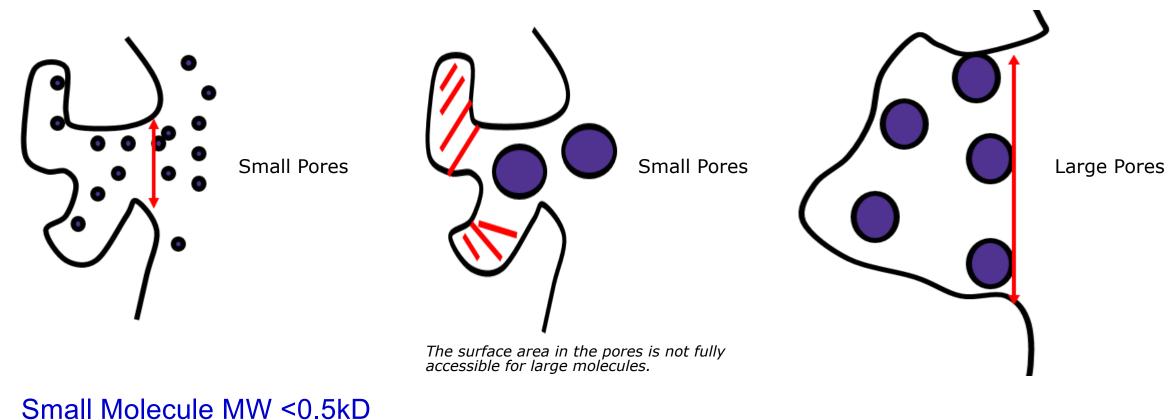
Sometimes multiple LC techniques are combined: orthogonal separation techniques confirm purity, orthogonal techniques may be required for difficult applications



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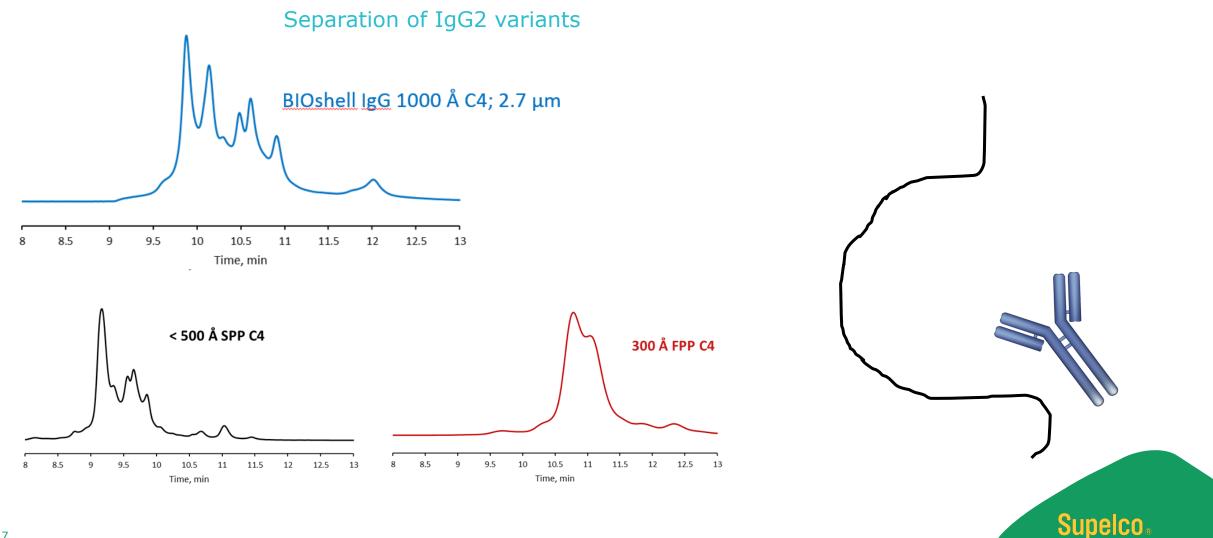
Large molecules require larger pores



Large Molecule / MW > 2.0kD

Pore Size Matters!

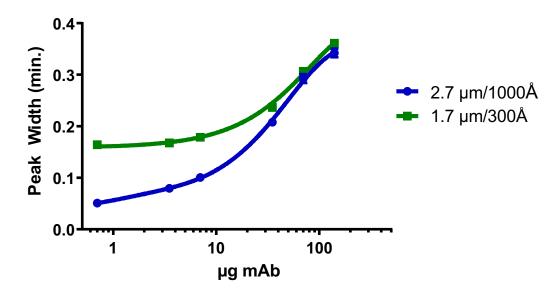
Trying to analyze intact proteins, mAbs, bsAbs or other large molecules >150kDa? BIOshell IgG 1000Å pore can offer high resolution separations!



Pore Size Matters!



Effect of Sample Mass on Peak Width



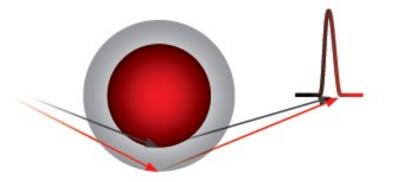
Conditions
Column: As indicated; 15 cm x 2.1 mm I.D., C4
Mobile Phase: [A] Water (0.1% DFA); [B] Acetonitrile (0.1% DFA)
Gradient: 27% B to 37% B in 10 min
Flow Rate: 0.5 mL/min
Column Temp.: 80 °C
Detector: UV, 280 nm
Injection: 0.1, 0.5, 1, 5, 10, and 20 μL
Sample: mAb, 7 mg/mL, water



Alternatives to smaller, fully porous particles

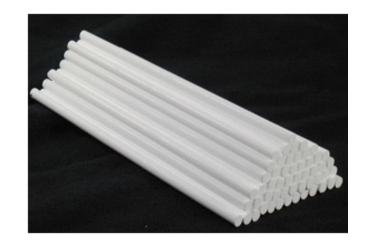
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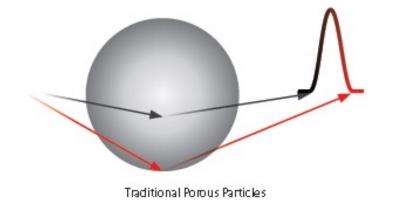
Ascentis® Express – Core-shell technology



Fused-Core Particles

Chromolith® – monolithic silica technology



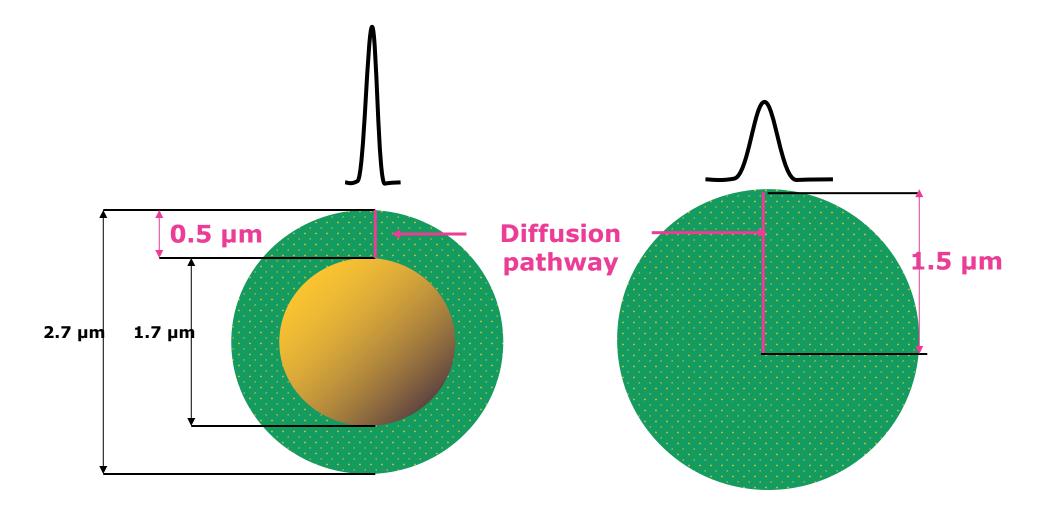


Mesopores

Macropore



Fused-Core provides higher efficiency



The shorter diffusion pathway facilitates the mass transfer (C term)!

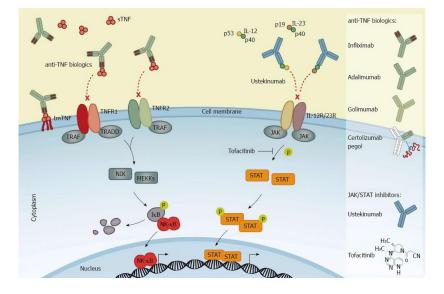
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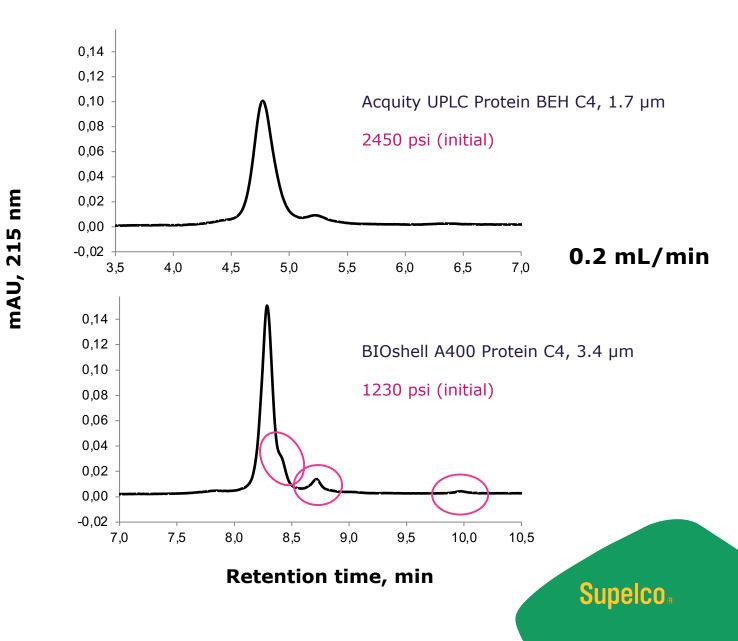
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FPP vs. SPP

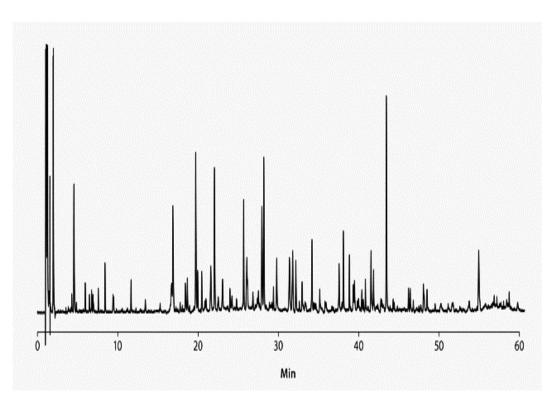
Humira (adalimumab)

Adalimumab, sold under the trade name **Humira** among others, is a medication used to treat rheumatoid arthritis, psoriatic arthritis, ankylosing spondylitis, Crohn's disease, ulcerative colitis, chronic psoriasis, hidradenitis suppurativa, juvenile idiopathic arthritis, and uveitis. In rheumatoid arthritis, adalimumab has a response rate similar to methotrexate, and in combination, it nearly doubles the response rate of methotrexate alone. Adalimumab is a TNF-inhibiting, anti-inflammatory, biologic medication. It binds to tumor necrosis factor-alpha (TNFa), which reduces the immune response. There is strong evidence that adalimumab increases the risk of life-threatening infections and cancers, particularly lymphoma.





Example of Fast Digestion Workflow: Peptide Map Results with Small Protein



column:BIOshell™ A160 Peptide C18; 15 cm x 2.1
mm I.D., 2.0 μmmobile phase:[A] 98:2 water:acetonitrile (both 0.1% TFA);
[B] 50:50 water:acetonitrile (both 0.1% TFA)gradient:0% B to 63% B in 60 minflow rate:0.3 mL/mincolumn temp::35 °Cdetector:UV, 215 nminjection:20 μLsample:Lysozyme tryptic digest, 10 μg/mL, water
(0.1% TFA)





Improving Peptide Separations: Peak Capacity



Peak Capacity Pc

• Pc (Gradient) = Duration of Gradient/mean Peak Width

Extraction of Peak Widths from 20 Peaks covering the whole range of the c-gram

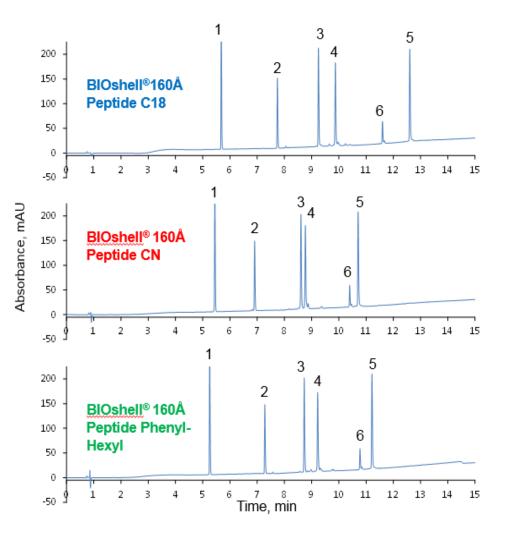
Column		t_g^*	w _{ave}	P _c	
BIOshell Peptide C18		41.3	0.1213	340	
Standard 5µ C18		47.2	0.1951	242	
	tg			\bigcirc	

* Gradient in column volumes (CV); while Peak Width in Minutes

Mean Peak Width on Fused-Core column is less than 40% compared to fully porous columns



Modification impact on separation



Chromatographic Conditions:

BIOshell[®] A160 Peptide 2.1 x 150 mm Columns: C18, 2.7 µm CN, 2.7 µm Phenyl-Hexyl, 2.7 µm Mobile Phase A: water/0.1% TFA Mobile Phase B: ACN/0.1% TFA 0-60% B in 15 min Gradient: Flow Rate: 0.4 mL/min 60 °C Temperature: 220 nm Detection: Injection: 2 µL

Peak Identities:

Tyr-Tyr-Tyr
Angiotensin II
Angiotensin 1-12
Melittin
Sauvagine
β-Endorphin



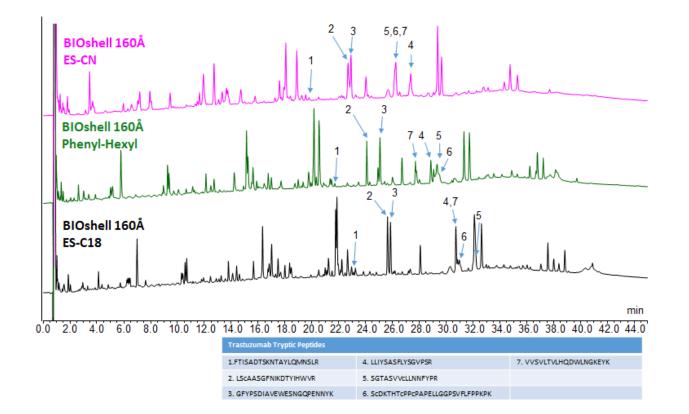


Trastuzumab Tryptic Digest:



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Effect of Phase Chemistry

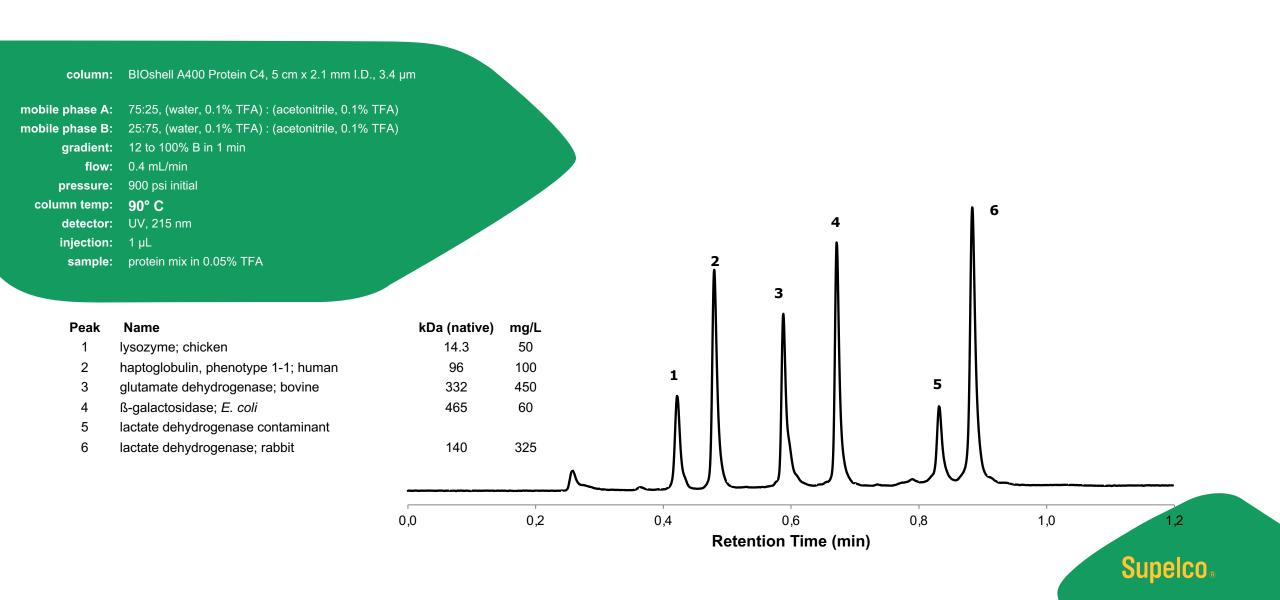


column:	As indicated; 10 cm x 2.1 mm I.D., 2.7 µm
mobile phase:	[A] Water (0.1% DFA); [B] Acetonitrile (0.1% DFA)
gradient:	Hold at 2% B for 2 min; 2% B to 50% B in 60 min
flow rate:	0.3 mL/min
column temp.:	60 °C
detector:	MSD
injection:	5 µL
sample:	Trastuzumab tryptic digest, 0.2 µg/mL, water

Muraco, C. E. "Breaking Up is Not So Hard to Do: Recent Advances in Peptide Mapping of Biotherapeutics." Oral Seminar given at HPLC 2018; July 31, 2018.

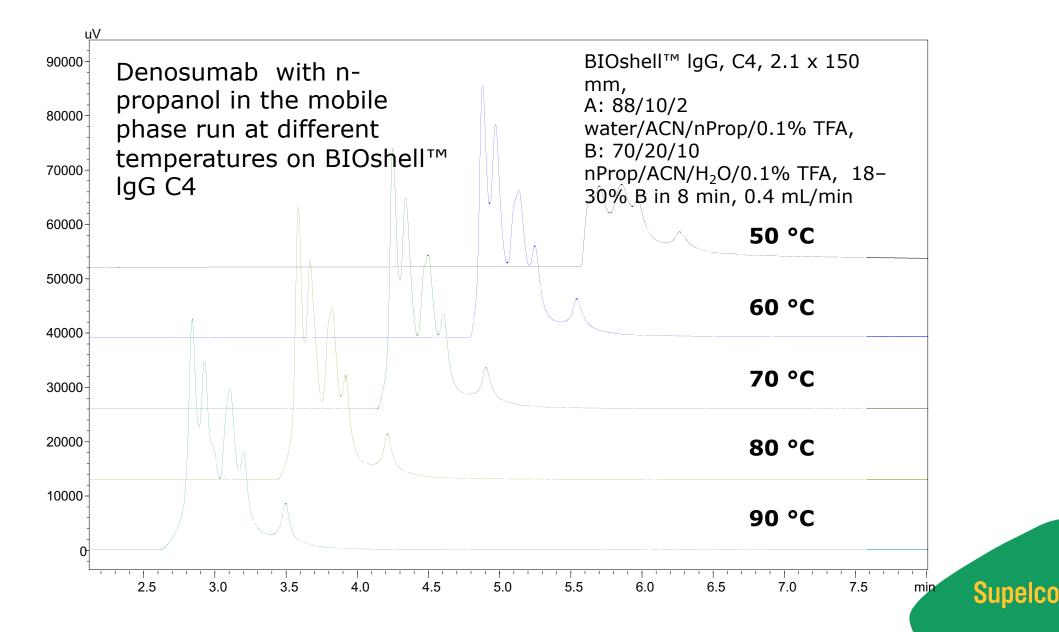
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Fast Protein Separation at High Temperature

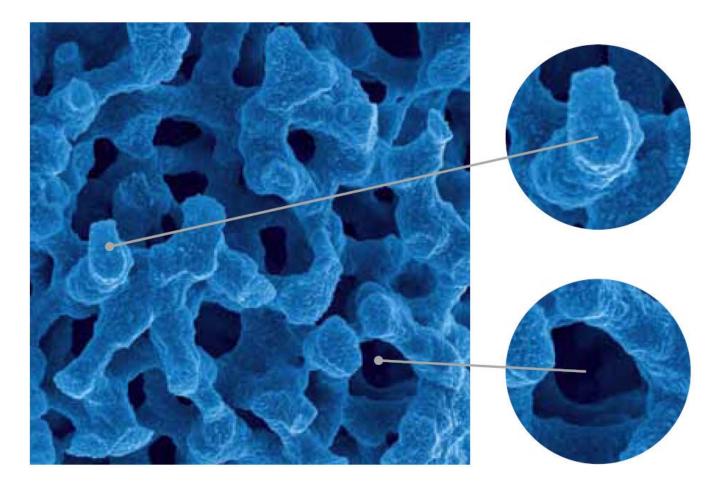


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Effect of Temperature on IgG2



Monolithic silica columns Bi-modual pore structure



Mesopores: Chromolith Performance: 130 Å Chromolith 2mm ID: 130 Å Chromolith HR: 150 Å

Macropores:

Chromolith Prep 3 μ m Chromolith Performance (3, 4.6, 10, 25 mm ID): 2 μ m Chromolith 2mm ID: 1.5 μ m Chromolith HR: 1.15 μ m

Pore volume Total porosity Surface area 1.0 mL/g >80 % 300 m2/g



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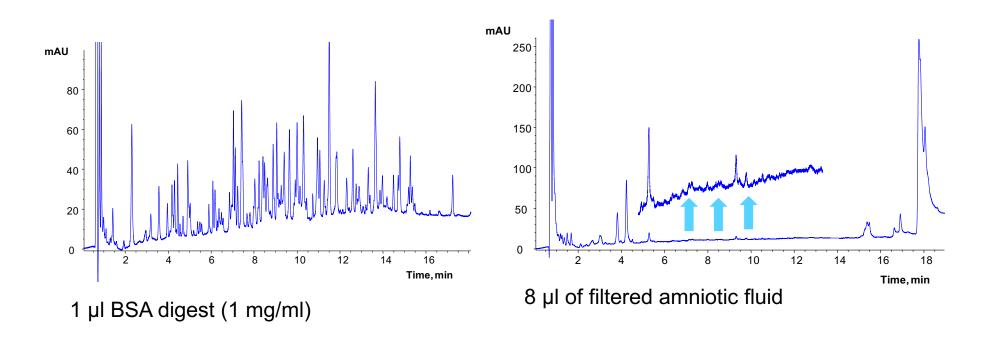


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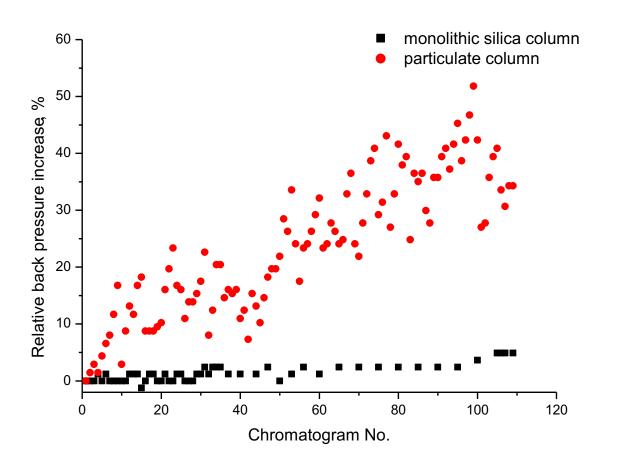
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Application: Proteomics Monolithic silica column RP-18e 100-2mm



EluentsA: 95% H₂O/5% ACN/0.1% TFA (v/v/v),
B: 5% H₂O/95% ACN/0.085% TFA (v/v/v);Gradientfrom 5% B to 50% B in 20 minFlow Rate0.3 ml/minDetectionUV 214 nm

Direct injection Human plasma



Changes in back pressure of the particulate (25-µm particles) and the monolithic silica columns injecting filtrated human plasma sample.

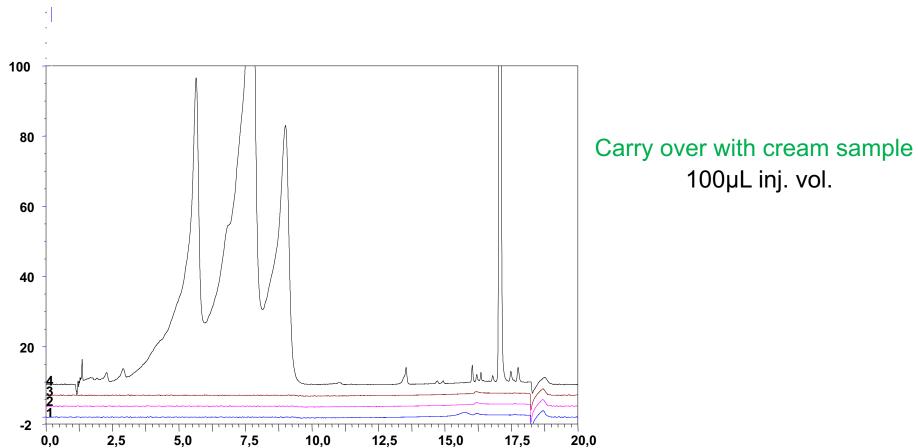
- Particulate column: 25 x 4 mm I.D. cm, 25µm RAM-SCX particles.
- Monolithic silica column: 5 x 4.6 mm I.D., Chromolith guard column.

Sample human plasma, 50 μ l per injection.





Applications UV-Filters in Sun-Lotion – Colipa S (QC-method)



0% Carry Over of UV-Filters!!!

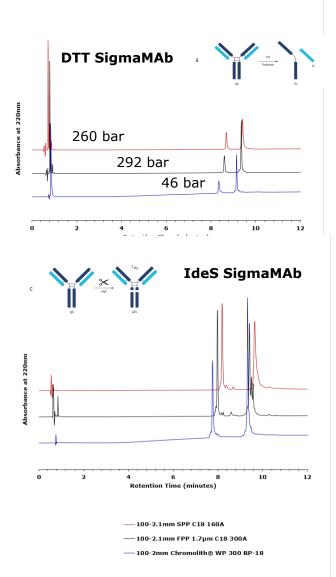


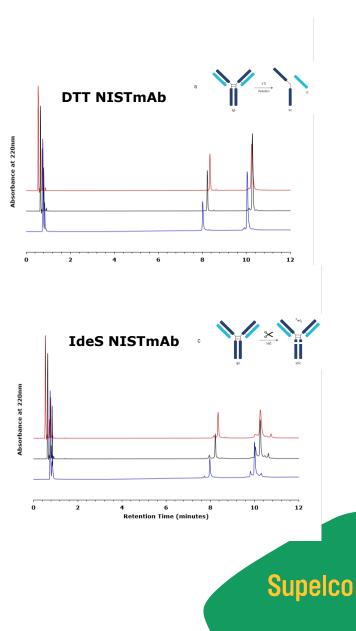


Antibody Fragment Analysis – vs. FPP and SPP Monolithic silica WP 300 RP-18 2 mm ID

Chromatographic conditions

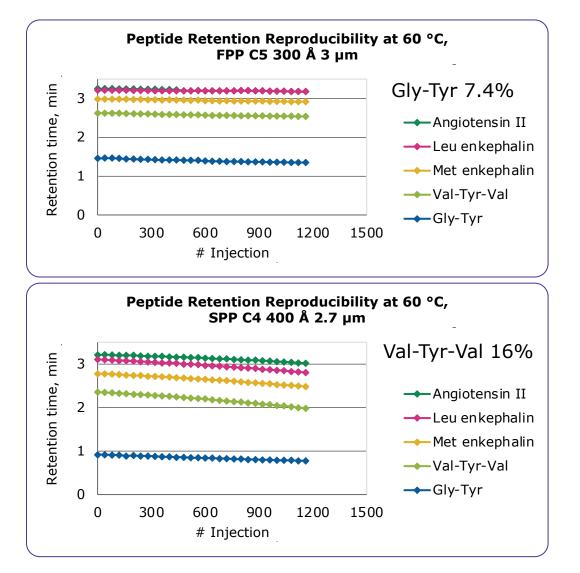
Columns:	Chromolith [®] WP 300 RP-18, 2 mm I.D. SPP, C18, 160 Å, 2.0 μm, 100-2.1 mm FPP, C18, 300 Å, 1.7 μm, 100-2.1 mm
Mobile Phase:	A: Water (0.1% (v/v) TFA) B: Acetonitrile (0.08% (v/v) TFA)
Gradient:	0 min 20% B 1 min 20% B 9 min 45% B
Detection:	UV, 220 nm
Temperature:	80 °C
Injection Volume:	1.0 μL
Flow rate:	380 µL/min
Sample:	SigmaMAb, 2 mg/mL (SiLu™ Lite Universal Antibody) NISTmAb, NIST® RM 8671
Sample preparation:	DTT digest: 60 μ L of 40 mM Dithiothreitol (DTT) solution was added in a PCR vial, 40 μ L mAb was added and incubated at 37 °C for 30 minutes creating LC and HC parts of the antibody. IdeS digest: 4 μ L IdeS-Protease and 56 μ L water were added in a PCR vial, 40 μ L mAb was added and incubated at 37 °C for 30 minutes creating F(ab') ₂ and scFc parts of the antibody.

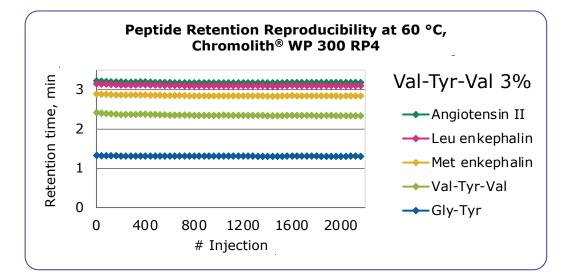






Stability of short chain columns





Mobile phase:	[A] Acetonitrile (0.08% TFA)
	[B] Water (0.1% TFA)
Gradient:	98% B to 55% B in 3 min
Flow rate:	1.5 mL/min
Detection:	UV, 220 nm
Temperature:	60 °C
Injection vol:	2 μL
Sample:	peptide standard mixture (H2016)
Column:	as indicated, 100 x 4.6 mm

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Monolithic silica WP 300 RP4 Influencing peak width and efficiency of cetuximab

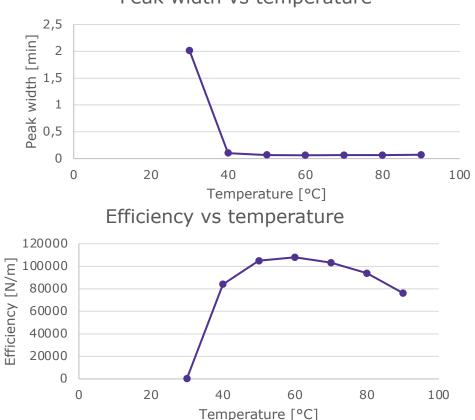
Temperature [°C]	Peak width 10% [min]	Separation efficiency [N/m]
30		_
40	0,103	84090
50	0,067	104918
60	0,062	107973
70	0,063	103188
80	0,064	93865
90	0,069	76228

Conditions: ACN 0,08%TFA/ Wasser 0,1%TFA 4/96 in 5min to 60/40, 2,2mL/min, UV220nm, 60°C, 0,5 μ L Inj.vol.

Column: Chromolith WP 300 RP4, 100x4.6mm (1.52260.0001)

Peak shape of biomolecules can be improved with increasing temperature. However for Chromolith WP300 RP4 and the separation of cetuximab a temperature of 60°C leads to the best results.

Nevertheless this is strongly depending on the protein.



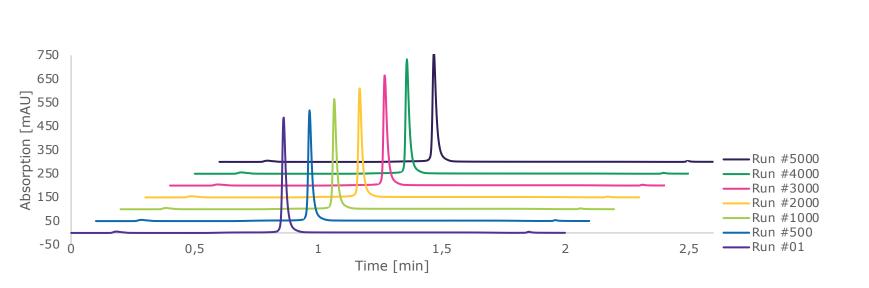


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Peak width vs temperature

Monolithic silica WP 300 Protein A: Stability test

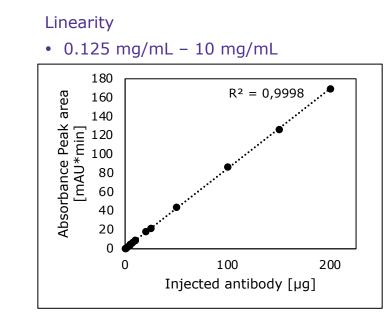




Stability is given for 10.000 pH shifts

- Performance was checked every 10th run with IgG
- RSD elution time IgG < 0.5%
- RSD peak area IgG < 1.1%

Reproducibility of 50 injections				
RSD elution time IgG	< 0.1%			
RSD peak area IgG	< 0.5%			



Stability test

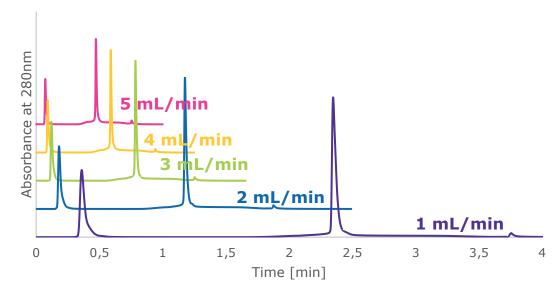
- 2.0 mL/min
- 280 nm
- 25°C
- 10 µl IgG (1 mg/mL)
- Buffer A: 100 mM sodium phosphate pH7.4
- Buffer B: 100 mM sodium phosphate pH2.5



Monolithic silica WP 300 Protein A: Flow rate



Antibody binding is not affected by flow rate



- high-speed separation at high flow rate due to excellent mass transfer properties of the monolithic skeleton
- separation of IgG demonstrates the extreme time savings and high separation efficiency made possible with Chromolith[®] protein A columns.

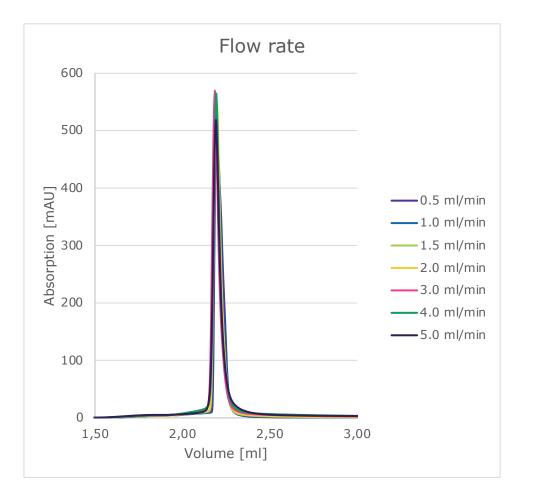
Monolithic column provides low column backpressure at high flow rates

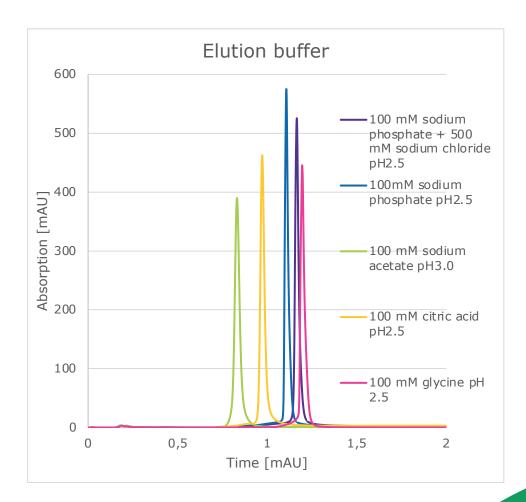
Flow rate	Unbound area	IgG area	Pressure [bar]
1 mL/min	39%	61%	3
2 mL/min	39%	61%	6
3 mL/min	39%	61%	10
4 mL/min	39%	61%	13
5 mL/min	39%	61%	21

- IgG was well separated with excellent peak symmetry
- At 5 ml/min the total analysis time is less than 1 minute and the net column backpressure is only 21 bar
- Antibody binding is not affected by flow rate

Monolithic silica WP 300 Protein A: Flow rate







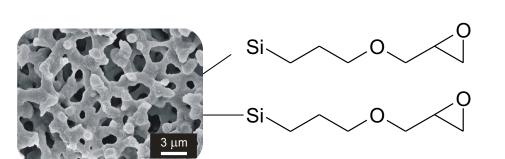
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Monolithic silica WP 300 Epoxy



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Product description



Silica type	High purity
Particle size	monolithic
Macropore size	~ 2 µm
Mesopore size	~ 30 nm (300 Å)
Surface area	~ 120 m²/g
Epoxide concentration	~ 3,2 µmol/m²

Pressure limit	200 bar
pH stability	1.5 – 7.5
immobilization	8.0 (up to 24 hours)
Operating temperature	2 – 45°C

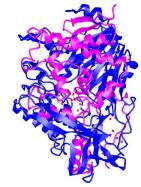
Shipping solution2-ProStorage temperature2 - 8

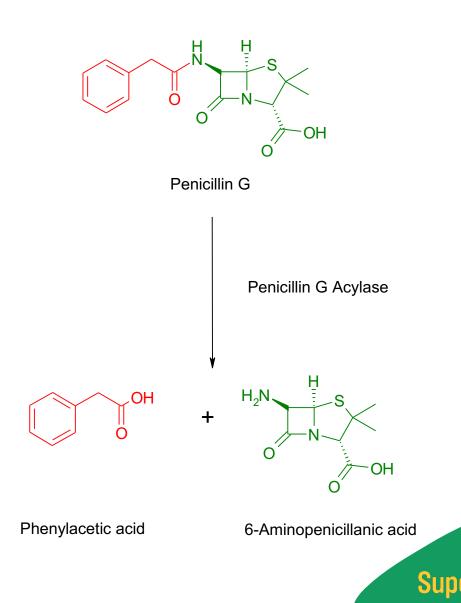
2-Propanol 2 – 8°C

Immobilization of penicillin acylase

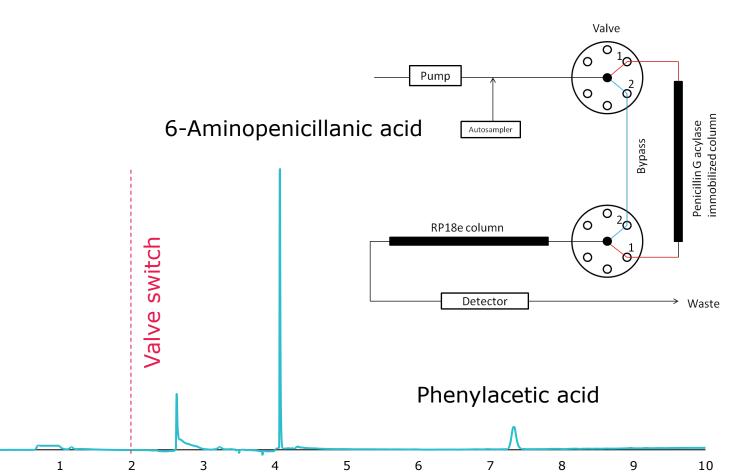


- According to Epoxy method
- Chromolith[®] WP 300 Epoxy 100-4.6mm
- 80 mg penicillin acylase dissolved in 25 ml 50mM sodium phosphate + 1.9M ammonium sulfate pH8.0
- Immobilization for 24 hours at 0.2 ml/min
- Quenching of remaining epoxide functions with glycine





Immobilization of penicillin acylase – Enzymatic bioreactor



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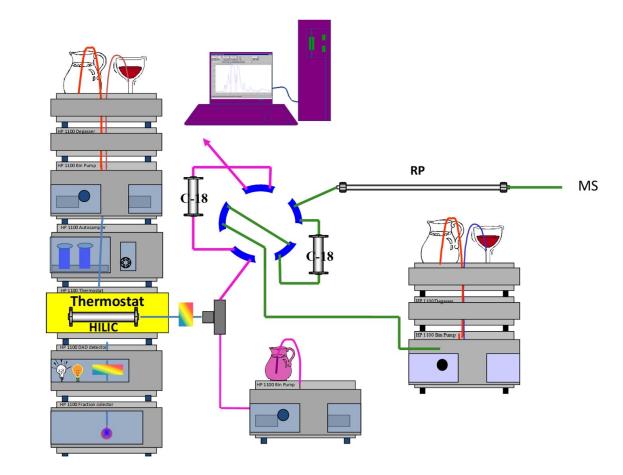
Chromatographic conditions					
Flow rate	1.0 ml/ı	min			
Temperature	23°C				
Detection	UV 225r	าท			
Eluent A	10mM s	10mM sodium phosphate pH7,0			
Eluent B	10mM sodium phosphate pH3,0				
Eluent C	Acetonit	rile			
Sample	1.0 µl P	enicillin (G (3.5 mg	g/ml)	
Gradient					
Time	Valve	А	В	С	
0.00	1	100	0	0	
2.00	1	100	0	0	
2.00	2	0	80	20	
4.00	2	0	80	20	
9.00	2	0	50	50	
9.50	2	0	50	50	
9.60	2	0	80	20	
15.00	2	0	80	20	

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2D separation: HILIC & RP MS

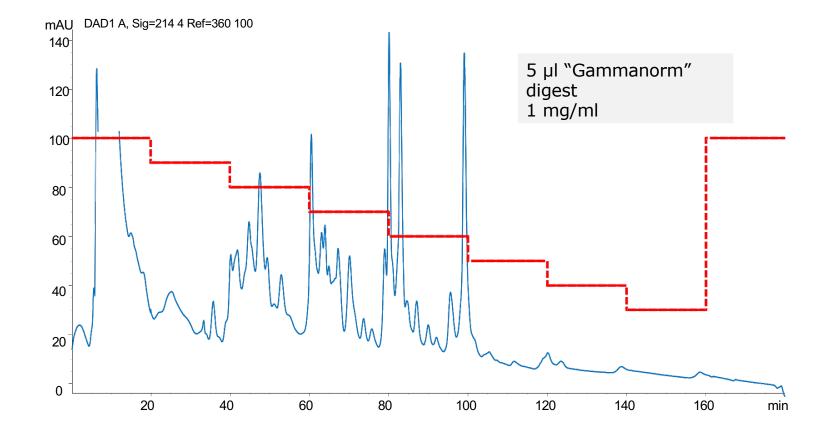






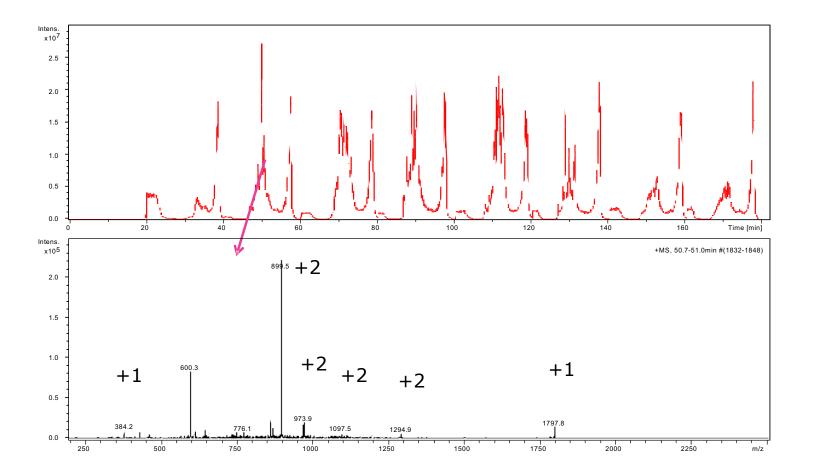
2D separation: 1st dimension - HILIC





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2D separation: **2**nd dimension RP MS



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Conclusions



- Pore size matters
- Superficially porous particles provides more efficiency, resolution and peak capacity
- Choosing right modification helps to achieve separation of coeluting substances
- Silica monoliths consist of macro- and mesopores, offering high permeability
 - SPP show highest separation efficiency
 - Silica monoliths show best column stability for more than 2000 injections
- Protein A immobilized silica monoliths enables robust and fast titer determination of immunoglobulines
 - Antibody binding is not affected by flow rate
 - Linearity up to 200 µg of injected antibody
- Immobilization of ligands onto epoxy-carrying monoliths leads to new degrees of freedom
 - Ligand binding via amino-groups using a simple, straightforward protocol
 - Various modes of chromatography are possible as well as the design of bioreactors or similar systems



Many thanks to our Chromatography R&D Groups in Darmstadt and Bellefonte and the Application labs in the different counties for providing the chromatographic data.

