



Reverse Phase



Agilent Technologies

How proteins separate on reverse-phase HPLC

- RP chromatography separates proteins through the interaction of the “hydrophobic foot” of the protein with a non-polar surface of the particle
- RP columns are nearly always based on silica particles
 - Mechanical stability, easy to make, surface can be modified, excellent peak shape & efficiency)
- Solvent
 - Organic modifier: Acetonitrile, isopropanol, methanol
 - Ion pair additive: Trifluoroacetic acid (TFA), Formic Acid, or Acetic.
- Gradient separation

Analysis & characterization of protein drugs by RP-HPLC

- RP HPLC plays a very important role in the analysis & characterization of protein therapeutic drugs
 - Verification of fidelity of primary sequence
 - Using peptide map with comparison to a reference standard
 - Determination of deamidation & oxidation
 - By means of peptide map comparison of native & stressed protein
 - Using an intact protein
 - Determination & confirmation of disulfide bonds
 - By peptide mapping comparing native & reduced protein
 - Characterization of glycosylation
 - Peptide mapping can determine glycopeptide (in conjunction with MS)

Choose The Initial Bonded Phase:

C18 C8 C3



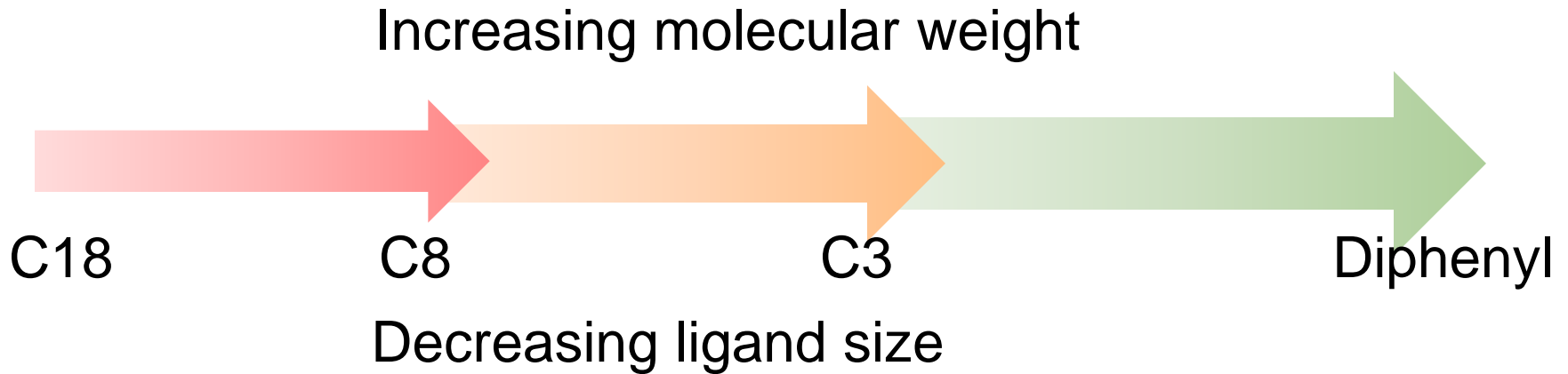
Buy Them All and Try Them All.....

Not really feasible, right?

How do you narrow it down?



Molecular Weight



- Larger molecular weights separate better with smaller ligands
 - Upper Mw of C18 = 70kDa
- Not much difference between C8, C3 & diphenyl
 - Upper Mw of C3/C8/DP = 180kDa

Pore Size

Generally speaking, the “go to pore” size for most protein applications using RP is 300 Å.

Smaller pore sizes are available for smaller proteins and peptides

Larger pore sizes are available for larger proteins and synthetic molecules



About Particle Size

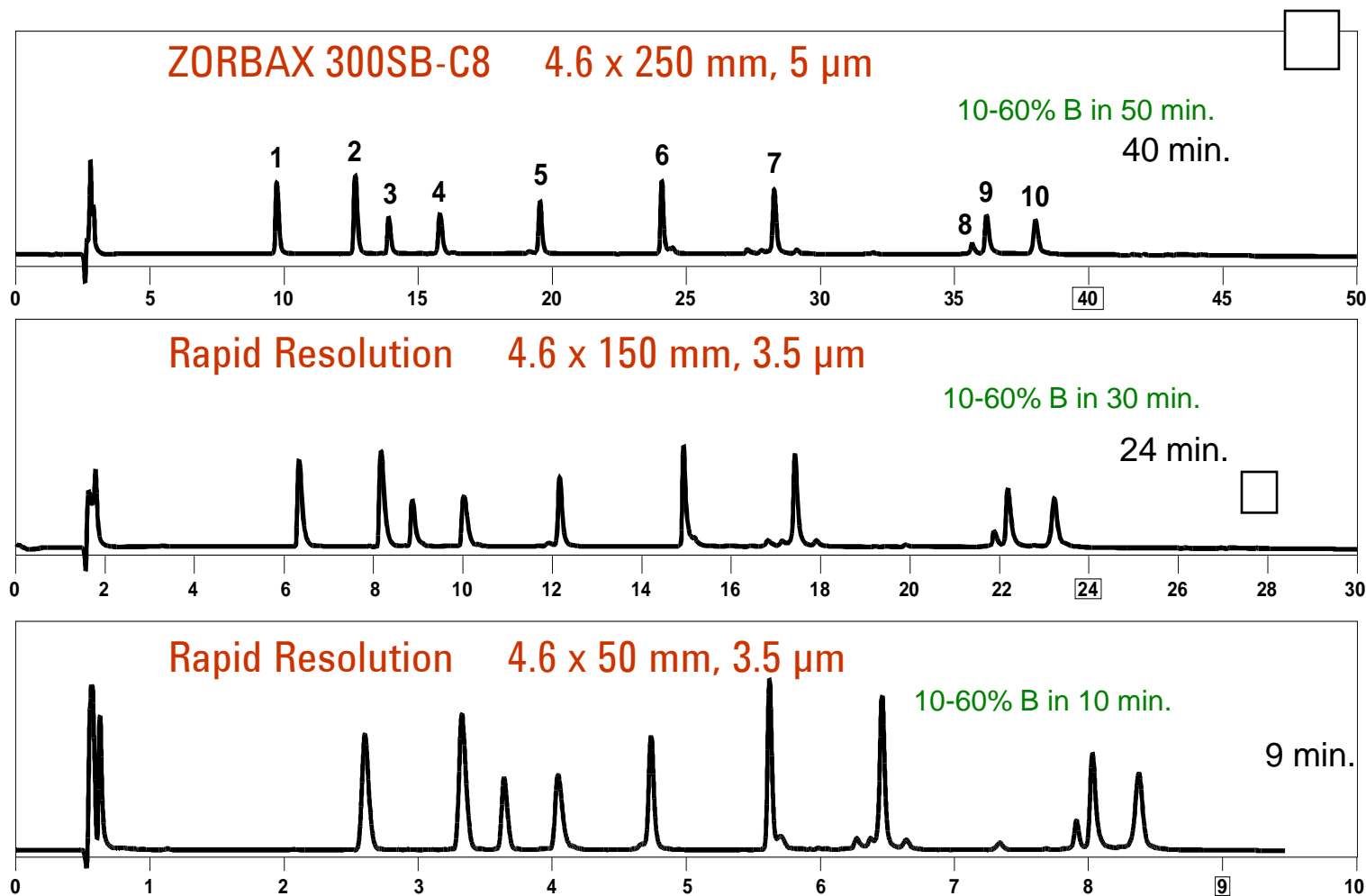
Smaller particle sizes will increase resolution power

Coupled with smaller column lengths, decrease time and increase throughput

Agilent offers many options down to 1.8 μm for RP



As Column Volume Decreases, Decrease Gradient Time (t_g) to Keep Gradient Retention (k^*) and Resolution Constant



Initial Separation Conditions

Mobile Phase: A: 95% H₂O/5% ACN, 01.% TFA

 B: 5% H₂O/95% ACN, 0.1% TFA

Gradient: 0-60% B in 60 min

Temp: 35- 40 C

Flow Rate: 1ml/min



Optimize Organic Modifier

In order of increasing elutropic force and decreasing polarity:

Water

Methanol

Acetonitrile

N-Propanol

THF



About Ion Pair Agents

- Typically TFA is used
- If LC/MS is used, can substitute Formic or Acetic acid

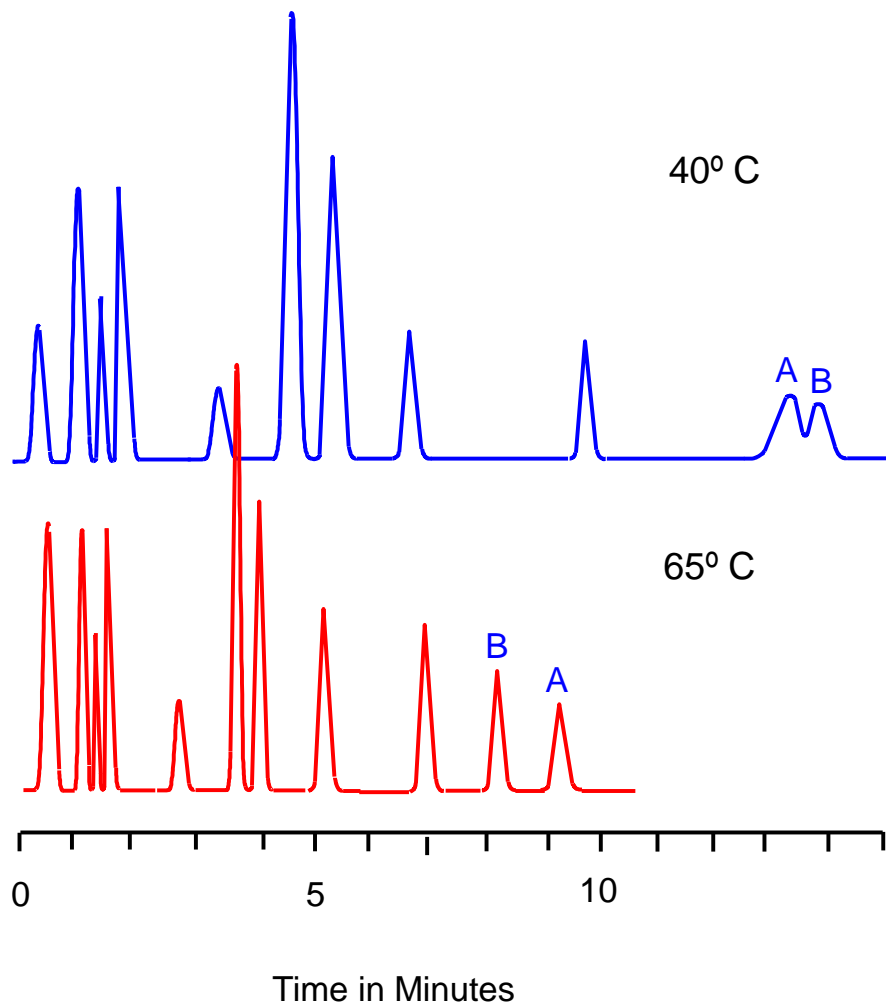
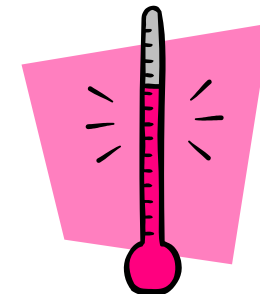


Optimize Temperature

- Higher column temperature can dramatically improve resolution and recovery
- Check manufacturer specs for compatibility
- Agilent Zorbax Stablebond columns are rated to 80 C



Effect of Column Temperature on Retention k and Selectivity α



1. Column temperature can be used to fine tune a separation by affecting both the retention k and selectivity α .
2. About a 1% increase in T leads to a 1 to 2% decrease in k .
3. Increase in T leads to decrease in Pressure due to decrease in mobile phase viscosity.
4. Increase in T also leads to decrease in peak widths.
5. Also, use of a thermostat column compartment improves retention time precision.

Optimize Mobile Phase pH

- Start with acidic pH first
- If not ideal, move to mid or high pH, check manufacturers specs for limits
- Selectivity will change because acidic amino acids will become negatively charged and basics may lose their charge
- Ammonium hydroxide is an excellent mobile phase for high pH separations using LC/MS



High pH Can be Used for Separating Hydrophobic or Other Low-Solubility Peptides

Comparison of A β Peptide RP-HPLC Separations at Low and High pH

TFA Conditions, 25°C
A- 0.1% TFA in water
B- 0.085% TFA in
80%AcN
33-45%B in 30 min.

TFA Conditions, 80°C
A- 0.1% TFA in water
B- 0.085% TFA in
80%AcN
29-41%B in 30 min.

NH₄OH Conditions, 25°C
A- 20 mM NH₄OH in water
B- 20 mM NH₄OH in
80%AcN
26-38%B in 30 min.

Column:
300Extend C18

ZORBAX

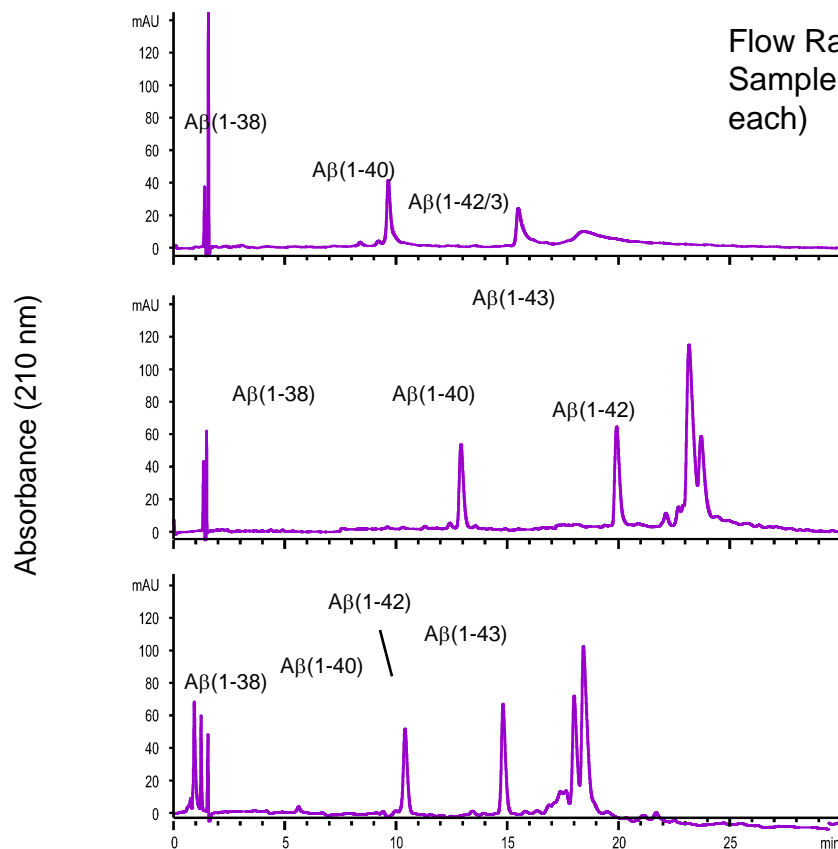
2.1 x 150 mm, 5 μ m

Flow Rate:

0.25 mL/min

Sample:
each)

5 μ L sample (100 pmol



Adjust Gradient Slope to Optimize Resolution

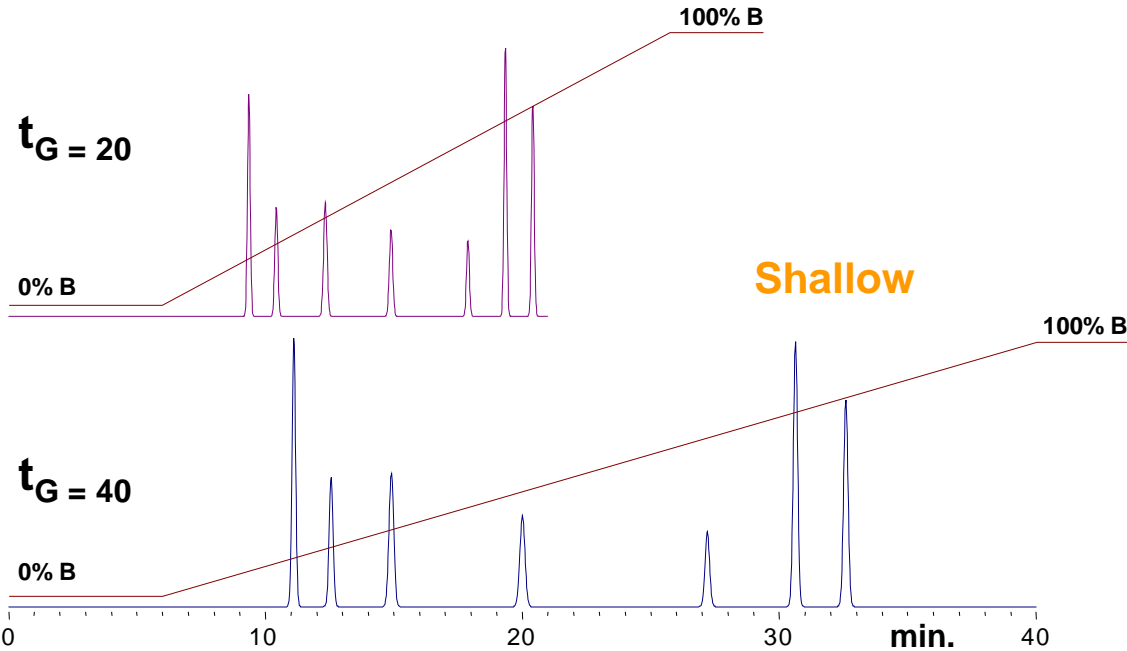
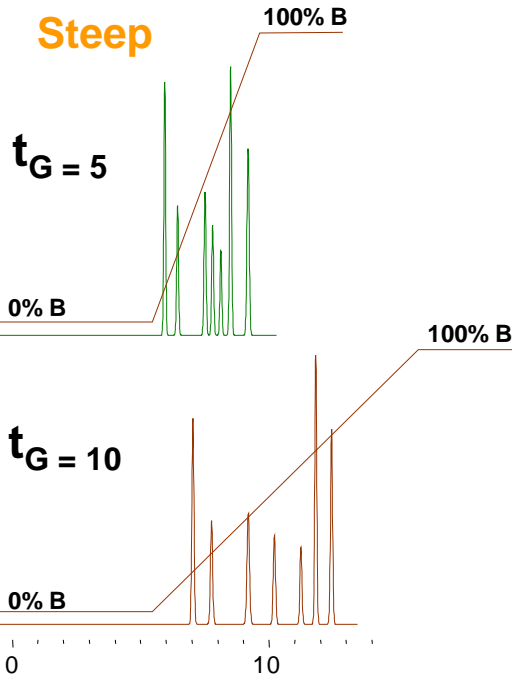
Accomplished by changing:

- gradient time

- % change in organic modifier over time



Gradient Slope



Agilent RP Column Choices for Biomolecules



Zorbax Silica

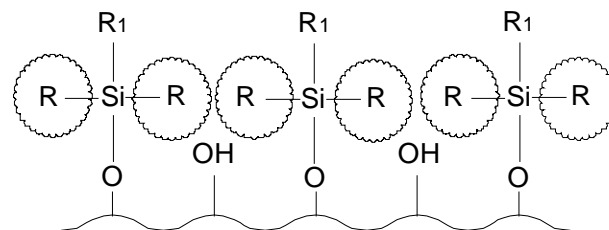
Zorbax Stablebond 300

300 Å pore size

available in C-3, C-8, C-18, and CN

non-endcapped

particle sizes: 3.5, 5, and 7



NEW!

Zorbax 300 SB RRHD for Proteins and Peptides!

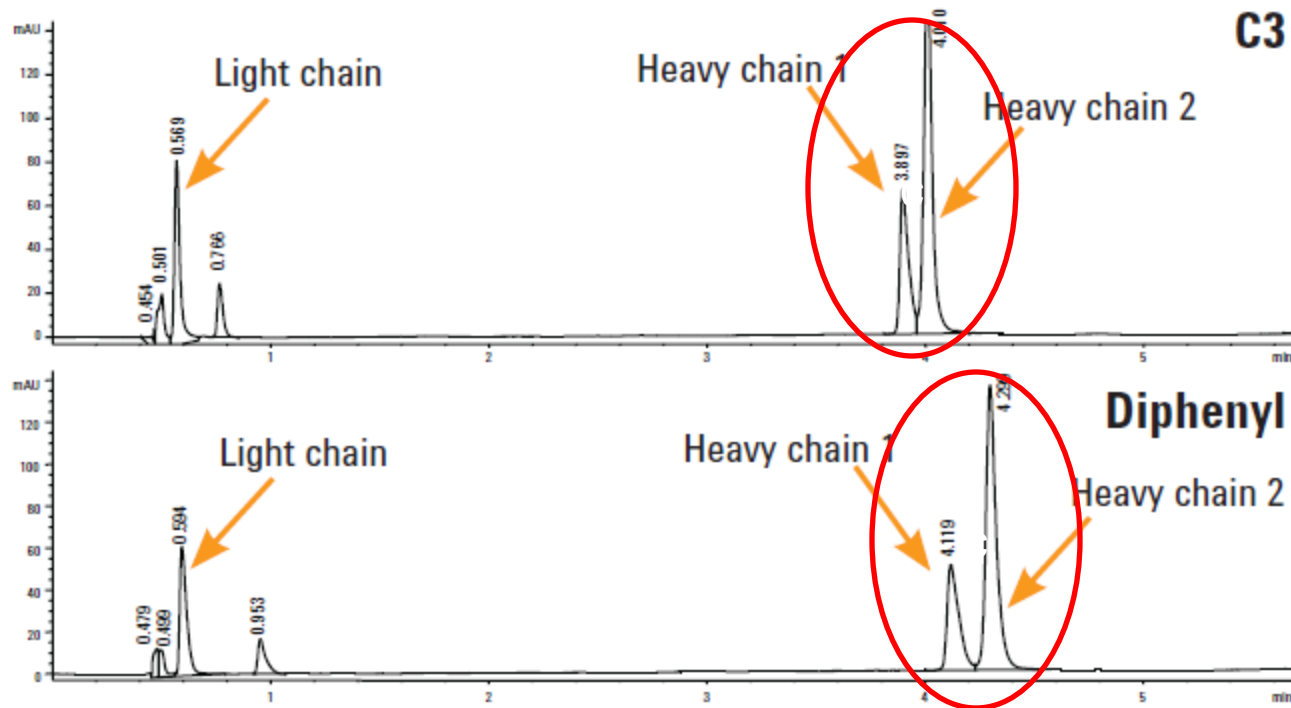
- Stablebond 300 silica
- C-18, C-8, C-3, HILIC and **unique diphenyl** bonded phase
- 1.8 um particle size
- 1200 Bar pressure limit for uHPLC



Diphenyl Selectivity

- Diphenyl provides alternate selectivity to C3
 - In addition to difference in hydrophobicity
- C18, C8 and C3 work on a purely hydrophobic interaction
- DP has π - π interactions also
- Additional affinity for aromatic amino acids and double bonds
 - *Orthogonality*

C3 vs Diphenyl



- Reduced IgG1
- 0.1% TFA gradient, 74°C
- Less hydrophobic DP column shows baseline resolution

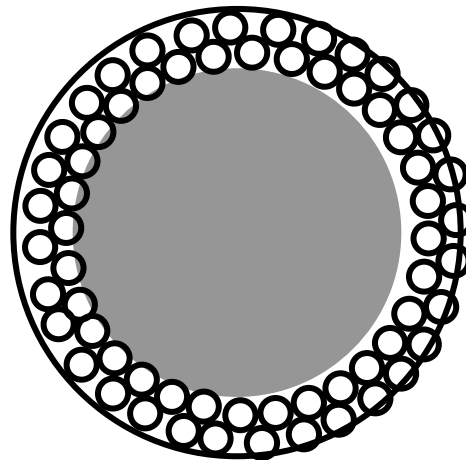
Poroshell 300

300 Å pore size

Stablebond chemistry

available in C-3, C-8, C-18, and C-18 Extend

5 µm particle size

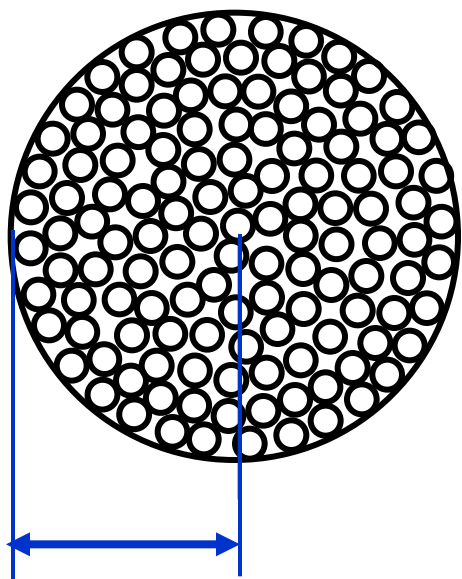


Comparison of Diffusion Distance

Totally porous silica vs. superficially porous silica

5 μm

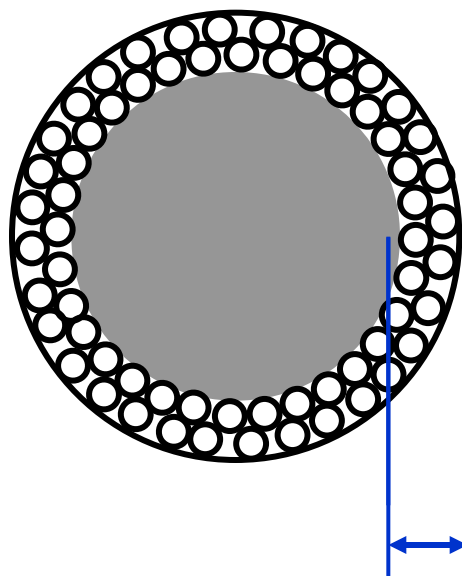
Totally Porous Particle



2.5 μm

5 μm

Superficially Porous Particle



0.25 μm

Required diffusion distance
for a macromolecule
reduced 10 fold !

AdvanceBio Peptide Mapping Column

A superficially porous column with a 2.7 μ m particle and C18 functionality which enables separation of hydrophilic through hydrophobic peptides to give superior resolution across the gradient range to efficiently resolve peptide fragments.

What are the compelling features?

- Peptide Mapping Resolving Power/Peak Capacity
- Enhance Resolution across a Wide Dynamic Range
- Fast Analysis Times
- Lower Pressure Drops than sub 2 μ m Columns
- Quality Checked for Peptide Performance



Peptide mapping

Peptide mapping is the single most important technique in analytical characterization of protein drugs. It is used to...

- Development (characterization)
 - Confirm primary structure by comparison of a product to a reference protein (detect point mutations, mis-translations & confirm genetic stability)
 - Identify location of disulfide bonds
 - Characterize & analyze degradation processes such as deamidation & oxidation
 - Isolate digest fragments for sequencing or further identification
 - Identify sites of glycosylation
- Quality control
 - Drug substance identity test
 - Drug substance purity test

AdvanceBio Peptide Mapping Column

Primary Benefit – Reduce Peptide Mapping Time without Losing Resolution

What is It? - A superficially porous column with a 2.7 μ m particle and C18 functionality which enables separation of hydrophilic through hydrophobic peptides to give superior resolution across the gradient range to efficiently resolve peptide fragments.

Major Features

- High Resolution of the Peptide Map
- Fast Analysis Times
- Lower Pressure Drops than sub 2 μ m Columns
- Quality Checked for Peptide Performance

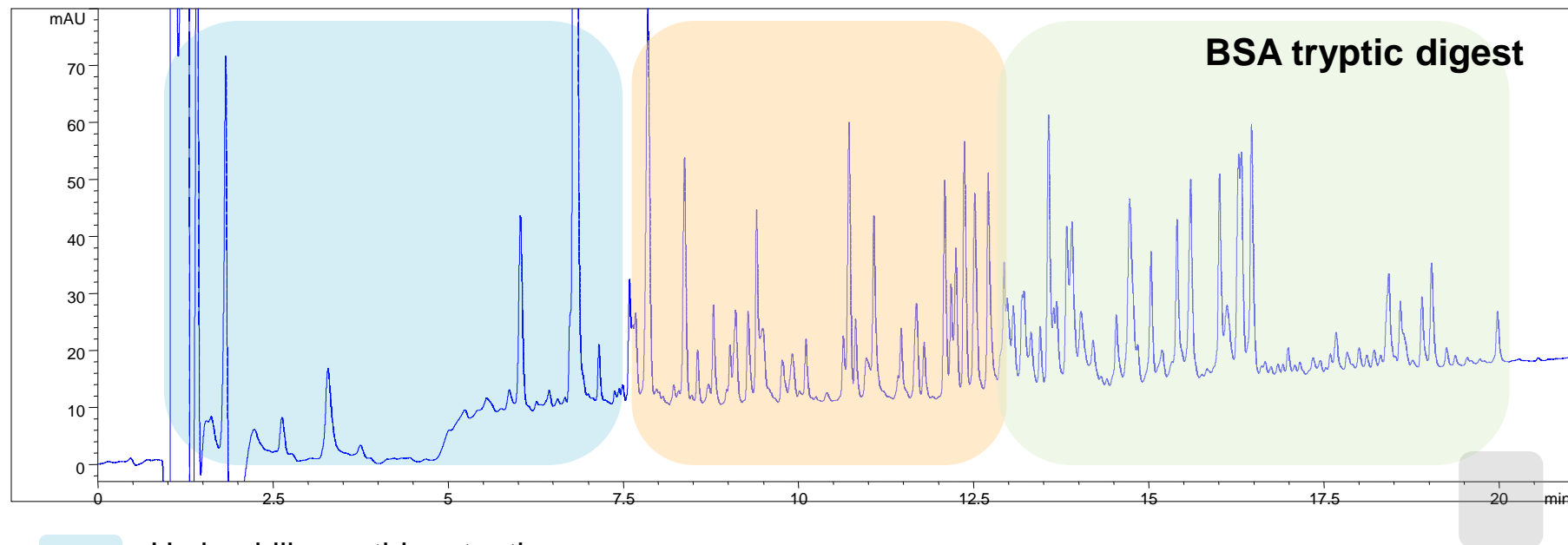


AdvanceBio Peptide Mapping Column Highlights

Peptide Mapping

2.1 x 150mm AdvanceBio Peptide Mapping Column

Mobile phase: A-water (0.1%TFA), B- ACN (0.08%TFA), 40 C, flow: 0.52mL/min



- Hydrophilic peptide retention
- Narrow Peaks w baseline resolution
- Hydrophobic peptide retention
- Reduced and fast analysis time



Critical and desired peptide mapping components to achieve fast, selective and highly efficient peptide separations across a wide dynamic range.

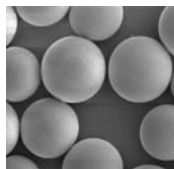
PLRP-S

Polystyrene divinylbenzene bead

Available in 100, 300, 1000, and 4000Å pore sizes

Particle sizes 3, 5, 8, 10, and higher

Various geometries from Nano, Capillary to preparative



Match to System Capabilities

Maximum Operating Pressure

400 bar

600 bar

1200 bar

ZORBAX RRHD 300Å 1.8 µm columns

Poroshell 300 columns

ZORBAX 300Å 3.5 and 5 µm columns

PLRP-S 3 and 5 µm columns

AdvanceBio 2.7 µm columns



Thank you!



Agilent Technologies