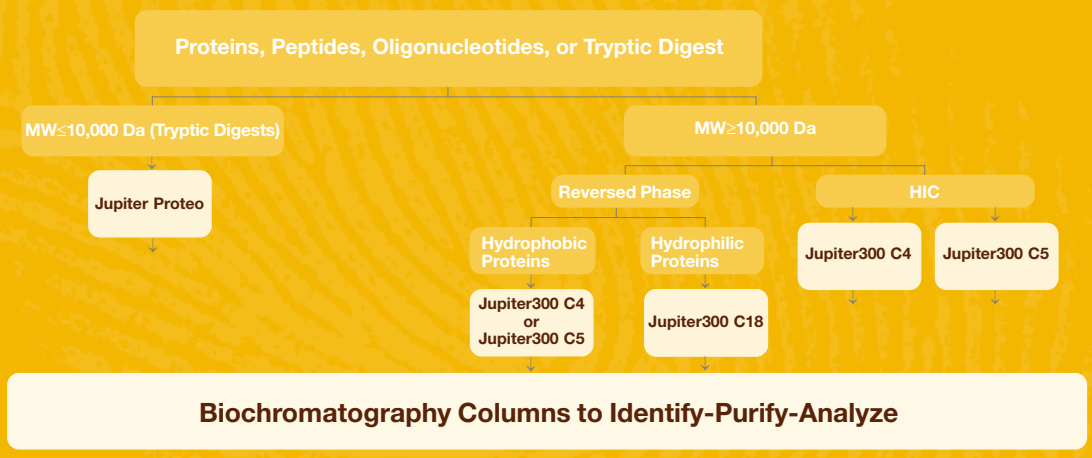
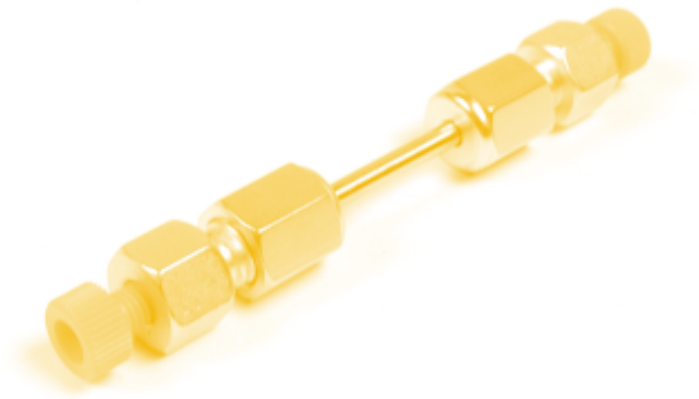
Jupiter™

HPLC columns for the proteomic era

phenomenex®


Proteins, Peptides, Oligonucleotides, or Tryptic Digest
MW≤10,000 Da (Tryptic Digests)
Jupiter Proteo
MW≥10,000 Da
Reversed Phase
HIC
Hydrophobic Proteins
Hydrophilic Proteins
Jupiter300 C4
Jupiter300 C5
Jupiter300 C4 or Jupiter300 C5
Jupiter300 C18
Biochromatography Columns to Identify-Purify-Analyze



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Jupiter™

IDENTIFY - PURIFY - ANALYZE ANY PROTEIN

A fingerprint is your unique physical identifier, just as tryptic digests can serve as “fingerprints” to identify proteins. With the number of protein characterization experiments increasing, the need for better data from protein digests is becoming common. Thus, we engineered Jupiter™ Proteo, a tryptic digests analysis column, to reveal more peaks, yield more data, and show more of the protein's “fingerprint”. The Jupiter™ column line consisting of Jupiter Proteo and Jupiter300™, a leading column for protein purification, now offers a total reversed phase biochromatography solution.

- Isolate and Purify Intact Proteins - Jupiter300™ proven to reproducibly analyze and purify large intact proteins and oligonucleotides *(FIGURE 2)*.
- Analyze Tryptic Digests - Jupiter Proteo engineered with the efficiency and peak capacity to reproducibly resolve complex tryptic digest samples. Figure 1 shows trypsin digested Cytochrom C genetic variants - the resolving power of Jupiter Proteo clearly illustrates differences between these genetic variants.

FIGURE 1
Isolate and Purify Intact Cytochrome C

APP ID 8715

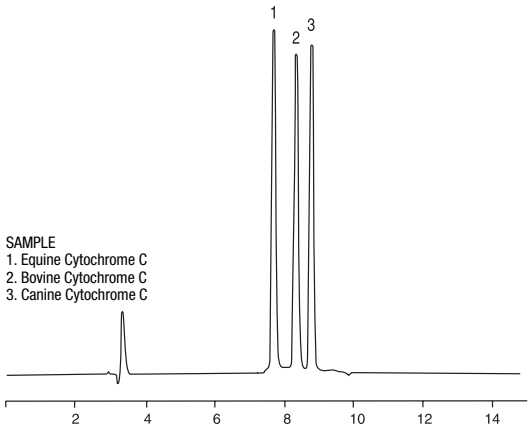
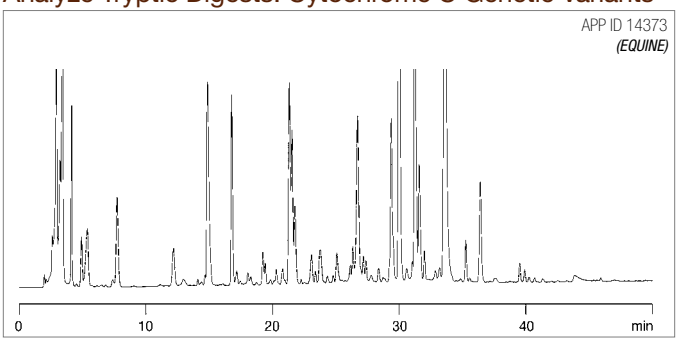
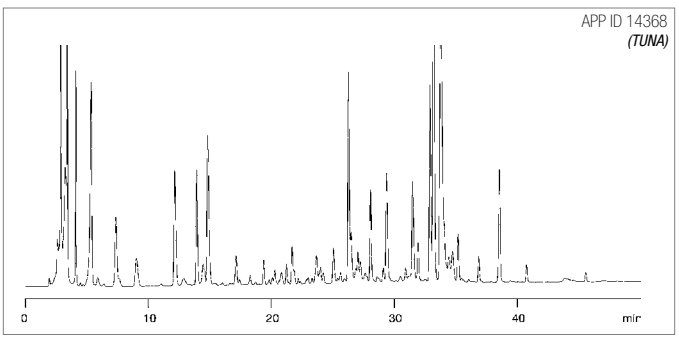
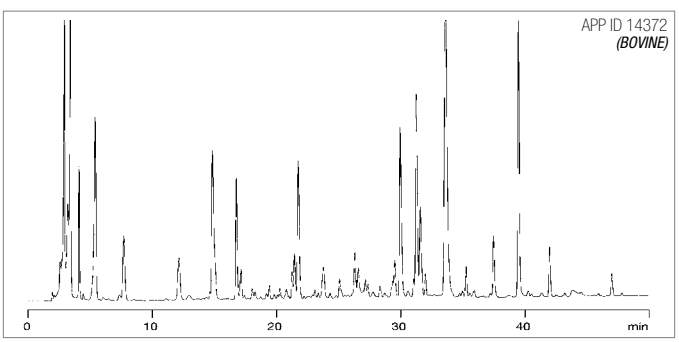
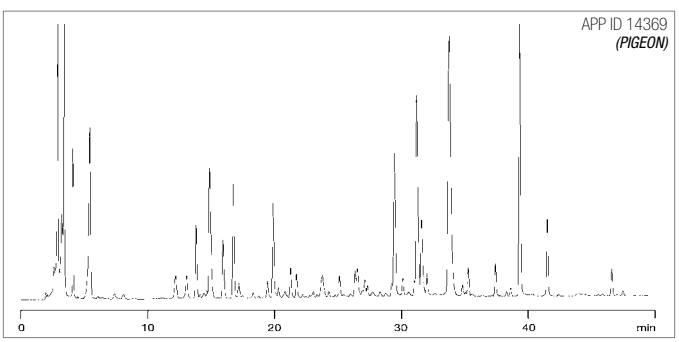


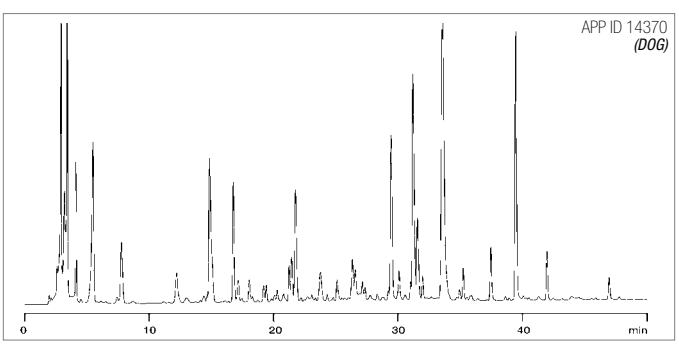
FIGURE 2
Analyze Tryptic Digests: Cytochrome C Genetic Variants

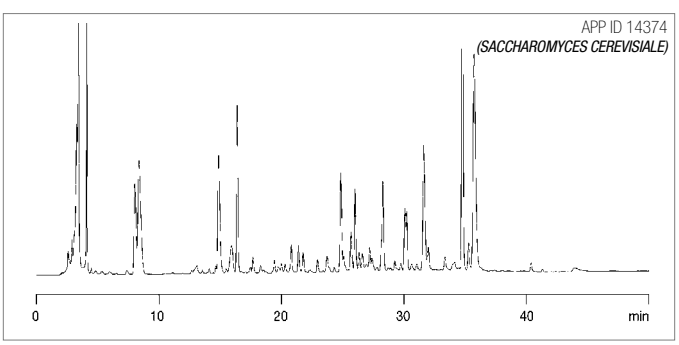






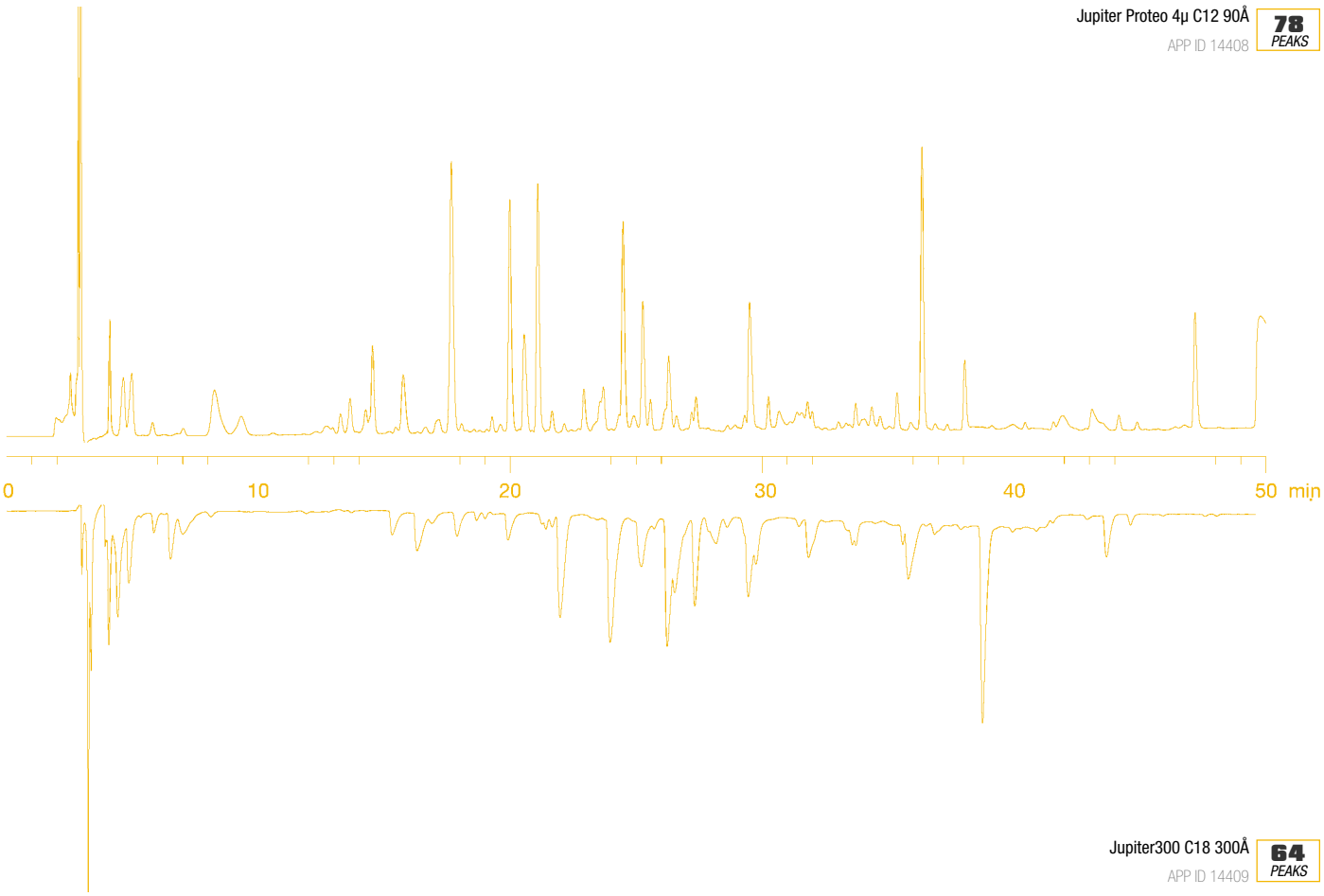






NEW JUPITER™ PROTEO - FOR TRYPTIC DIGESTS AND PEPTIDES.

FIGURE 3
Compare: 300Å C18 vs 90Å Jupiter Proteo (Myoglobin Tryptic Digest)



Traditionally, 300Å columns have been used for the analysis of intact proteins, peptides and tryptic digests. 300Å silica has low surface area, which provides good retention and resolution of intact proteins, but results in poor retention and column efficiencies necessary for analysis of tryptic digests.

Jupiter Proteo breaks all traditions and optimizes column parameters to provide extreme performance *(FIGURE 3)*. Utilizing a 90Å high-surface area silica maximizes stationary phase interaction; 4µ silica particles provide high column efficiencies. Additionally, the unique C12 bonded phase with proprietary end-capping has been engineered to:

- Sharpen peak symmetry with a 25% higher bonded phase coverage as compared to C18 ligands for greater resolution.
- Increase peak capacity for greater sample/ bonded phase interaction *(FIGURE 3)*

CONDITIONS

FIGURE 1
Intact Cytochrome C

APP ID: 8715
Columns: Jupiter300 5µ C18 300Å
Dimensions: 250 x 4.6mm
Order No.: 00G-4053-E0
Mobile Phase: A) 0.1% TFA in Water
B) 0.1% TFA in Acetonitrile
Gradient: A/B (75:5) to A/B (45:55) in 15 min (2% B/min)
Flow Rate: 1mL/min
Detection: UV @ 220nm
Sample: 1. Equine cytochrome c
2. Bovine cytrochrome c
3. Canine cytochrome c

FIGURE 2
Cytochrome C Genetic Variants

APP ID: 14368-14374
Columns: Jupiter 4µ Proteo 90Å
Dimensions: 250 x 4.6mm
Order No.: 00G-4396-E0
Mobile Phase: A) 0.012% TFA in Water
B) 0.01% TFA in Acetonitrile
Gradient: A/B (95:5) for 5 min, then to A/B (60:40) in 55 minutes
Flow Rate: 1mL/min
Temperature: 22°C
Detection: UV @ 210nm
Sample: Tryptic map of Cytochrome C genetic variant – see chromatogram for species

FIGURE 3
Myoglobin Tryptic Digest

APP ID: 14408, 14409
Dimensions: 250 x 4.6mm
Mobile Phase: A) 0.012% TFA in Water
B) 0.01% TFA in Acetonitrile
Gradient: A/B (95:5) for 5 min, then to A/B (60:40) in 55 minutes
Flow Rate: 1mL/min
Temperature: 22°C
Detection: UV @ 210nm
Sample: Myoglobin Tryptic Digest

RESOLVE 100 + PEAKS

Just as every ridge of a fingerprint confirms the identity of its owner, every peak in a tryptic digest further characterizes the intact protein. Thus, we developed a column for maximum peak counts. High-resolution separations of complex samples are achieved by:

- High column efficiencies similar to 3µ materials, but at low backpressures similar to 5µ materials.
- 475m^2/g surface area increases bonded-phase/ sample interaction and peak capacity.

Jupiter Proteo resolves more peaks, at higher efficiencies, a feature that is critical as large peak numbers demand greater resolution *(FIGURES 4-5)*

Determining peak counts - The large number of peaks in a given tryptic digest makes counting peaks visually both inaccurate and subjective. For a more accurate approach, peak counting was performed using HP ChemStation™ software. Four different integration parameters at different sensitivity settings were used in calculating the number of peaks and an average. The parameters changed within each method were: minimum peak area, minimum peak height, peak width, and threshold. The table below describes the parameters used for each calculation.

Method	Threshold	Peak Width	Min Area	Min Height
1	1.0	0.1	10.0	20.0
2	2.0	0.2	10.0	20.0
3	3.0	0.3	20.0	10.0
4	3.0	0.3	20.0	50.0

FIGURE 4
Myoglobin Tryptic Digest Comparisons

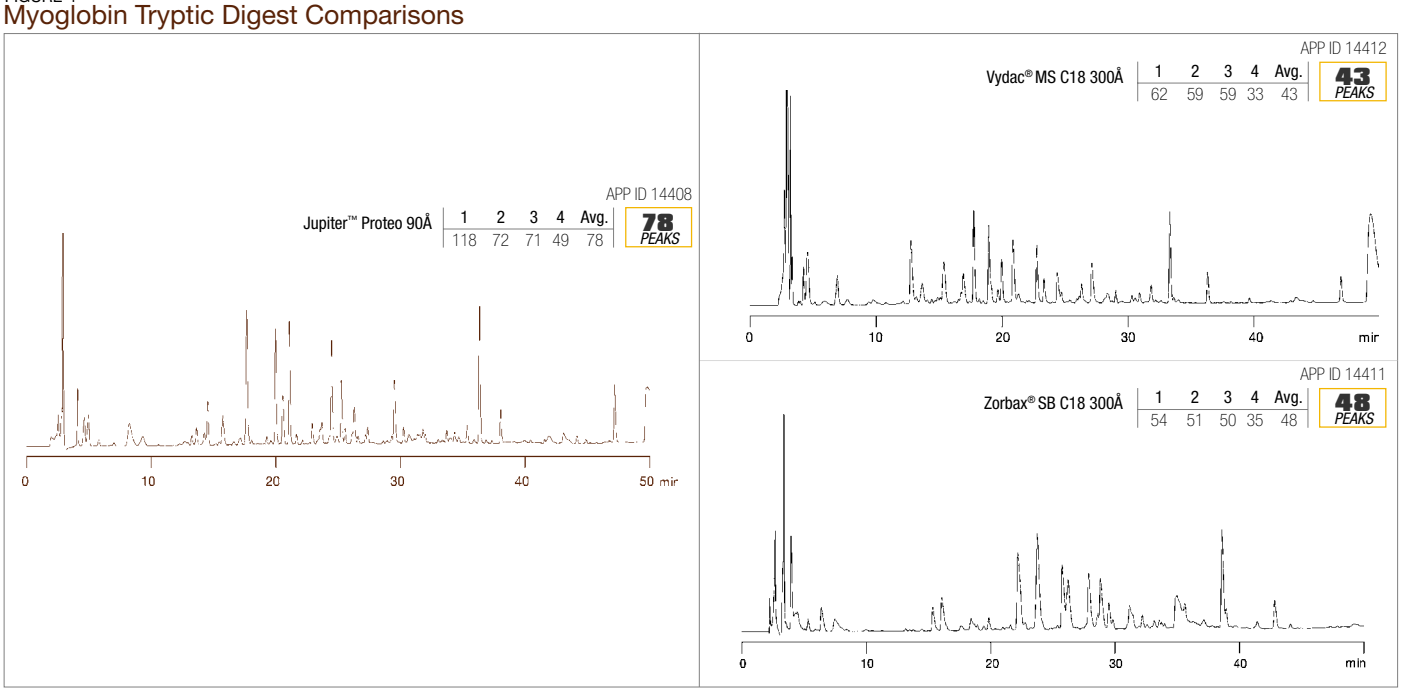
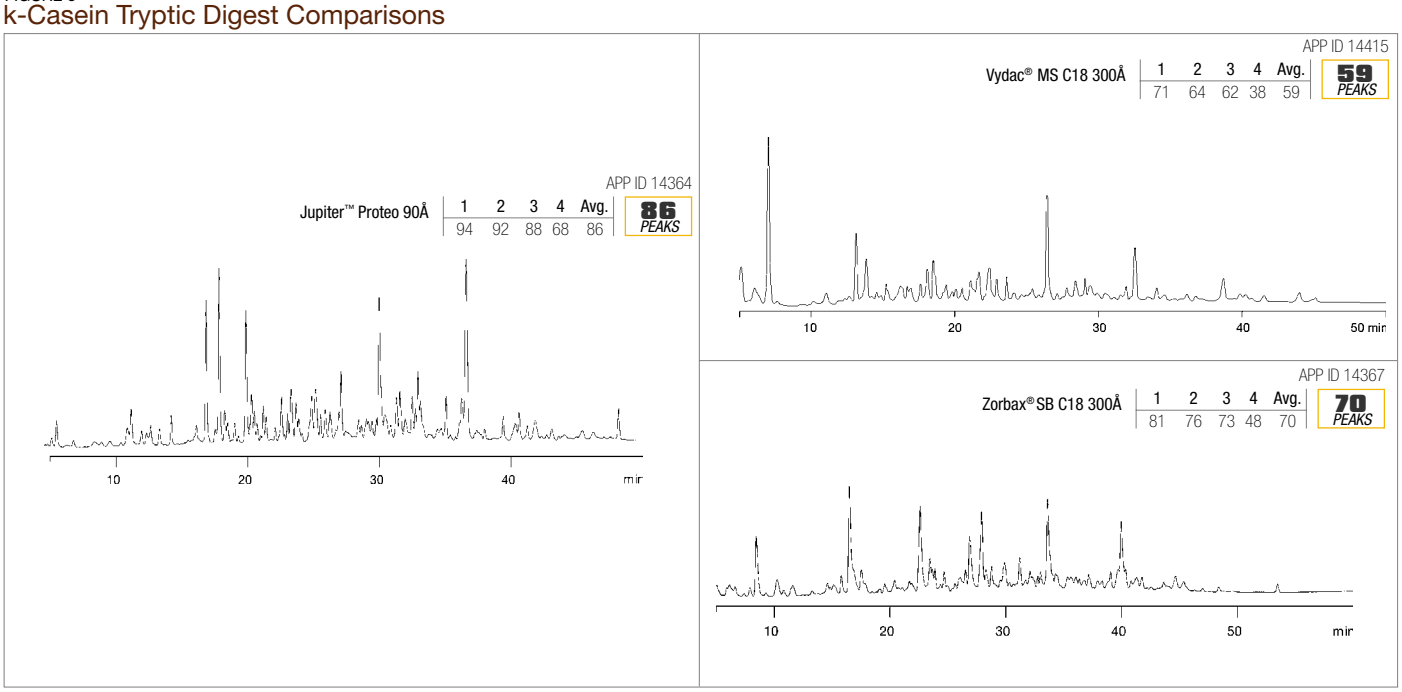


FIGURE 5
k-Casein Tryptic Digest Comparisons



EASILY MONITOR OXIDATION AND DEAMINATION

The shelf life of a protein product is a major concern in the biotechnology industry as it may be subject to inactivation from deamination or oxidation. Oxidation is commonly seen with methionine due to its readily oxidized sulfur group. A tryptic digest of ß-Lactoglobulin reveals early eluting peaks of a more polar peak representing the oxidation product *(FIGURE 6)*. Deamination of asparagine forms aspartic acid which is less polar and elutes slightly later in a chromatographic profile. RNase is readily susceptible to deamination and the deamination peaks are easily resolved by Jupiter Proteo *(FIGURE 7)*. Monitoring protein oxidation and deamination peaks within the jungle of a tryptic digest can be difficult without adequate resolution, thus Jupiter Proteo was engineered with one goal: high resolution.

FIGURE 6
Oxidation of β-Lactoglobulin

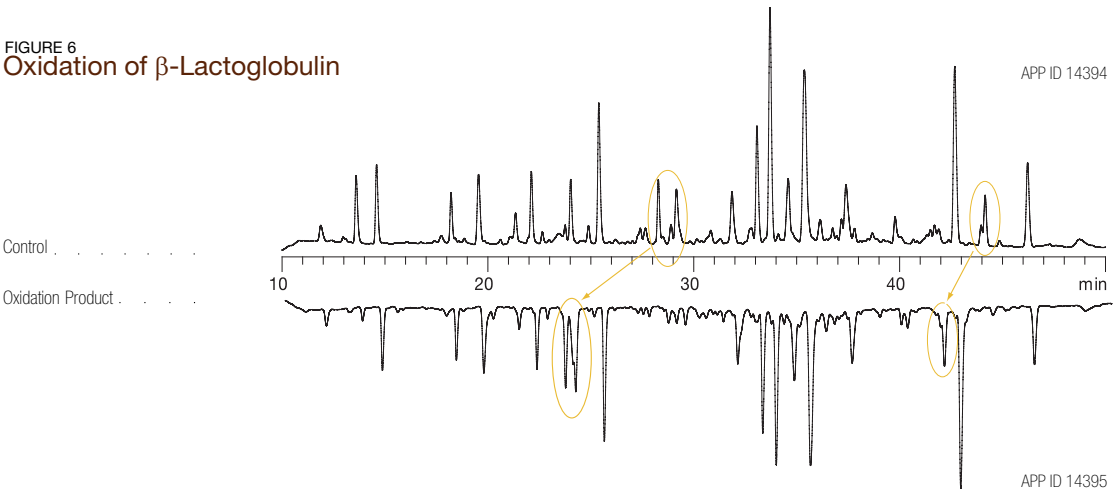
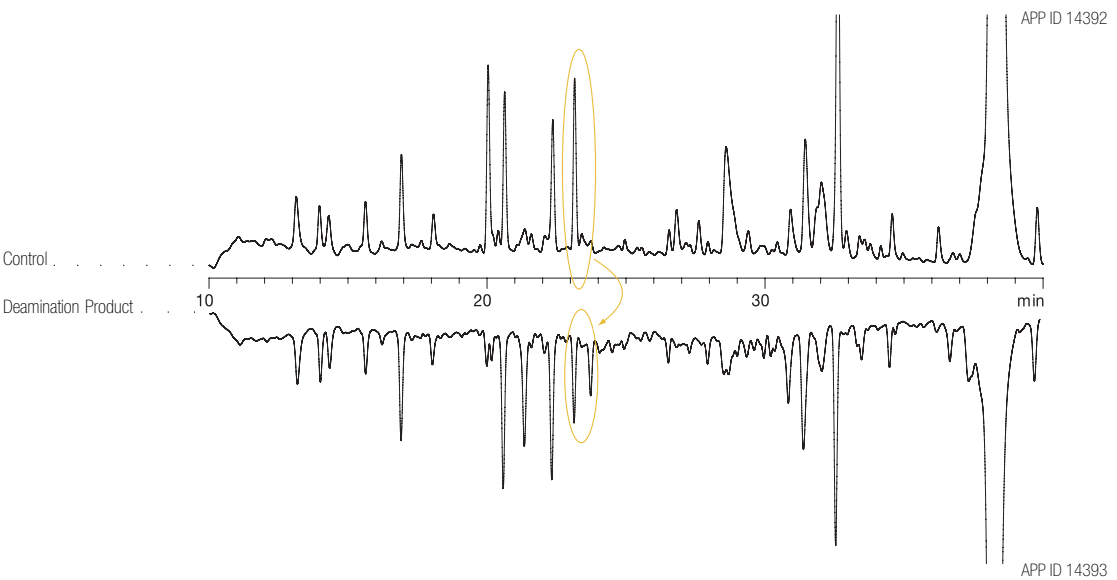


FIGURE 7
Deamination of RNase



CONDITIONS

FIGURE 4
Myoglobin Tryptic Digest

APP ID: 14408, 14411-14412
Columns: Jupiter 4µ Proteo 90Å
Vydac 5µ MS C18 300Å
Zorbax 5µ SB-C18 300Å
Dimensions: 250 x 4.6mm
Mobile Phase: A) 0.012% TFA in Water
B) 0.01% TFA in Acetonitrile
Gradient: A/B (95:5) for 5 min, then to A/B (60:40) in 55 minutes
Flow Rate: 1mL/min
Temperature: 22°C
Detection: UV @ 210nm
Sample: Myoglobin Tryptic Digest

FIGURE 5
Tryptic Digest of k-Casein

APP ID: 14364, 14367, 14415
Columns: Jupiter 4µ Proteo 90Å
Vydac 5µ MS C18 300Å
Zorbax 5µ SB-C18 300Å
Dimensions: 250 x 4.6mm
Mobile Phase: A) 0.012% TFA in Water
B) 0.01% TFA in Acetonitrile
Gradient: A/B (95:5) for 5 min, then to A/B (60:40) in 55 minutes
Flow Rate: 1mL/min
Temperature: 22°C
Detection: UV @ 210nm
Sample: k-Casein Tryptic Digest

FIGURE 6
Tryptic Digest of Oxidized and Control β-Lactoglobulin

APP ID: 14394, 14395
Columns: Jupiter 4µ Proteo 90Å
Dimensions: 250 x 4.6mm
Order No.: 00G-4396-E0
Mobile Phase: A) 0.012% TFA in Water
B) 0.01% TFA in Acetonitrile
Gradient: A/B (95:5) for 5 min, then to A/B (60:40) in 55 minutes
Flow Rate: 1mL/min
Temperature: 22°C
Detection: UV @ 210nm
Sample: Top Chromatogram – β-Lactoglobulin tryptic digest Bottom Chromatogram – Oxidated β-Lactoglobulin tryptic digest

FIGURE 7
Tryptic Digest of Deaminated and Control RNase

APP ID: 14392, 14393
Columns: Jupiter 4µ Proteo 90Å
Dimensions: 250 x 4.6mm
Order No.: 00G-4396-E0
Mobile Phase: A) 0.012% TFA in Water
B) 0.01% TFA in Acetonitrile
Gradient: A/B (95:5) for 5 min, then to A/B (60:40) in 55 minutes
Flow Rate: 1mL/min
Temperature: 22°C
Detection: UV @ 210nm
Sample: Top Chromatogram – RNase tryptic digest
Bottom Chromatogram – Deaminated RNase tryptic digest

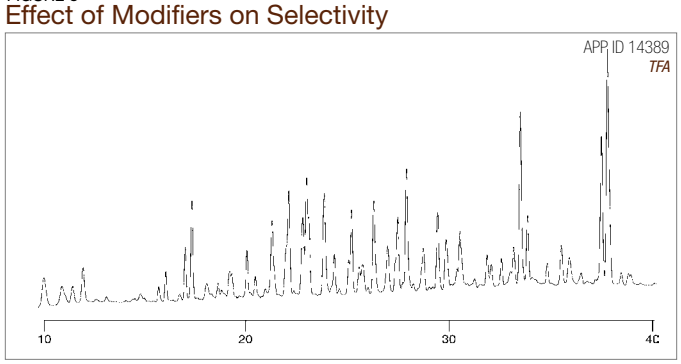
MODIFIER COMPATIBILITY + PH STABILITY = BETTER RESOLUTION

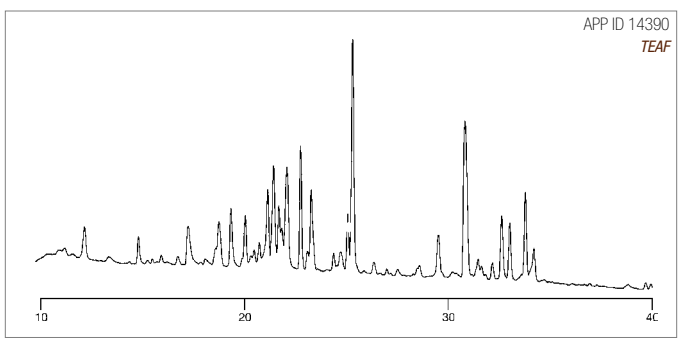
Wide mobile phase flexibility allows you to operate under conditions to provide optimal separations. Jupiter Proteo ensures resolution and selectivity by providing:

- Remarkable performance in MS-buffers (TFA, TEAF, Formic acid) *(FIGURE 8)*.
- Excellent peak shape down to 0.01% TFA *(FIGURE 9)*.

Simply adjust the gradient profile to increase retention *(FIGURE 10)*. Jupiter Proteo widens your operating pH range from 1.5 to 10 (2-8 for ordinary silica columns). The result is greater method flexibility and easier column regeneration.

FIGURE 8
Effect of Modifiers on Selectivity





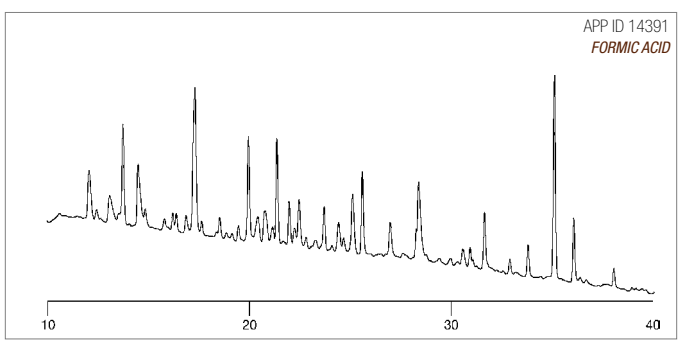
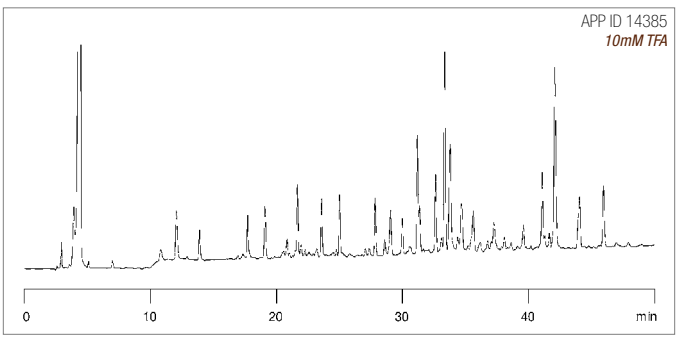
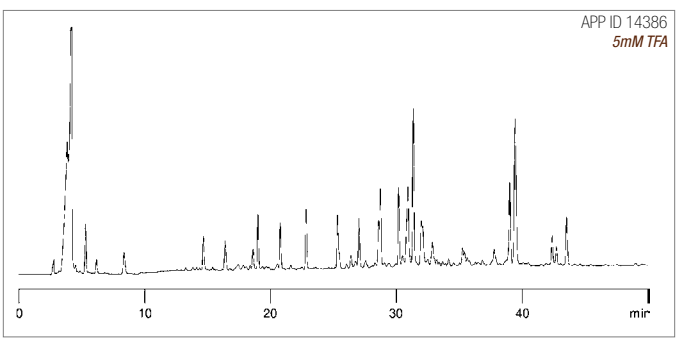
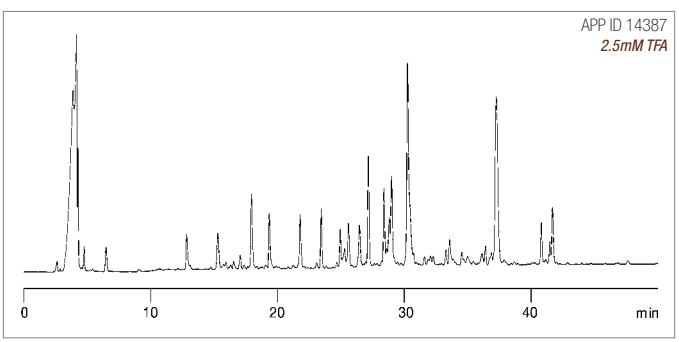
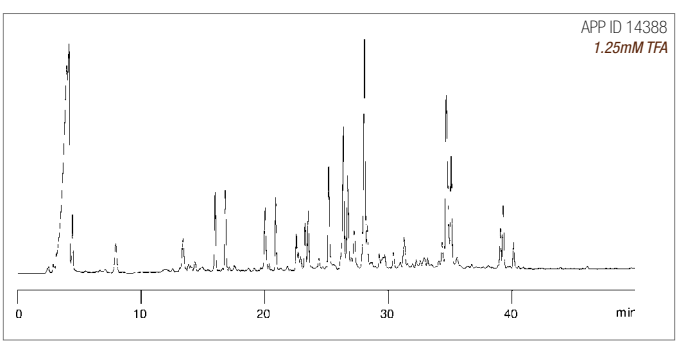


FIGURE 9
Buffer Concentration Effect on Resolution









CONDITIONS

FIGURE 8
Effect of Modifiers on Selectivity

APP ID: 14389 14390 14391
Columns: Jupiter 4u Proteo 90Å
Dimensions: 250 x 4.6mm
Order No.: 00G-4396-E0
Mobile Phase: A) 5mM modifier in Water
B) 5mM modifer in Acetonitrile
(see chromatograms for modifiers)
Gradient: A/B (95:5) for 5 min, then to A/B (60:40) in 55 minutes
Flow Rate: 1mL/min
Temperature: 22°C
Detection: UV @ 210nm
Sample: Myoglobin Tryptic Digest

FIGURE 9
Buffer Concentration Comparison

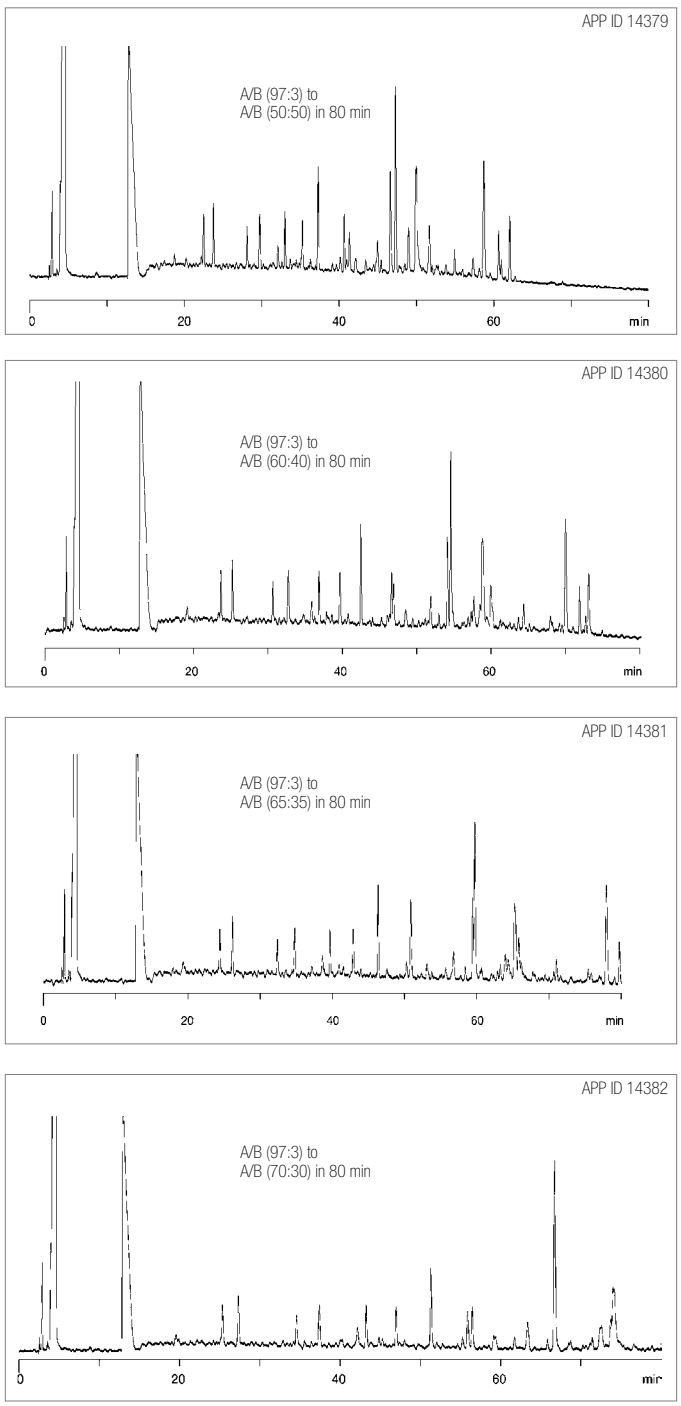
APP ID: 14385-14388
Columns: Jupiter 4µ Proteo 90Å
Dimensions: 250 x 4.6mm
Order No.: 00G-4396-E0
Mobile Phase: A) TFA in Water
B) TFA in Acetonitrile
(see chromatograms for TFA concentrations)
Gradient: A/B (95:5) for 5 min, then to A/B (60:40) in 55 minutes
Flow Rate: 1mL/min
Temperature: 22°C
Detection: UV @ 210nm
Sample: Myoglobin Tryptic Digest

FIGURE 10
Gradient Optimization

APP ID: 14379-14382
Columns: Jupiter 4u Proteo 90Å
Dimensions: 250 x 4.6mm
Order No.: 00G-4396-E0
Mobile Phase: A) 0.012% TFA in Water
B) 0.01% TFA
in Acetonitrile
Gradient: A/B (97:3) for 10 min, then see chromatogram for gradient profile
Flow Rate: 1mL/min
Temperature: 22°C
Detection: UV @ 210nm
Sample: β-Lactoglobulin Tryptic Digest

RESOLVE PEPTIDE & INSULIN VARIANTS

FIGURE 10
Retention Optimization By Gradient Profile Manipulation



Jupiter Proteo can be used to resolve peptides of MW ≤10,000 Da, and often are able to separate peptides of only 1-2 amino acid difference. Figure 11 compares the resolution of five peptide standards with amino acid sequences that differ in hydrophobicity by one methyl group each. Comparing the differences with respect to efficiency, selectivity, and resolution allows us to monitor the overall column performance; Jupiter Proteo fully resolves each peptide. Sharper peaks with greater resolution are obtained with Jupiter Proteo as compared to the competition. This is also illustrated in the separation of insulin and its degradation and deamination products *(FIGURE 12)*.

FIGURE 11
Comparison of Methylene Selectivity

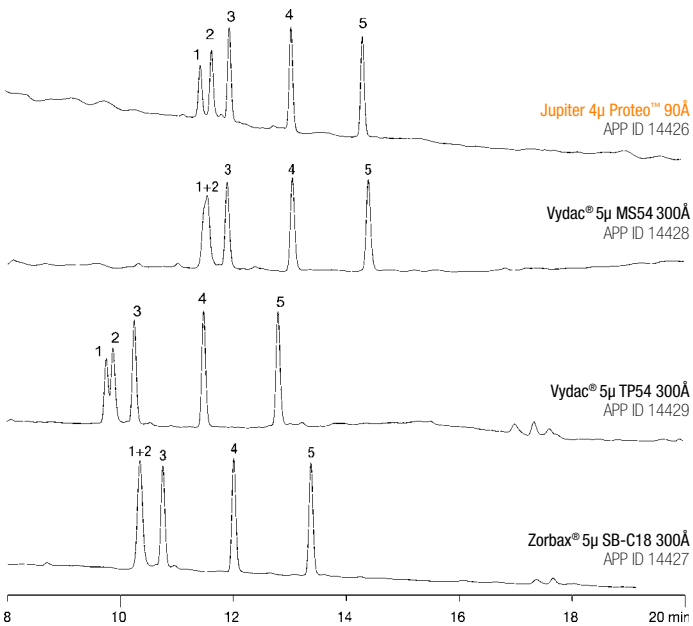


FIGURE 12
Insulin, Its Degradation and Deamination Products

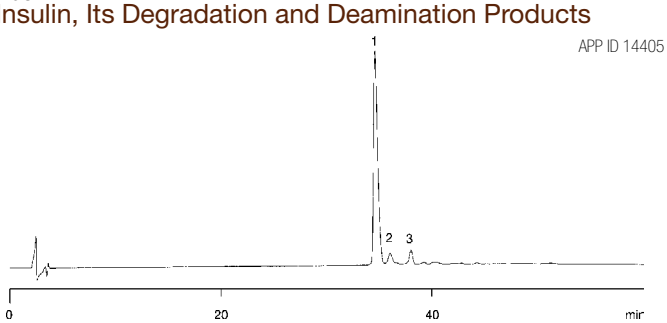


FIGURE 11
Comparison of Methylene Selectivity

APP ID: 14426, 14427, 14428, 14429
Columns: Jupiter 4µ Proteo 90Å
Vydac 5µ MS54 300Å
Vydac 5µ TP54 300Å
Zorbax 5µ SB-C18 300Å
Dimensions: 250 x 4.6mm
Mobile Phase: A) 0.1% TFA
B) 0.085% TFA in Acetonitrile
Gradient: A/B (95:5) to
A/B (55:45) in 20 minutes
Flow Rate: 1mL/min
Temperature: 22°C
Detection: UV @ 214nm
Sample: 1. NH_2-Arg-Gly-Gly-Ala-Gly-Gly-Leu-Gly-Leu-Gly-Lys-Amide
2. Ac-Arg-Gly-Gly-Gly-Gly-Gly-Leu-Gly-Leu-Gly-Lys-Amide
3. Ac-Arg-Gly-Ala-Gly-Gly-Gly-Leu-Gly-Leu-Gly-Lys-Amide
4. Ac-Arg-Gly-Val-Gly-Gly-Gly-Leu-Gly-Leu-Gly-Lys-Amide
5. Ac-Arg-Gly-Val-Val-Gly-Gly-Leu-Gly-Leu-Gly-Lys-Amide

FIGURE 12
Insulin, Its Degradation and Deamination Products

APP ID: 14405
Column: Jupiter 4µ Proteo 90Å
Dimension: 250 x 4.6mm
Order No: 00G-4396-E0
Mobile Phase: A) 0.012% TFA in Water
B) 0.01% TFA in Acetonitrile
Gradient: A/B (85:15) to A/B (70:30) in 45 min
Flow Rate: 1mL/min
Temperature: 40°C
Detection: UV @ 210nm
Sample: 1. Insulin
2. Insulin Deamination Product
3. Insulin Degradation Product

JUPITER300™ - A COLUMN FOR INTACT PROTEINS AND OLIGONUCLEOTIDES

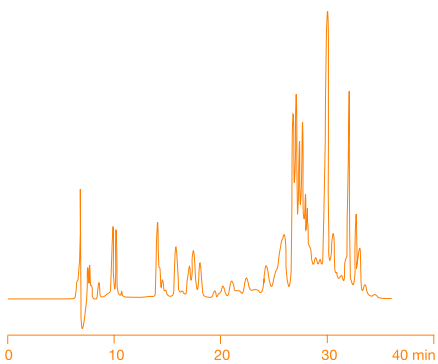
Jupiter300™ HPLC columns have proved their performance to biochromatographers world-wide. Jupiter 300's reliability result from:

- Super-smooth, high-mechanical-strength silica that reduces fine formation during the packing process and ensures highly efficient columns with longer column life.
- Dense bonded phase surface coverage for low non-specific adsorption of proteins, producing high yields
- A wide operating pH range from 1.5 to 10 allows native proteins to maintain bioactivity during the run and permit high pH washes for easy column regeneration.
- Low phase bleed and exceptional performance at low buffer concentrations (0.01% TFA) provides great LC/MS results
- 5, 10 and 15µ particles facilitate the quick scale-up to preparative/process purifications

FIGURE 13
Wheat Protein Extract*

Column: 5µ C18, 300Å, 250 x 4.6mm
"Previously, we were working with a Vydac #218TP54 reversed phase column. However, we became dissatisfied with the results obtained with the Vydac column due to poor reproducibility as well as poor resolution. We purchased the Jupiter300 C18 300A column a few months ago and have been quite impressed with its performance. The Jupiter300 column provides better separation of the proteins. As for reproducibility, the control profiles have not changed since day one of its use."

Jupiter300™ APP ID 8703



Vydac® APP ID 7005

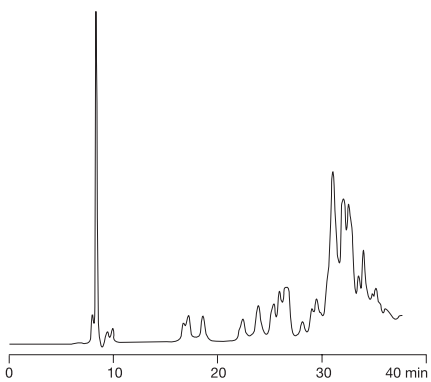
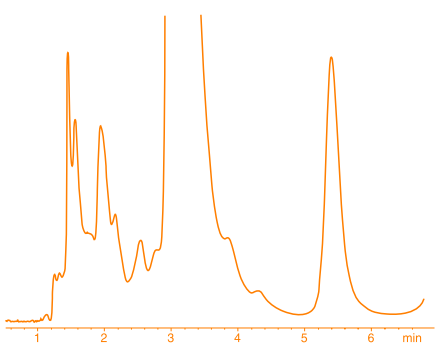


FIGURE 14
Protoporphyrins*

Column: 10µ C4, 300Å, 150 x 4.6mm
"In comparing Phenomenex's Jupiter300 column with Vydac C4, I found a significant improvement in peak shape and symmetry. This was true not only for small peaks, but also for peaks 30 times larger as well."

Jupiter300™ APP ID 9034



Vydac® APP ID 9035

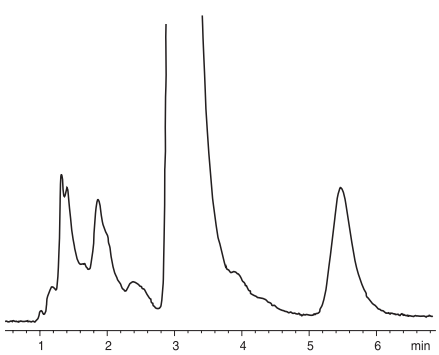
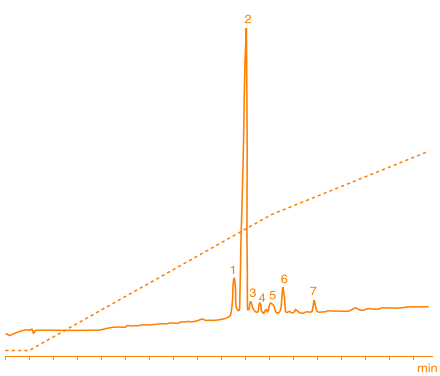


FIGURE 15
13mer Synthetic Peptide*

Column: 5µ C18, 300Å, 150 x 4.6mm
"As a Core Facility we synthesize a large number of peptides. Since their introduction, the Jupiter300 columns from Phenomenex have become our first choice for use in purification, as they consistently give better resolution than other columns in their class."

Jupiter300™ APP ID 9032



Vydac® APP ID 9033

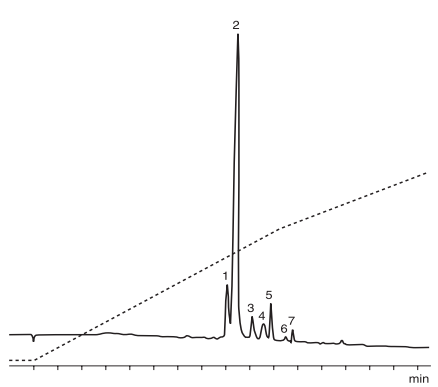


FIGURE 16
Recombinant Proteins*

Column: 5µ C4 300Å, 250 x 4.6mm
"In comparison to another C4 column for the analysis of a recombinant protein, the Jupiter was much more rugged: typically hundreds of injections and even with storage in 0.1% TFA."

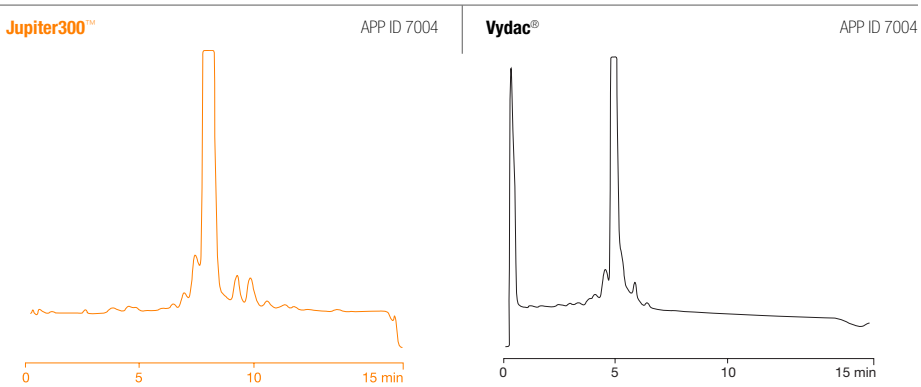
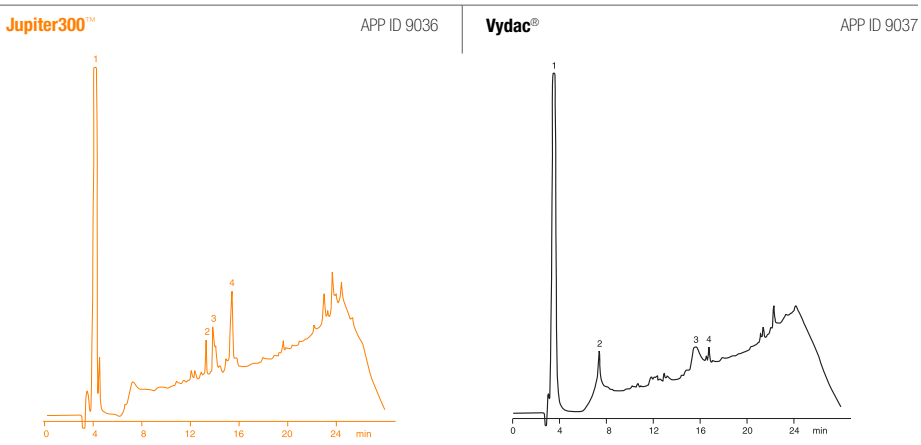


FIGURE 17
HAS*

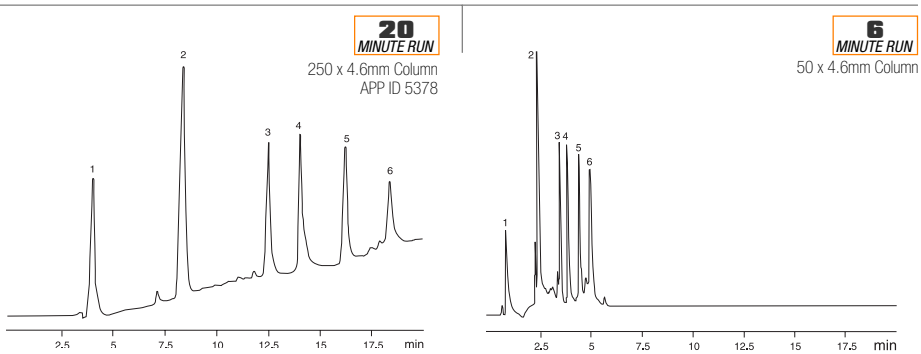
Column: 5µ C18, 300Å, 250 x 4.6mm
"I ran the same sample on a Jupiter™ column and a Vydac column. The Vydac column I used for this comparison is actually newer; however, the Jupiter™ column resolved better and showed much improvement over peak shape. It almost looks like two different samples."



REDUCE ANALYSIS TIME BY 70%

FIGURE 18
Protein Separation on Jupiter300™ 300Å C4

For large proteins, column length has little effect on retention. Using a 50 x 4.6mm column a 70% reduction in analysis time can be achieved over a 250 x 4.6mm column. Solvent consumption is also reduced so results are achieved not only faster but also at a lower cost.



CONDITIONS

FIGURE 13,14, 15, 16, 17
**DATA ABOVE SUPPLIED BY CUSTOMERS. CONDITIONS ARE PROPRIETARY FOR BOTH COLUMNS. MAY NOT BE REPRESENTATIVE OF ALL APPLICATIONS.*

FIGURE 18
Protein Separation of Jupiter C4 300Å
Conditions for 250 x 4.6 mm Column

APP ID:	5378
Columns:	Jupiter300 5µ C4 300Å
Order No.:	00G-4167-E0
Mobile Phase:	A)0.1% TFA in Water B)0.1% TFA in Acetonitrile
Gradient:	A/B (95:5) to A/B (74:26) in 7 min, then to A/B (66:a34) in 3 min, then to A/B (46:54) in 10 min
Flow Rate:	1mL/min
Detection:	UV @ 220nm

Conditions for 50 x 4.6mm column

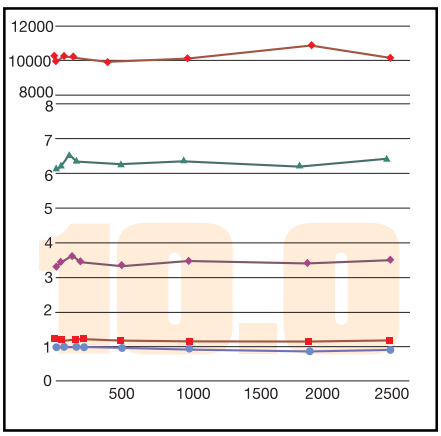
Dimensions:	50 x 4.6mm
Order No.:	00B-4167-E0
Mobile Phase:	A)0.1% TFA in Water B)0.1% TFA in Acetonitrile
Gradient:	A/B (100:0) to A/B (80:20) in 1 min, then to A/B (65:35) in 1.5 min, then to A/B (53.5:46.5) in 1.5 min, then hold for 2 min
Flow Rate:	1mL/min
Detection:	UV @ 220nm

Sample: 1. Alkaline Phosphatase
2. Cyanocobalamin
3. RNase
4. Insulin
5. Transferrin
6. Trypsin Inhibitor

STABLE FROM pH 1.5 TO 10

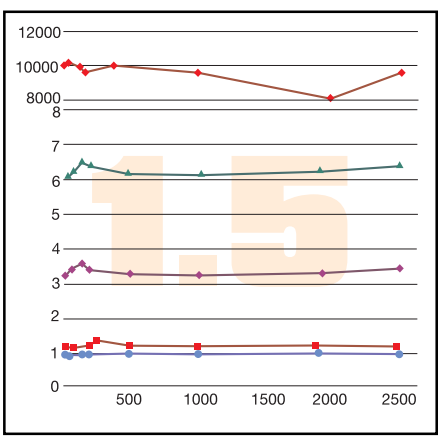
A wide pH range means more than just longer column life, it means method development opportunities. Jupiter300 is stable from pH 1.5 to 10 for over 2500 hours *(FIGURE 19)* and shows good peak shape down to 0.01% TFA *(FIGURE 21)*. A wide pH range allows for manipulations of the mobile phase pH for improvement of selectivity *(FIGURE 20)*. Changing the mobile phase pH can also provide confirmation of purity by revealing additional evidence of impurities. Performing a high pH wash (pH 9 -10) easily removes contaminates and regenerates column performance.

FIGURE 19
Stability of Jupiter300 C18 at pH 1.5 and 10



Hours of Exposure

Test Conditions: Column flushed in 20mM Na_2HPO_4 (pH 10.0) in Water/ Acetonitrile (50:50)



Hours of Exposure

Test Conditions: Column flushed in 0.1% TFA (pH 1.5) in Water/ Acetonitrile (50:50)

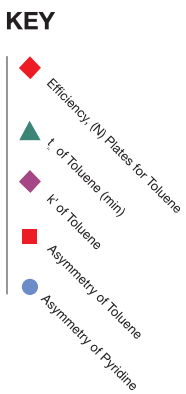


FIGURE 20
Effect of pH on Bradykinin Separation

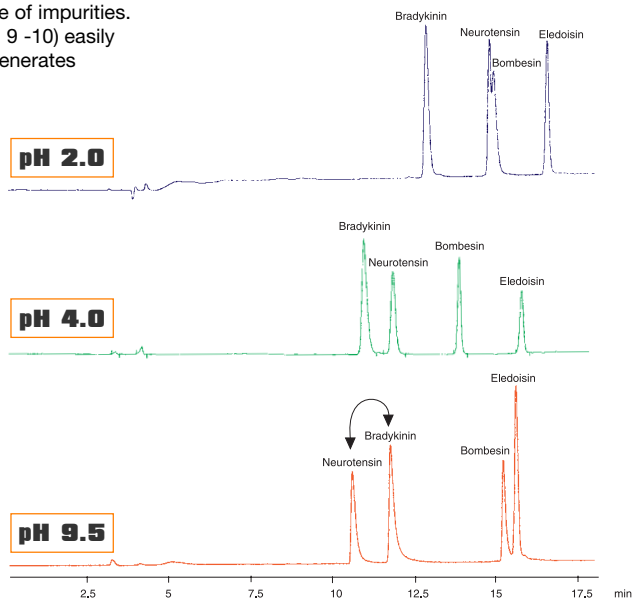
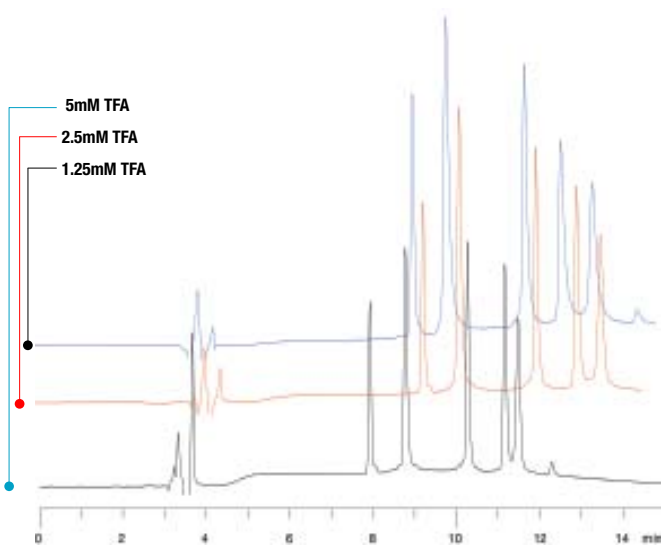


FIGURE 21
Effect of Buffer Concentration on Protein Separation



CONDITIONS

FIGURE 20
Effect of pH on Bradykinin Separation

APP ID: 8724
Column: Jupiter300 5µ C1 300Å
Dimensions: 250 x 4.6mm
Order No.: 00G-4053-E0
Flow Rate: 1.0 mL/min
Detection: UV @ 215nm
Sample: 1. Bradykinin
2. Bombesin
3. Neurotension
4. Eledoisin

FIGURE 21
Effect of Buffer Concentration on Separation

APP ID: 14185-14187
Column: Jupiter300 5µ C4 300Å
Dimensions: 250 x 4.6mm
Order No.: 00G-4167-E0
Mobile Phase: A) Water with TFA (B) Acetonitrile with TFA (see chromatograms for TFA concentration)
Gradient Profile: A/B (75:25) to A/B (5:95) in 20 min
Flow Rate: 1.0 mL/min
Temperature: 35°C
Detection: UV @ 214nm
Sample: 1. Insulin
2. Trypsinogen
3. Lactalbumin
4. Myoglobin
5. Carbonic anhydrase

QUICKLY SCALE-UP TO PROCESS PURIFICATIONS

Jupiter300 10 and 15µ medias are manufactured with the same bonding and base silica as 5µ media - they are not "prep-variants". This ensures quick direct scale up from analytical methods to production purifications. The benefits are:

- High mechanical-strength silica for better packing
- Large loading capacity for higher sample recovery *(FIGURE 23)*
- Resistance to silica particle sheering and fine formation at high packing pressures and flow rates
- Easy column cleaning and regeneration as a result of 1.5 to 10 pH stability

The strength of Jupiter silica is demonstrated by examining its resistance to sheering after packing in a Dynamic Axial Compression (DAC) column. Jupiter silica maintains its smooth uniform structure, while other silicas show fines of crushed silica particles *(FIGURE 22)*. With a low percentage of silica fines the column bed is more stable, backpressure is lower, and fouling is reduced. This allows Jupiter to maintain performance for longer periods.

Packed columns up to 100mm ID as well bulk media are available. Custom columns larger than 100mm ID are also available upon request.

FIGURE 22
High Mechanical Strength Silica Resists Sheering

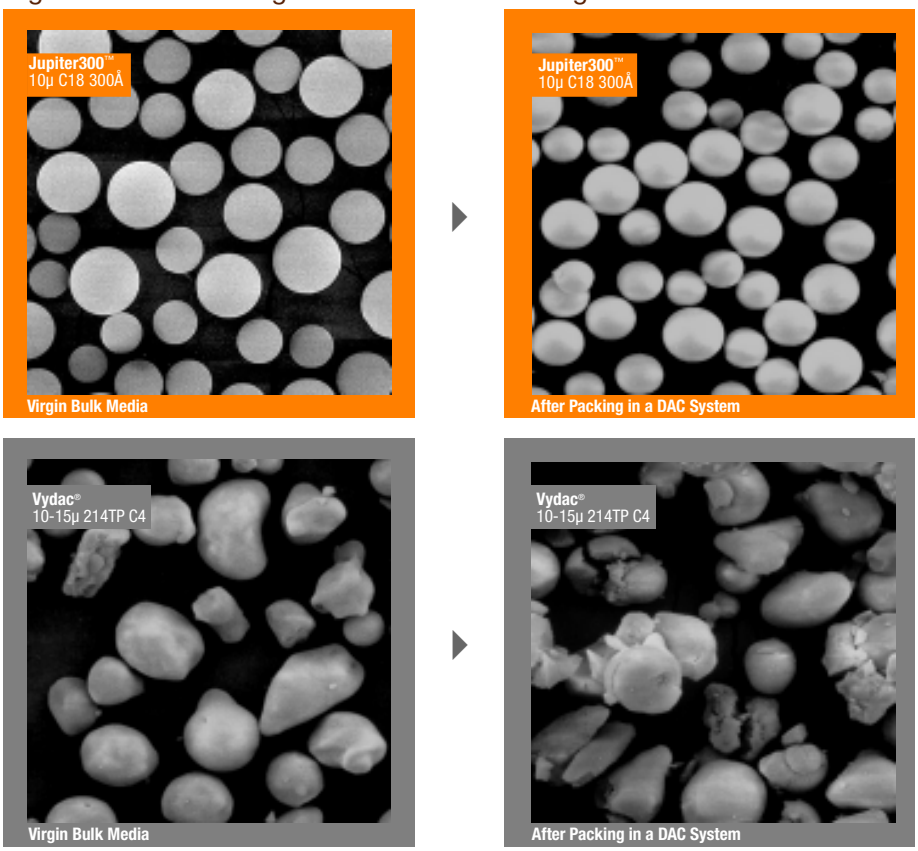
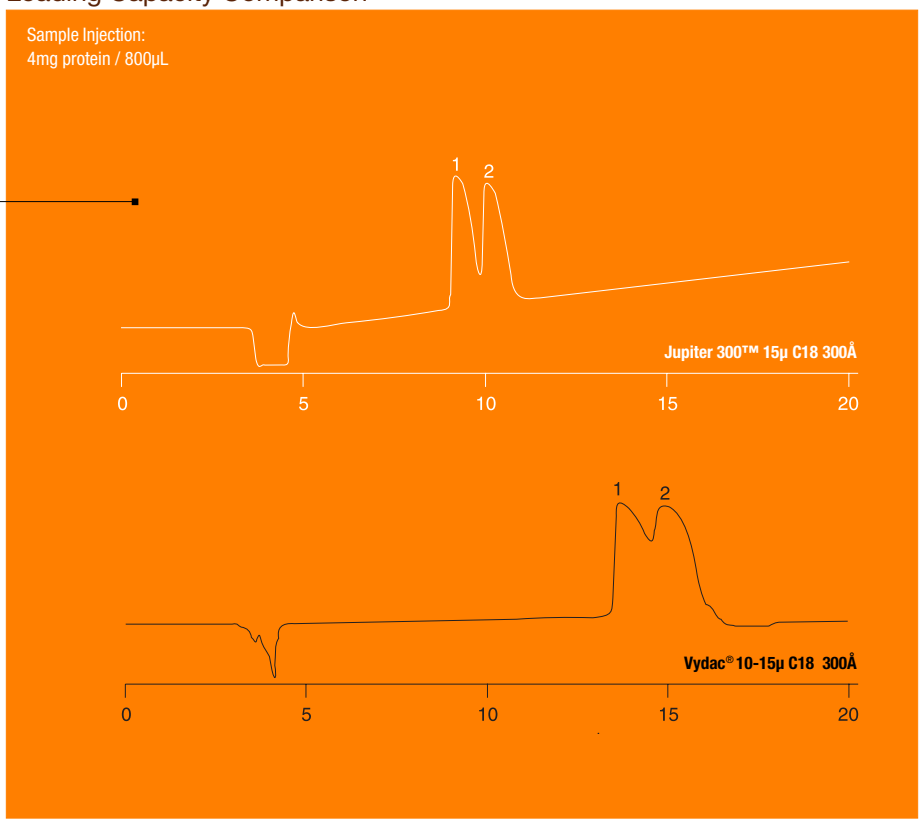


FIGURE 23
Loading Capacity Comparison



Sample Recovery as a function of peak area

Peak Area (mAU/s)

	Equine Cytochrome C	Bovine Cytochrome C
Jupiter™	**89420**	**89253**
Vydac®	44412	58078

CONDITIONS

FIGURE 23
Loading Capacity Comparison
Conditions for all columns:

Dimensions: 250 x 4.6mm
Mobile Phase: A: 0.1% TFA in Water,
B: 0.1% TFA in Acetonitrile
Gradient: A/B(75:25) to A/B(35:65) in 20min
Flow Rate: 1 mL/min
Detection: UV @ 280nm
Sample: 4mg protein/800µL of
1. Equine Cytochrome C
2. Bovine Cytochrome C

TECHNICAL DATA

Jupiter™ Proteo and Jupiter300 packings are monitored and tested for reproducibility. Tight control is maintained over silica particle consistency, size and smoothness. Over 25 individual tests are performed on every batch of Jupiter material to ensure consistent and reproducible chromatography *(FIGURES 25 AND 26)* - each test result is reported in the Material Validations Document (MVD) that accompanies every 4µ Jupiter Proteo and 5µ Jupiter300 analytical column.

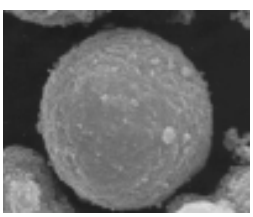
Material Characteristics

	Jupiter Proteo™	Jupiter300™
Particle Size	4, 10µ	5, 10, 15µ
Bonded Phase(s)	C12 with proprietary endcapping	C4, C5, C18
End-capping	Yes - (proprietary, non-polar)	Yes(non-polar)
Pore Size	90Å	300Å
pH Stability	1.5 to 10	1.5 to 10
Surface Area	475m^2/g	170m^2/g
Application	Tryptic digest and peptides	Intact Proteins
Sample Molecular Weight Range	≤10,000 Da	≥10,000 Da

FIGURE 24
Silica comparison
JUPITER™ 5µ C18 300Å

12,000X

VYDAC® 5µ C18 300Å



JUPITER™ PROTEO 4µ 90Å

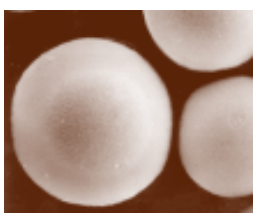


FIGURE 25
Batch-to-Batch Reproducibility of Jupiter™ 4µ Proteo 90Å

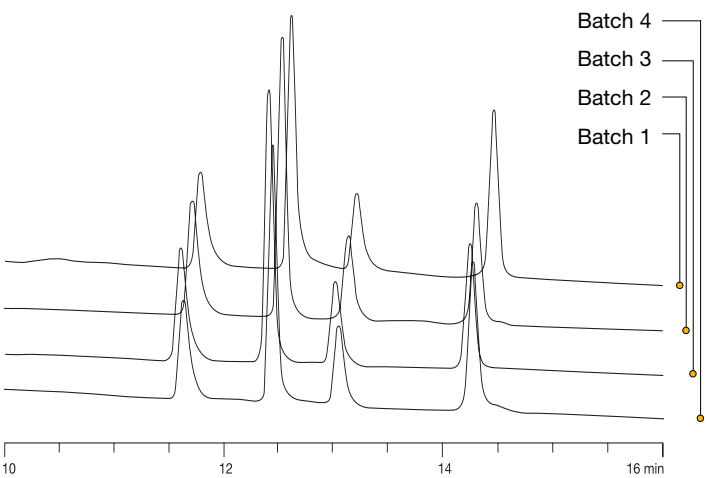
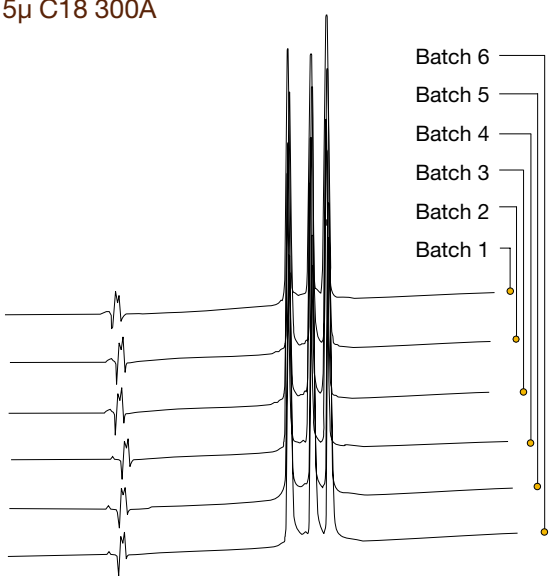


FIGURE 26
Batch-to-Batch Reproducibility of Jupiter300™ 5µ C18 300Å



CONDITIONS

FIGURE 25
Batch-to-Batch Reproducibility of Jupiter 4µ Proteo 90Å

Column: Jupiter 4µ Proteo 90Å
Dimensions: 250 x 4.6mm
Order No: 00G-4396-E0
Mobile Phase: A) 0.1% TFA in Water
B) 0.08% TFA in Acetonitrile
Gradient: A/B (95:5) to A/B (5:95) in 20min 1.0mL/min
Flow Rate: 1.0mL/min
Detection: UV @ 210nm
Sample: 1. Bradykinin (300µg/mL)
2. Angiotensin III (100µg/mL)
3. Neurotensin (300µg/mL)
4. Eledoisin (250µg/mL)

FIGURE 26
Batch-to-Batch Reproducibility of Jupiter300 5µ C18 300Å

Column: Jupiter 5µ C18 300Å
Dimensions: 250 x 4.6mm
Order No: 00G-4053-E0
Mobile Phase: A) 0.1% TFA in Water
B) 0.1% TFA in Acetonitrile
Gradient: A/B (75:25) to A/B (45:55) in 15min (2% B/min)
Flow Rate: 1.0 mL/min
Detection: UV @ 220nm
Sample: 1. Equine Cytochrome c
2. Bovine Cytochrome c
3. Canine Cytochrome c

JUPITER300™ / JUPITER™ PROTEO
ORDERING INFORMATION

Capillary Columns

4µ & 5µ Columns (mm)

Phases	50 x 0.30	150 x 0.30	250 x 0.30	50 x 0.50	150 x 0.50	250 x 0.50
5µ C4 300Å	00B-4167-AC	00F-4167-AC	00G-4167-AC	00B-4167-AF	00F-4167-AF	00G-4167-AF
5µ C18 300Å	00B-4053-AC	00F-4053-AC	00G-4053-AC	00B-4053-AF	00F-4053-AF	00G-4053-AF
4µ Proteo 90Å	00B-4396-AC	00F-4396-AC	00G-4396-AC	00B-4396-AF	00F-4396-AF	00G-4396-AF

SecurityGuard™Cartridges require universal holder Order No.: KJO-4282

4µ & 5µ Capillary Columns (mm) (Cont.)

Phases	50 x 0.70	150 x 0.70	250 x 0.70
5µ C4 300Å	00B-4167-AG	00F-4167-AG	00G-4167-AG
5µ C18 300Å	00B-4053-AG	00F-4053-AG	00G-4053-AG
4µ Proteo 90Å	00B-4396-AG	00F-4396-AG	00G-4396-AG

4µ & 5µ Microbore and Minibore Columns (mm) — SecurityGuard™ Cartridges

Phases	150 x 1.0	50 x 2.0	150 x 2.0	250 x 2.0	4 x 2.0mm	4 x 3.0mm
5u C4 300Å	00F-4167-A0	00B-4167-B0	00F-4167-B0	00G-4167-B0	AJ0-4329	AJ0-4330
5µ C5 300Å	00F-4052-A0	00B-4052-B0	00F-4052-B0	00G-4052-B0	AJ0-4326	AJ0-4327
5µ C18 300Å	00F-4053-A0	00B-4053-B0	00F-4053-B0	00G-4053-B0	AJ0-4320	AJ0-4321
4µ Proteo 90Å	00F-4396-A0	00B-4396-B0	00F-4396-B0	00G-4396-B0	AJ0-6073	AJ0-6074
					for ID: 2.0-3.0mm	3.2-8.0mm

Analytical and Preparative Columns

4µ & 5µ Columns (mm) — SecurityGuard™Cartridges

Phases	50 x 4.6	150 x 4.6	250 x 4.6	250 x 10	250 x 15	250 x 21.2	250 x 30	4 x 2.0mm	4 x 3.0mm
5u C4 300Å	00B-4167-E0	00F-4167-E0	00G-4167-E0	00G-4167-N0	00G-4167-AK	00G-4167-P0	00G-4167-U0	AJ0-4329	AJ0-4330
5µ C5 300Å	00B-4052-E0	00F-4052-E0	00G-4052-E0	00G-4052-N0	00G-4052-AK	00G-4052-P0	00G-4052-U0	AJ0-4326	AJ0-4327
5µ C18 300Å	00B-4053-E0	00F-4053-E0	00G-4053-E0	00G-4053-N0	00G-4053-AK	00G-4053-P0	00G-4053-U0	AJ0-4320	AJ0-4321
4µ Proteo 90Å	00B-4396-E0	00F-4396-E0	00G-4396-E0	00G-4396-N0	00G-4396-AK	00G-4396-P0	00G-4396-U0	AJ0-6073	AJ0-6074
								for ID: 2.0-3.0mm	3.2-8.0mm

10µ Columns (mm) — SecurityGuard™Cartridges

Phases	250 x 4.6	250 x 10	250 x 15	250 x 21.2	250 x 30	250 x 50	4 x 2.0mm	4 x 3.0mm
C4 300Å	00G-4168-E0	00G-4168-N0	00G-4168-AK	00G-4168-P0	00G-4168-U0	00G-4168-V0	AJ0-4329	AJ0-4330
C5 300Å	00G-4054-E0	00G-4054-N0	00G-4054-AK	00G-4054-P0	00G-4054-U0	00G-4054-V0	AJ0-4326	AJ0-4327
C18 300Å	00G-4055-E0	00G-4055-N0	00G-4055-AK	00G-4055-P0	00G-4055-U0	00G-4055-V0	AJ0-4320	AJ0-4321
Proteo 90Å	00G-4397-E0	00G-4397-N0	00G-4397-AK	00G-4397-P0	00G-4397-U0	00G-4397-V0	AJ0-6073	AJ0-6074
							for ID: 2.0-3.0mm	3.2-8.0mm

15µ Columns (mm) — SecurityGuard™Cartridges

Phases	250 x 4.6	250 x 10	250 x 15	250 x 21.2	250 x 30	250 x 50	250 x 100	4 x 2.0mm	4 x 3.0mm
C4 300Å	00G-4169-E0	00G-4169-N0	00G-4169-AK	00G-4169-P0	00G-4169-U0	00G-4169-V0	00G-4169-W0	AJ0-4329	AJ0-4330
C5 300Å	00G-4056-E0	00G-4056-N0	00G-4056-AK	00G-4056-P0	00G-4056-U0	00G-4056-V0	00G-4056-W0	AJ0-4326	AJ0-4327
C18 300Å	00G-4057-E0	00G-4057-N0	00G-4057-AK	00G-4057-P0	00G-4057-U0	00G-4057-V0	00G-4057-W0	AJ0-4320	AJ0-4321
								for ID: 2.0-3.0mm	3.2-8.0mm

Other Dimensions available upon request.

Bulk Packings

10µ

Phases	100g	1kg	5kg	10kg	50kg	100kg
C4 300Å	04G-4168	04K-4168	04L-4168	04M-4168	04N-4168	04P-4168
C5 300Å	04G-4054	04K-4054	04L-4054	04M-4054	04N-4054	04P-4054
C18 300Å	04G-4055	04K-4055	04L-4055	04M-4055	04N-4055	04P-4055
Proteo 90Å	04G-4397	04K-4397	04L-4397	04M-4397	04N-4397	04P-4397

15µ

Phases	100g	1kg	5kg	10kg	50kg	100kg
C4 300Å	04G-4169	04K-4169	04L-4169	04M-4169	04N-4169	04P-4169
C5 300Å	04G-4056	04K-4056	04L-4056	04M-4056	04N-4056	04P-4056
C18 300Å	04G-4057	04K-4057	04L-4057	04M-4057	04N-4057	04P-4057

Method Validation and Method Development Kits

Order No.	Description	Unit	Price
KH0-4155	Jupiter C4 Method Validation Kit (3 each of 250 x 4.6mm Columns from 3 Separate Batches)	3/pk	
KH0-4154	Jupiter C5 Method Validation Kit (3 each of 250 x 4.6mm Columns from 3 Separate Batches)	3/pk	
KH0-4153	Jupiter C18 Method Validation Kit (3 each of 250 x 4.6mm Columns from 3 Separate Batches)	3/pk	
KH0-3983	Jupiter Bioseparation Method Development Kit (1 each of 250 x 4.6mm 5µ C4, C5, C18)	3/pk	
KH0-7274	Jupiter Bioseparation Method Development Kit (1 each of 250 x 4.6mm 5µ C5, C18 & 4µ Proteo)	3/pk	

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FAX:	(310) 328-7768	(310) 328-7768	(310) 328-7768	01625-501796	06021-58830-11	09-4780952	1800 553 923