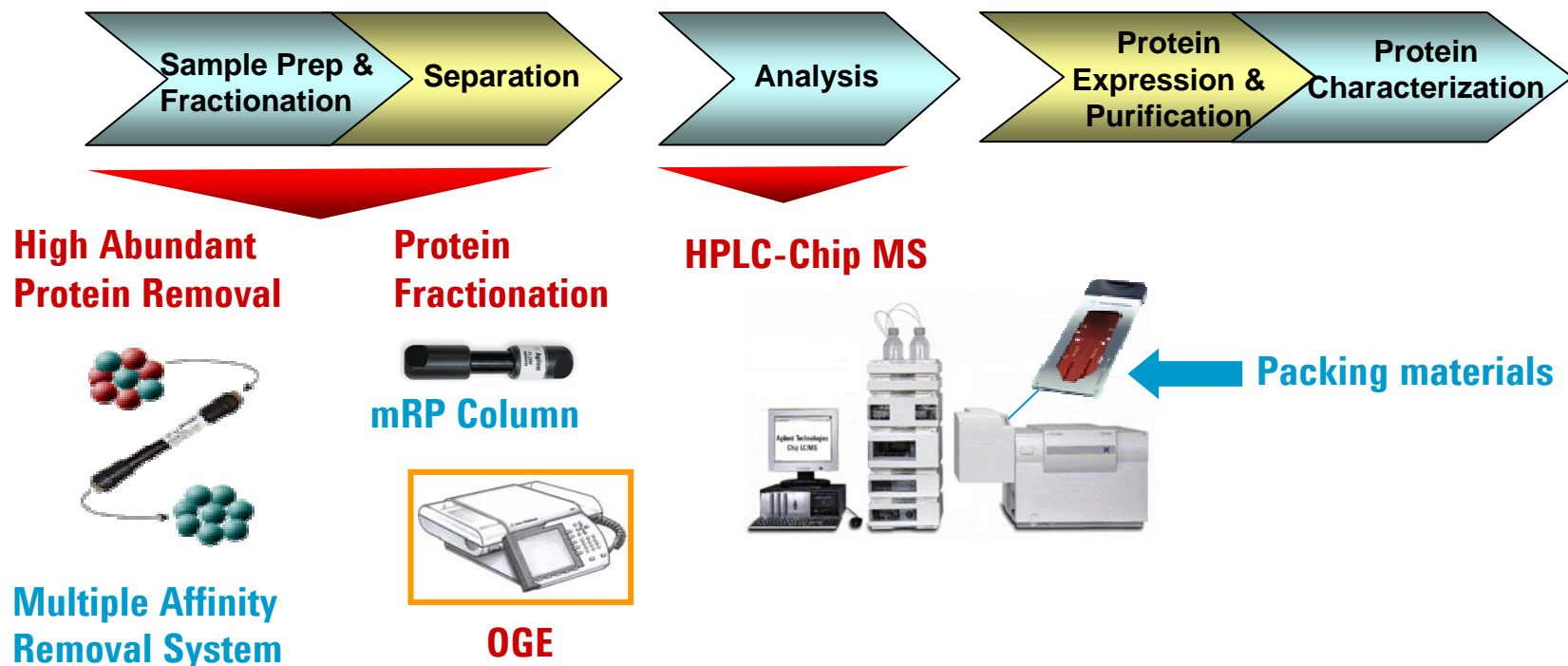


New Sample Preparation and Protein Fractionation Techniques



What is New in Protein Sample Preparation and Separation?



Focus:

- Recovery of sample (fewest number of steps, return of sample)
- Selectivity
- Reproducibility (run to run, lot to lot of product)
- Reliability and increased productivity



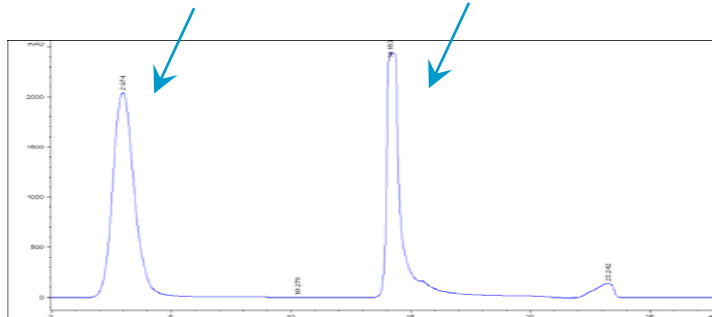
The Multiple Affinity Removal System

A polyclonal antibody based system to rapidly deplete multiple high abundant proteins in serum/plasma/CSF.

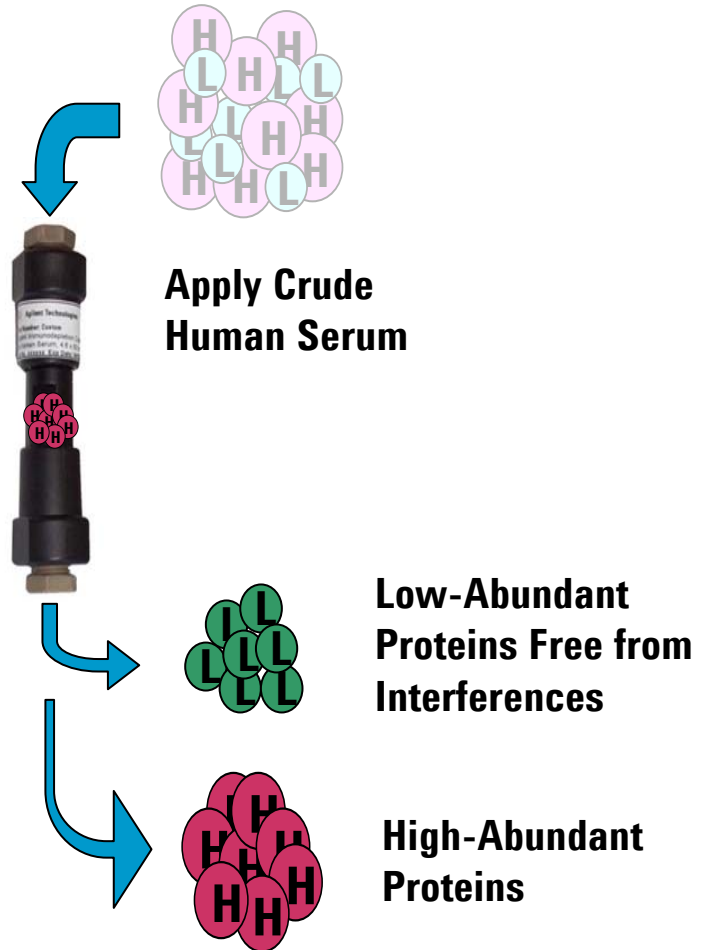
- ➡ Launched in August 2003
- ➡ Individual Ab Materials are mixed in selected percentages and packed into a column format
- ➡ Agilent continues to innovate and lead this market

Unbound Fraction (low abundant proteins)

Bound Fraction (high abundant proteins)



Total Run Time (30 min)



The Agilent Multiple Affinity Removal System

➤ Selectivity

Only native human plasma proteins are used as antigens. This ensures highest selectivity for epitopes in “real samples”. Our antibodies are so selective that species cross-reactivity is very low.

Our buffers are specifically formulated to minimize protein-protein interactions resulting in highest possible selectivity of binding (minimize any possible protein-protein interactions, such as with albumin)

➤ Reproducibility

Run to run:

- Coupling chemistry of antibodies to column beads is designed for longest possible lifetime of Antibodies resulting in excellent run to run reproducibility. Only native protein antigen is used for affinity purification resulting in reproducible antibody selection.
- Buffers for affinity purification of our polyclonal antibodies are designed to disruption unwanted protein-protein interactions (such as with albumin) resulting in reproducible epitope selection.

Lot to lot: Manufacturing processes have been engineered to provide excellent lot to lot reproducibility



The Agilent Multiple Affinity Removal System

➤ Ease of Use

LC column: Automated single pass, 2 buffer, 30 minute total run time to deplete 80 uL of human plasma/serum (4.6 x 100 mm column) at 98-99% efficiency. Larger column sizes available on request.

Spin tube: 2-step re-usable system, 10 minute total run time to deplete 15 uL of human serum/plasma

➤ Compatibility with Downstream Analysis

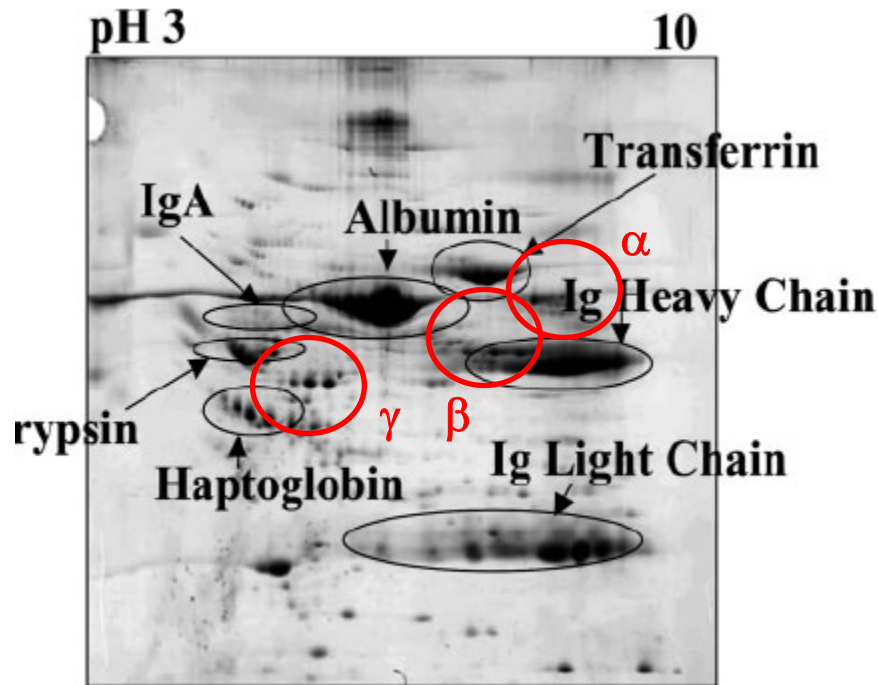
1D gel: Proteins elute in buffer system immediately ready for application for 1DGE

HPLC: Proteins can be simultaneously concentrated, desalted, and fractionated on our new mRP column

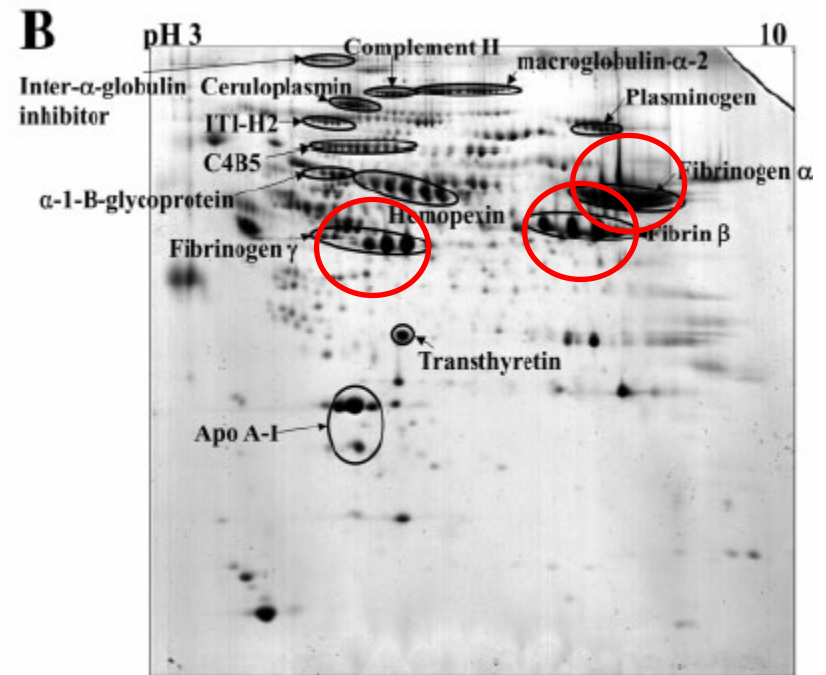
MS: There are no detergents present in our buffers



Why Multiple Affinity Removal System?



Plasma



Plasma after Top-6 Depletion

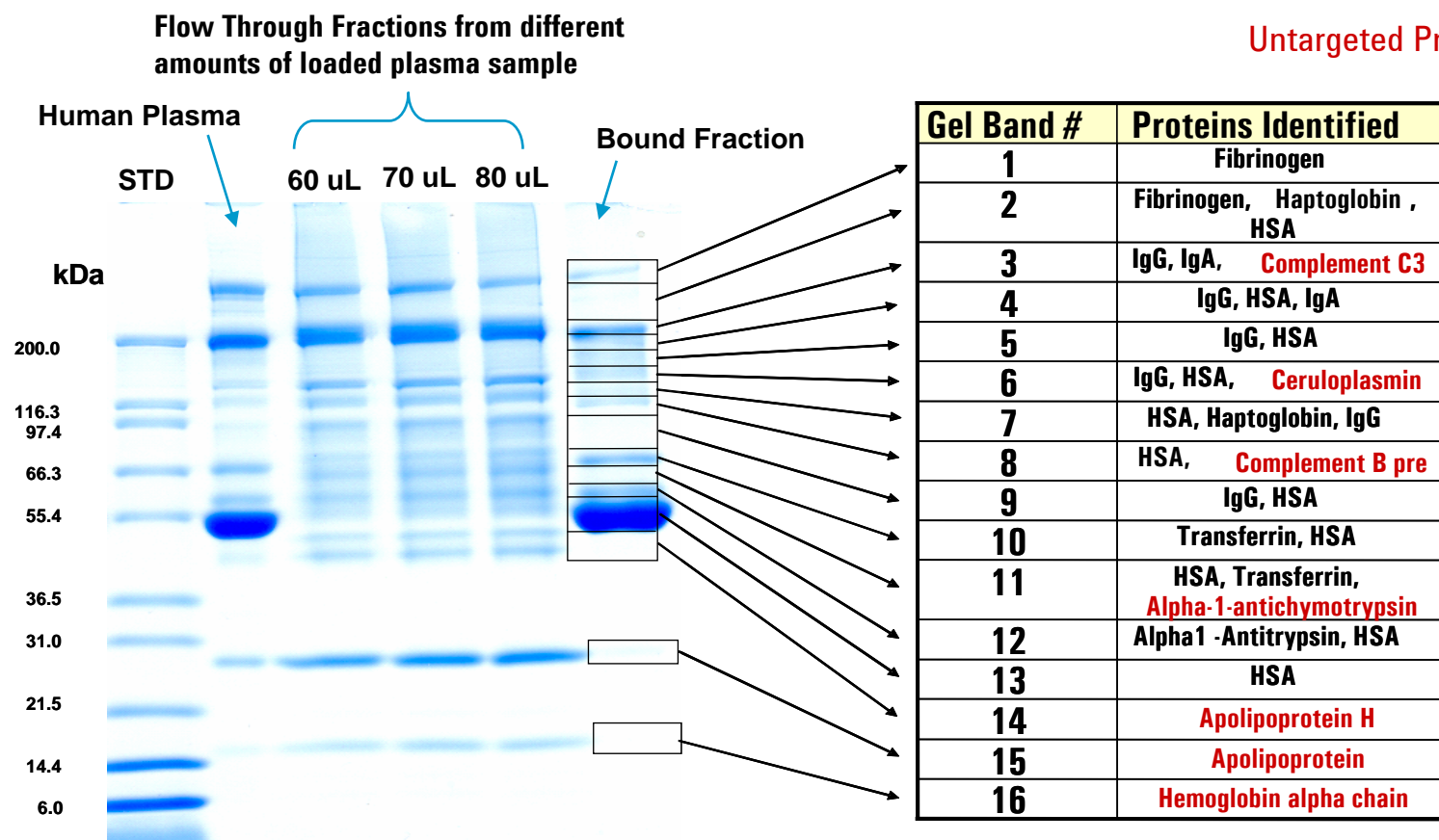
Data: Dr. Y.K. Paik

Agilent Multiple Affinity Removal System: Where Are We? & What is Next?



Selectivity of Plasma-7 Column

Proteins Identified in Bound Fraction by LC/MS/MS



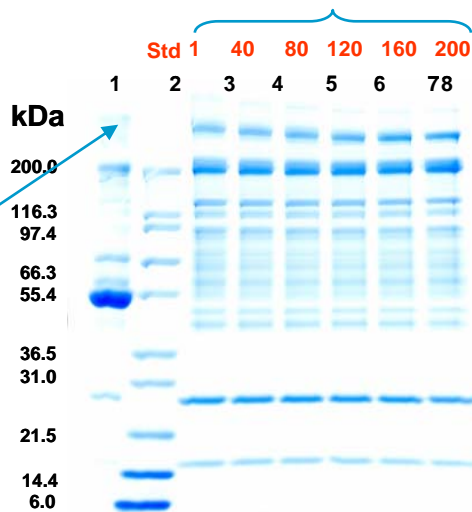
ELISA analysis indicate **99.4%** depletion of Fibrinogen from 60, 70 and 80 uL of a plasma load on a 4.6x100mm column

Reproducibility from Run to Run

Comparison of runs 40, 80, 120, 160, & 200

SDS-PAGE analysis of the flow-through fractions from multiple runs on a Human Plasma 7 column

Bound Fraction
(Bands excised for
confirmation of ID
by MS/MS)



- 1- Human Plasma
- 2- Mark12 Standards
- 3- Flow-through Fraction, Run 1
- 4- Flow-through Fraction, Run 40
- 5- Flow-through Fraction, Run 80
- 6- Flow-through Fraction, Run 120
- 7- Flow-through Fraction, Run 160
- 8- Flow-through Fraction, Run 200

10 µg of protein/well

4-20% SDSPAGE

**Column performs
reproducibly for 200 runs!**



mRP-C18 High-Recovery Protein Fractionation Column



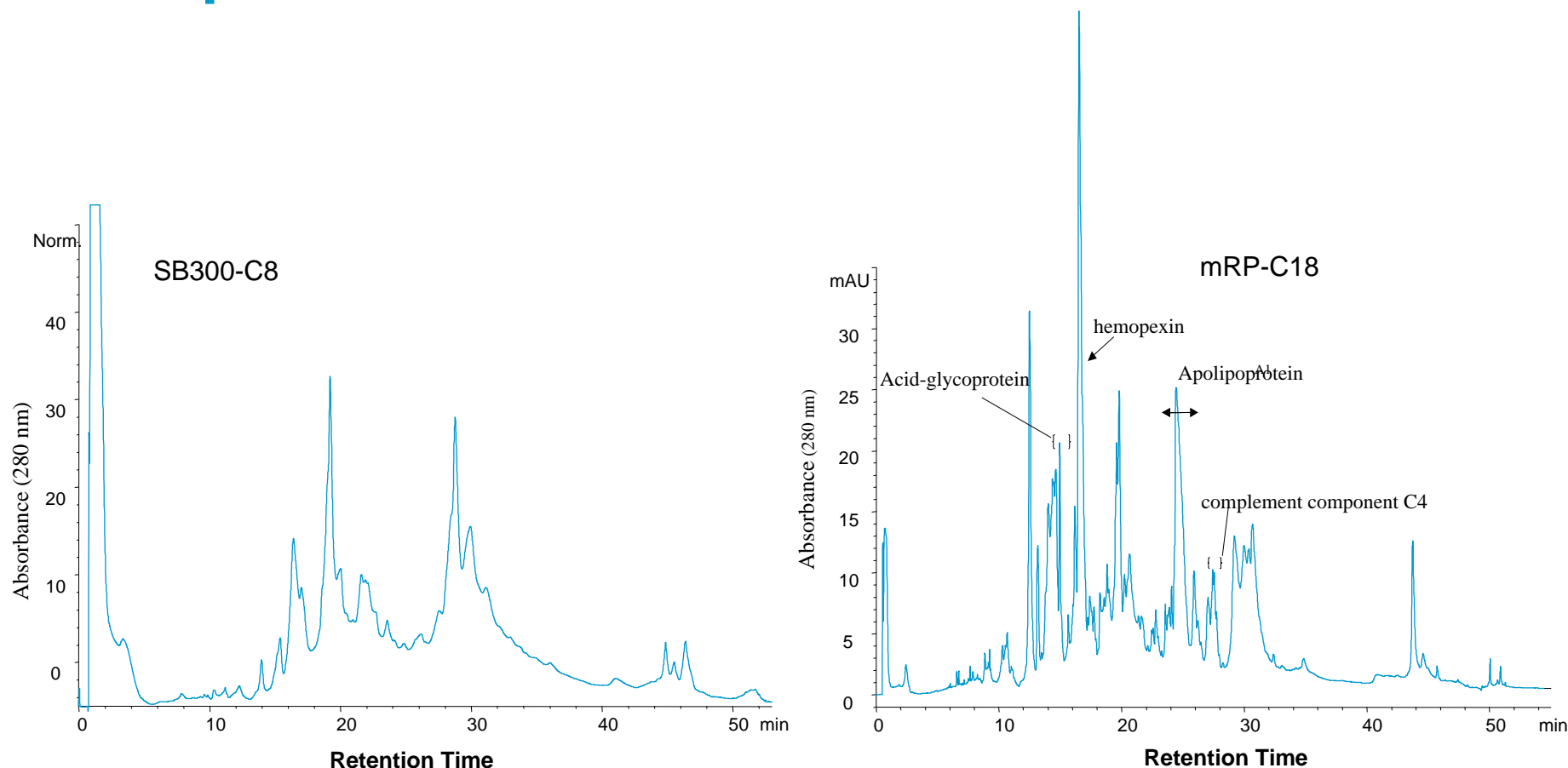
mRP (macroporous reverse-phase)

What is it? Reverse Phase column for protein separation and fractionation. The silica based particles and recommended LC methods have been optimized for:

- Highest recoveries of protein samples (95% - 99% of loaded sample)
- Highest resolution separations
- Reproducibility
- High sample loading capacity (3X higher than most standard RP columns)
- Lifetime



Comparison of mRP with Zorbax SB300-C8



Sample: 270ug flow-through (6M urea/5.0% AcOH) of immunodepleted human serum from Multiple Affinity Removal System column

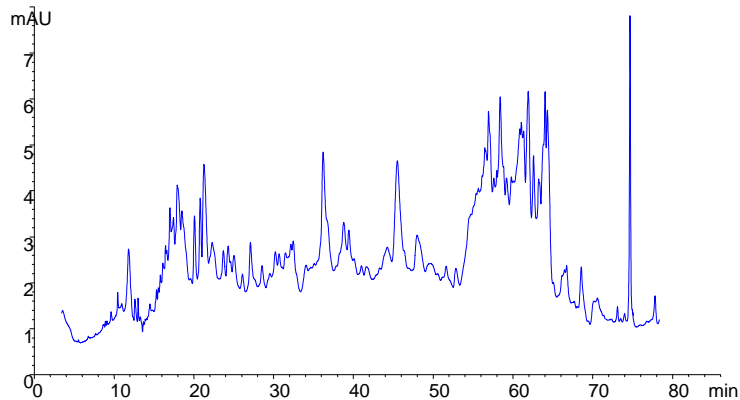
Columns: Panel A – Zorbax SB300-C18 (300 Å, 5.0µm), 4.6 mm x 50 mm i.d., SS; Panel B – mRP-C18 (macroporous, 5µm), 4.6 mm x 50 mm i.d., PEEK, 0.75mL/min., DAD 280nm

Mobile Phase & Conditions: A-0.1% TFA/water, B-0.08%TFA/ACN, Temp 80° C, gradient:5-30%B in 5min., 30-55%B in 33min., 55-100%B in 4min.

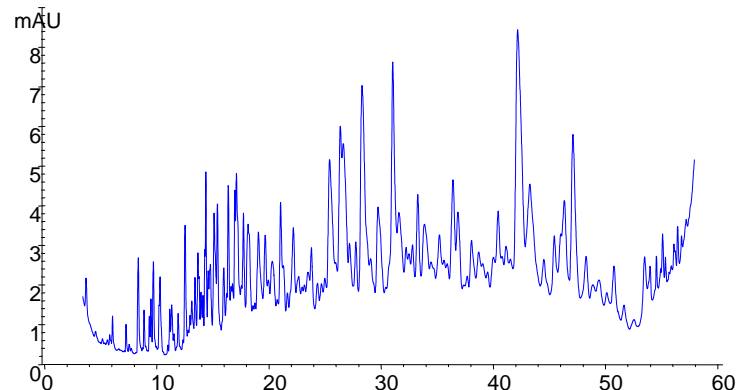
1D SDS PAGE: Collected 36 fractions (1.0 min. time slices) from immunodepleted human serum RP separation

Protein Fractionation on mRP

(4.6 x 50mm mRP-C18)

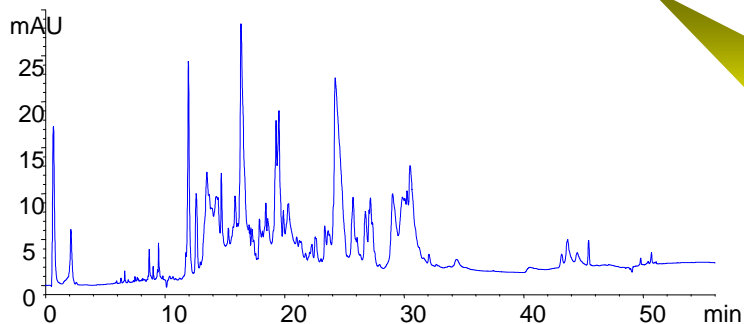


HeLa Membrane Prep

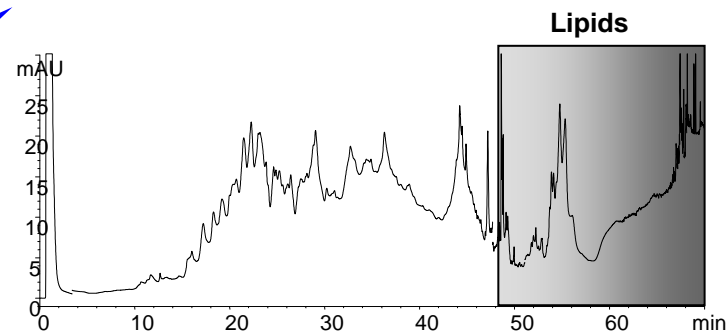


HeLa cell lysate (352ug)

*Highest
Recovery*



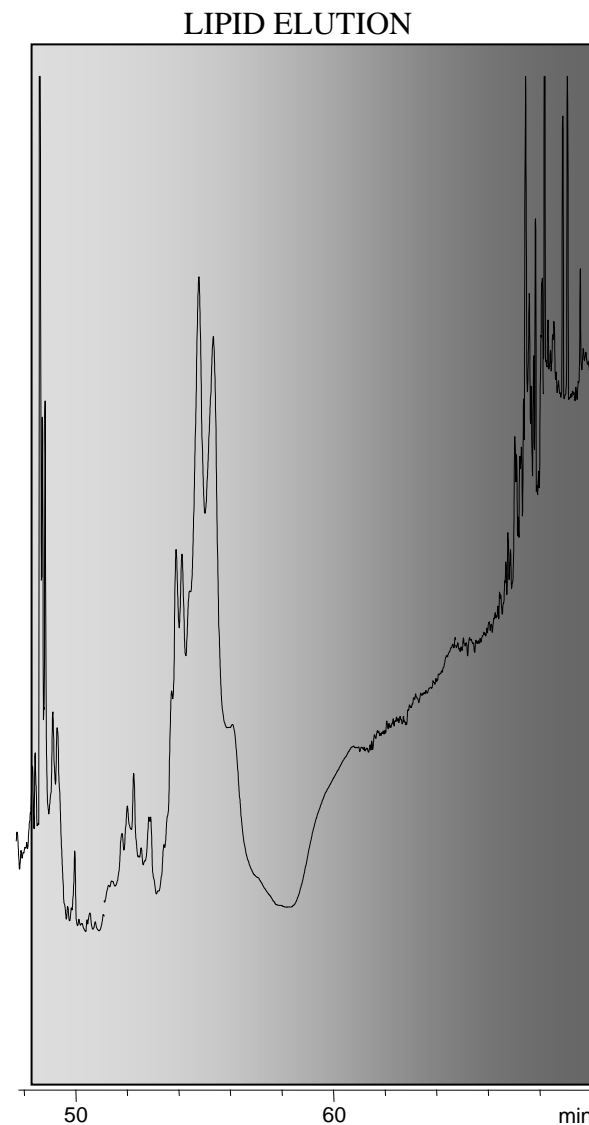
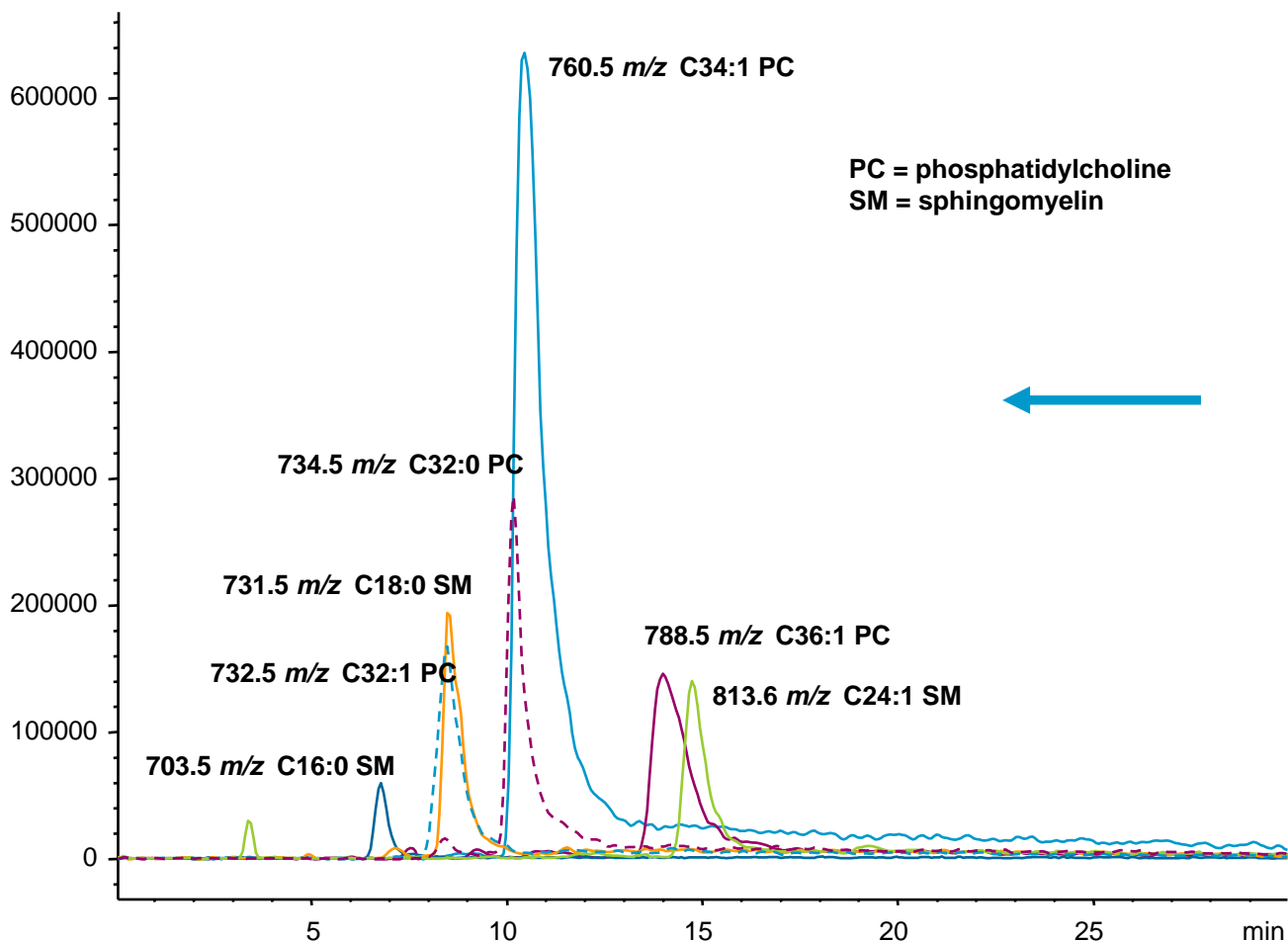
"Top-6" depleted human serum



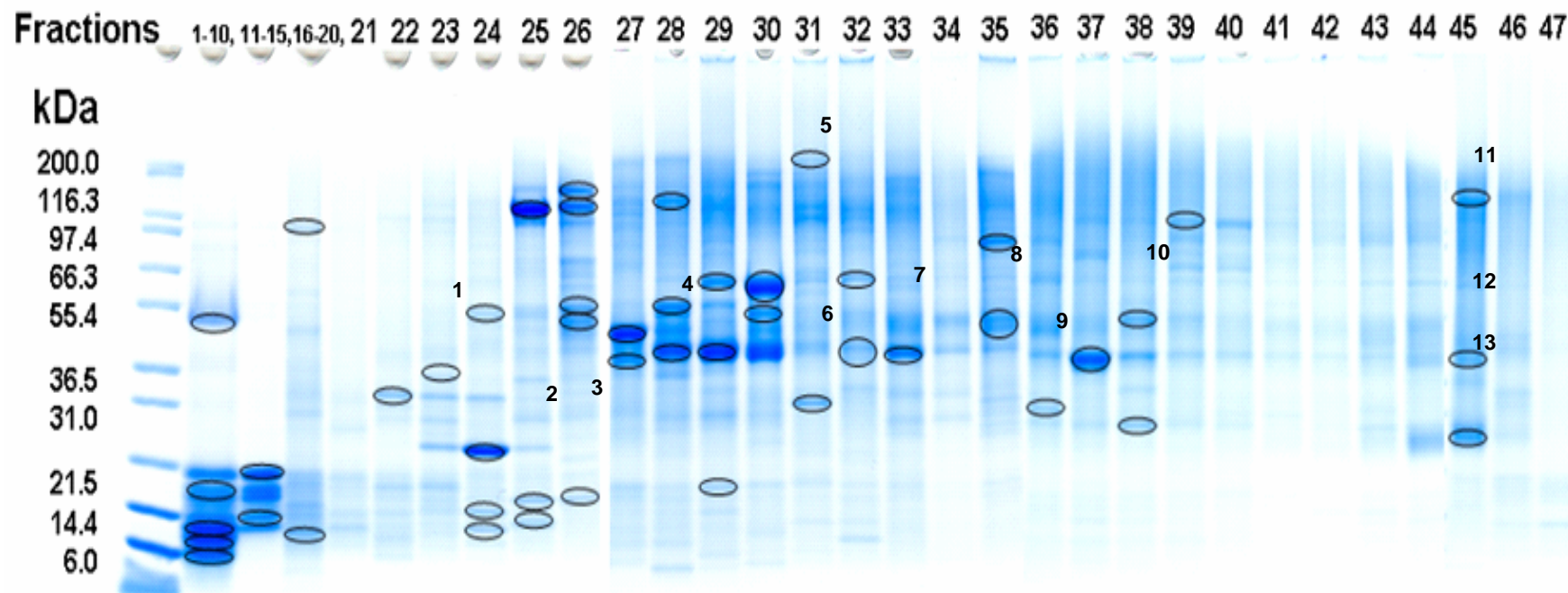
Human Brain membrane lipid Raft prep (500ug)



Preliminary LC-MS data of the lipid fraction isolated from the human brain membrane rafts sample



Lipid Raft Sample: mRP Fractionation followed by 1D-SDS PAGE Fractionation

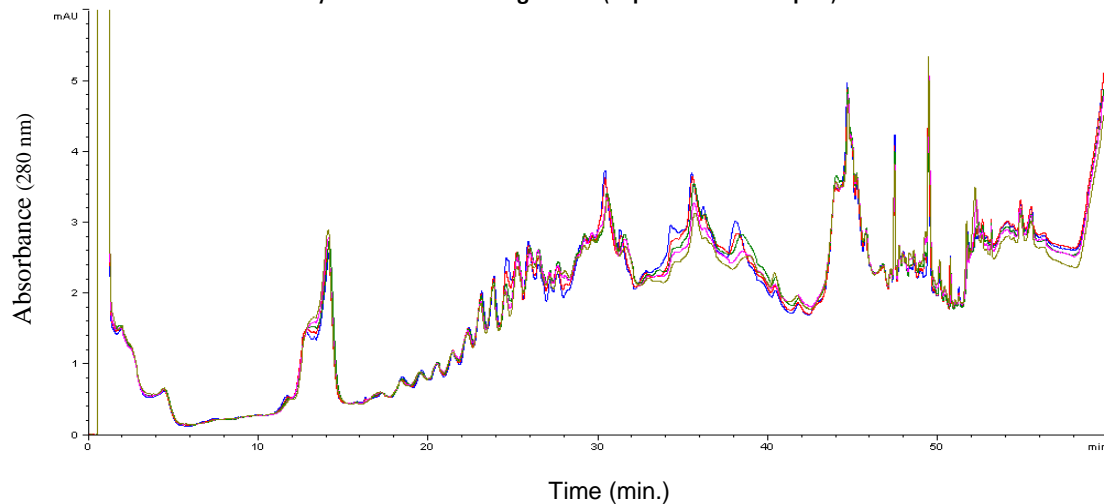


Selected Excised Bands Which are Intregal Membrane Proteins

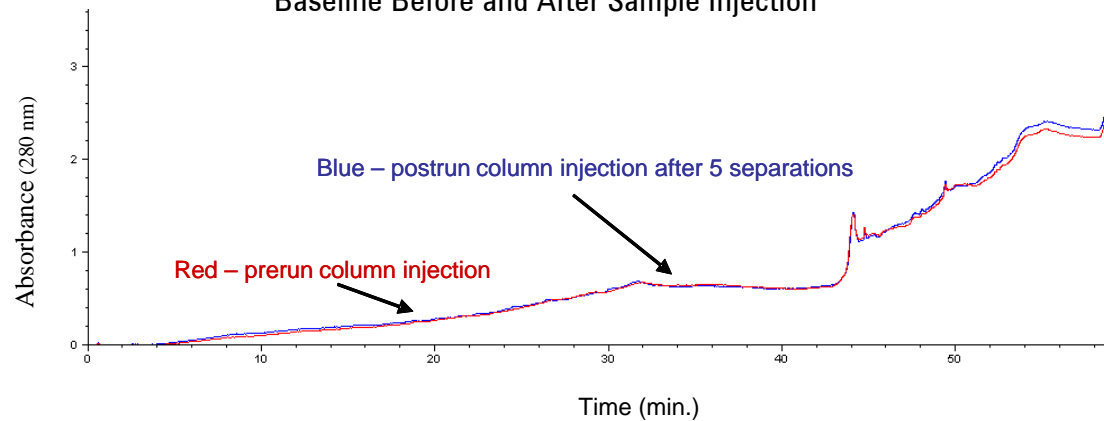
- | | | | |
|----|---|-----|--|
| 1. | Voltage-Dependent Anion Selective Channel Protein 1 | 8. | ATP Synthase alpha chain |
| 2. | Cytochrome C Oxidase subunit IV (COX IV) | 9. | Vacuolar ATP Synthase Subunit D |
| 3. | Cytochrome C Oxidase subunit IV (COX IV) | 10. | Vacuolar ATP Synthase Subunit B |
| 4. | 2',3'-Cyclic-Nucleotide 3''-Phosphodiesterase (CNP) | 11. | Contactin Associated Protein |
| 5. | Spectrin Alpha Chain, Brain (Alpha-II Spectrin) | 12. | Vacuolar ATP Synthase Subunit C |
| 6. | Vacuolar ATP Synthase Subunit E | 13. | ATP Synthase Chain B |
| 7. | Creatine Kinase, B Chain | 14. | Thy-1 Membrane Glycoprotein Precursor (Thy1) |

Lipid Raft Sample: Reproducibility and Baseline Stability

Overlay of 5 Chromatograms (Lipid Raft Sample)



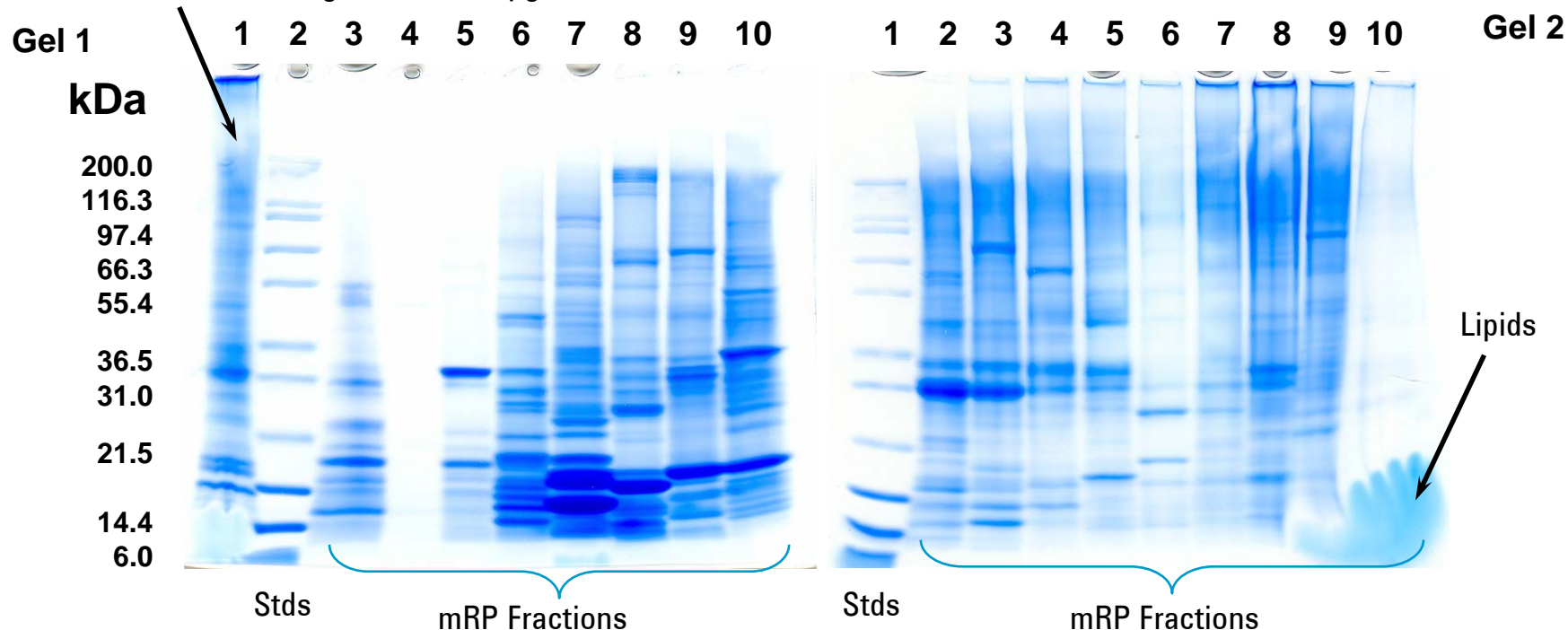
Baseline Before and After Sample Injection



Hela Cell Membrane mRP Fractions followed by 1D-SDS PAGE Fractionation

4.6 x 50mm mRP

Hela membranes, starting material, 22 µg



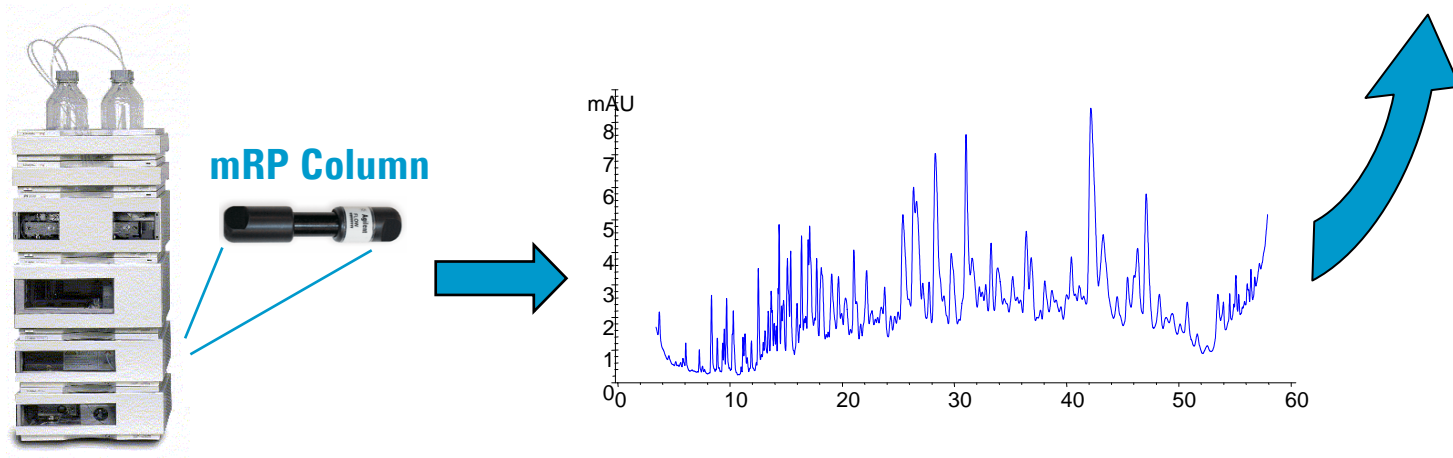
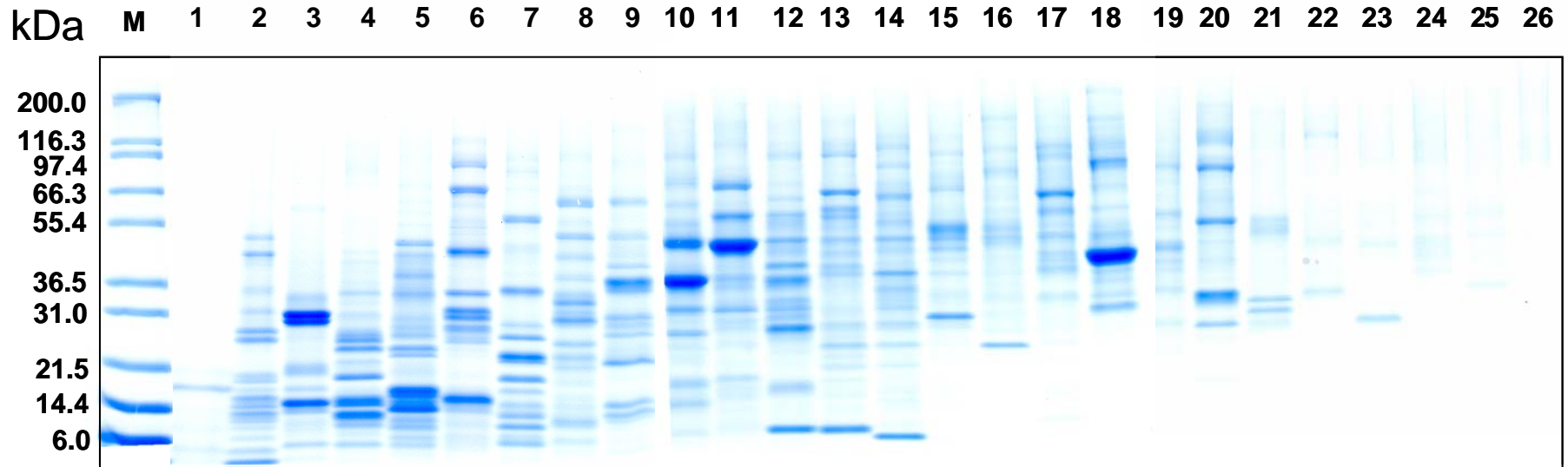
Identification performed by chip-based nano LC/MS/MS from excised gel bands

Sample (216 gel bands from mRP)	Total Acquisition Time (hrs)	# MS/MS Spectra Collected	# Distinct Peptides Matched	# Total Proteins Identified	# Membrane Proteins Identified	# Integral Membrane Proteins Identified
HeLa Membranes	108	486,700	3841	688	364	286



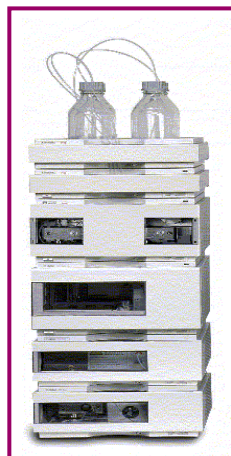
Hela Cell Lysate mRP Fractionation followed by 1D-SDS PAGE Fractionation

4.6 x 50mm mRP C18 column



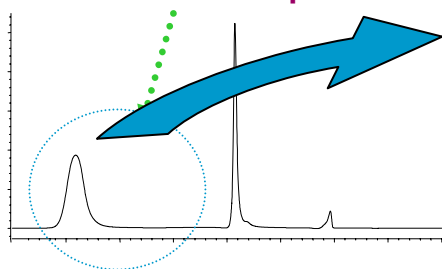
For Plasma/Serum Biomarker Discovery: Combine “Top-6” and mRP Fractionation

Removal of 6 most abundant proteins ➔ Fractionation of lower abundance proteins



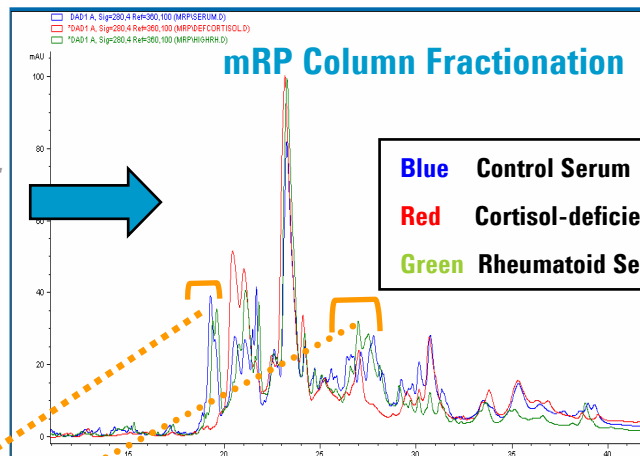
MARS Immunodepletion

Low abundance proteins



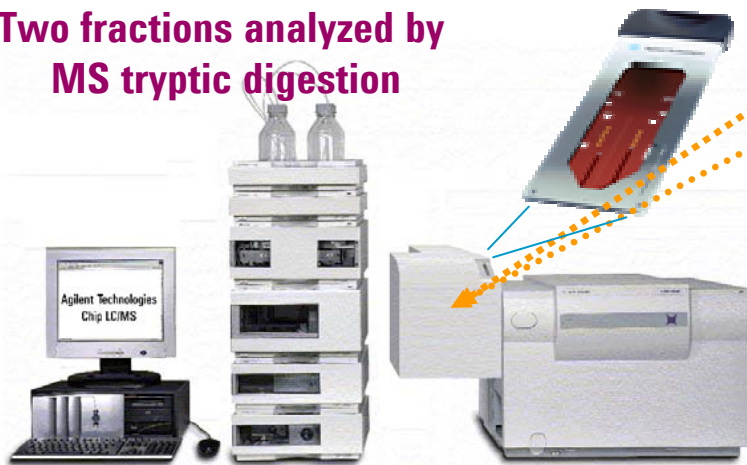
Simultaneously:

- Concentrate
- Desalt
- Fractionate



Blue Control Serum
Red Cortisol-deficient Serum
Green Rheumatoid Serum

Two fractions analyzed by
MS tryptic digestion



LC/MSD Trap XCT

Spectrum Mill

serum #	def. Cor	Rheumatoid	total	# Unique	Score	Protein
spectra #	spectra #	spectra #	intensity	Peptides		
14	0	4	3.09E+07	12	178.37	H factor 1 (complement)
8	0	9	1.94E+07	8	115	apolipoprotein H (beta-2-glycoprotein I)
0	3	1	0.00E+00	3	39.47	ceruloplasmin
0	0	2	0.00E+00	2	30.34	complement component 1 inhibitor precursor
2	0	0	8.65E+00	2	28.61	apolipoprotein C-III precursor
1	0	2	1.84E+00	2	27.34	complement factor B preproprotein
0	0	2	0.00E+00	2	24.99	hemopexin
0	0	2	0.00E+00	2	24.77	alpha-1-acid glycoprotein 2 precursor



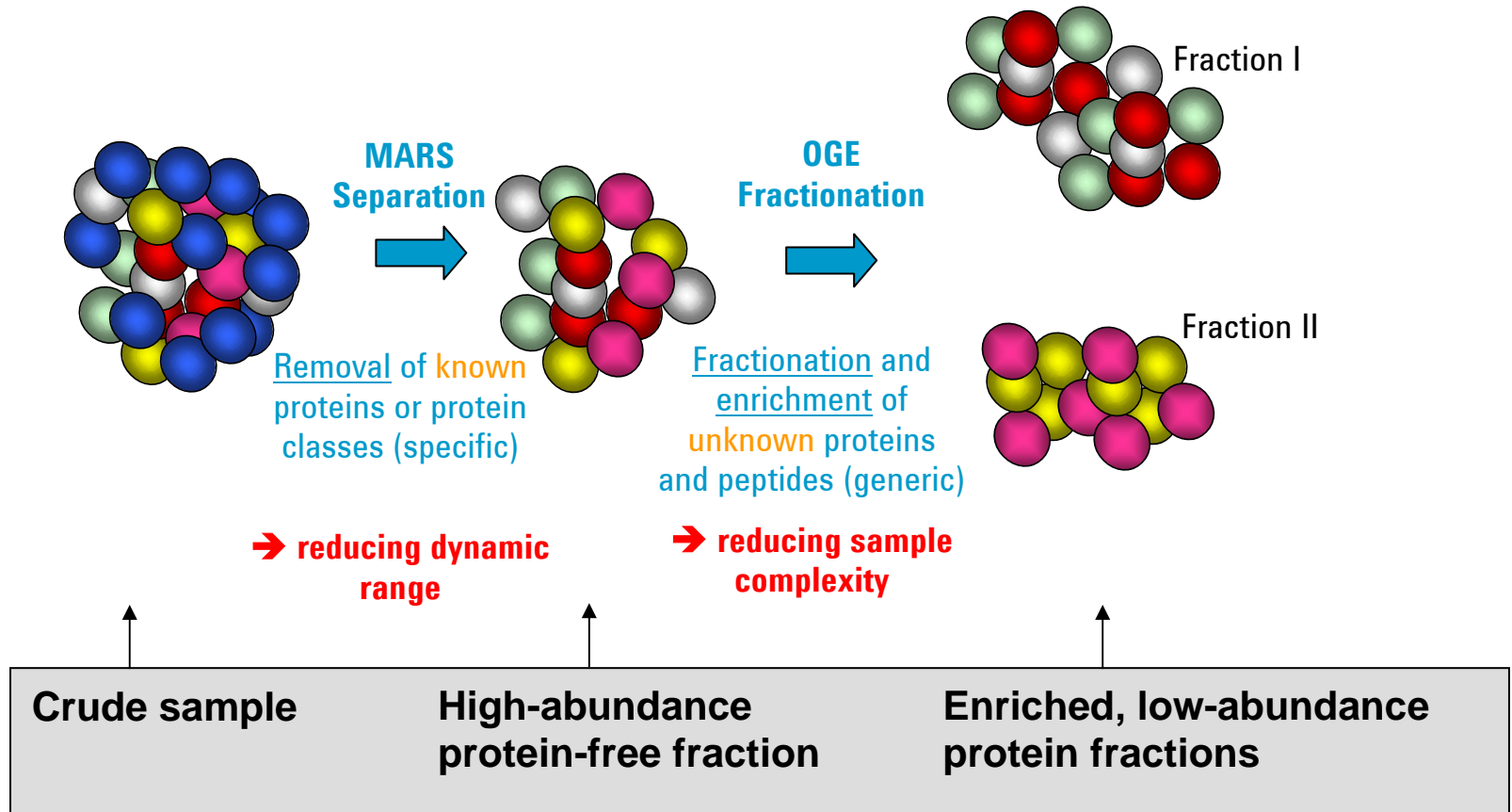
Off-Gel Electrophoresis

Technology and Applications



Strategy

Towards Low Abundance Proteins with Immunodepletion & OGE

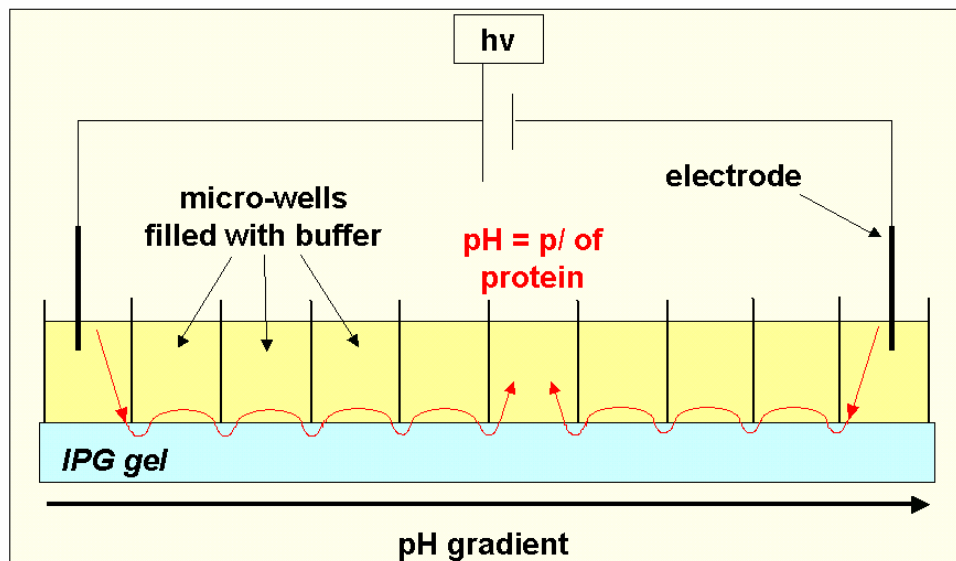


MARS: Multiple Affinity Removal System

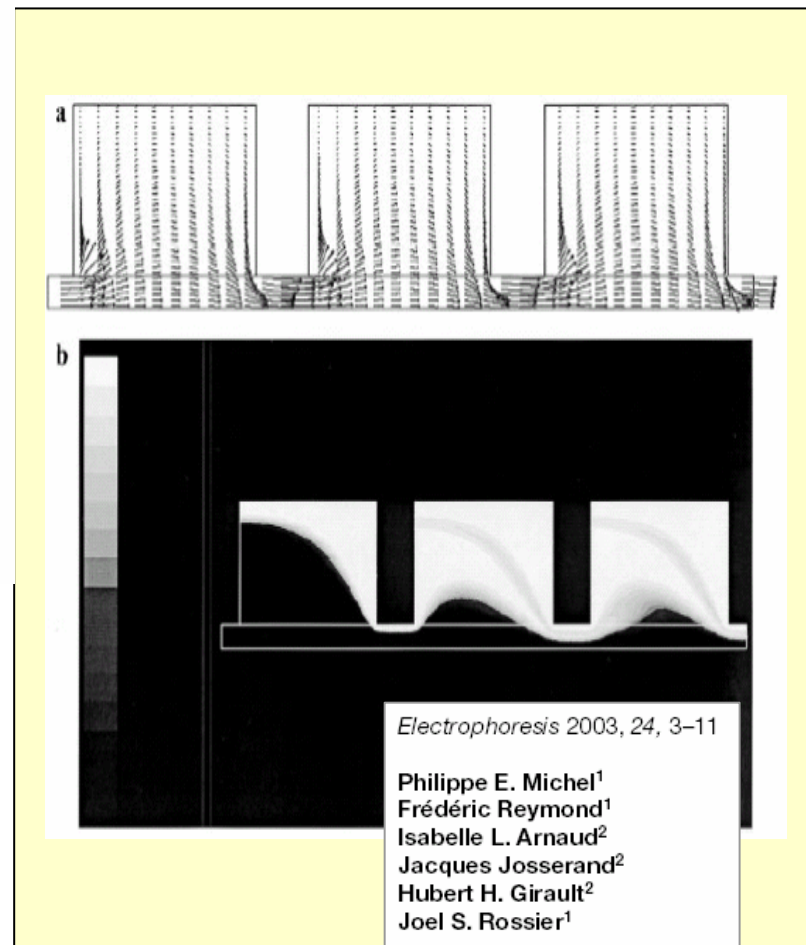
OGE: Off-Gel Electrophoresis



pl-based Fractionation: Off-Gel-Electrophoresis

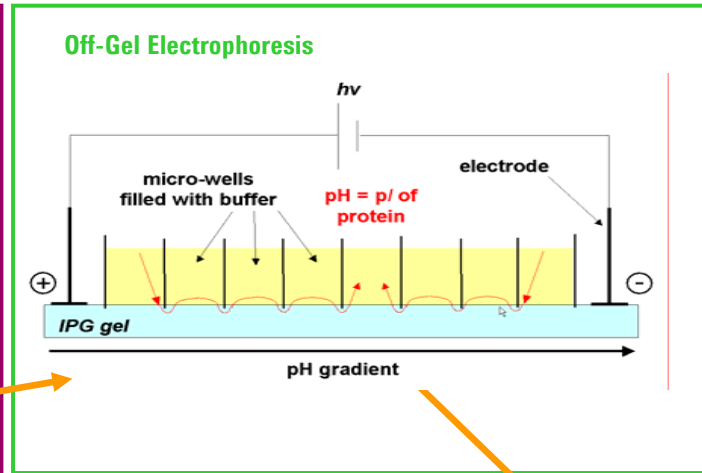
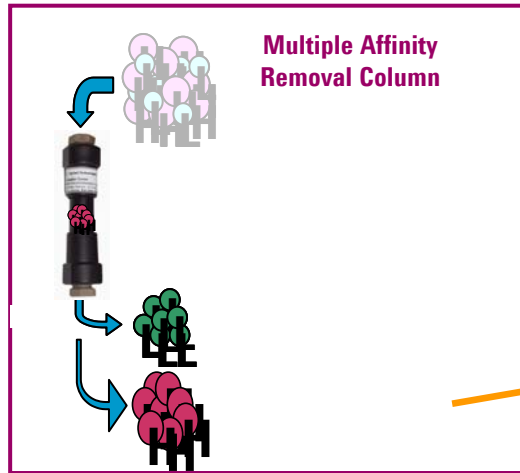


pH gradient	immobilized (IPG gels)
Number of fractions	≤ 30
Fraction volume	0.05 - 0.1 ml
Resolution	0.05-0.5 pH
Separation time	5 - 20 h

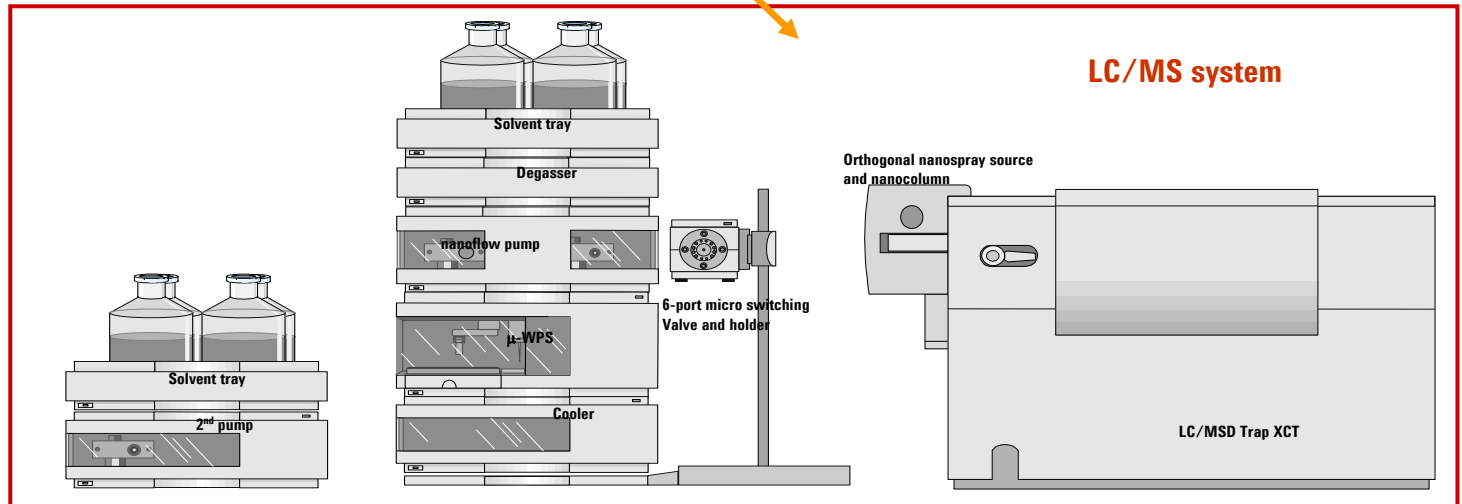


Plasma Proteome Workflow

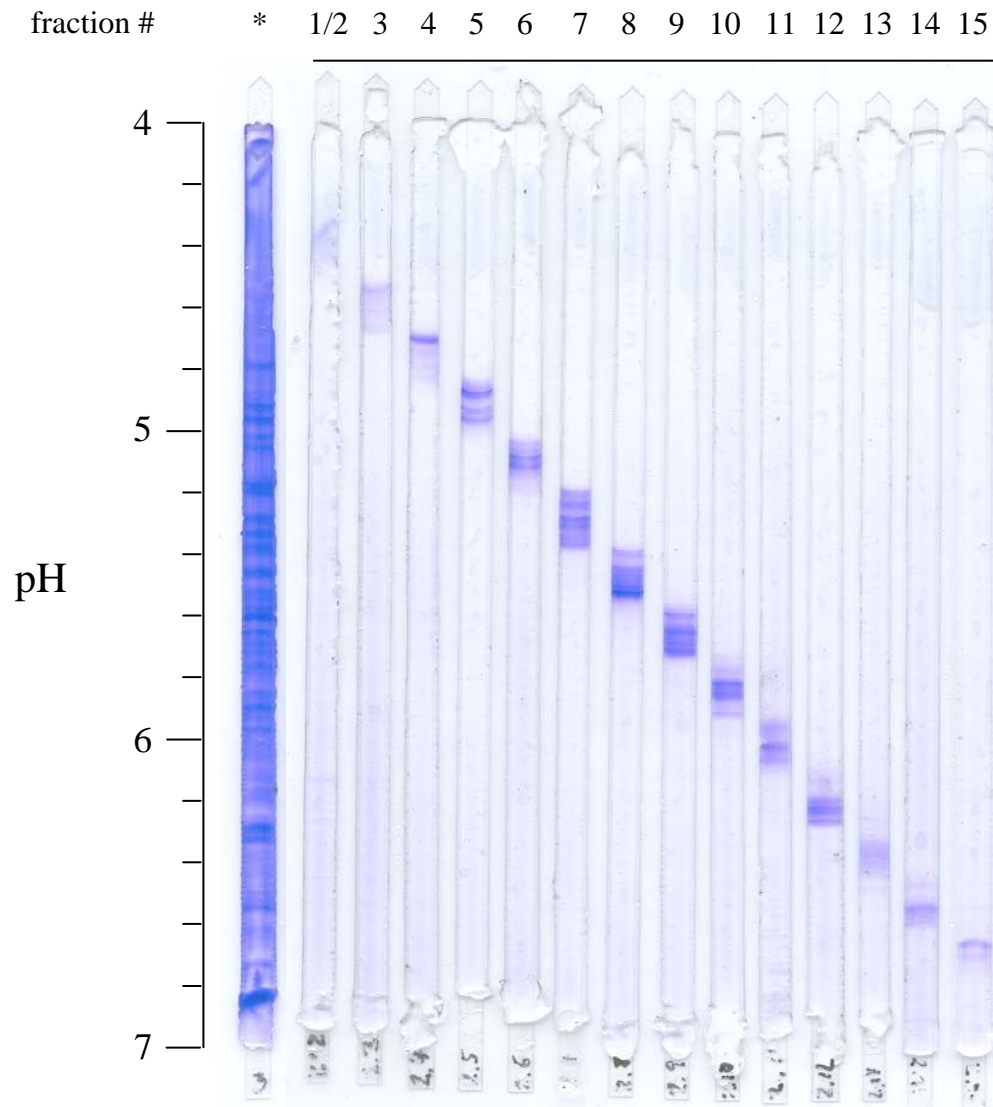
Immunodepletion, OGE, LC/MS



Workflow and instrumental setup of the immunoaffinity column, OGE and LC/MS system



Analysis of OGE Fractions by 1D Electrophoresis



E. coli cell extract

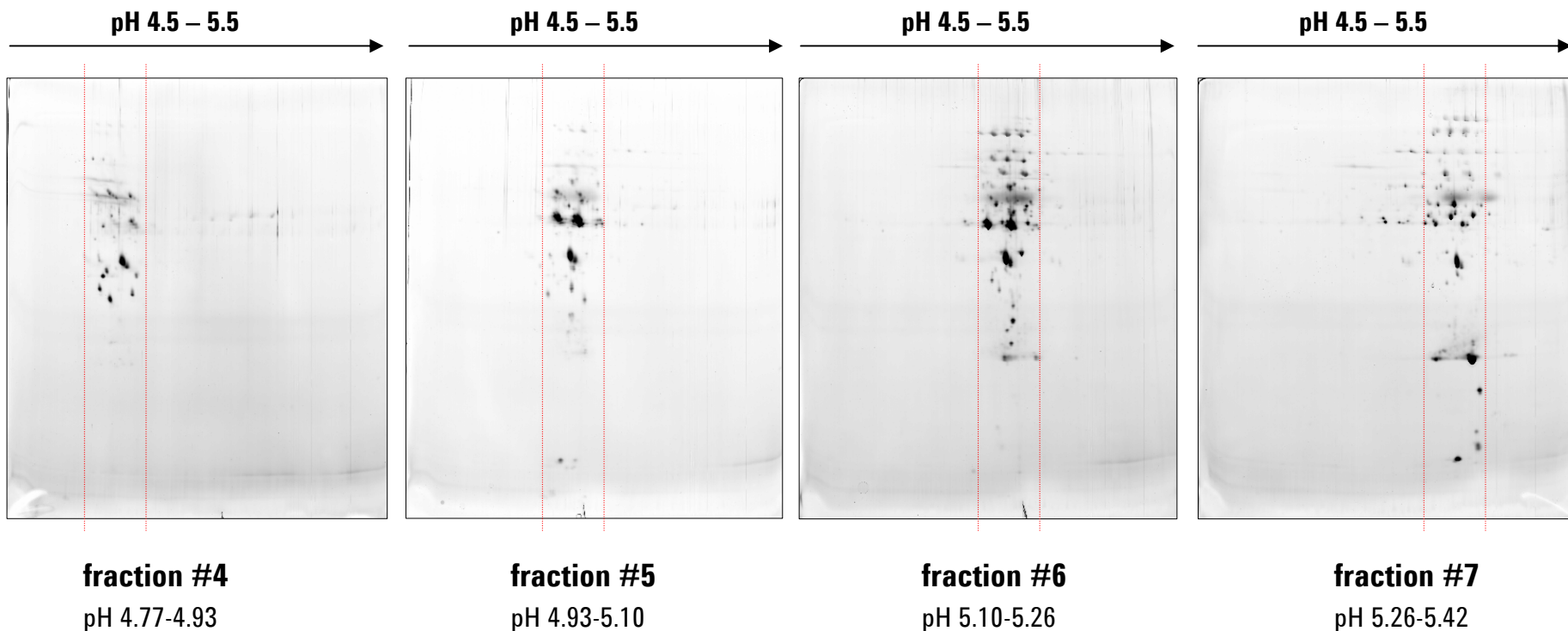
Coomassie Brilliant Blue stain

* unfractionated sample



Analysis of OGE Fractions by High Resolution 2DE Albumin-Depleted Human Plasma, Silver Stain; Experiment done by Lab of Prof. Tissot/CHUV

target: Δ pH 0.16



→ almost no overlap between fractions

Applications

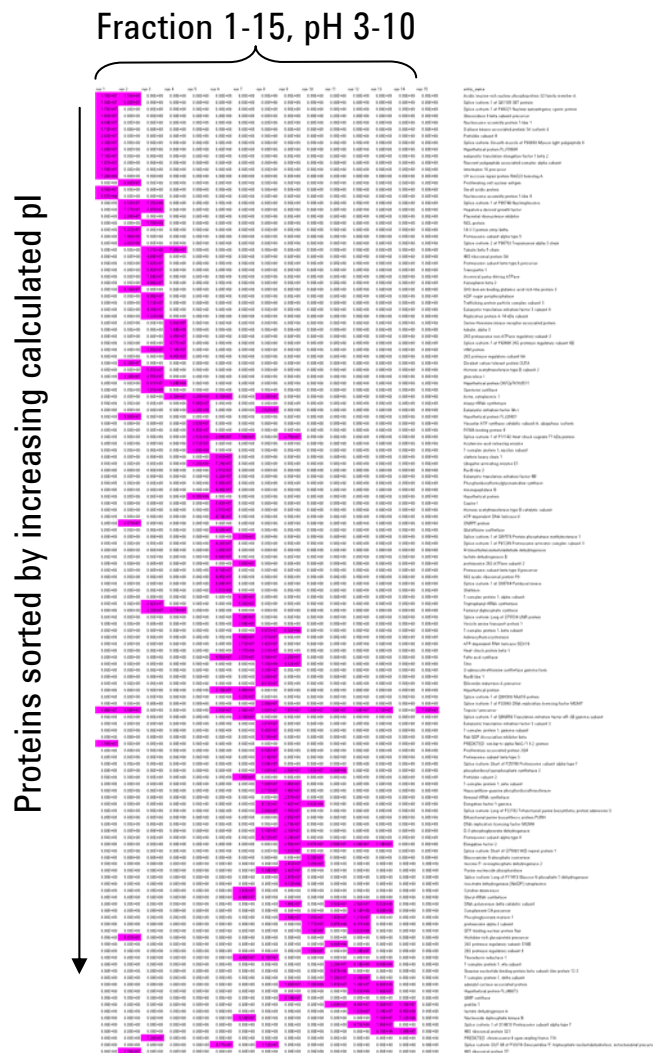
Protein Samples:

- Immunodepleted serum/plasma
- Cerebrospinal fluid (CSF)
- HeLa proteasome cell extract
- Mammalian macrophage cell extract
- preB 697 cell extract
- Bacterial lysates
 - *E. coli*
 - *H. influenzae*

Peptide samples



OGE Fractionation of a Protein Fraction from HeLa S3 Cell Extract* analyzed by Chip-LC/MS



Prefractionation of this cell extract leads to significantly greater number of proteins identified:

144 proteins total for 15 OGE fractions

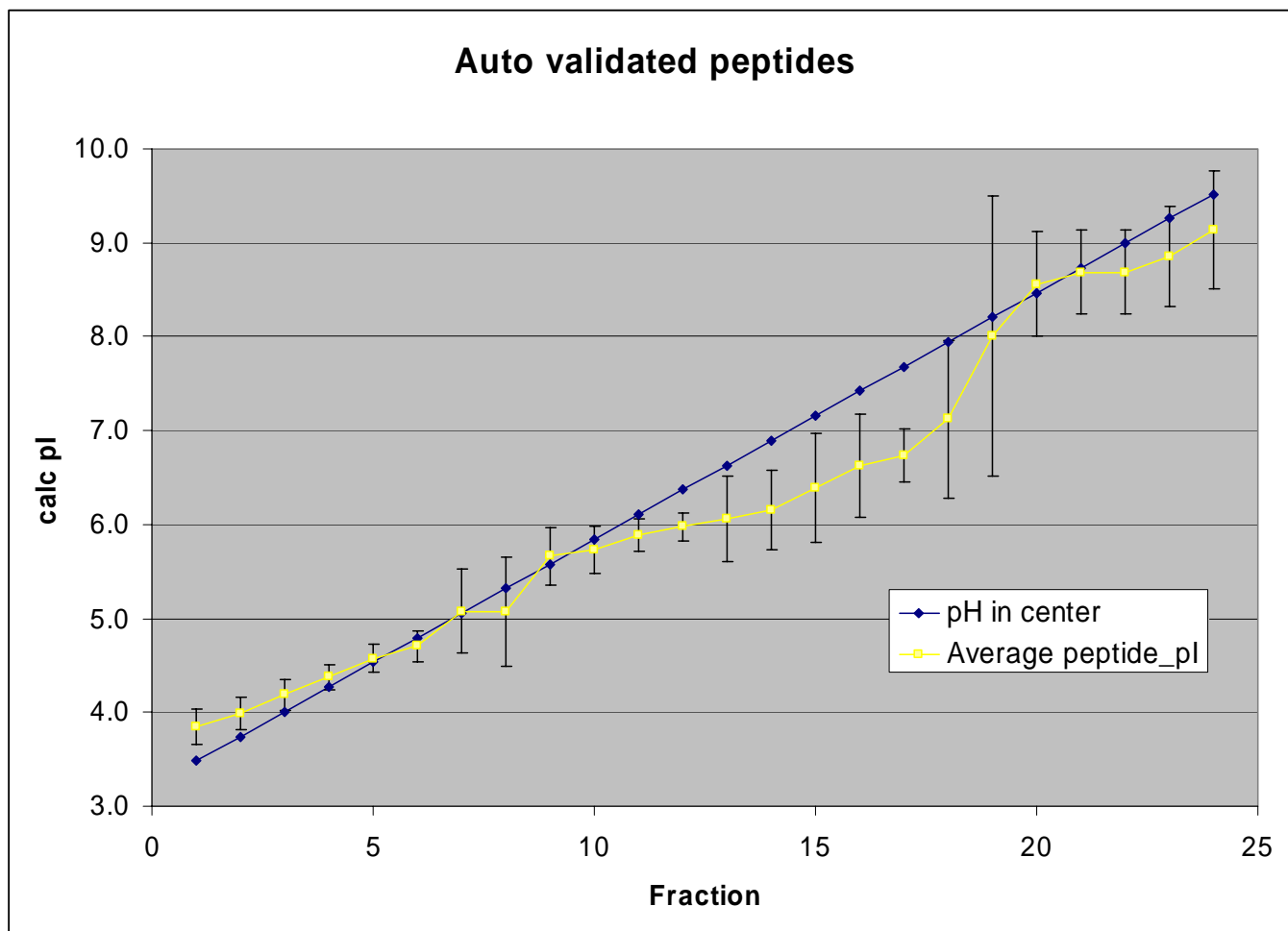
20 proteins total for 15 injections of unfractionated sample

* binding to anion exchange resin



OGE Fractionation of Peptides - E.Coli Tryptic Digest

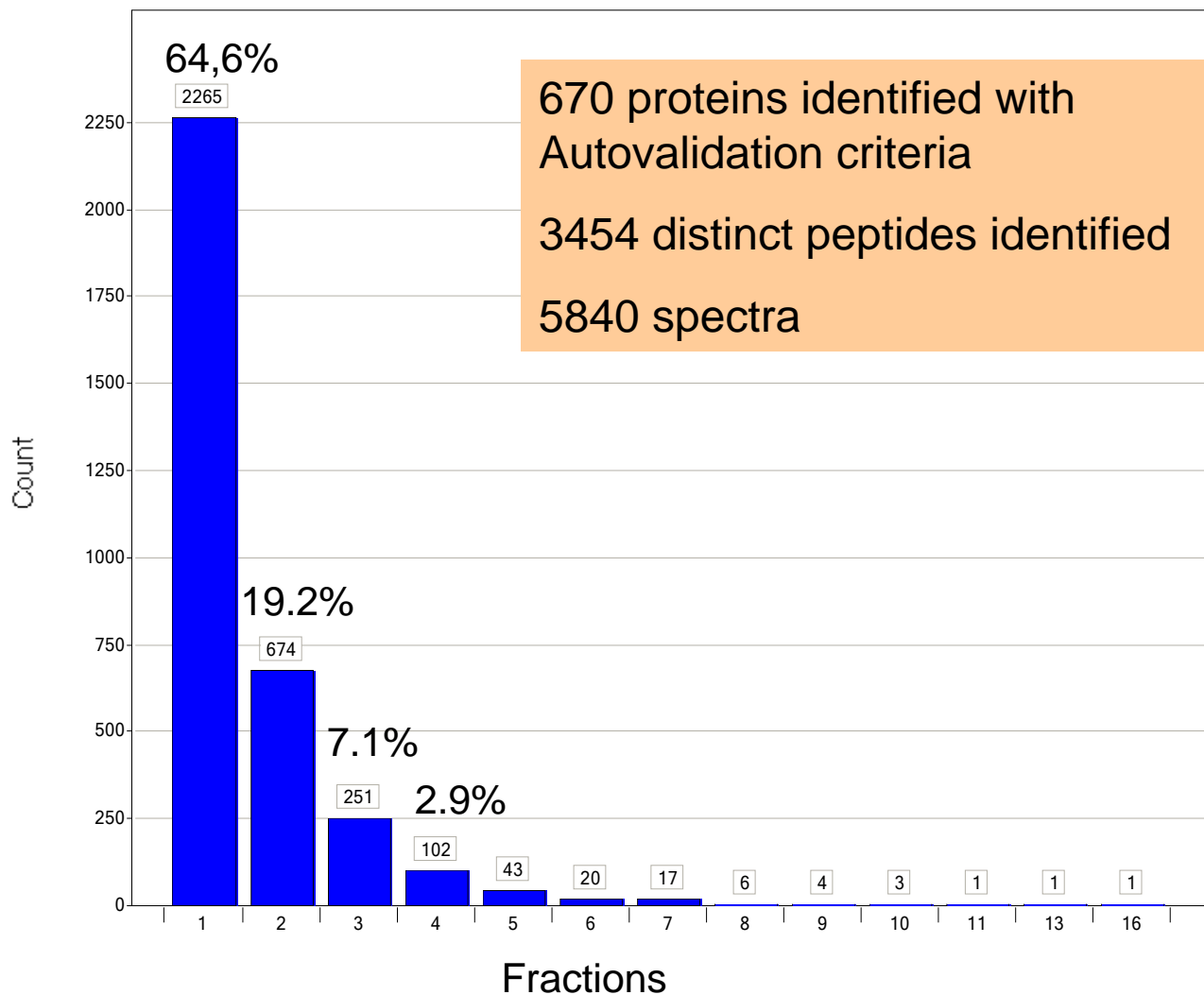
Average Peptide pI with Standard Deviation for Autovalidated Peptides



OGE Fractionation of Peptides - E.Coli Tryptic Digest

Number of Peptide Identifications in Number of Fractions

Bar Chart



670 proteins identified with
Autovalidation criteria
3454 distinct peptides identified
5840 spectra

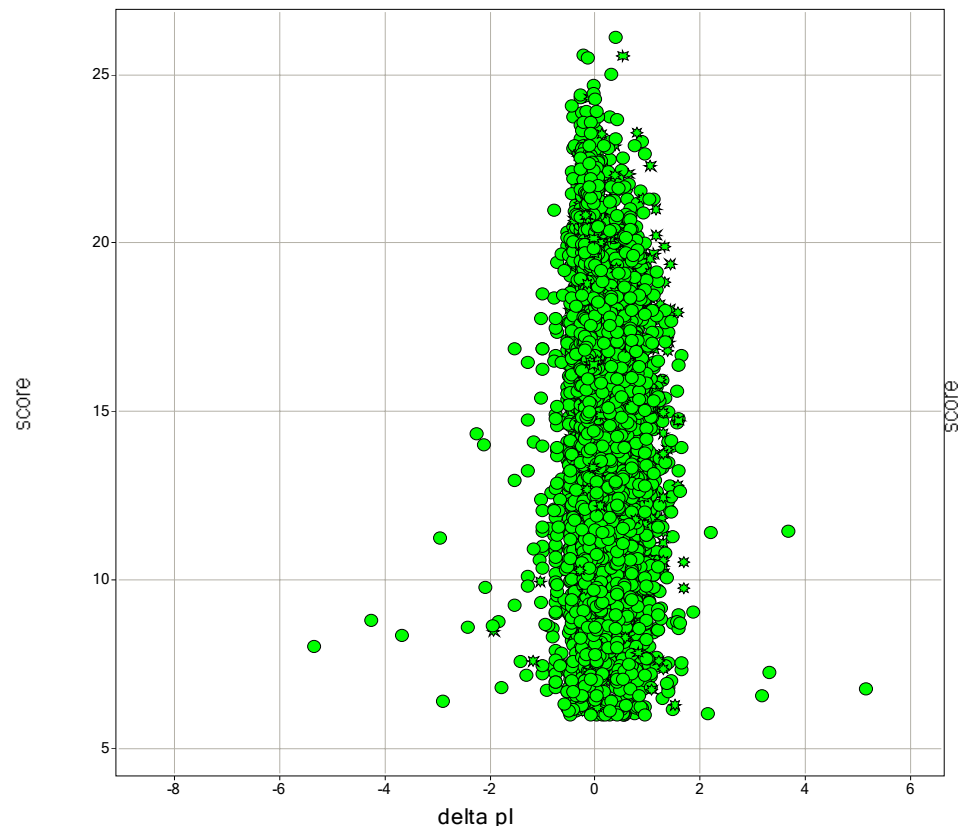
=> The majority of
peptides are found in
only 1 or 2 fractions!



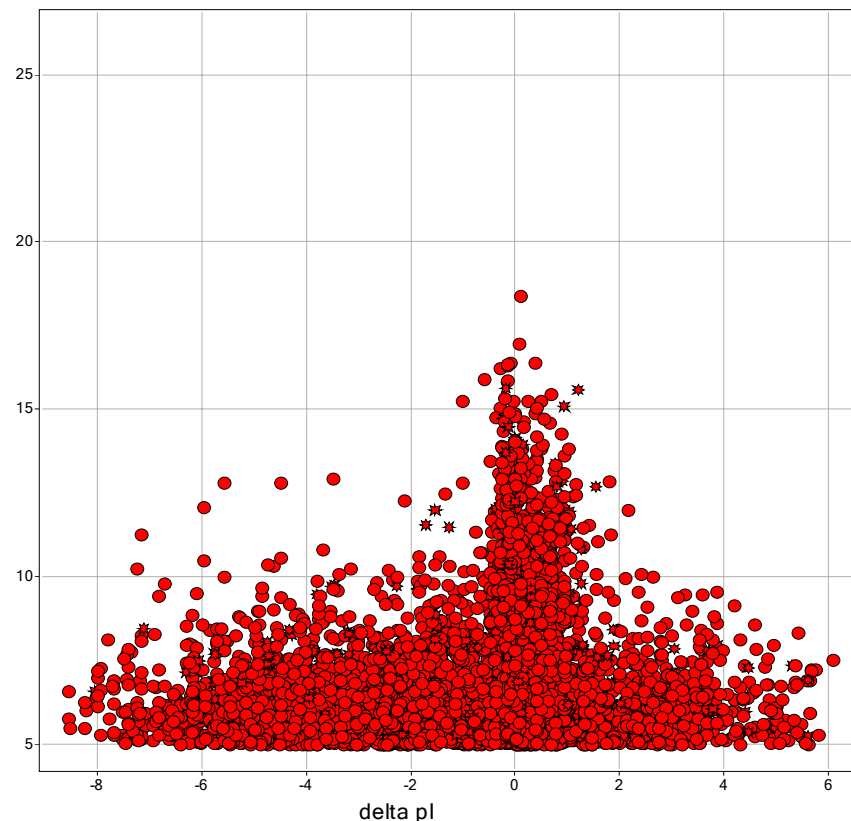
OGE Fractionation of Peptides

Trypsin Digested *E-Coli* Lysate

Peptide scores plotted against delta pl (3454 peptides, 5840 spectra, valid after autovalidation)



Peptide scores plotted against delta pl (5251 spectra, not valid after autovalidation)

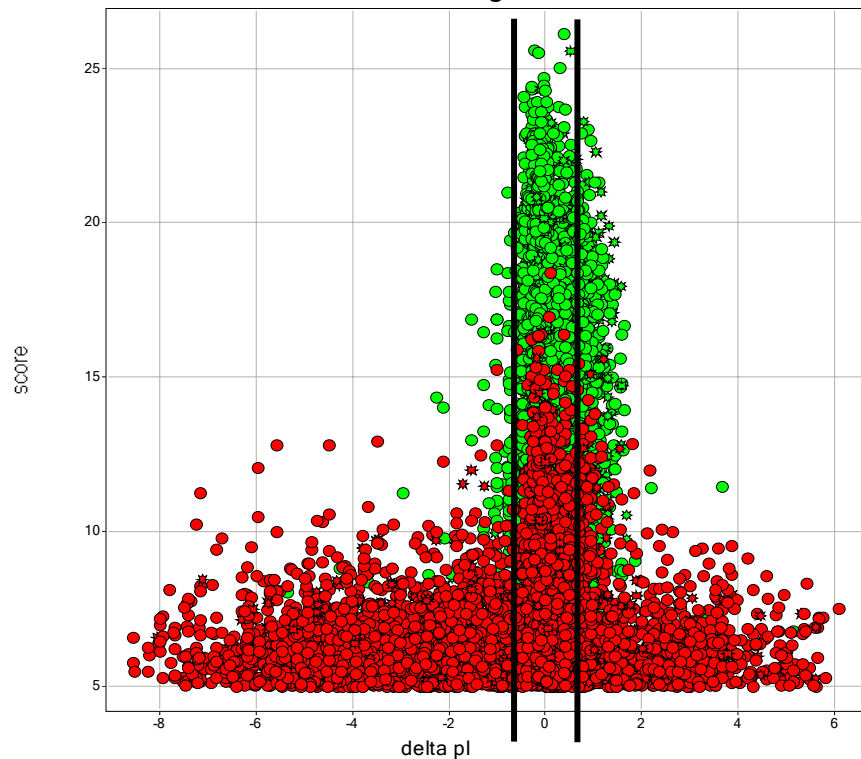


Can be used to search for charged PTM's, peptides with high delta pl and high score are possible candidates.

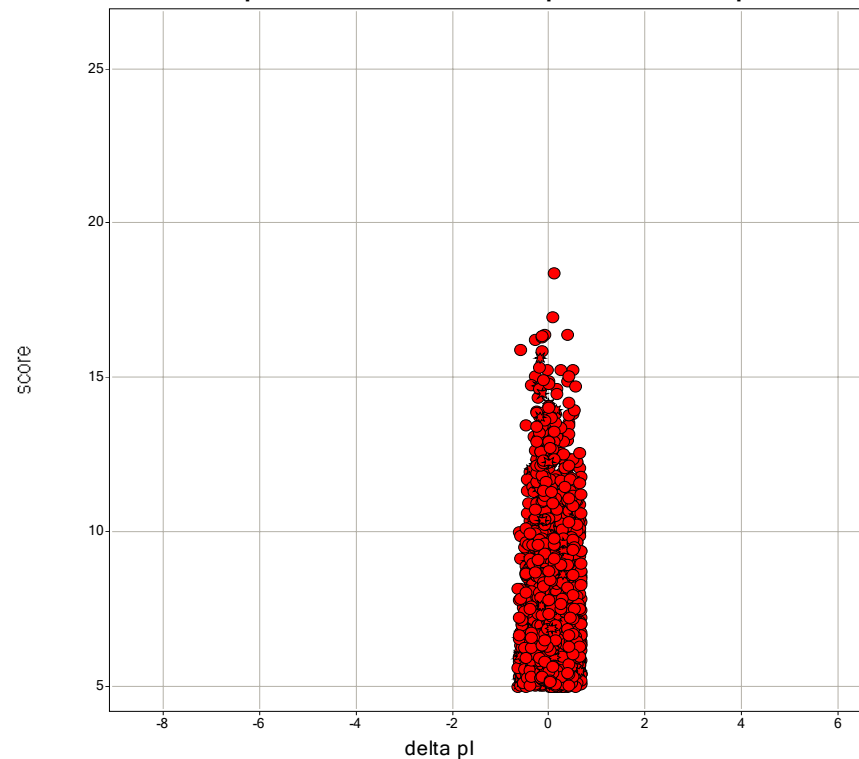
OGE Fractionation of Peptides

Trypsin Digested *E-Coli* Lysate

Peptide scores plotted against delta pI (11091 spectra, valid after autovalidation = green, not validated = red)



Peptide scores plotted against delta pI (1964 not validated spectra within ± 0.63 pH of center pH of well)



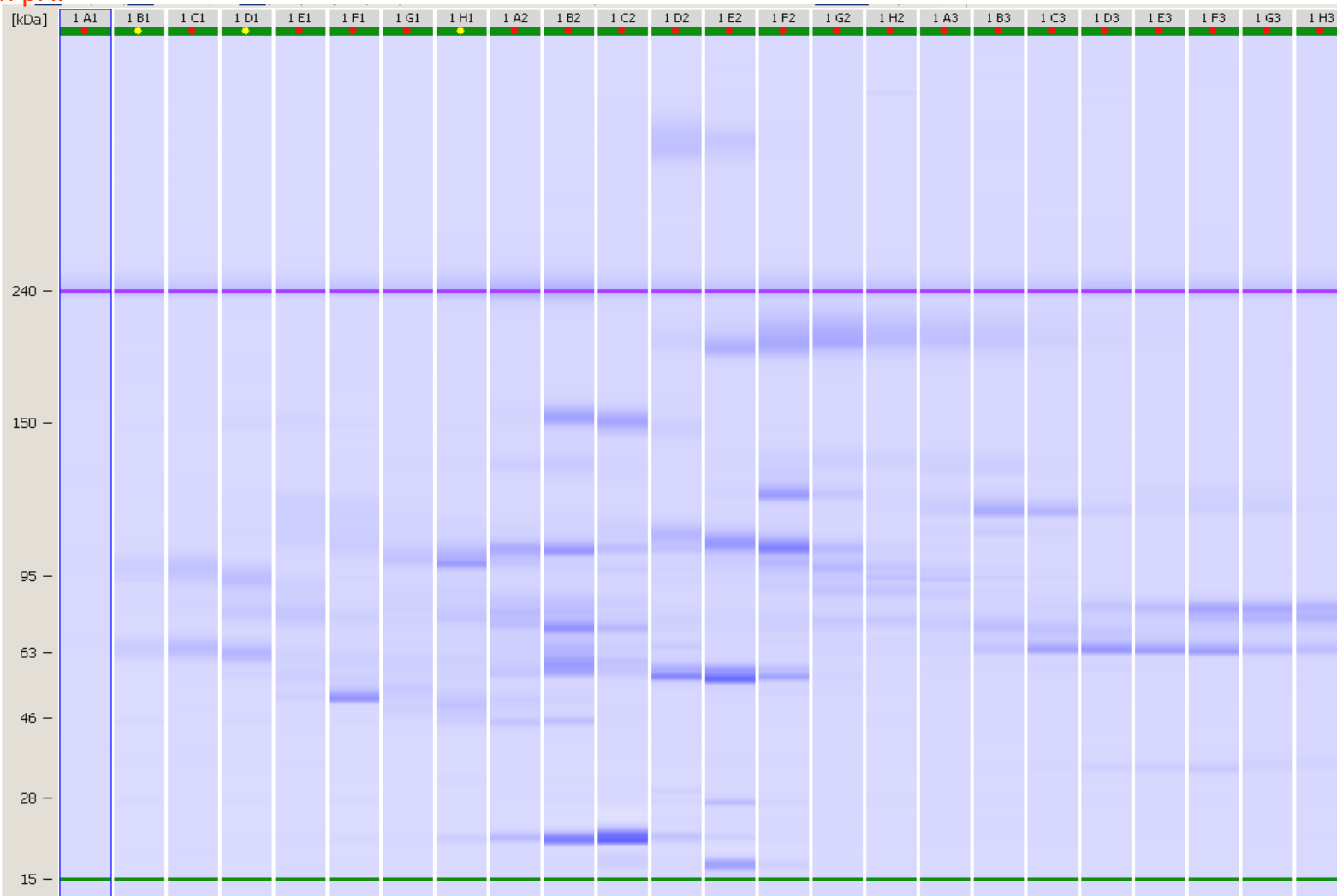
~35% of spectra not autovalidated are within ± 0.5 pH.

Using this information, up to 20% more peptides can be identified!



Pseudo 2D Gel: OGE Fractions of Human Serum analyzed with the Protein 200-HT2 Assay on Agilent's 5100 ALP

fraction pH: 4.21 4.32 4.43 4.54 4.66 4.77 4.88 4.99 5.11 5.22 5.33 5.44 5.56 5.67 5.78 5.89 6.01 6.12 6.23 6.34 6.46 6.57 6.68 6.79



Outlook

- Protein prefractionation by immunodepletion, mRP and OGE enables a deeper dive into the plasma proteome and provides methods compatible with LC-MS based analysis.
- All prefractionation methods and tools integrate well together minimizing sample loss due to excessive sample manipulations
- OGE provides PTM-grade resolution of proteins and peptides and delivers fractions in solution (LC/MS compatibility)
- The mRP column provides highest recovery of protein samples (95+%) even on challenging protein samples such as integral membrane proteins
- The Multiple Affinity Removal System provides the highest sample capacity per ml resin and longest column lifetime when compared to other products. This translates to the lowest cost per ml of depleted sample.
- The Multiple Affinity Removal System also provides the greatest ease of use, highest selectivity and reproducibility (run to run, lot to lot) compared to any equivalent product.



Further Information

Bioreagents catalog – 5989-3431EN "The 2005-2006
Bioreagents Product and Resource Guide"

CD Compendium – Bioseparations 5989-4047EN

Weblink: <http://www.agilent.com/chem>

