



# Screening and Optimization Designs to Improve Method Performance and Robustness

John F. Kauffman, Ph.D.

Daniel J. Mans, Ph.D.

FDA Division of Pharmaceutical Analysis

IFPAC 2015

**Disclaimer:**

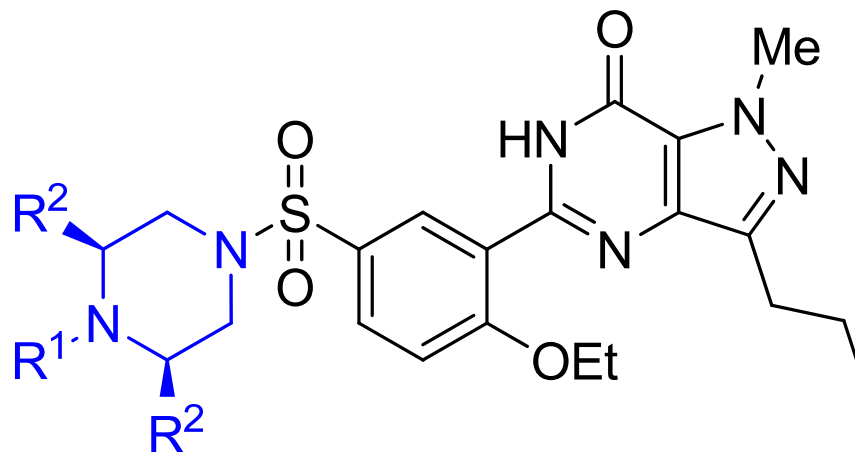
The findings and conclusions in this presentation have not been formally disseminated by the Food and Drug Administration and should not be construed to represent any Agency determination or policy.



## Research Problem Statement

- FDA will develop a method using the QbD paradigm, and transfer the method to an EMA lab.
  - Begin with a harmonized compendial method and apply QbD concepts to improve the method
  - Method: HPLC analysis of sildenafil and analogues of sildenafil

# Sildenafil and some Analogues



- $R^1 = \text{Me}; R^2 = \text{H}$  Sildenafil  
 $R^1 = \text{CH}_2\text{CH}_3; R^2 = \text{H}$  homosildenafil  
 $R^1 = \text{CH}_2\text{CH}_2\text{OH}; R^2 = \text{H}$  Hydroxyhomosildenafil  
 $R^1 = \text{H}; R^2 = \text{H}$  *N*-desmethylsildenafil  
 $R^1 = \text{H}; R^2 = \text{CH}_3$  *N*-desmethylsildenafil  
 $R^1 = \text{cyclopentyl}; R^2 = \text{H}$  Cyclopentynafil

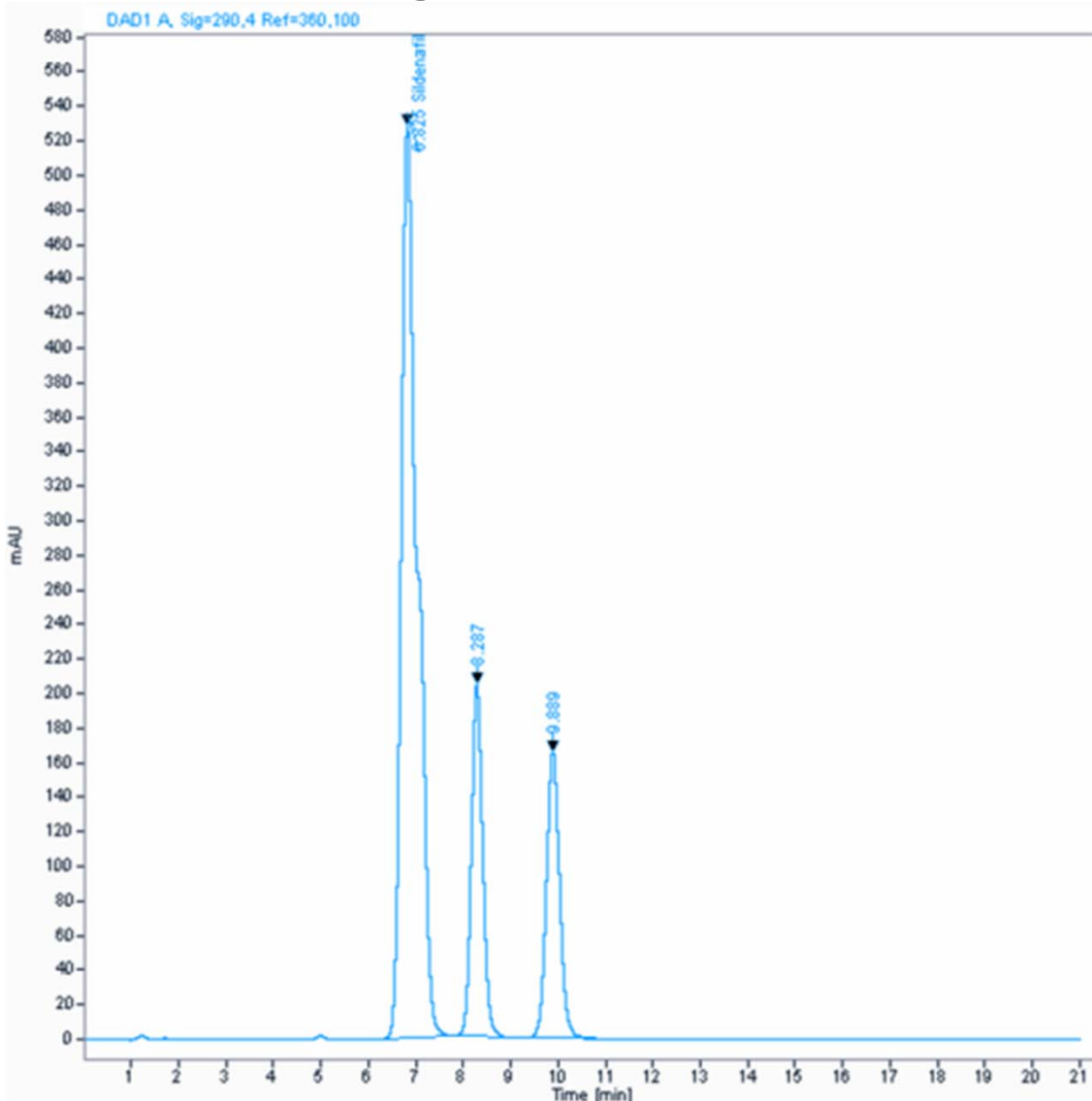
\*Pre-existing analogue library prepared for rapid screening surveillance program;  
Harmonized Method exists



## Example ATP

- The method will separate 6 compounds with high specificity (HPLC resolution  $\geq 1.5$ )
- Quantify each compound at levels from 25 ug to 100 mg per gram of finished product.
  - Multiple dilutions may be required
- Repeatability:  $\leq 2\%$  over six replicates
- Accuracy: within  $\pm 15\%$  of the true value at 25 ug and within  $\pm 2\%$  of the true value at 100 mg, with 95% confidence.

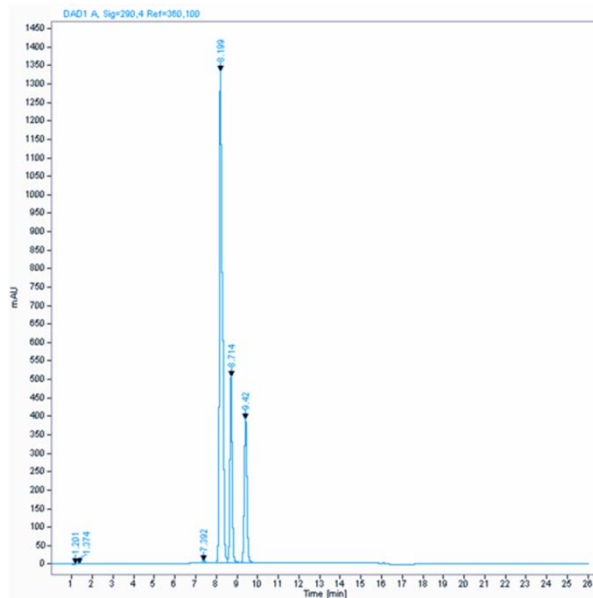
# Starting Point: USP Method for Sildenafil



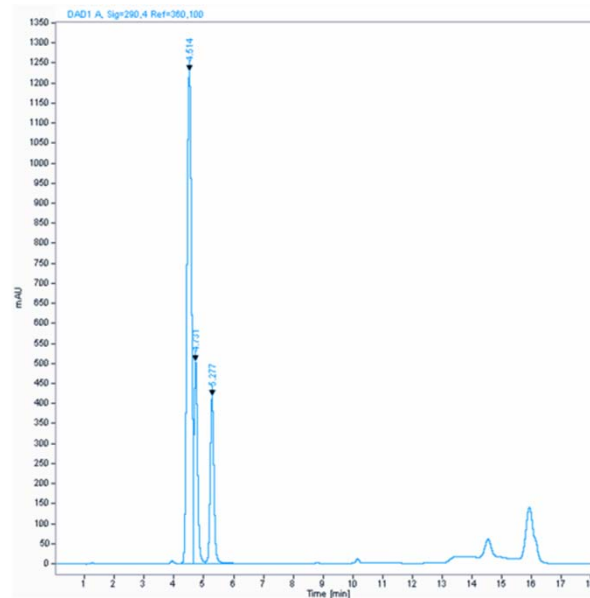
- Isocratic: 57/28/15  
Buffer/Methanol/CH<sub>3</sub>CN  
(Buffer = Phosphoric acid,  
pH 3 with triethylamine)
- C18 column
- 30 °C
- Poorly separated:  
6 compounds → 3 peaks

# Initial Studies: Mobile Phase Evaluation

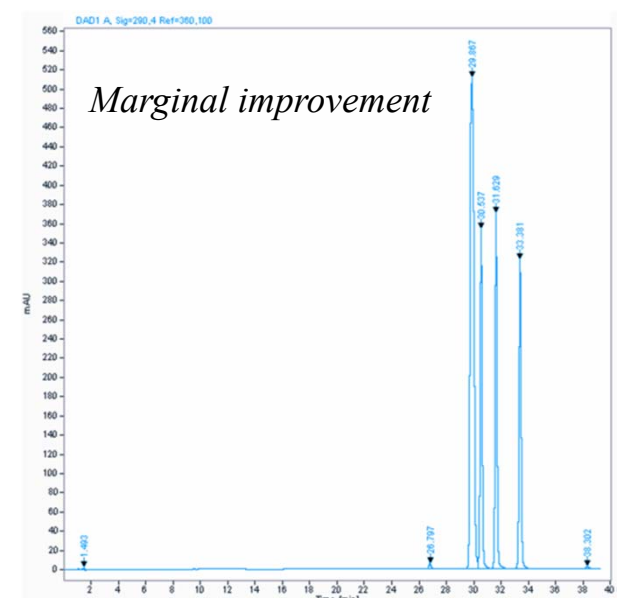
- Change from Isocratic to Gradient (A=Buffer, B=MeOH/CH<sub>3</sub>CN)? Remove CH<sub>3</sub>CN? Remove Methanol?



A=Buffer  
B=MeOH/CH<sub>3</sub>CN (25/17)



A=Buffer  
B=MeOH



A=Buffer  
B=ACN



## Summary and Conclusion of Initial Screen

- 6 columns screened (4 C18, 2 PFP): Results did not conform with theoretical expectations
- Varied combinations of mobile phases and gradient times
- Began to investigate pH effects: 4.5 vs. 3.0  
→ affords separation of the 6 components but does not meet criteria of the ATP
- ❖ Time consuming and tedious one-variable-at-a-time conventional approach. Difficult to keep track of numerous generated method files.



# A Systematic QbD Approach

- Develop screening designs to evaluate diverse method options
- Use DOE methodology to predict optimal conditions
- Use statistical analysis to determine ranges of acceptable operating parameters - Robustness
- Implemented using S-Matrix Fusion QbD Software

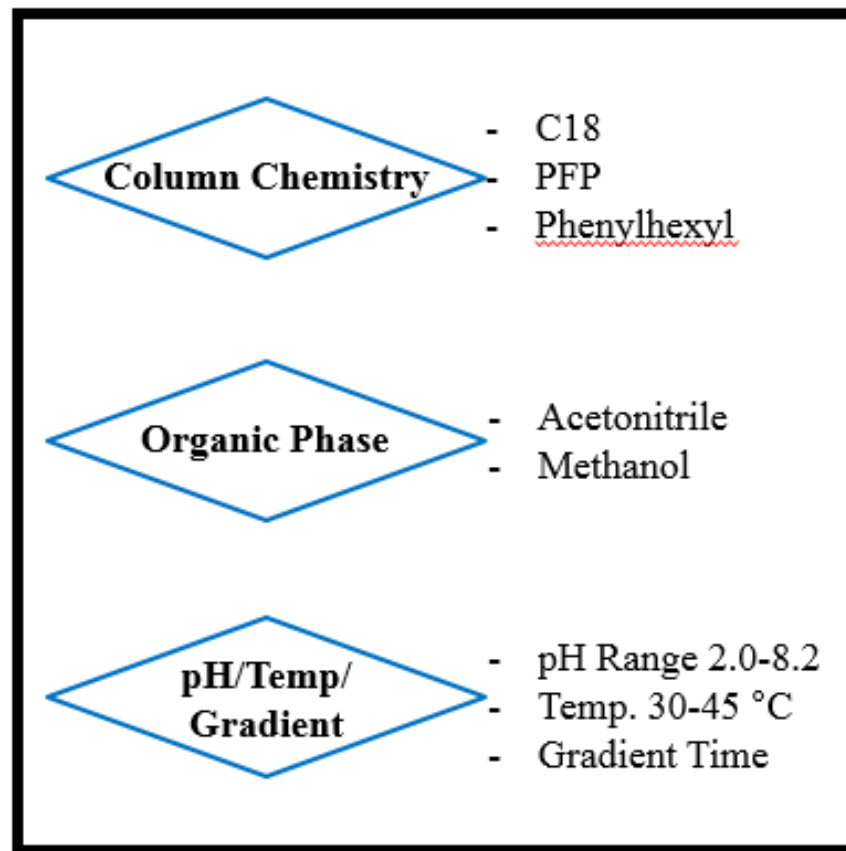


## Three Screening Designs

- 1. Broad screen of 3 columns, 2 organic phases, pH and gradient time. (37 experiments)
  - Purpose: Identify the best column, pH range
- 2. Fix column and screen 2 organic phases, most promising pH range, gradient time (19 experiments)
  - Purpose: Select most promising organic phase, further narrow pH range
- 3. Fix column and organic phase, screen pH, gradient time, column temperature (16 experiments)
  - Purpose: Final method, operable design region

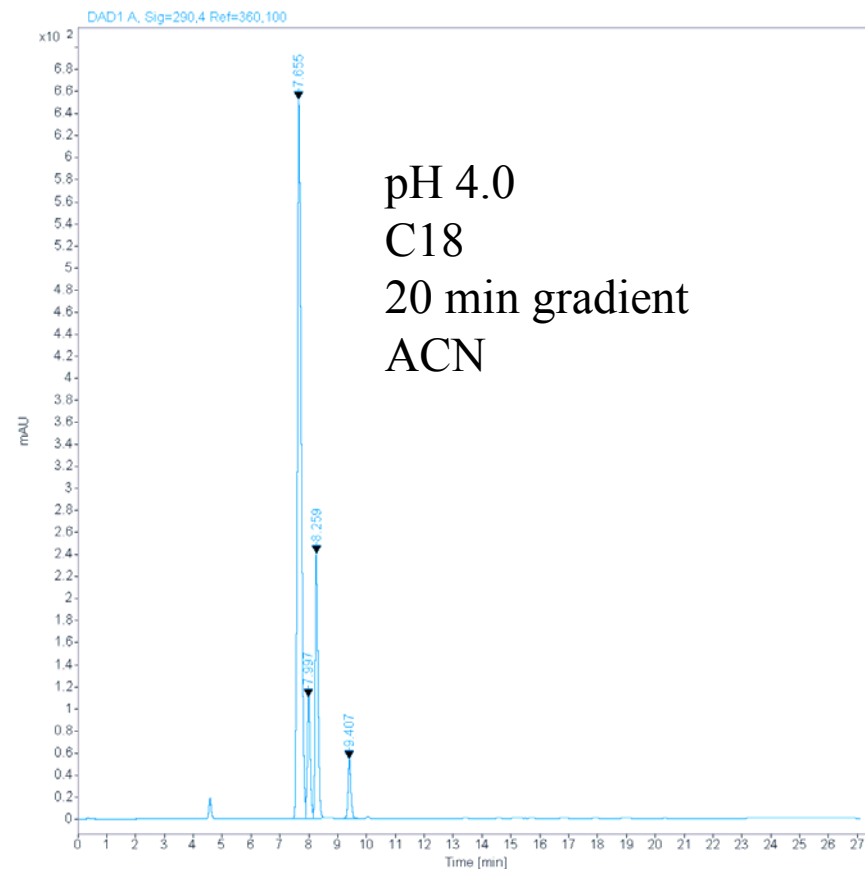
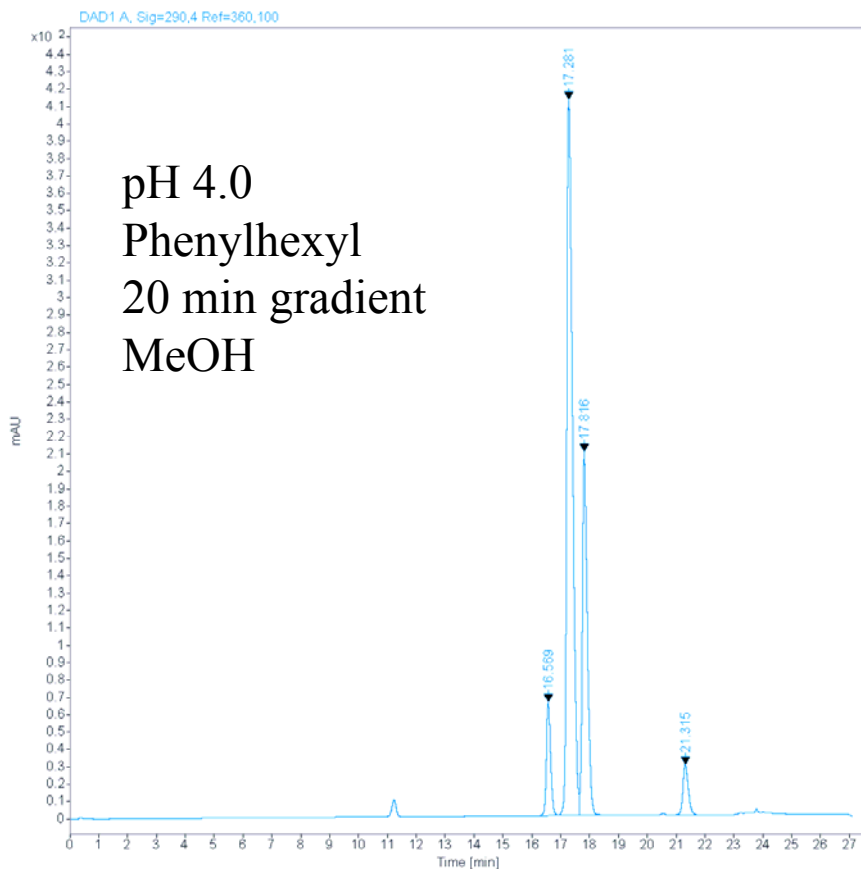
## Screen 1: Best Column (37 Experiments)

- Columns: analytical columns of same ID and length from same supplier
- Mobile Phase
  - MeOH and ACN
  - 10 mM buffer @ pH 4.0, 5.0, 6.0, 7.0, 8.2
- Gradient Time: 4-20 minutes (10-55% organic)
- Fixed column temperature (30 °C)



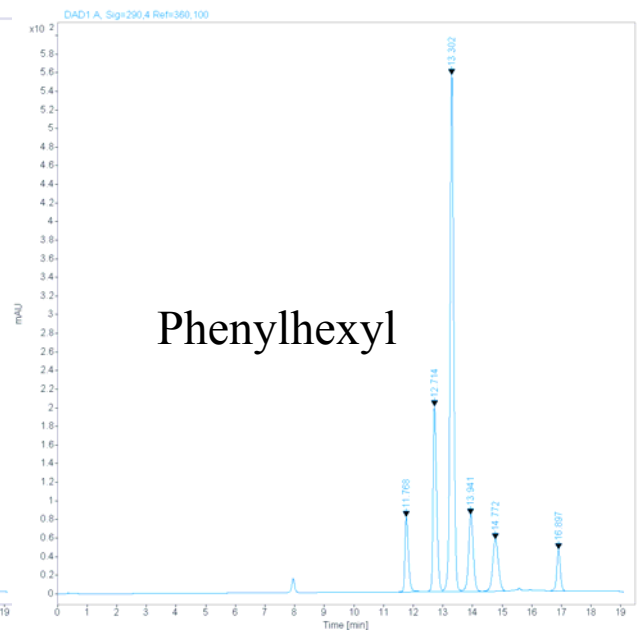
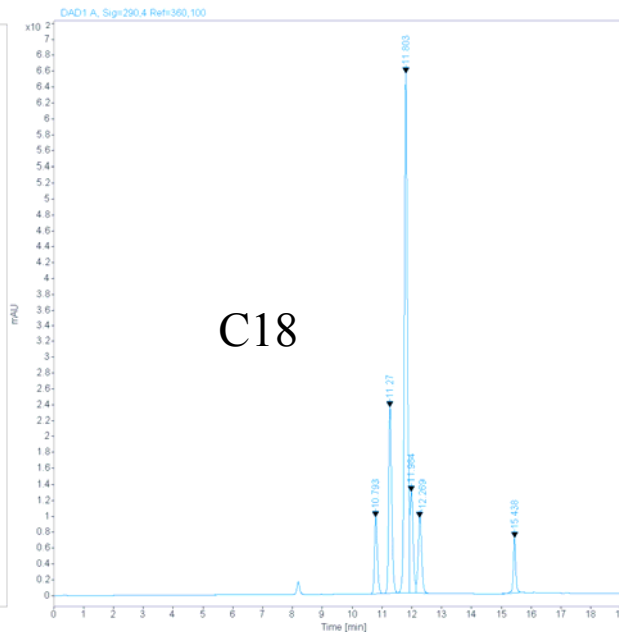
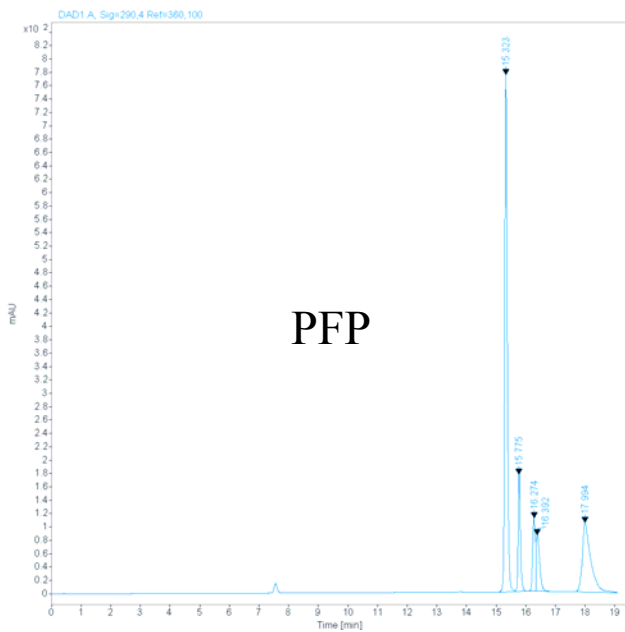
# Column Screening: A Few Examples

- Low pHs (3.0, 4.0) gave the least # peaks (recall USP pH 3.0)



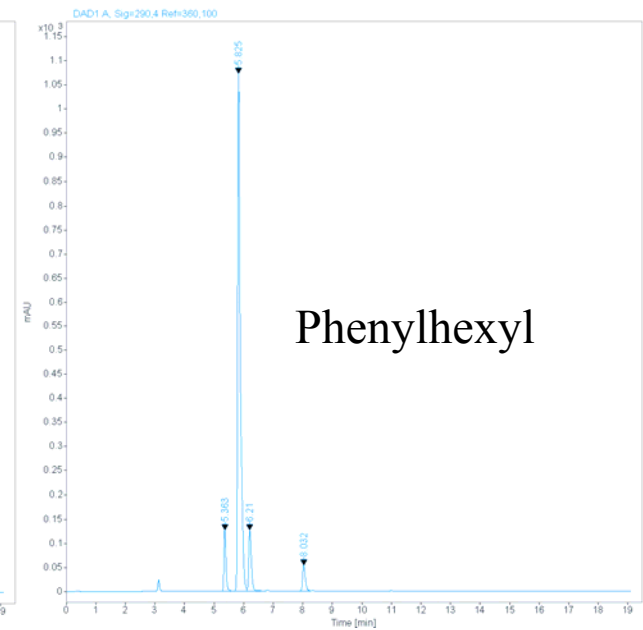
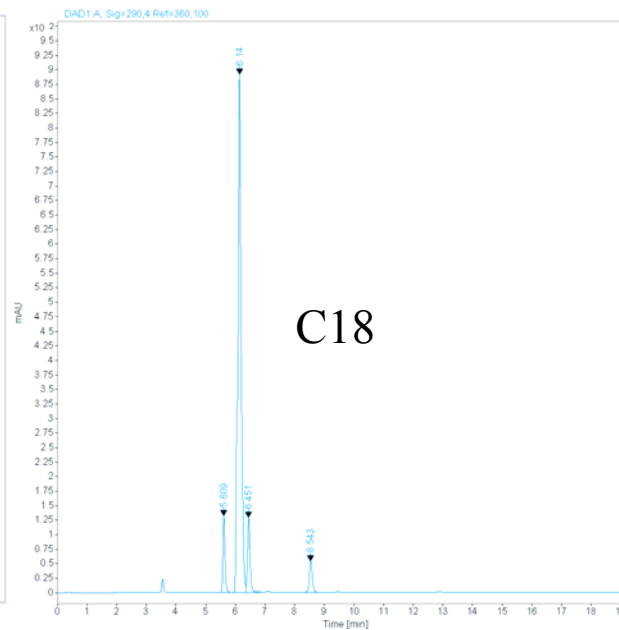
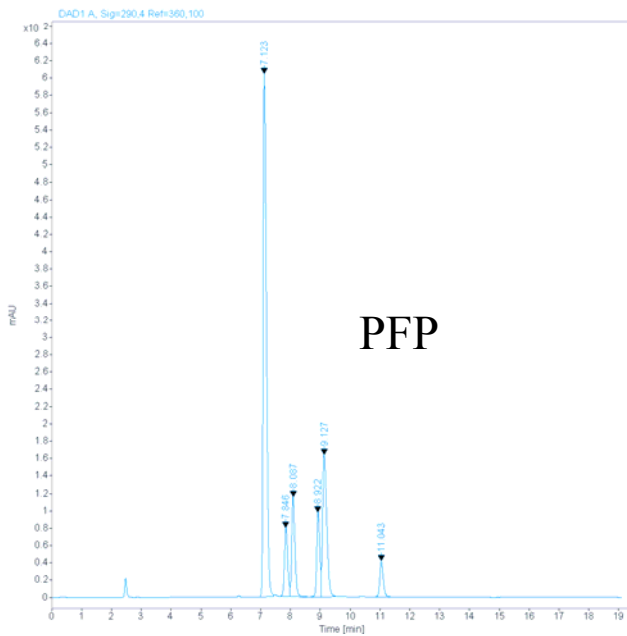
# Column Screening: A Few Examples

- Constant: pH 5.0, MeOH, 12 min gradient

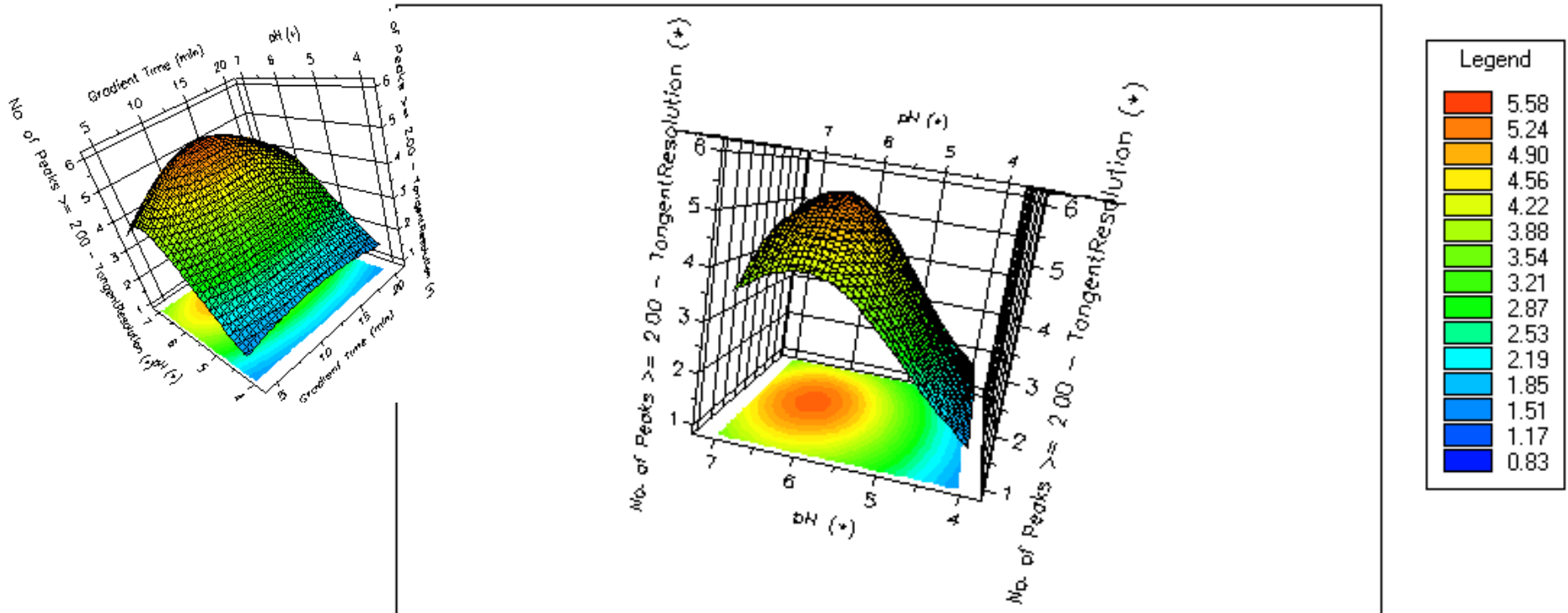


# Column Screening: A Few Examples

- Constant: pH 5.0, ACN, 12 min gradient

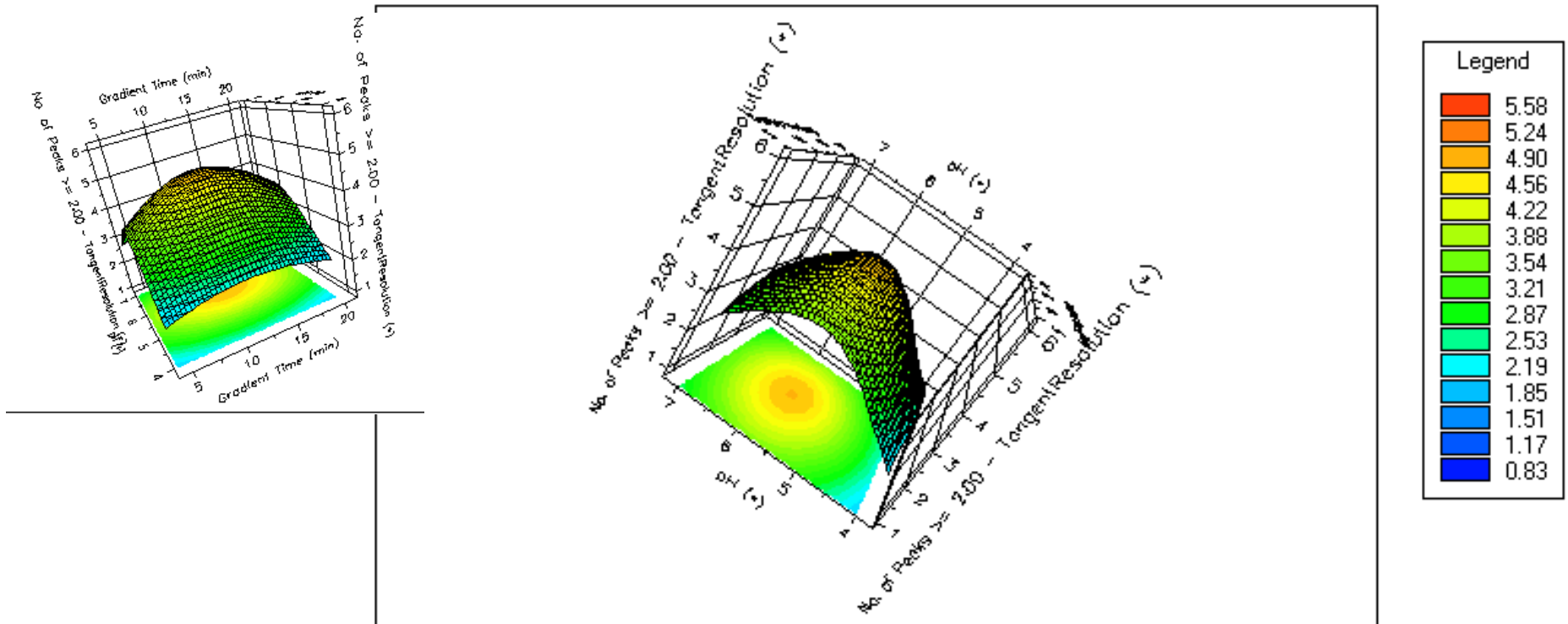


## Number of peaks with resolution $\geq 2$ : ACN Phenylhexyl



*Modeling predicts pH  $\sim$ 6-6.5 optimal for ACN with 10-17 min gradient times (using the resolution  $\geq 2.00$  metric)*

## Number of peaks with resolution $\geq 2$ : MeOH Phenylhexyl



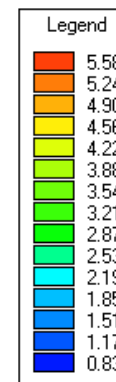
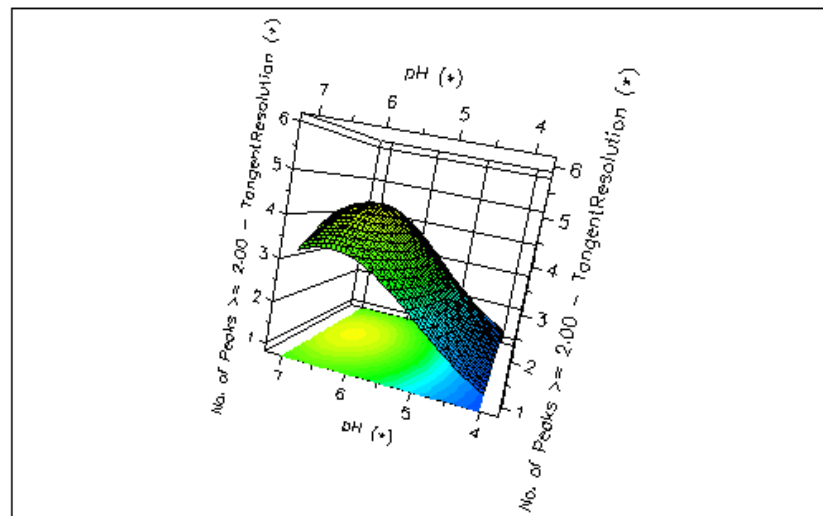
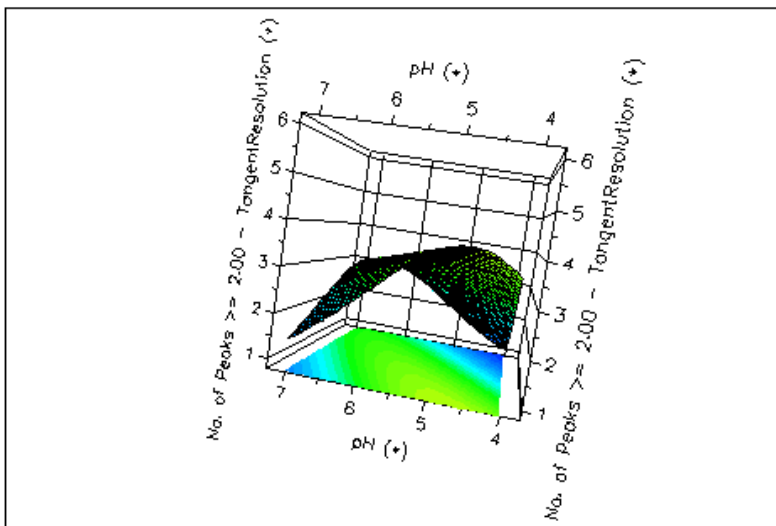
*Modeling predicts pH 5.5-6.0 optimal for MeOH with 10-17 min gradient times*

By comparison PFP and C18 have about 4 peaks with resolution  $\geq 2.00$

MeOH PFP

MeOH C18

Fusion AE Graph



**Best Overall Answer: Phenylhexyl**

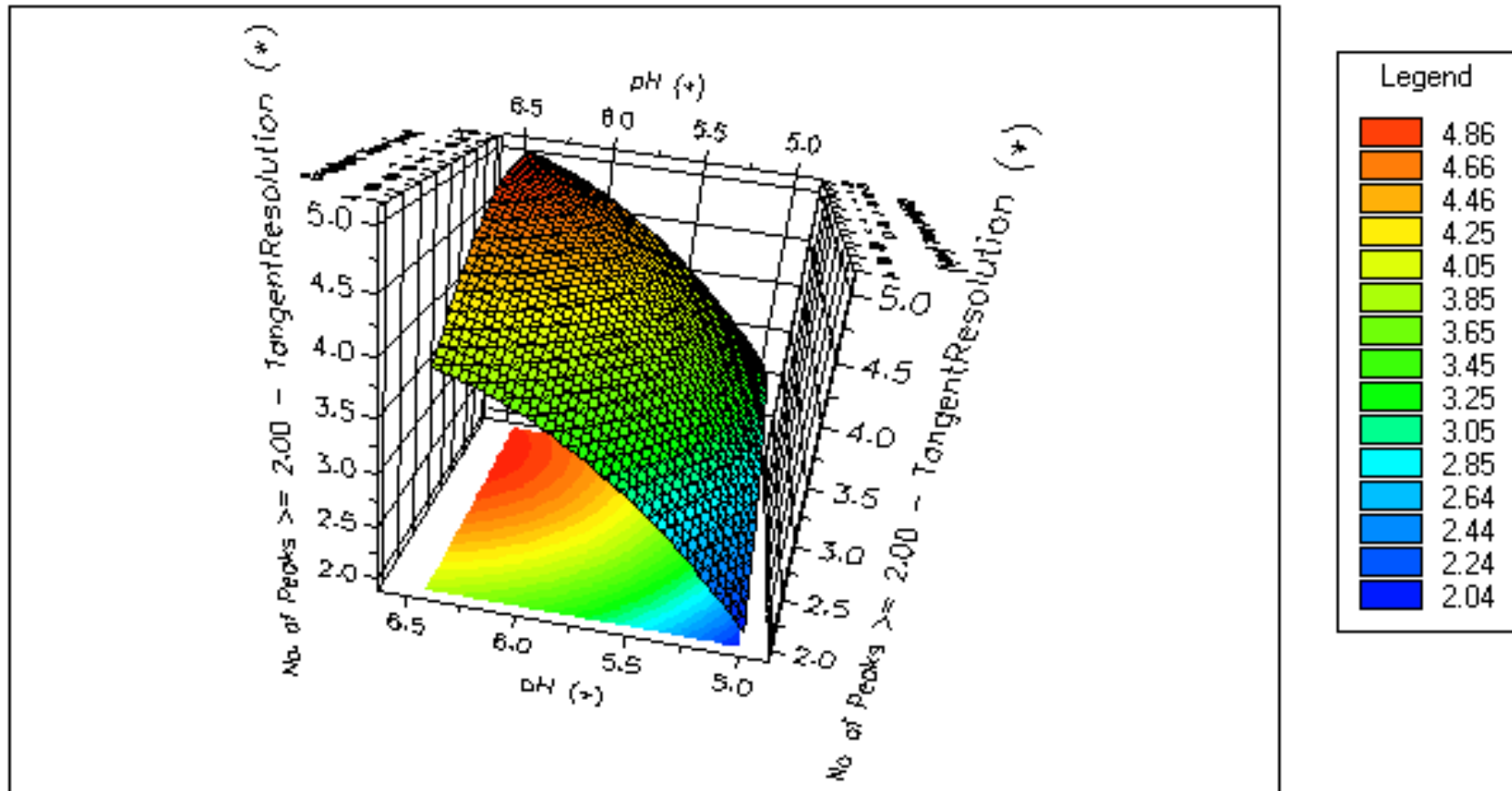




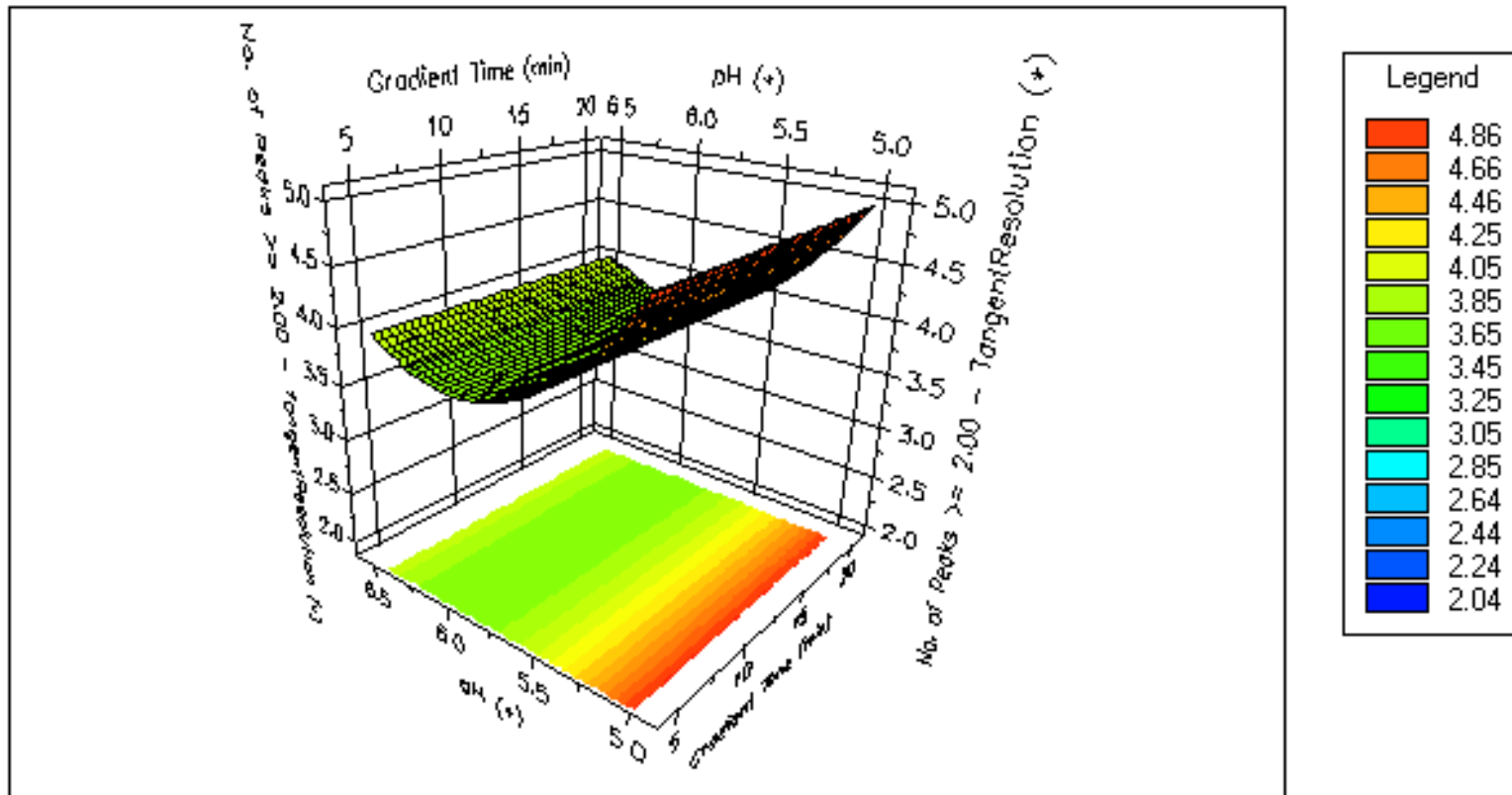
## Screen 2 (19 Experiments)

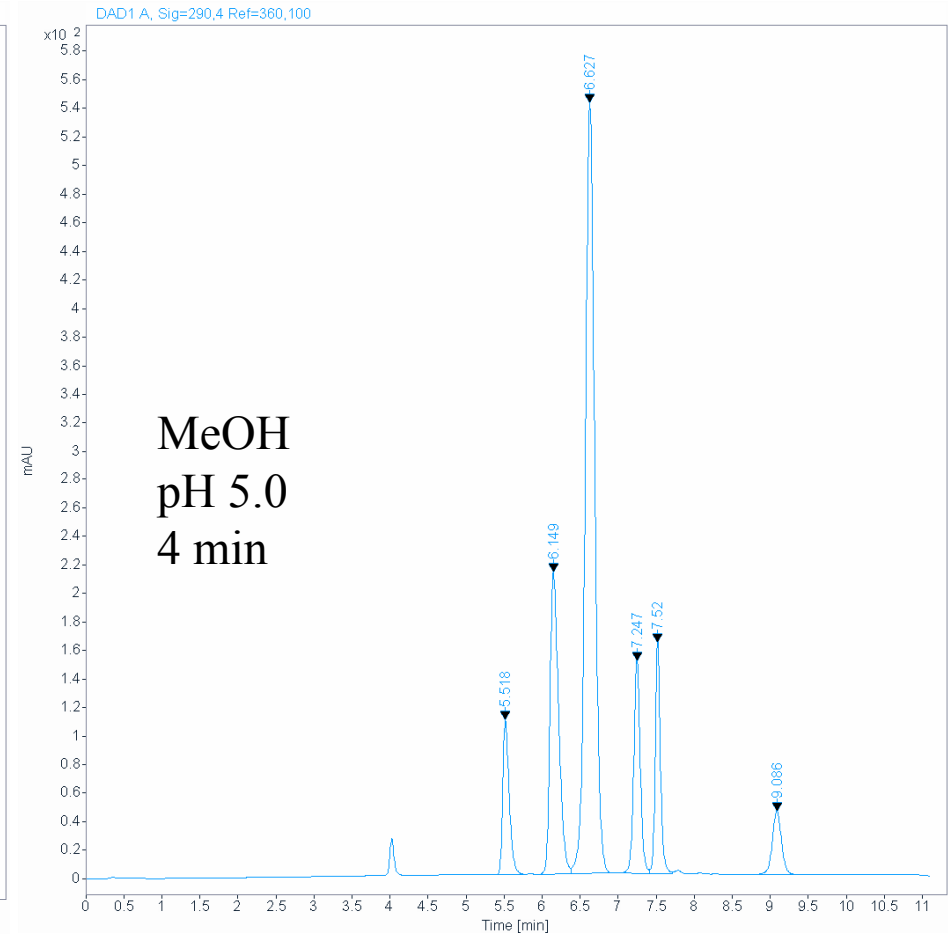
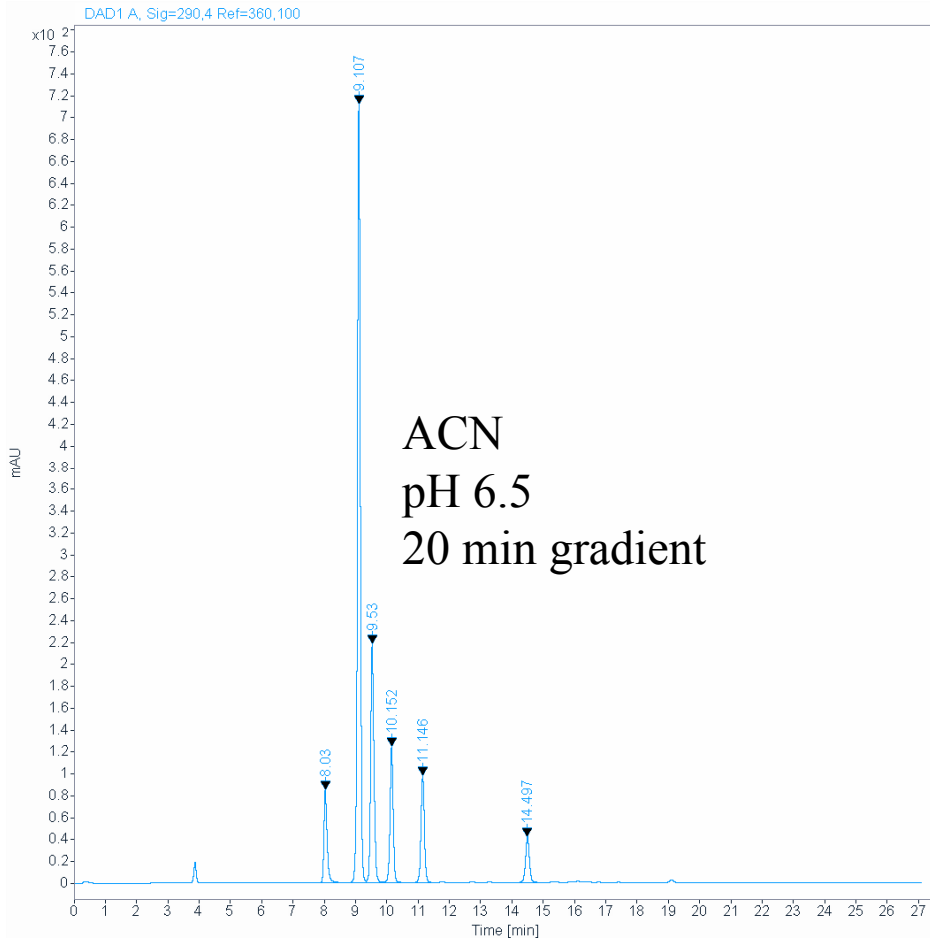
- Phenylhexyl column
- pH 5.0, 5.5, 6.0, 6.5
- ACN vs. MeOH
- Gradient Time: 4-20 minutes (10-55% organic gradient)

# Number of peaks with resolution $\geq 2$ : ACN Phenylhexyl



# Number of peaks with resolution $\geq 2$ : MeOH Phenylhexyl





- Phenylhexyl elution order of Peaks 2 & 3 (L→R) changes between MeOH and ACN
- Peak Areas also change
- Both solvents viable for the ATP, ACN chosen for # plates, sharpness of peaks, and slightly better resolution



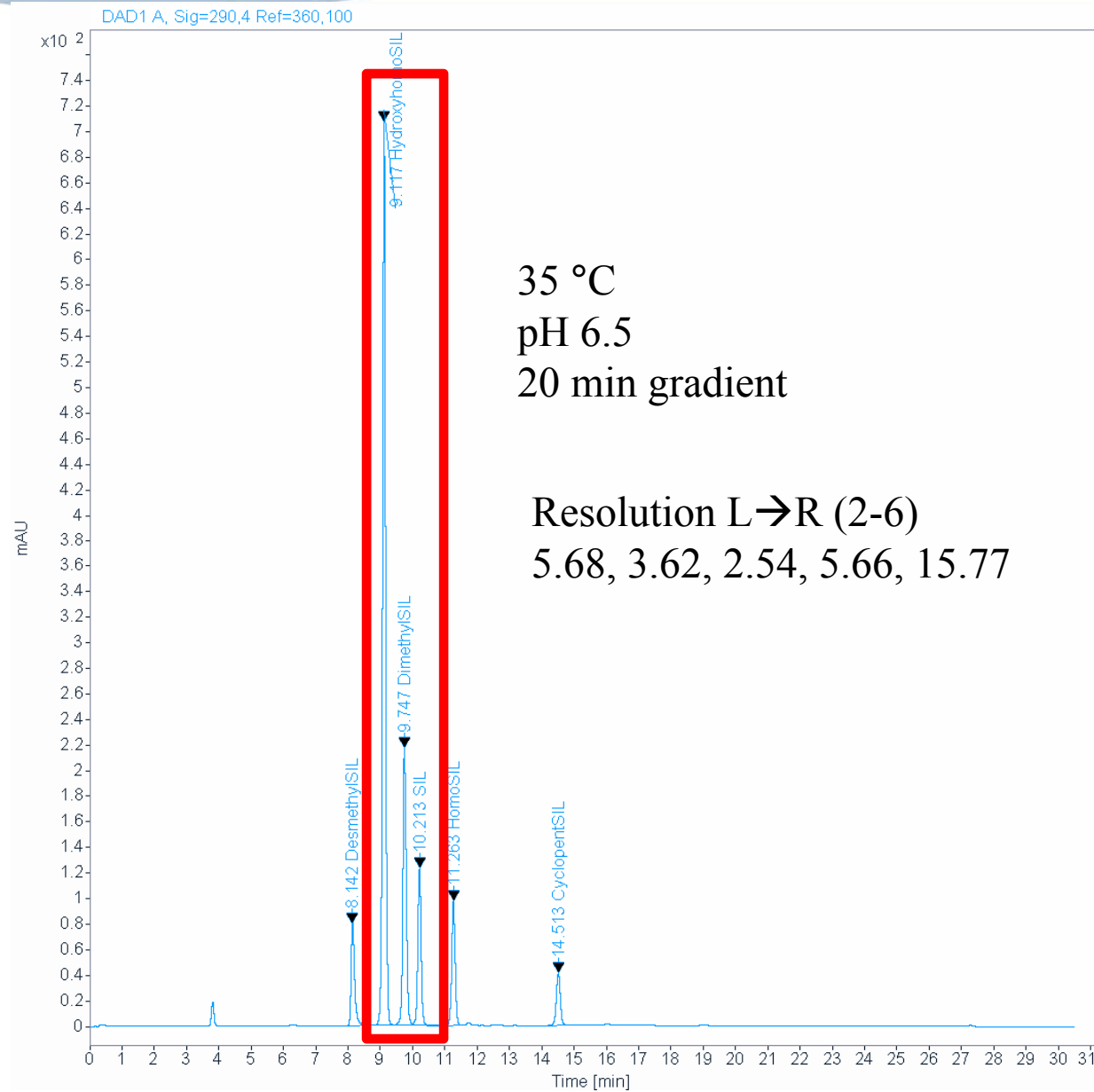
## Screen 3 (16 Experiments)

- Phenylhexyl & ACN constant
- pH 5.90, 6.10, 6.30, 6.50
- Column temp 30, 35, 40, 45 °C
- Gradient Time: 10-20 minutes (10-55% organic gradient)



## Sample of Screen 3 Experiments

Run No.	Sequence No.	Gradient Time	Oven Temperature	pH	No. of Peaks
Condition Column - 1	1	2	30	5.9	
1	1	20	30	5.9	5
2	1	10	30	5.9	6
3	1	10	30	5.9	6
Condition Column - 2	1	2	35	6.11	
4	1	15	35	6.11	6
5	1	15	35	6.11	6
6	1	17.5	35	6.11	6
7	1	12.5	40	6.11	6
Condition Column - 3	1	2	45	5.9	
8	1	15	45	5.9	5
Condition Column - 4	1	2	45	6.11	
9	1	20	45	6.11	6
10	1	10	45	6.11	6
Condition Column - 5	1	2	45	6.11	
Condition Column - 6	2	2	30	6.51	
11	2	15	30	6.51	6





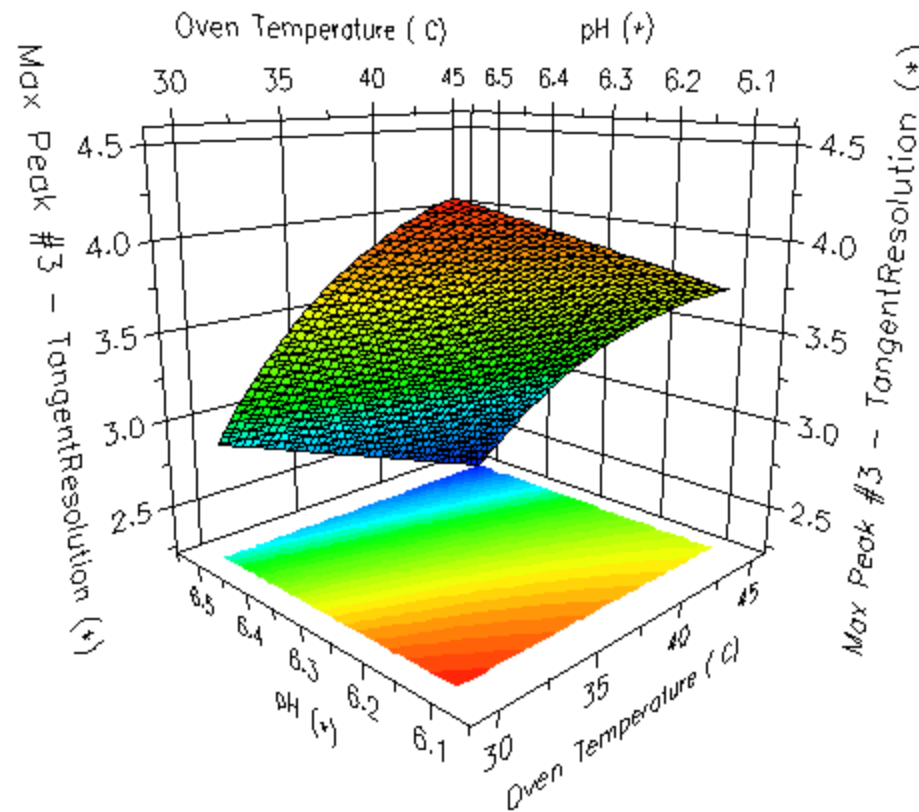
## Example of a Resolution Model Eqn.

- Peak 3 resolution

$$R = 3.0607 + 0.4109(\text{GT}) - 0.3367(\text{Temp}) \\ - 0.7772(\text{pH}) - 0.2013(\text{pH})^2$$



# Example of a Resolution Model Eqn. Predicted Response



## Analysis of Robustness

- Method capability: Resolution criteria

$$C_{pk} = \frac{R - LSL_{ATP}}{3\sigma}$$

$\sigma$  = response standard deviation

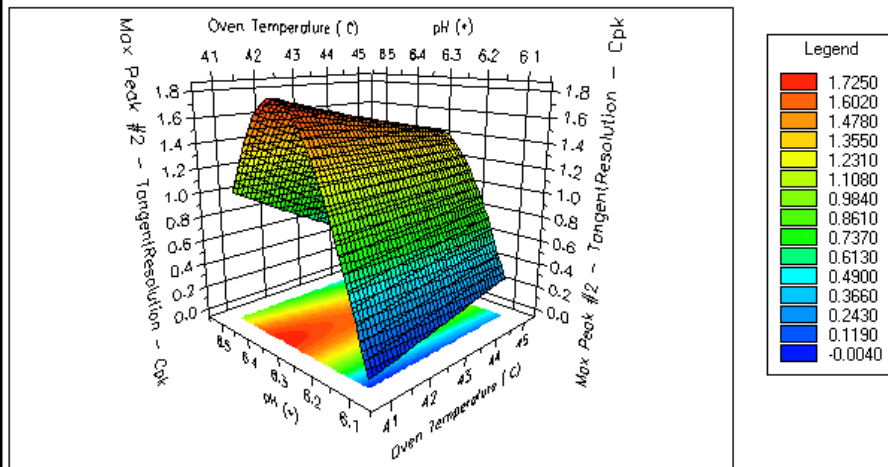
- Monte Carlo simulation using model equation estimates  $\sigma$  for specified response
  - pH  $\pm$  0.1, Temp  $\pm$  2°C, Gradient  $\pm$  0.25 min
  - Normally distributed
- Require  $C_{pk} \geq 1.33 \rightarrow R - 1.5 \geq 4\sigma$ .



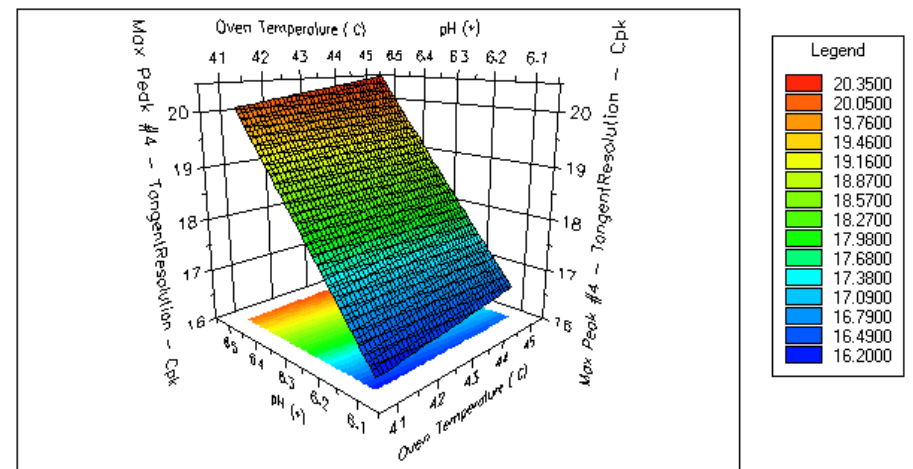
$C_{pk}$  of Res<sub>1-2</sub> : Range = 0 - 1.75, Robust region at surface ridge, sensitive to pH\*Temp.

$C_{pk}$  of Res<sub>3-4</sub> : Range > 16, linear in pH but not Temp.

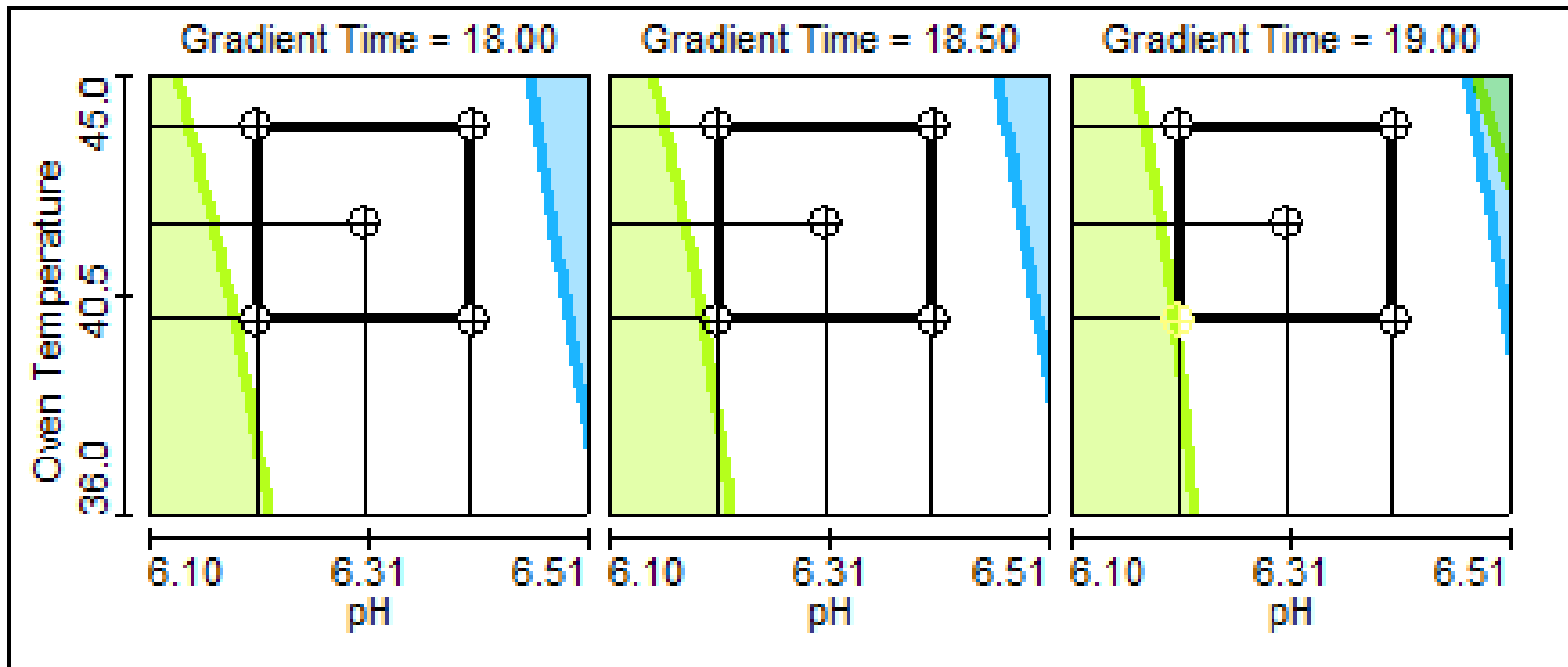
Peak 2 resolution Cpk: Gradient Time – 20 min.



Peak 4 resolution Cpk: Gradient Time – 20 min.



# Method Robustness: Operable Region



- Corners:  $C_{pk} = 1.33$  for Resolutions 2, 3 and 4
- Ranges: pH  $6.30 \pm 0.1$ , Gradient  $18.5 \pm 0.5$  min, Temp  $42 \pm 2$  °C

## Optimal Conditions

- Phenylhexyl is the best column
  - Literature methods use C18
- Acetonitrile gives best peak shape and resolution.
  - MeOH/Phenylhexyl can support a method that meets the ATP. This is extremely useful information for method understanding
- Gradient time, pH, column temperature have been optimized



## Future Work and Interesting Questions

- Method validation for quantitative work
- Further exploration of method robustness and ruggedness
- Designing methods and models that incorporate multiple columns and organic phases



## Acknowledgements

- **Sergey Arzhantsev: IT support**
  - Making Fusion work with Agilent ChemStation implemented on OpenLab ECM
- **Richard Verseput: S-Matrix support**
- **Cindy Buhse: Acting Director, CDER/OPQ  
Office of Testing and Research**



**U.S. Food and Drug Administration**  
Protecting and Promoting Public Health

[www.fda.gov](http://www.fda.gov)

**Thank You!**