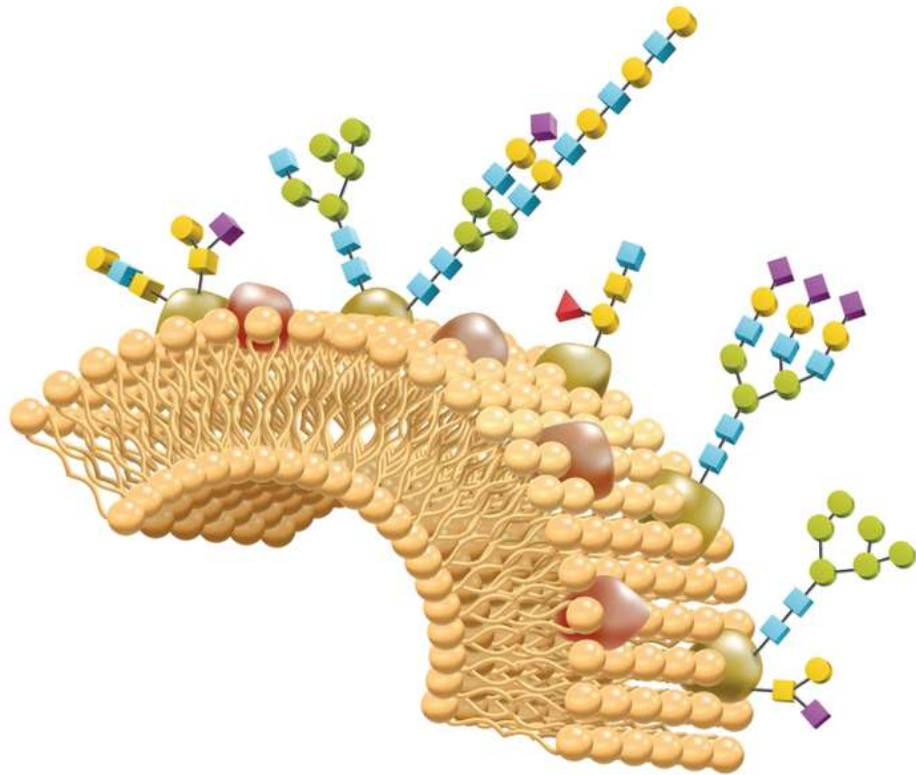


# Enhancing Glycopeptide Detection, Identification, and Characterization through PGC-Incorporated LC-MS

**Pittcon 2021**

Graham Delafield  
University of Wisconsin - Madison

# Introduction



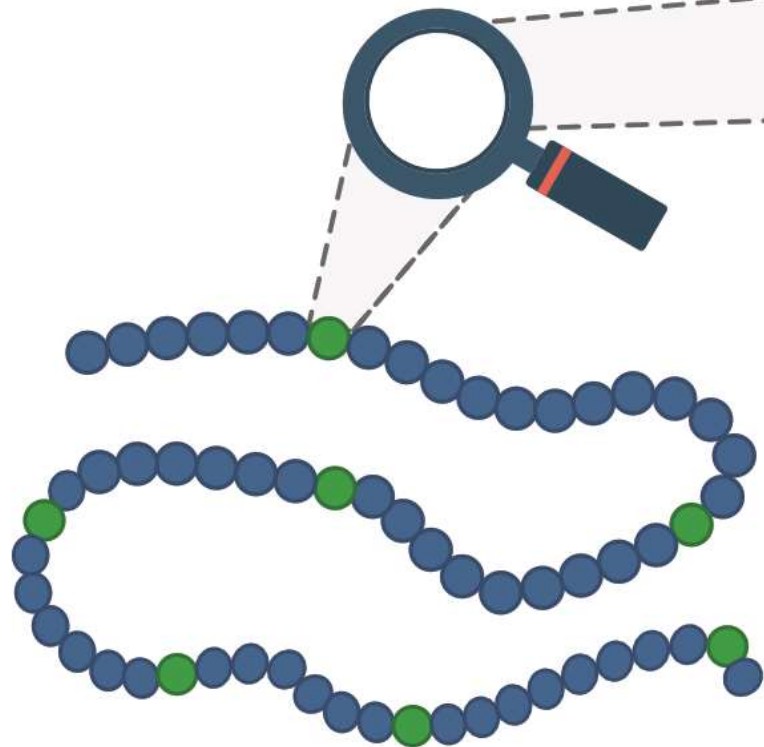
## Function

Cellular communication and immune response  
Intrinsic/extrinsic signaling pathways  
Protein folding and viability

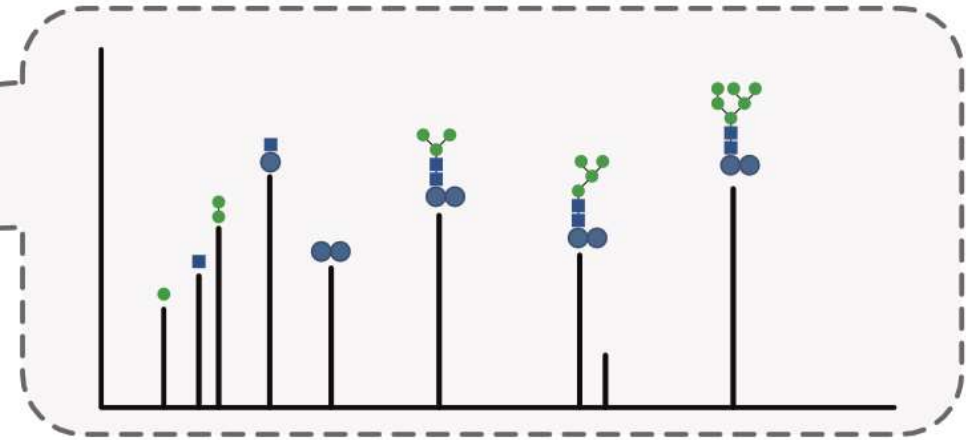
## Disease

Target for pathogen invasion  
Altered expression during disease propagation  
Aberrant profiles across numerous disease

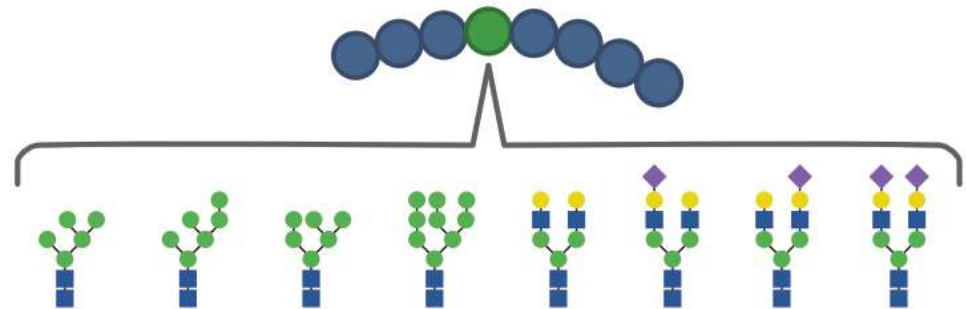
# Glycoproteomic Need



Glycosite Identification



Adequate Fragmentation



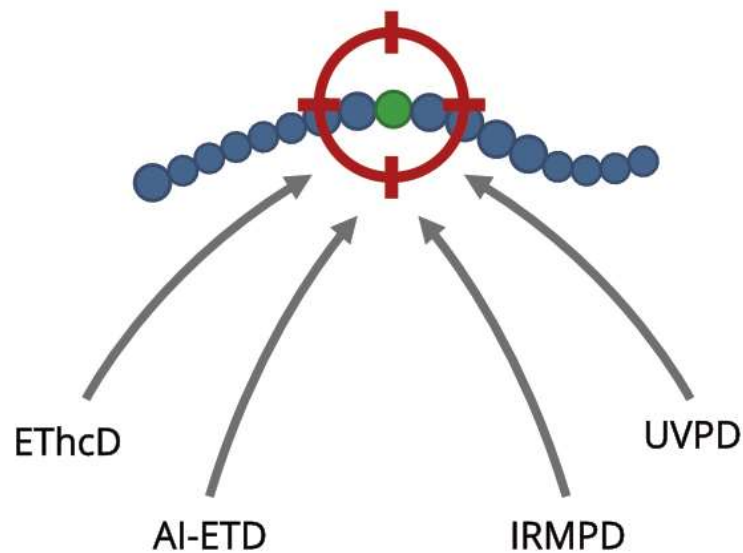
Microheterogeneity Profiling

# Areas of Interest

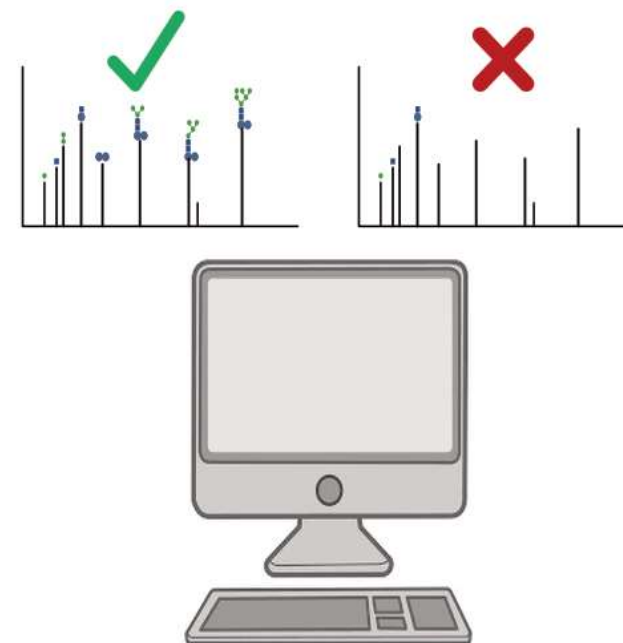
Enrichment



Dissociation



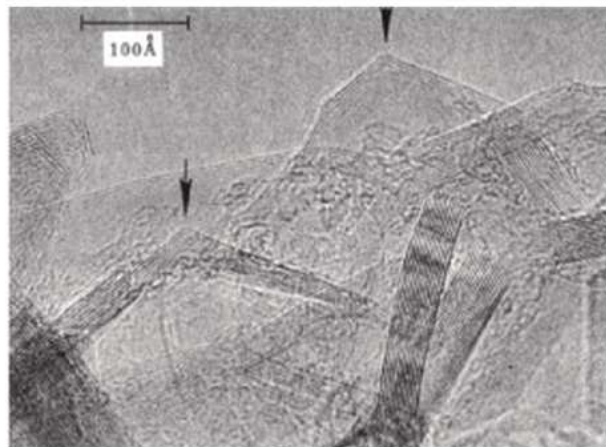
Spectral Scoring



# Alternative Separation



RPLC C18

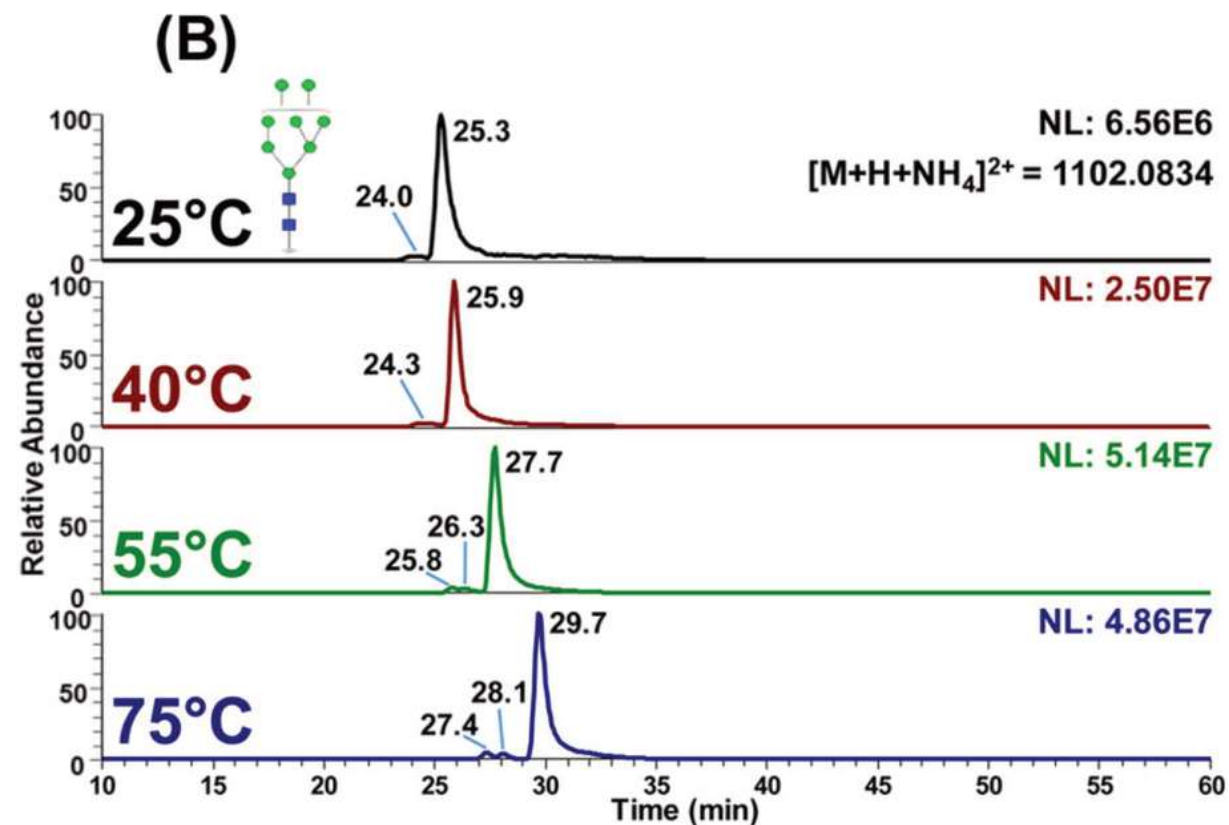
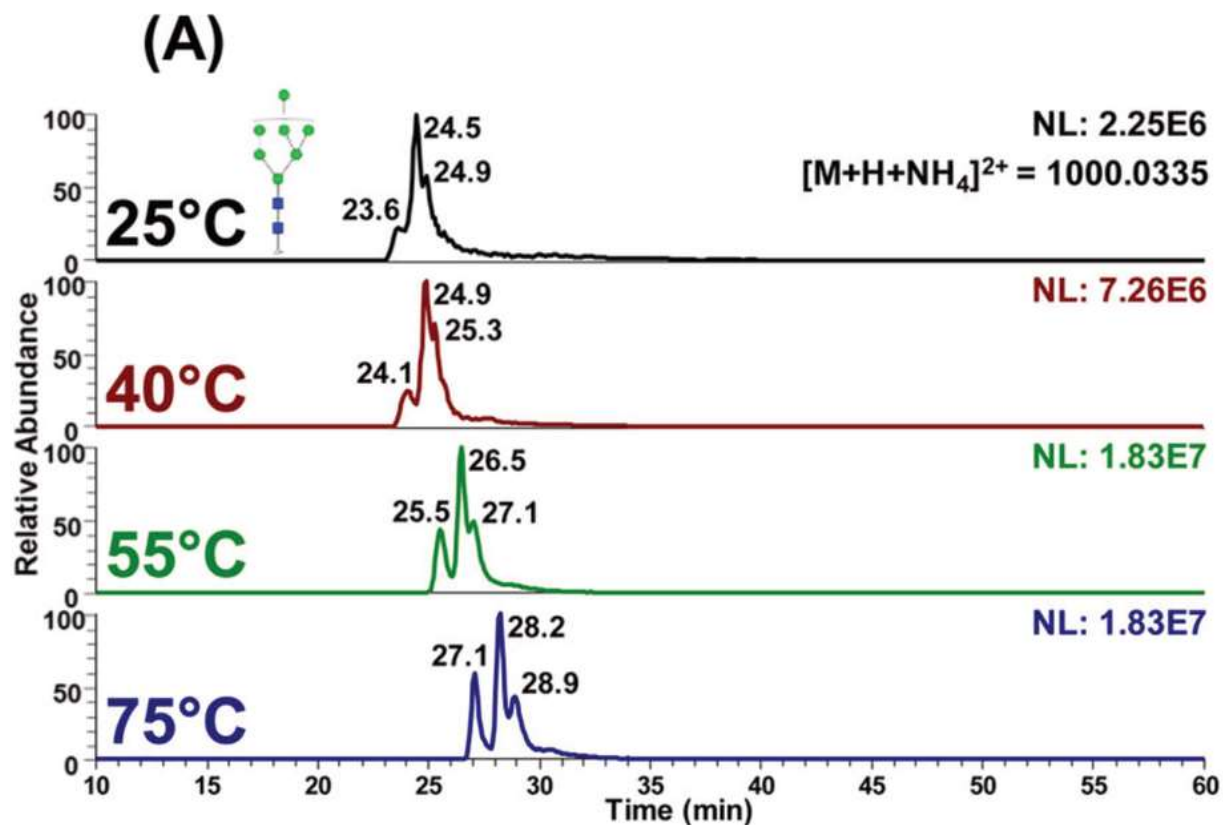


PGC

## Porous Graphitic Carbon (PGC)

1. Polar and electrostatic interactions
2. Solvent flexibility, compatible with traditional buffer systems
3. Improved glycan retention and separation

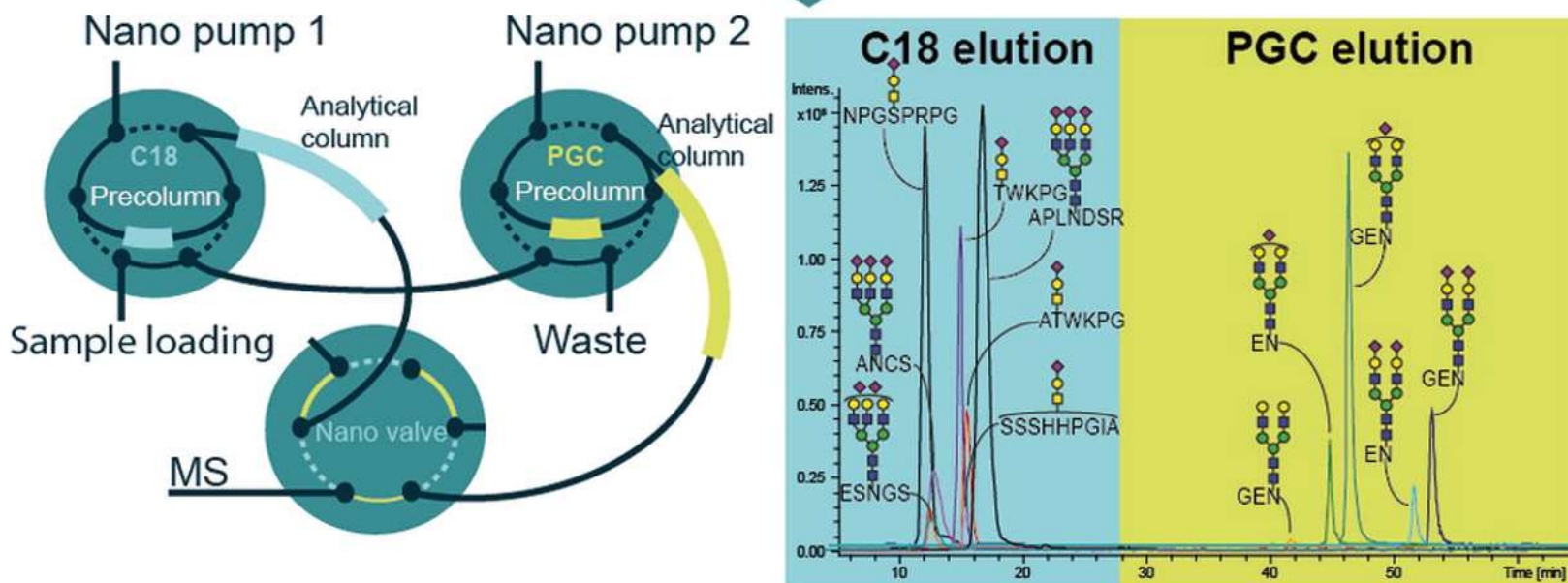
# PGC Application



# PGC Application

1.) N- and O-glycopeptides after Pronase treatment

2.) C18-PGC-LC



3.) QTOF-MS/MS with lower- and enhanced-energy CID

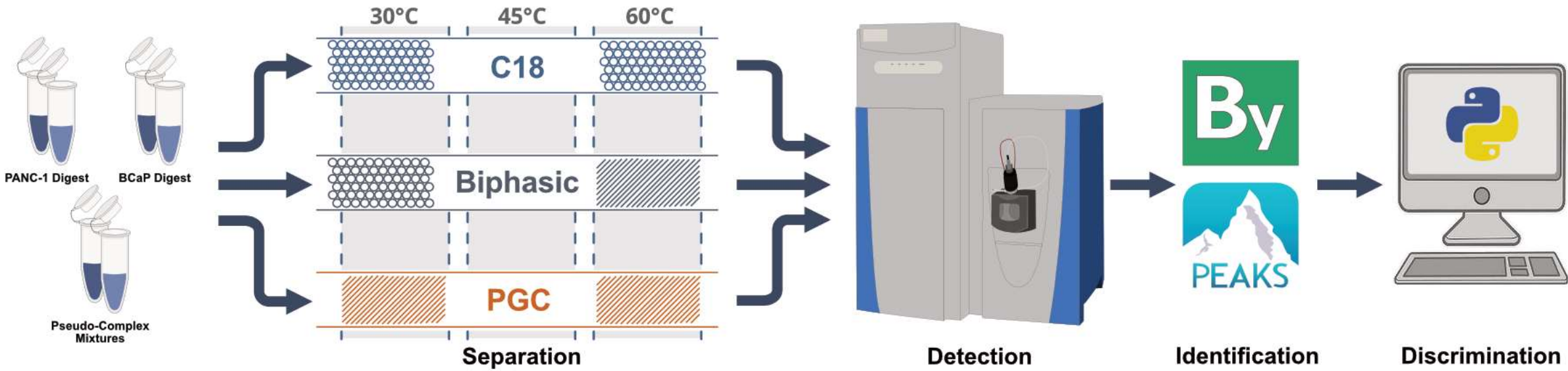
# Knowledge Gap

Searching for a compliment to traditional liquid phase separations that provides:

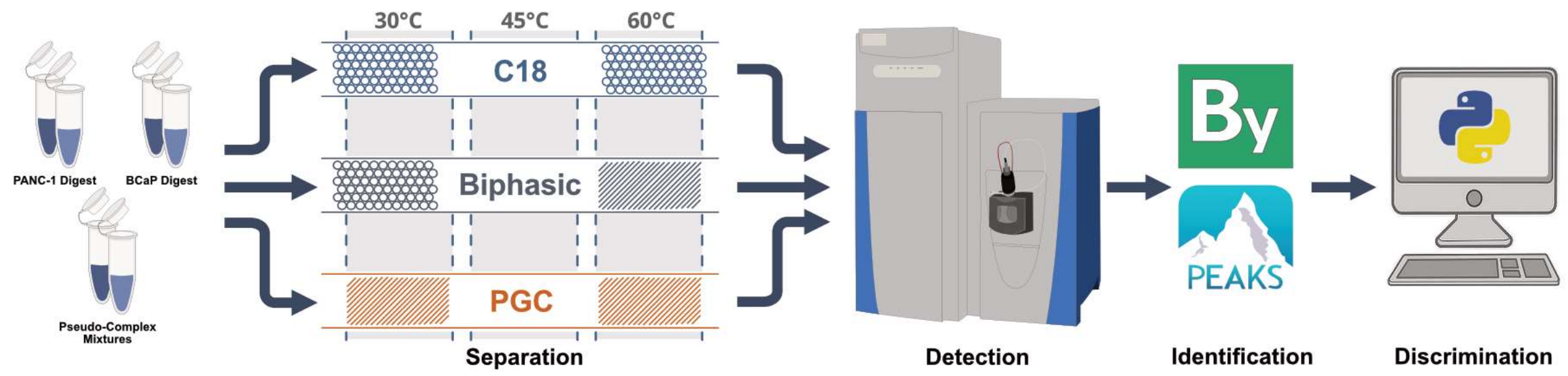
1. Access to proteome components traditionally missed in RPLC analyses
2. Expanded glycoproteome coverage
3. Improved liquid-phase separation of isomeric glycopeptides
4. Path toward facile characterization of disease-specific analytes



# Methodology

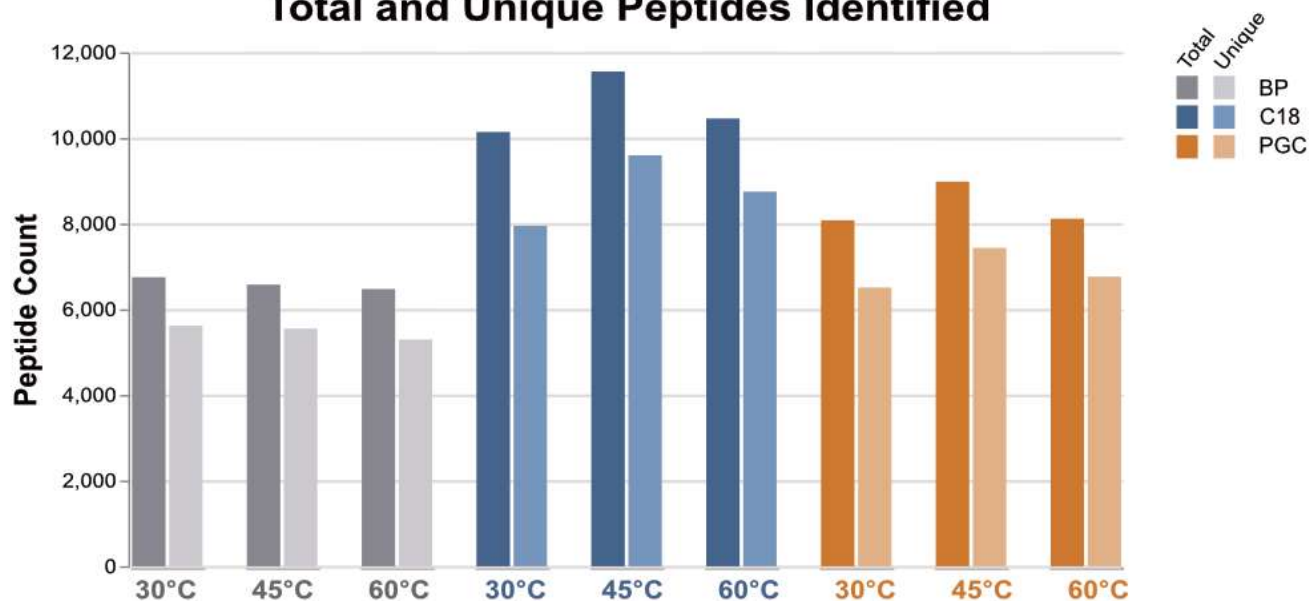


# Methodology

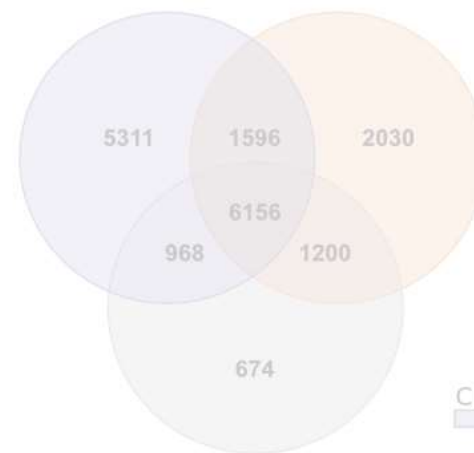


# Proteome Coverage

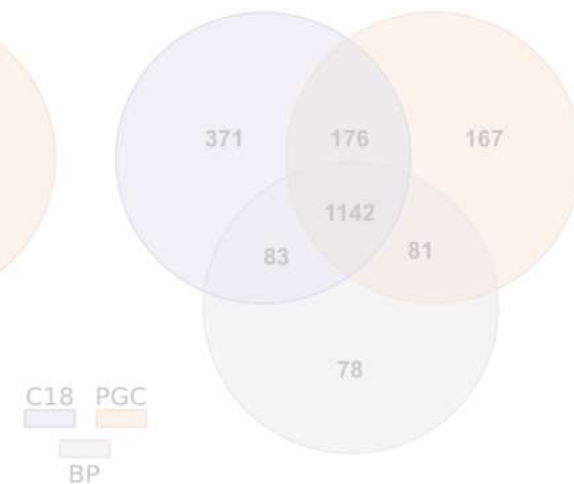
**Total and Unique Peptides Identified**



**Peptide Overlap**

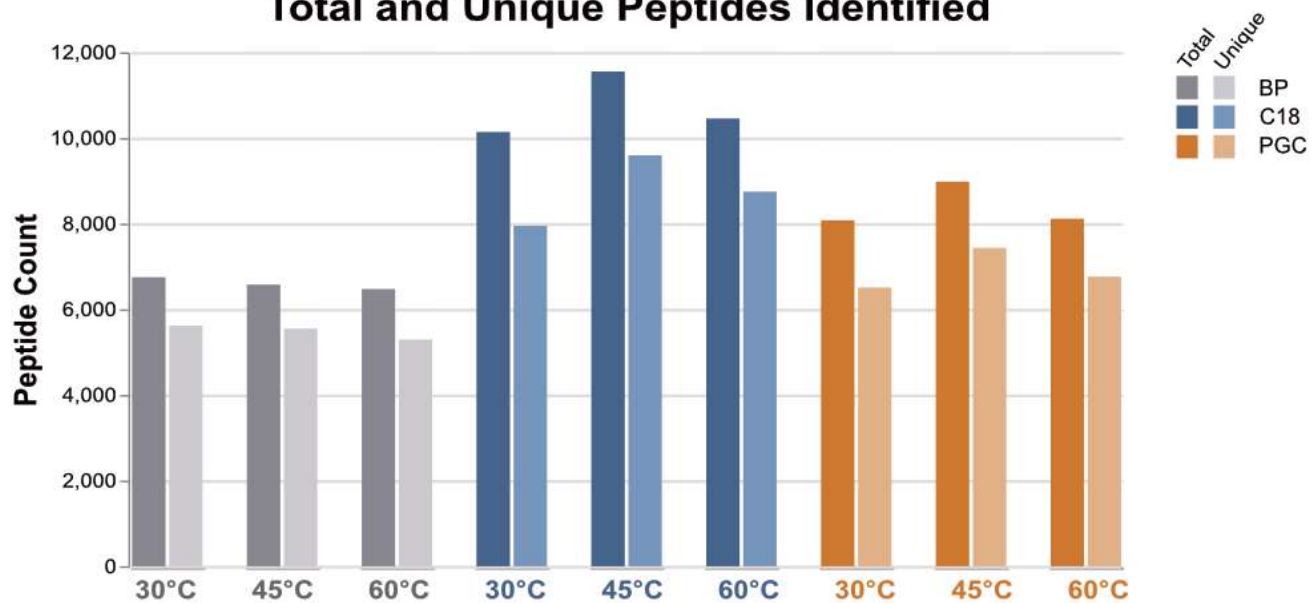


**Protein Overlap**

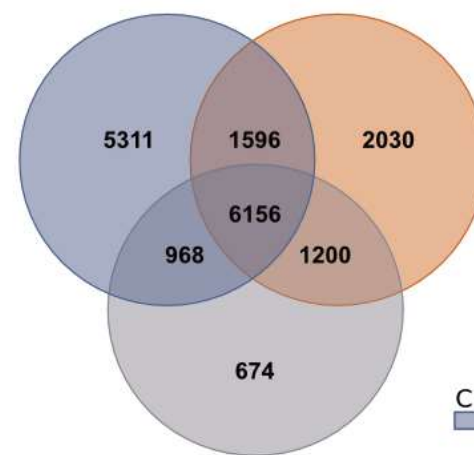


# Proteome Coverage

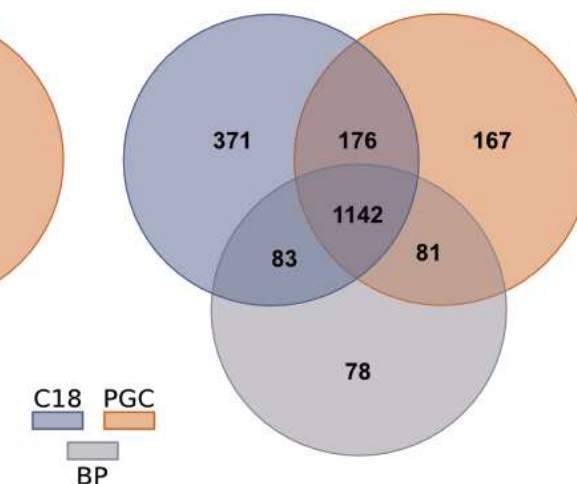
**Total and Unique Peptides Identified**



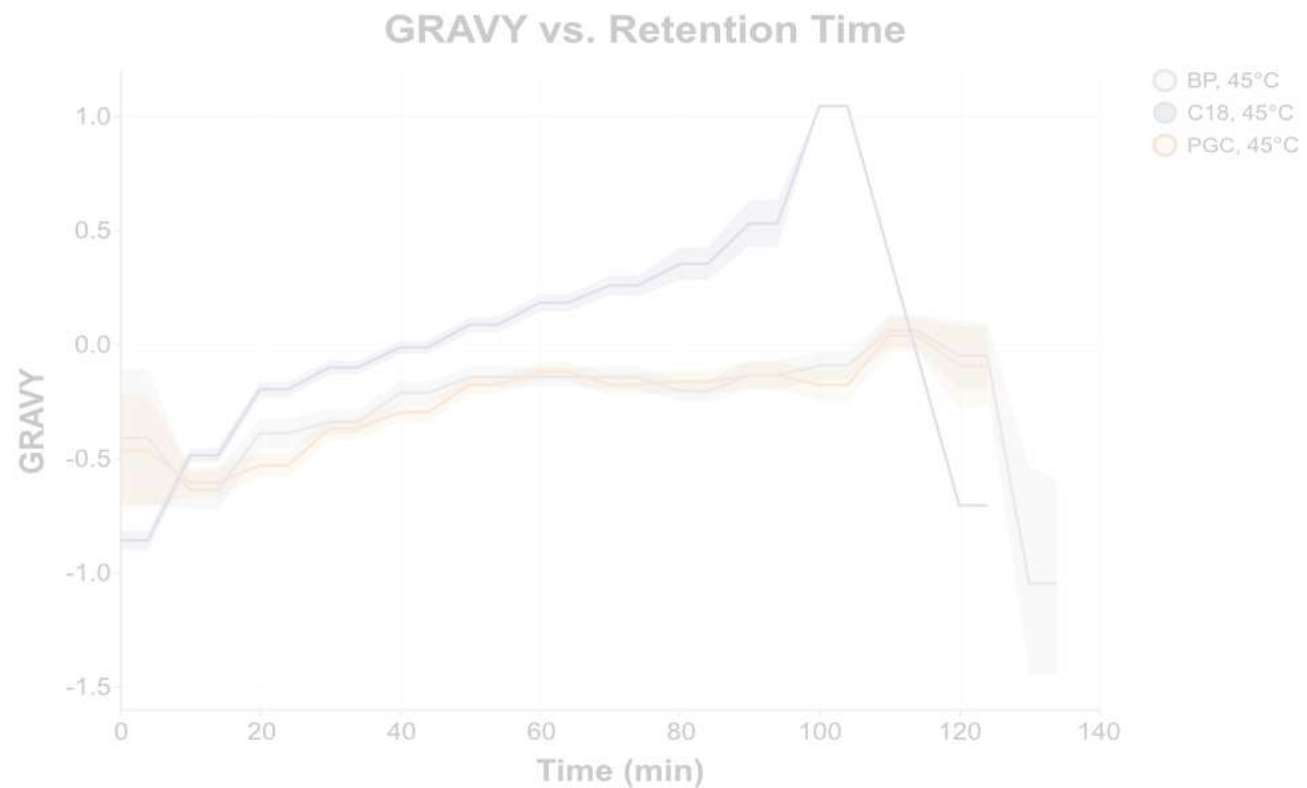
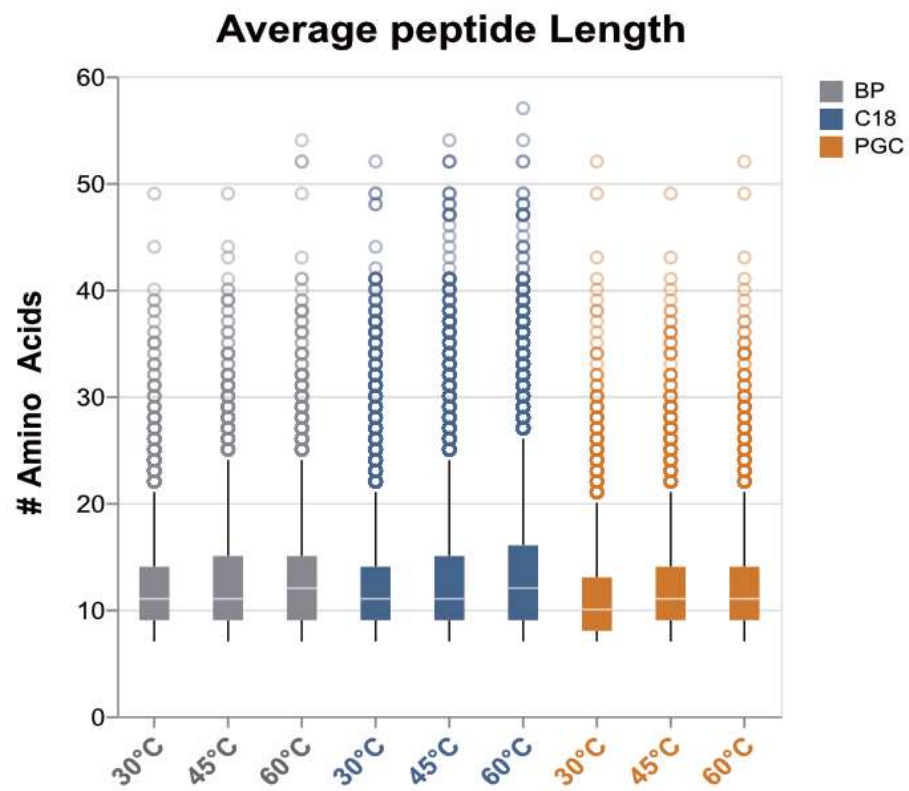
**Peptide Overlap**



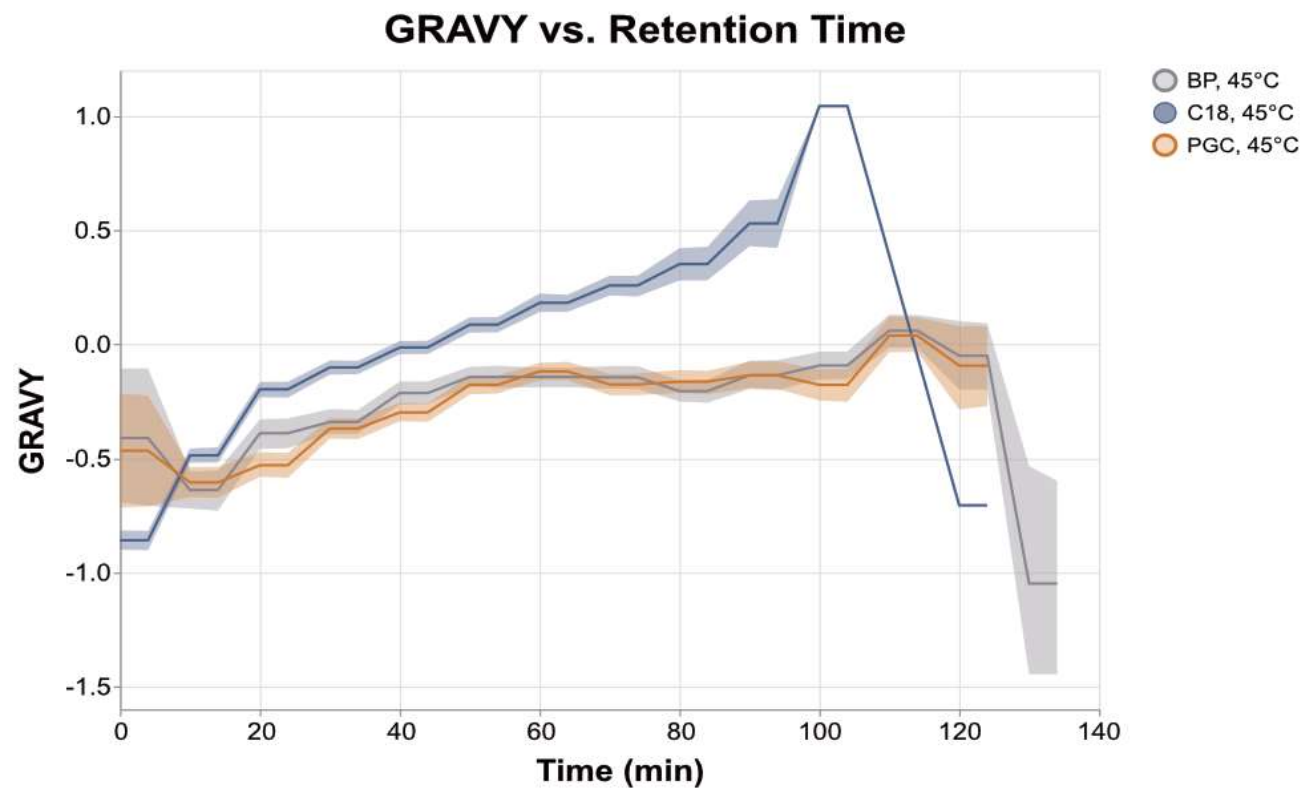
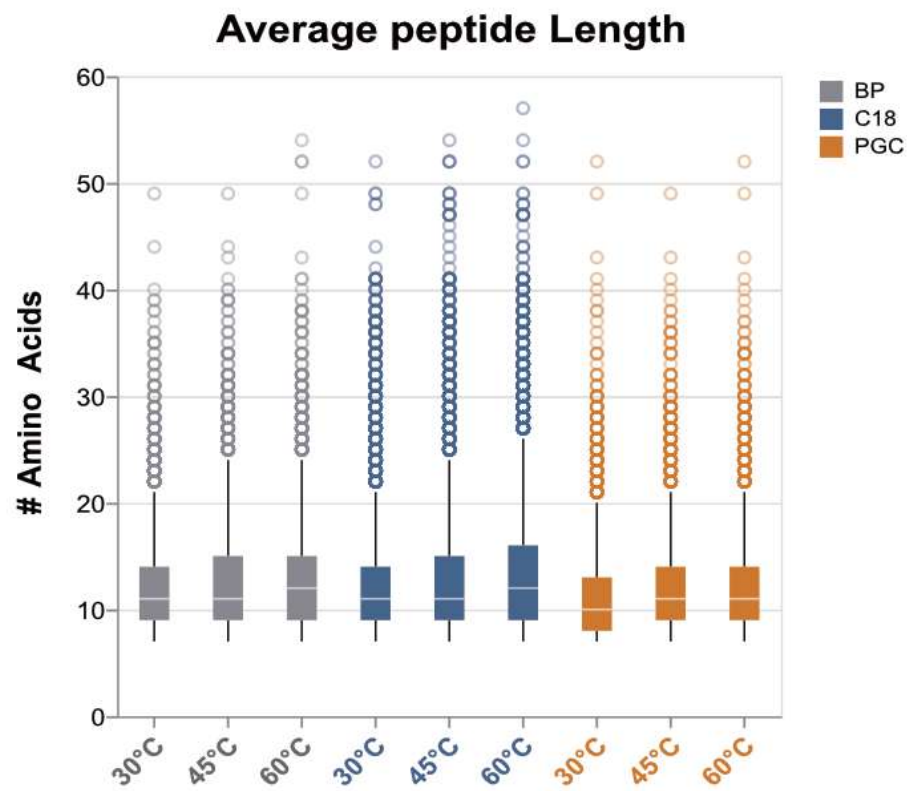
**Protein Overlap**



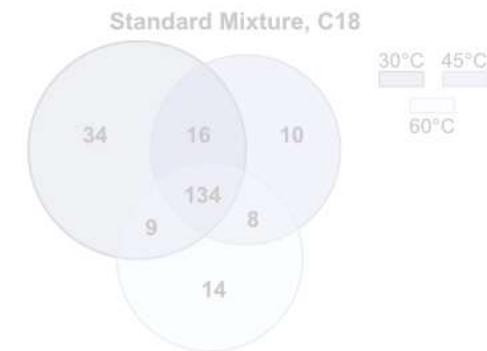
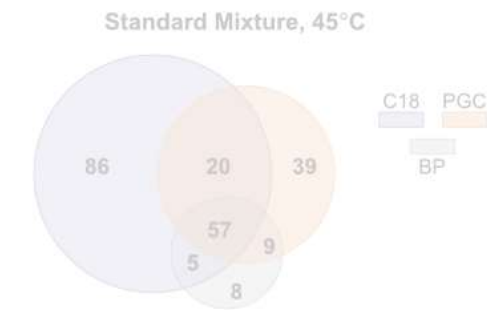
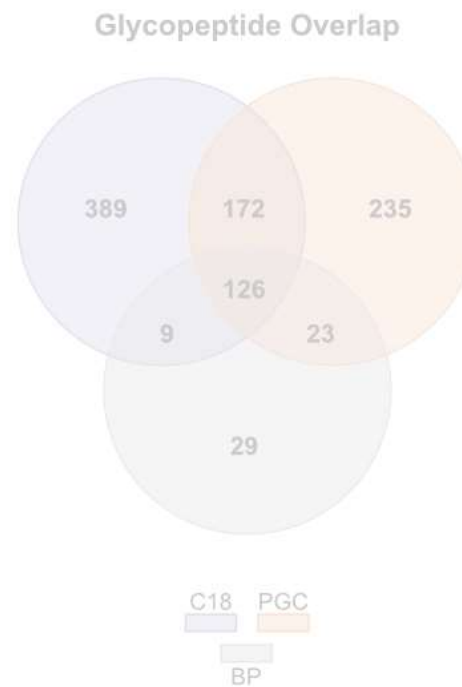
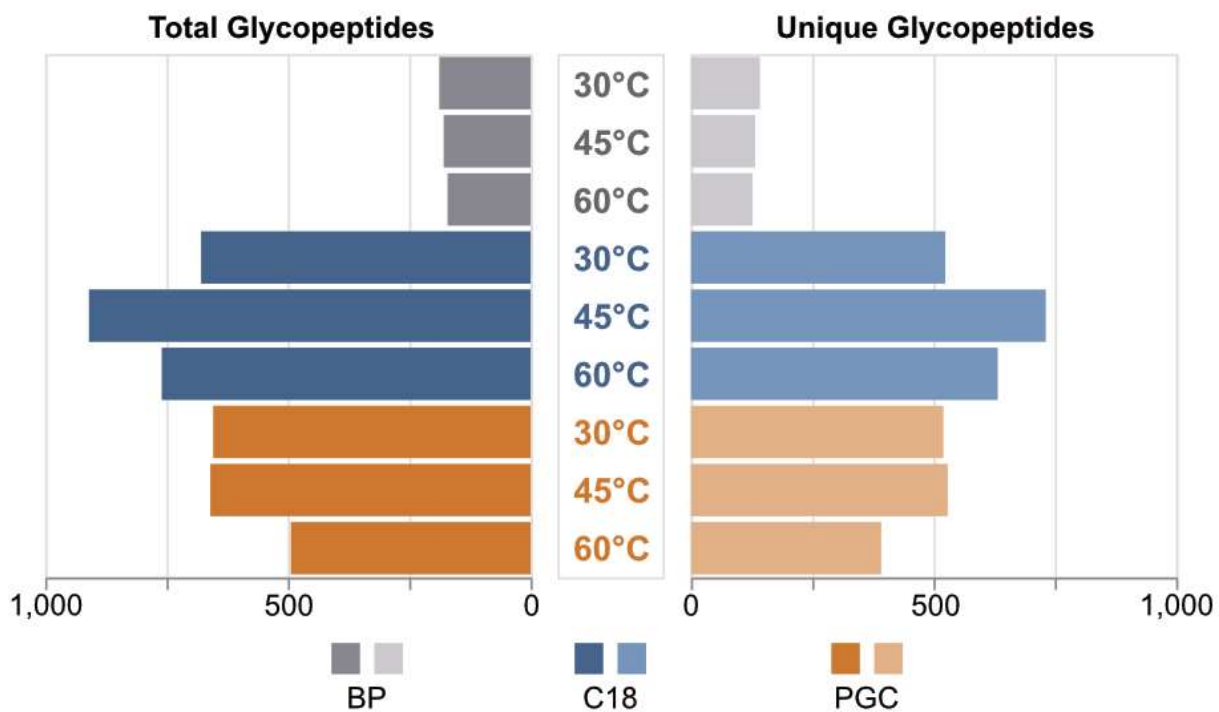
# Peptide Character



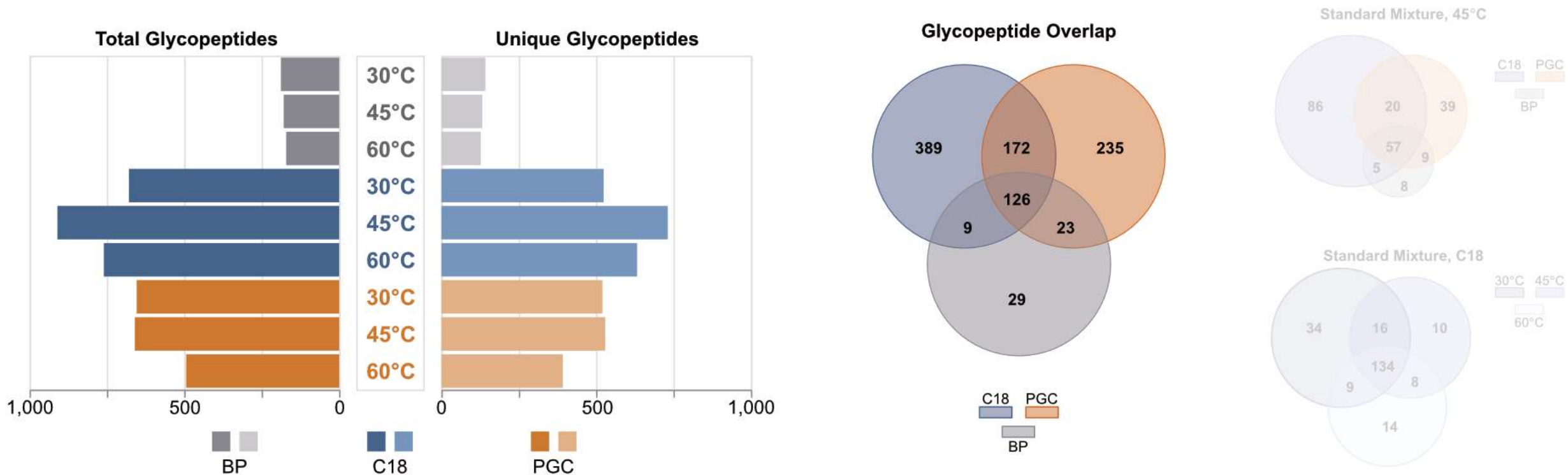
# Peptide Character



# Glycopeptide Detection

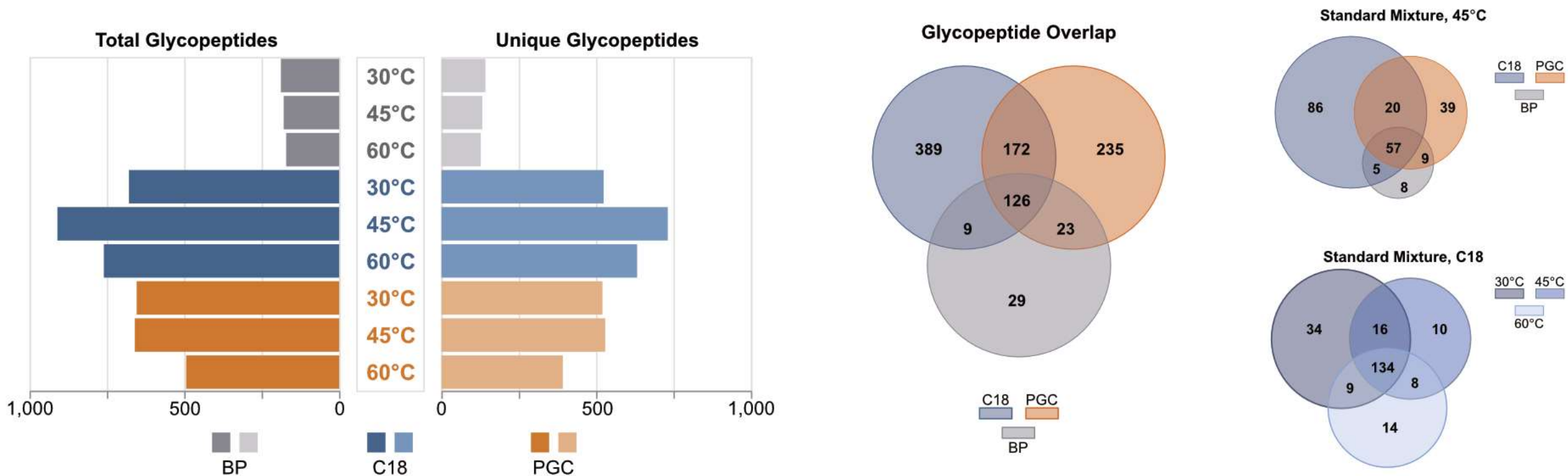


# Glycopeptide Detection

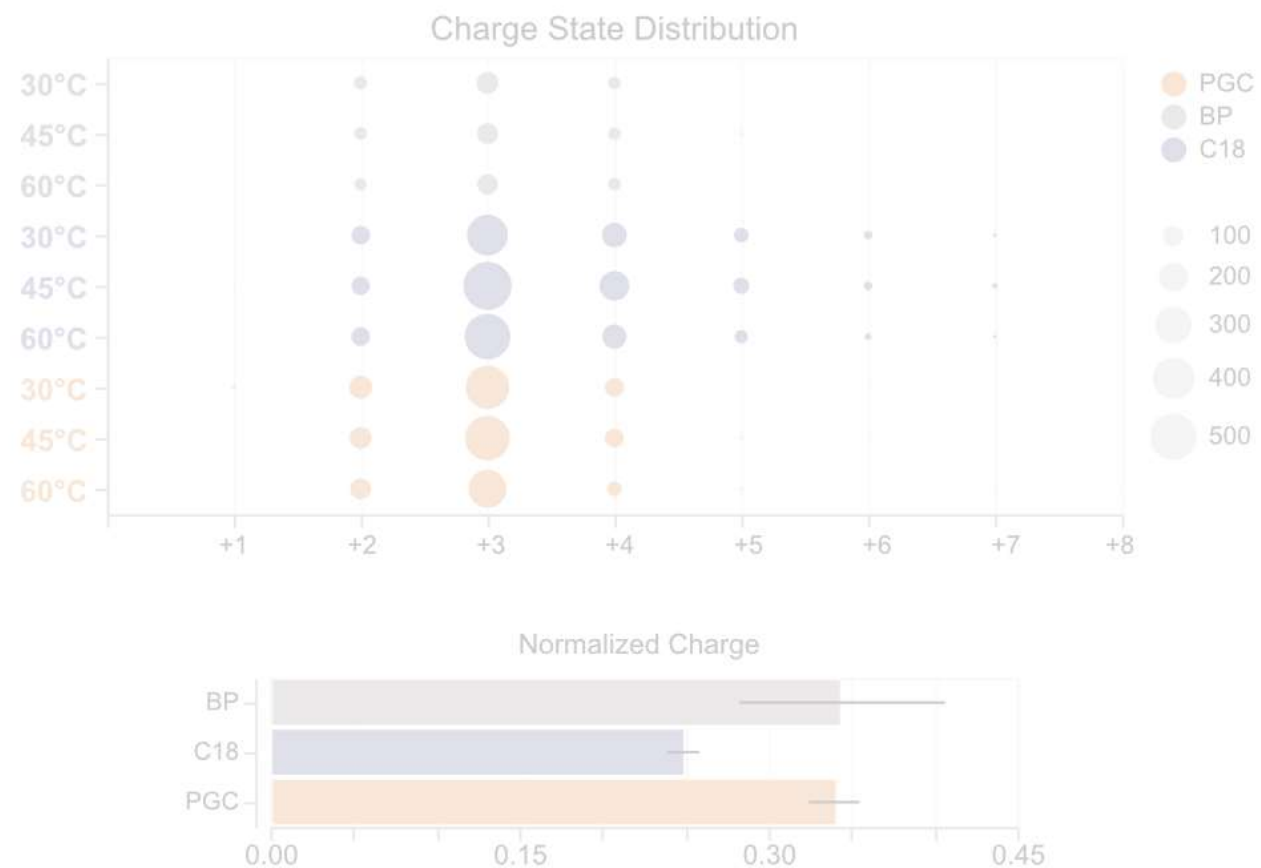
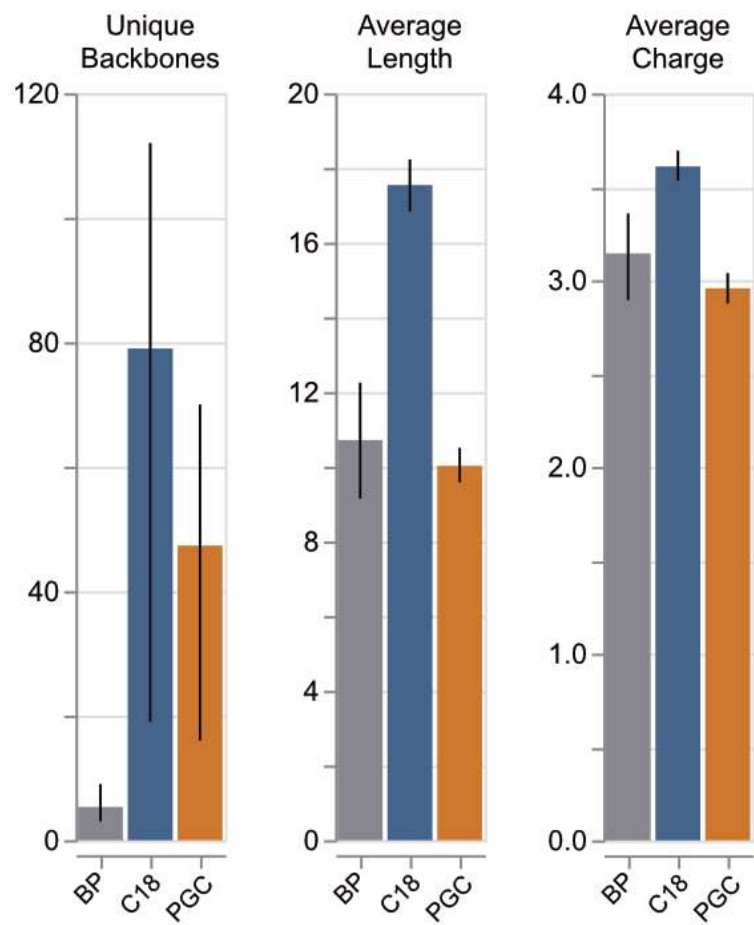




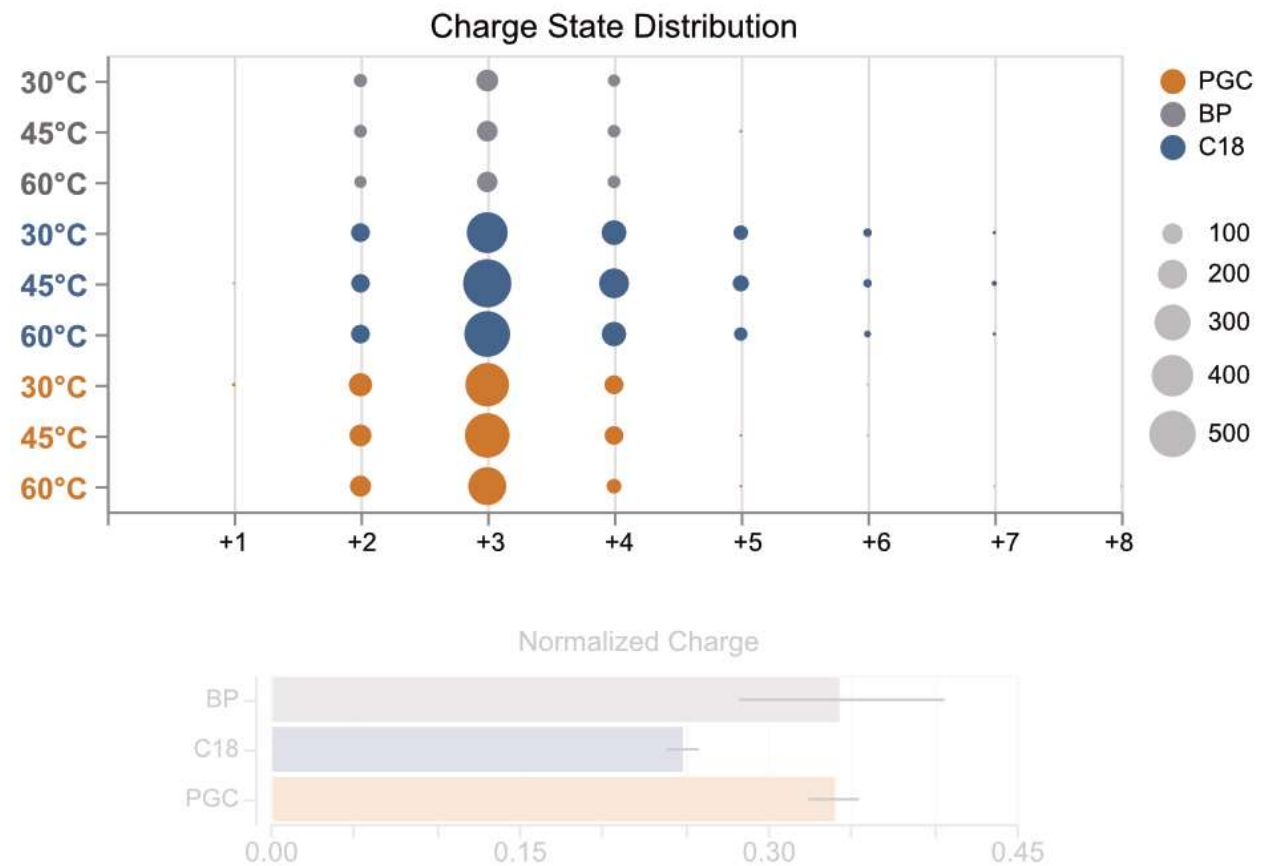
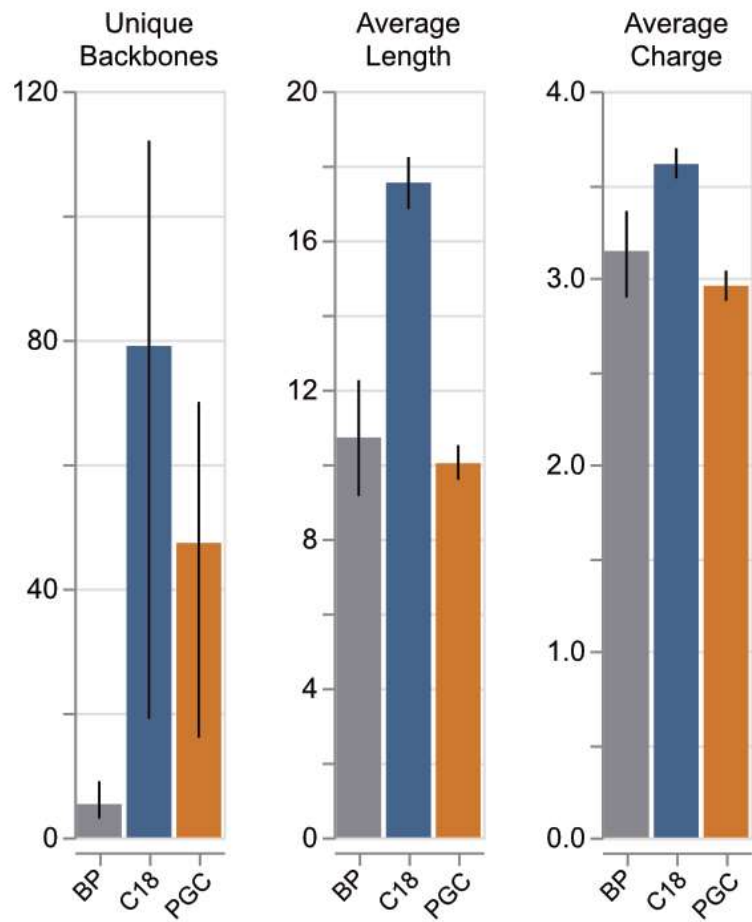
# Glycopeptide Detection



# Peptide-level Differences

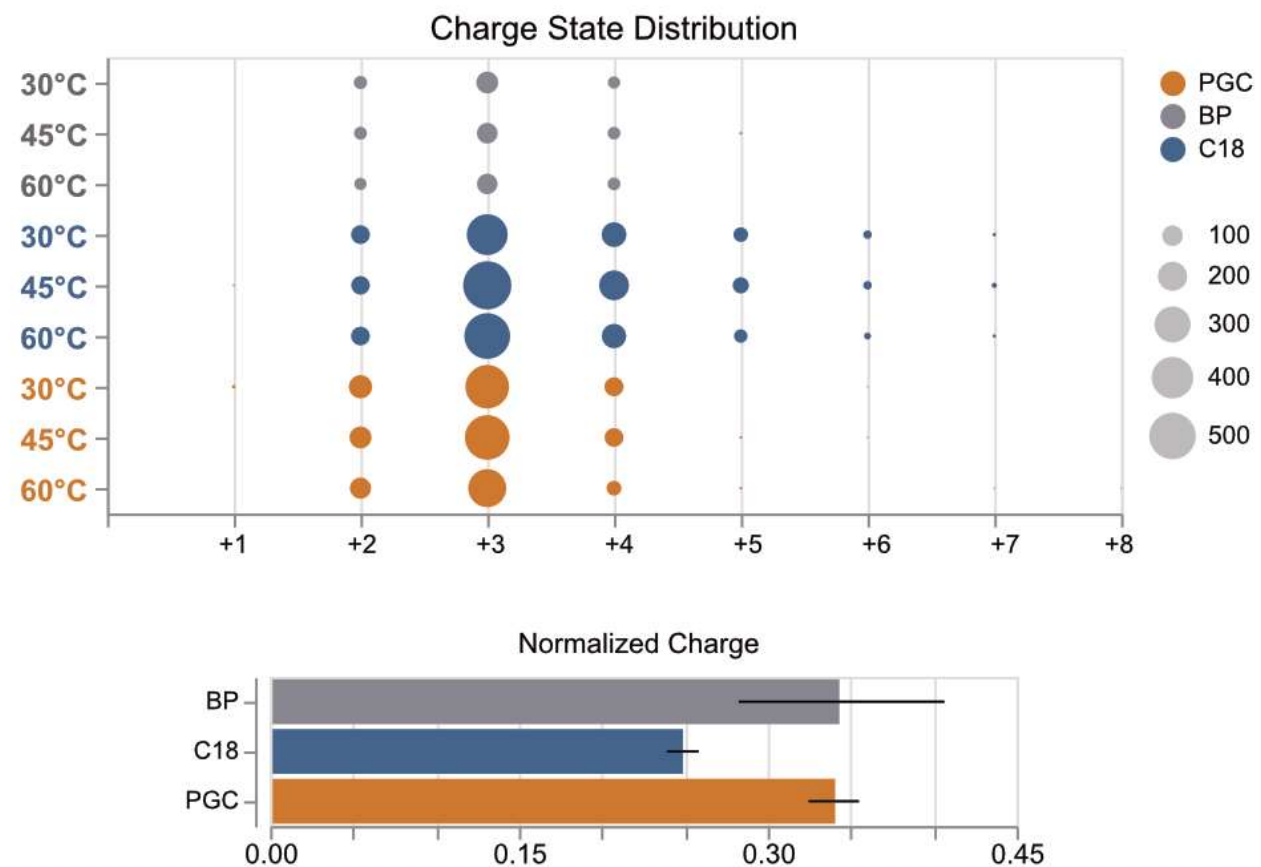
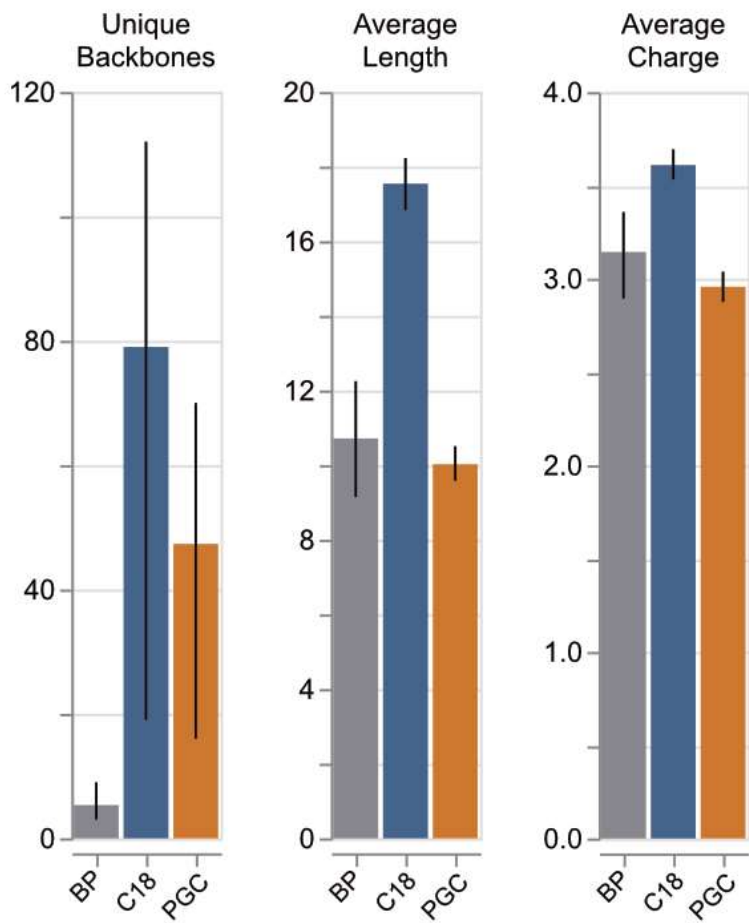


# Peptide-level Differences

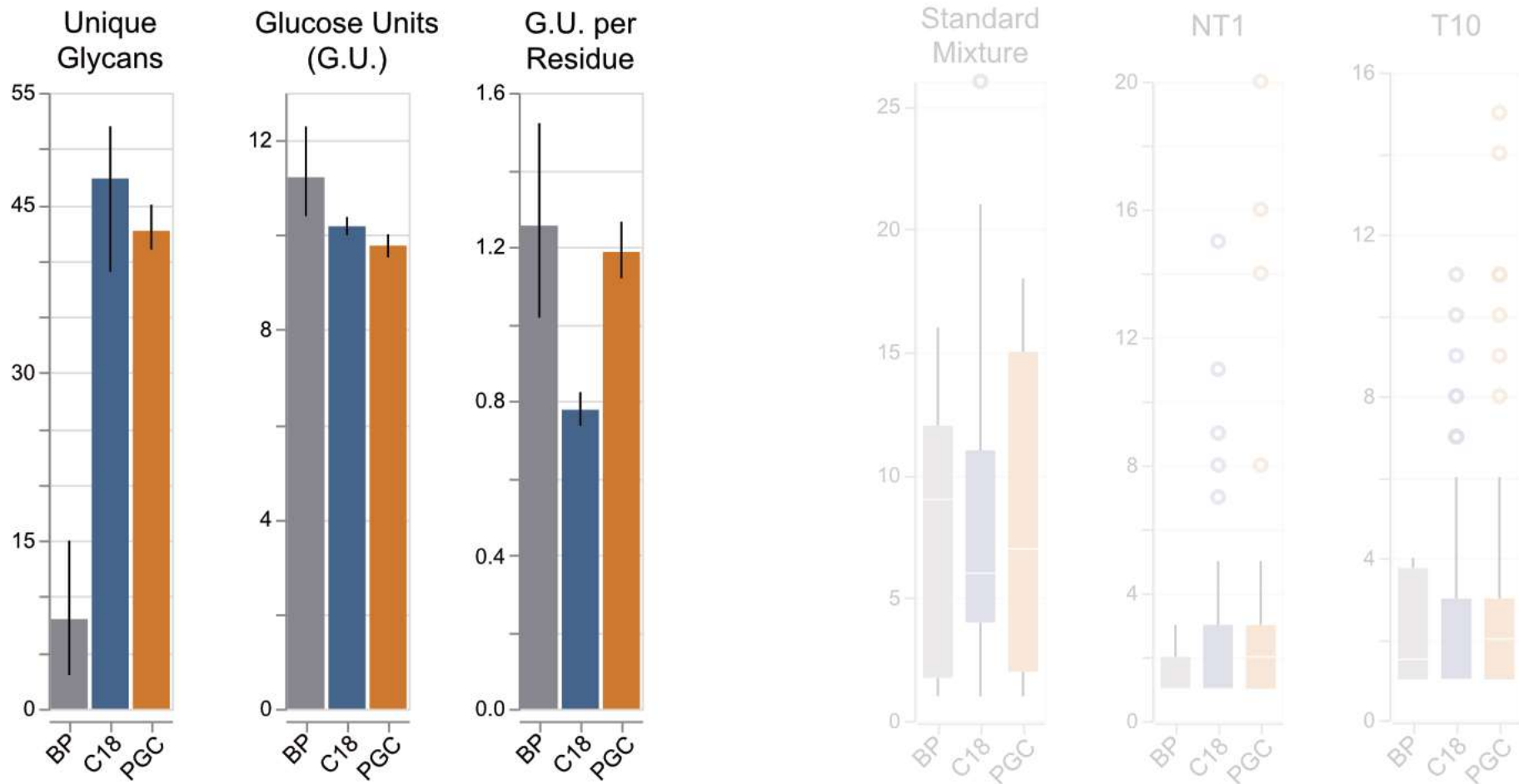




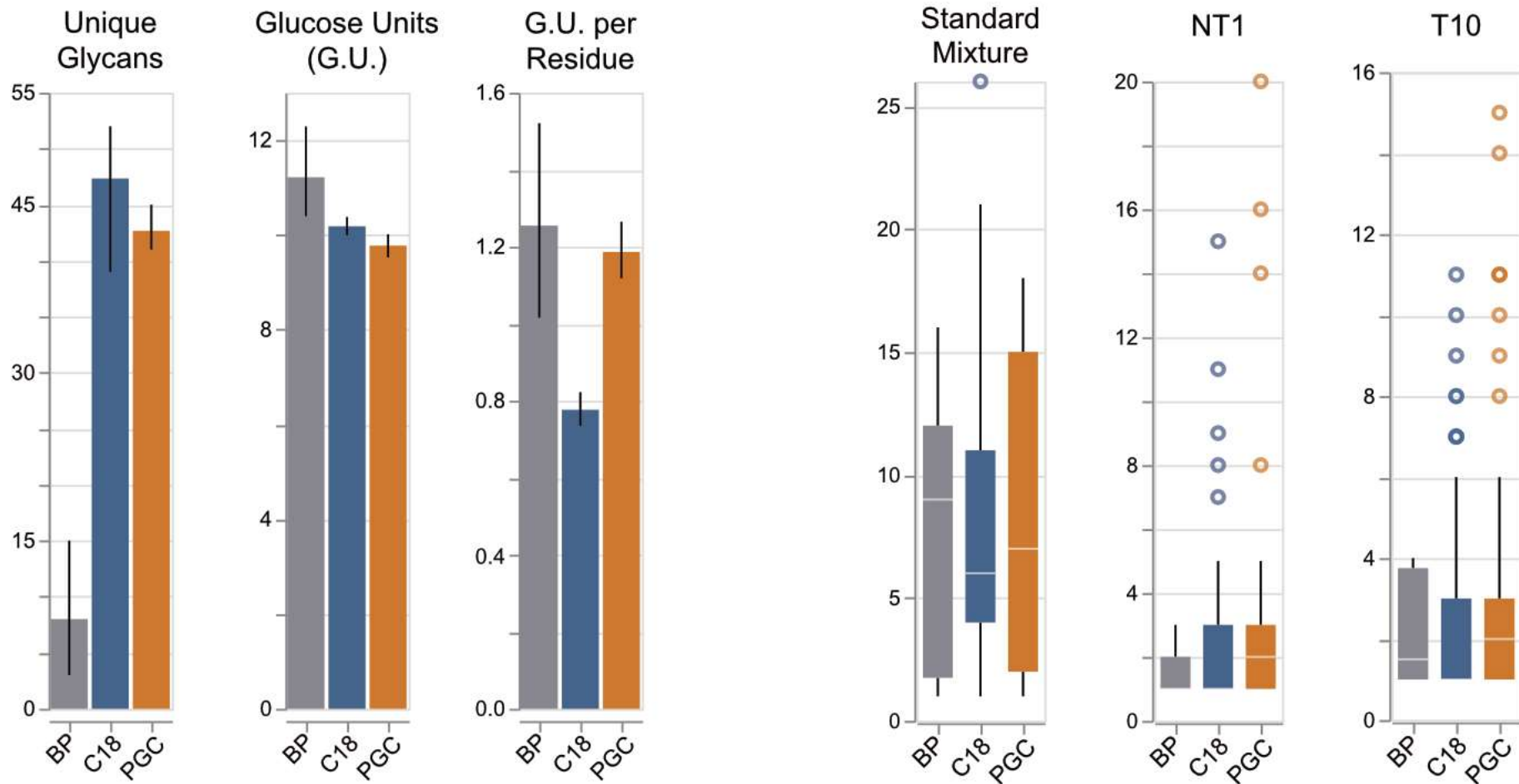
# Peptide-level Differences



# Glycan-level Differences

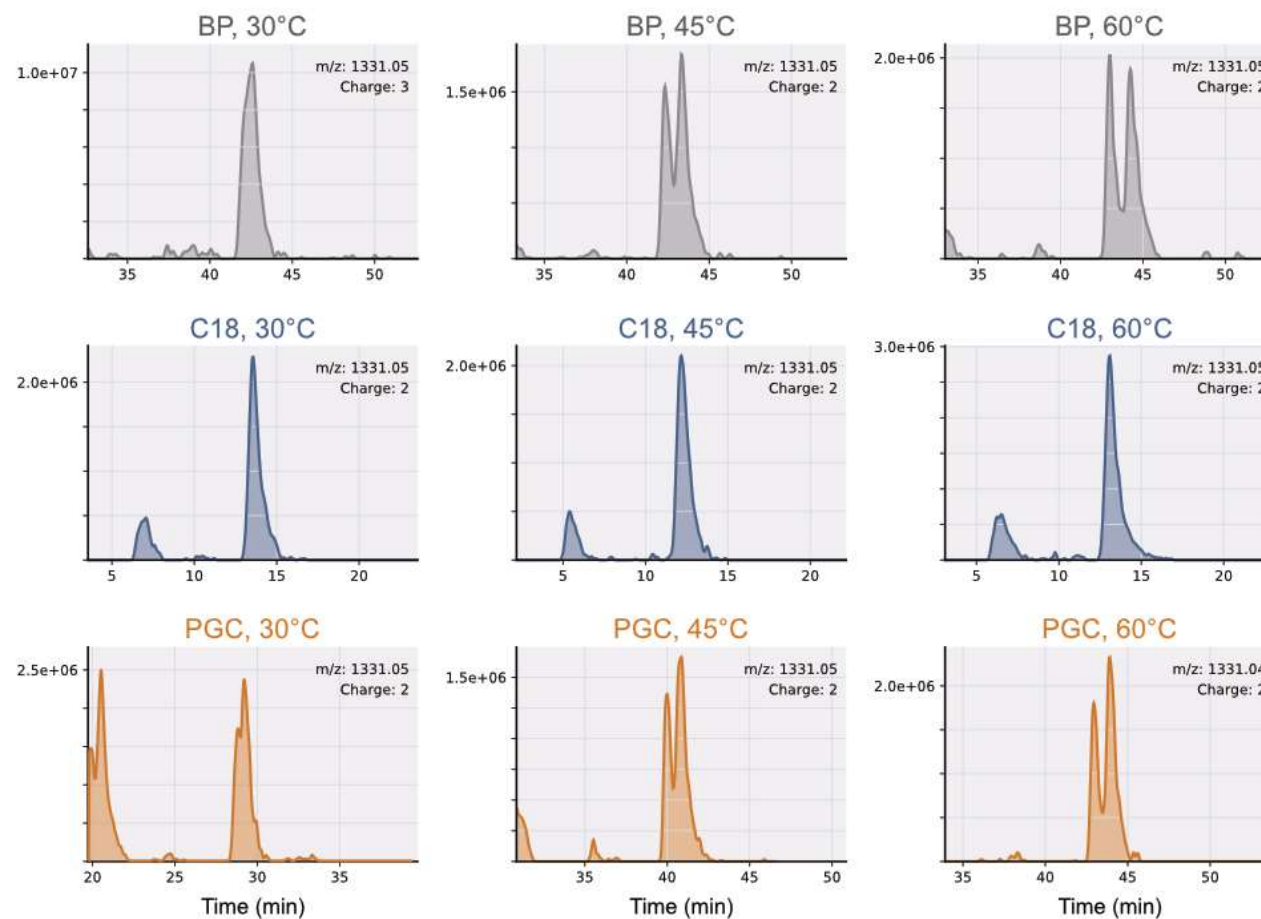


# Glycan-level Differences



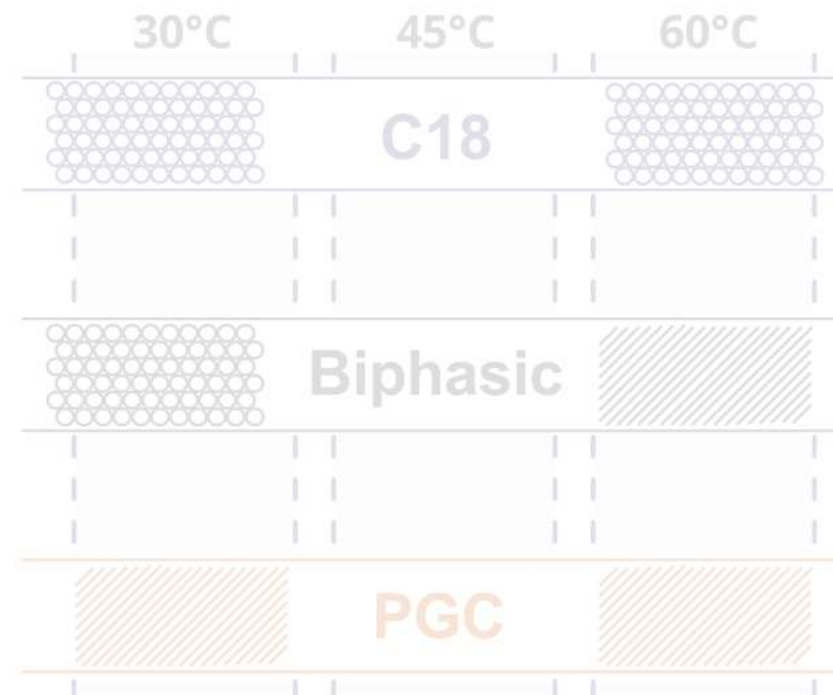
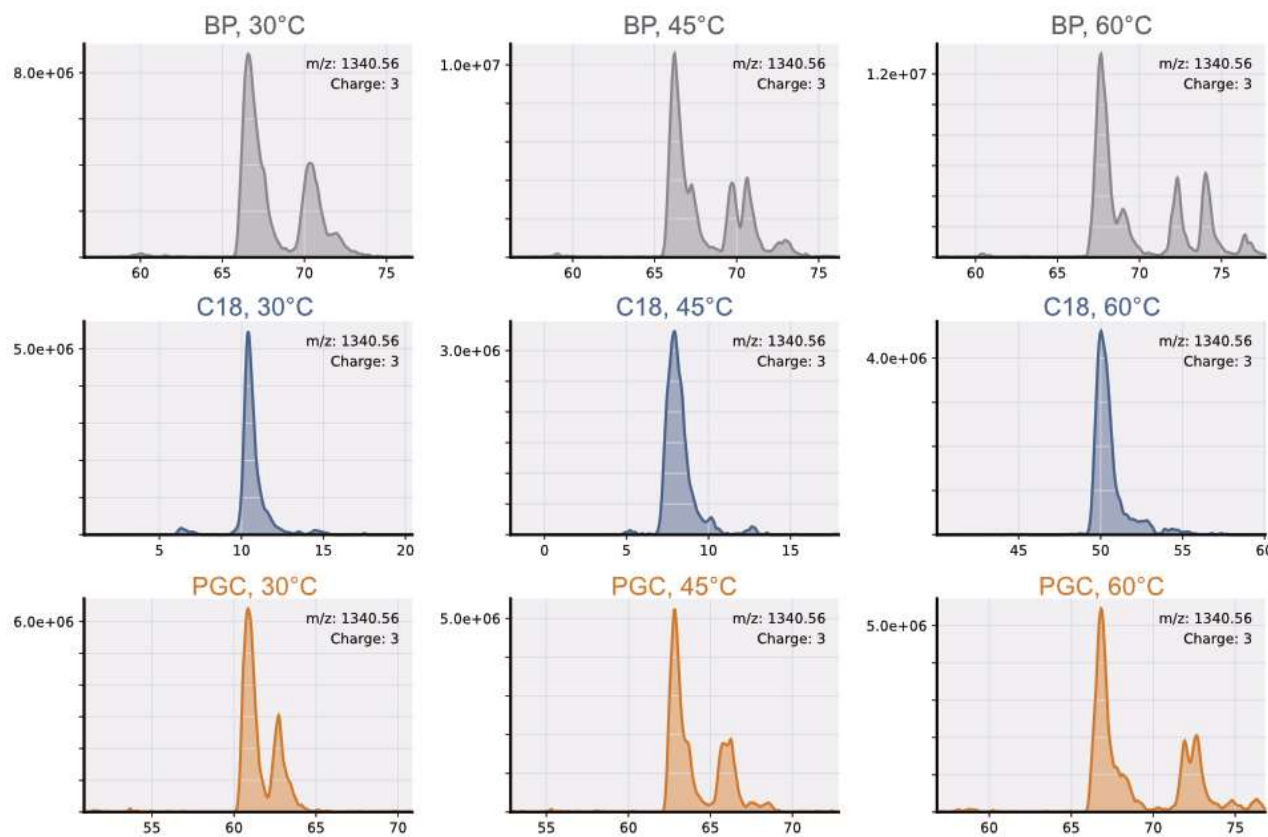
# Liquid-phase Resolution

QNGTLSK + HexNAc(4)Hex(5)NeuAc(1)



# Liquid-phase Resolution

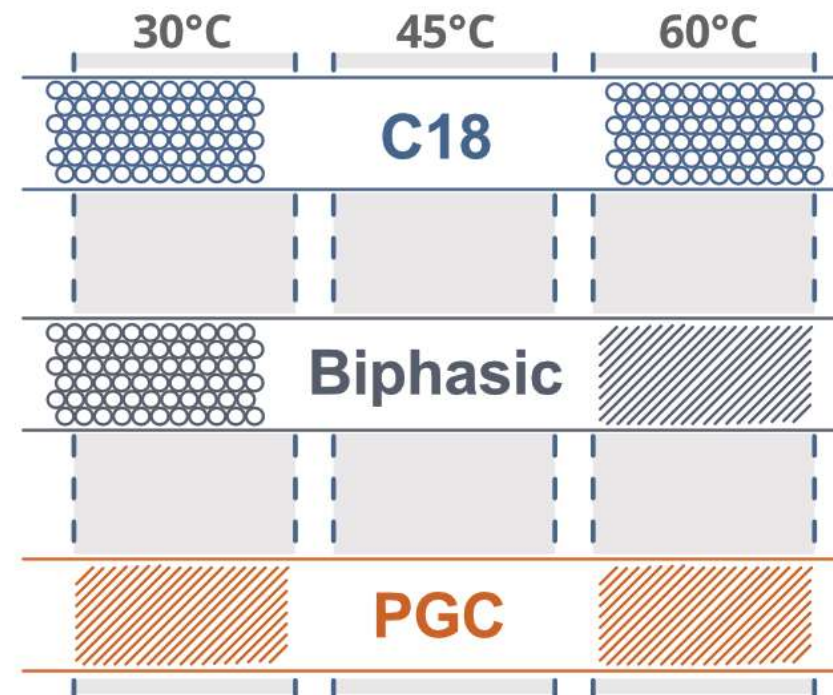
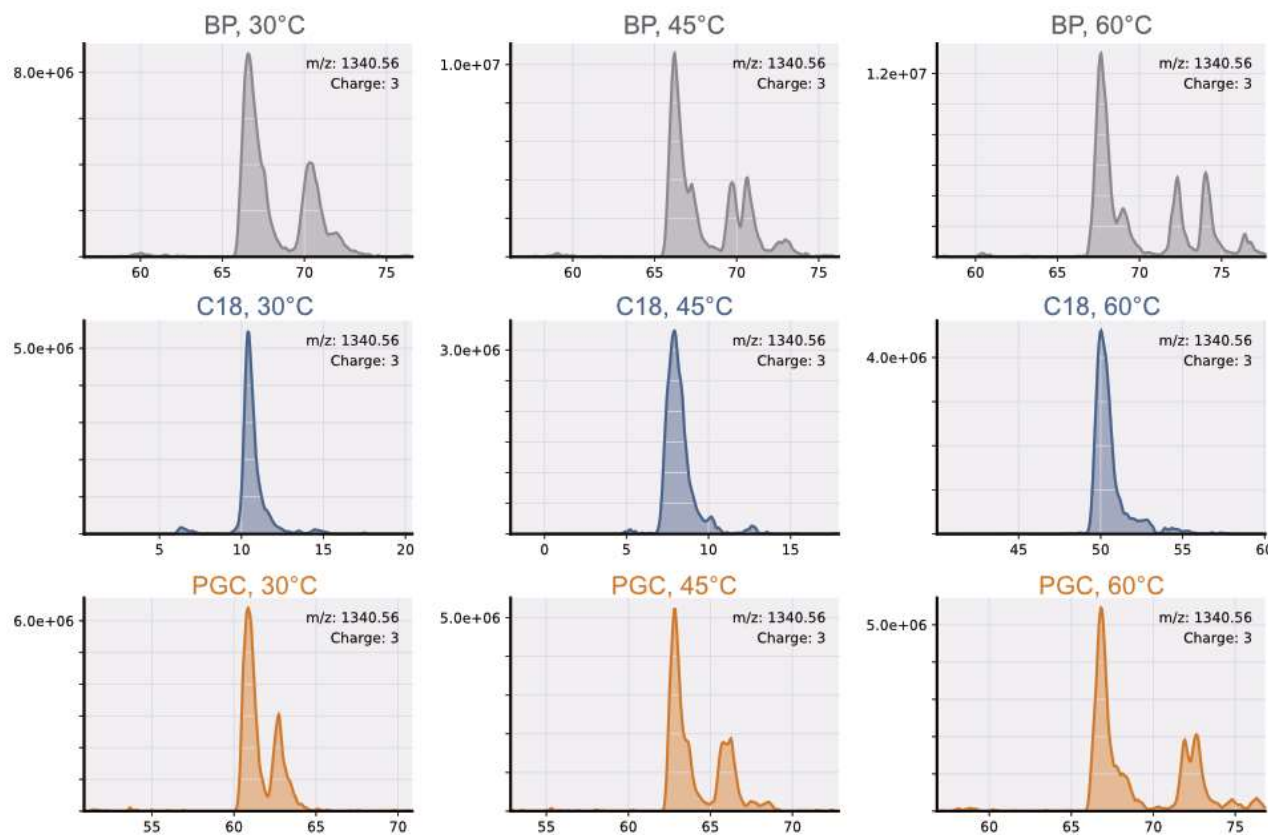
LCPDCPLLAPLNSDR + HexNAc(5)Hex(6)NeuAc(1)





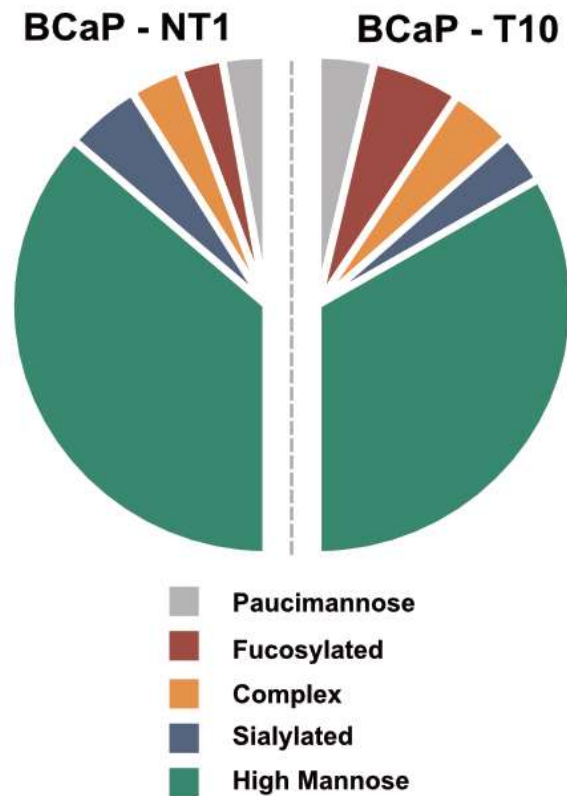
# Liquid-phase Resolution

LCPDCPLLAPLNSDR + HexNAc(5)Hex(6)NeuAc(1)

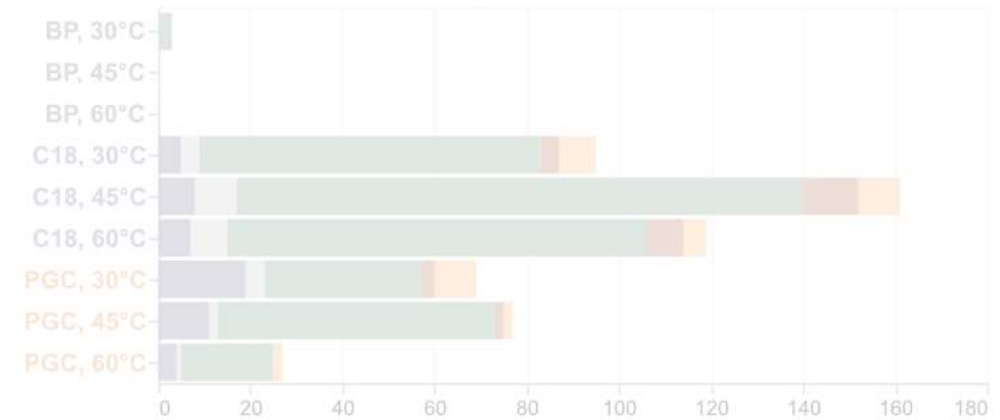


1. Common for high mannose and complex glycans with mismatched antennae
2. Concentration-dependent

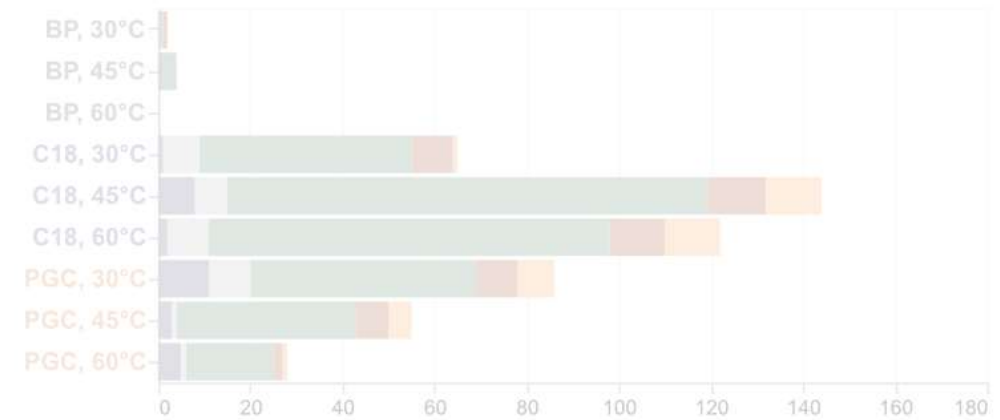
# Glycoproteome Profiles



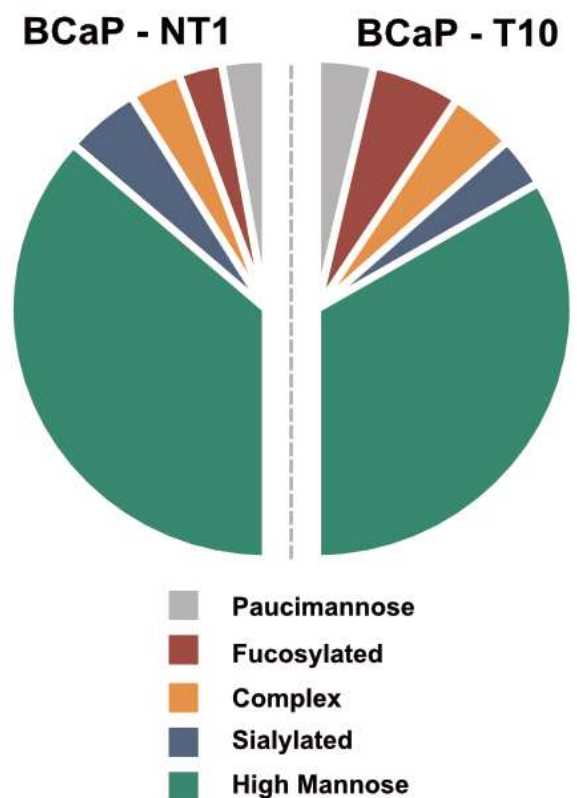
Glycans in NT1



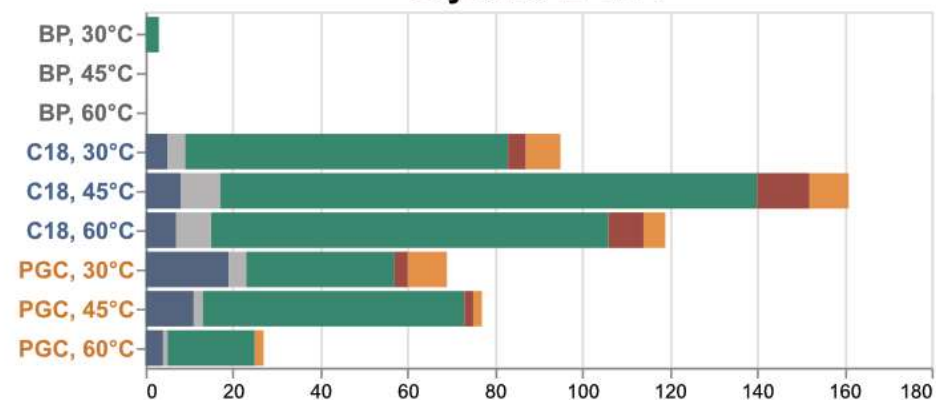
Glycans in T10



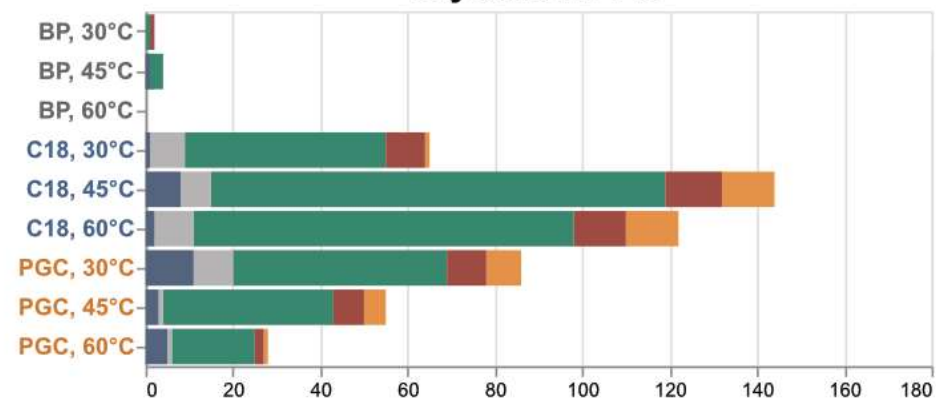
# Glycoproteome Profiles



**Glycans in NT1**



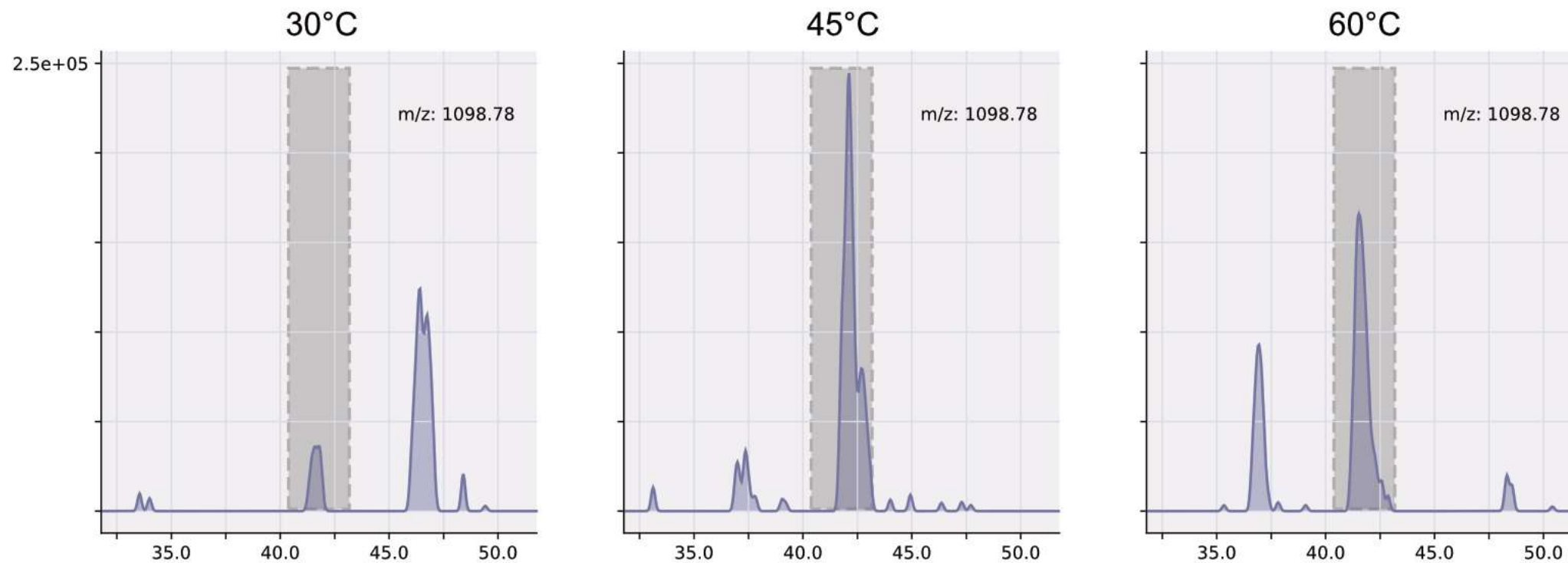
**Glycans in T10**



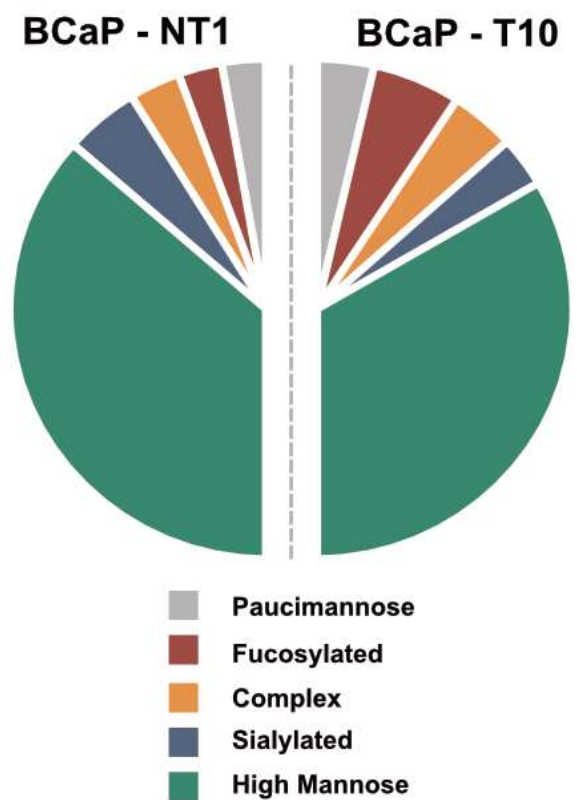


# Peak Height

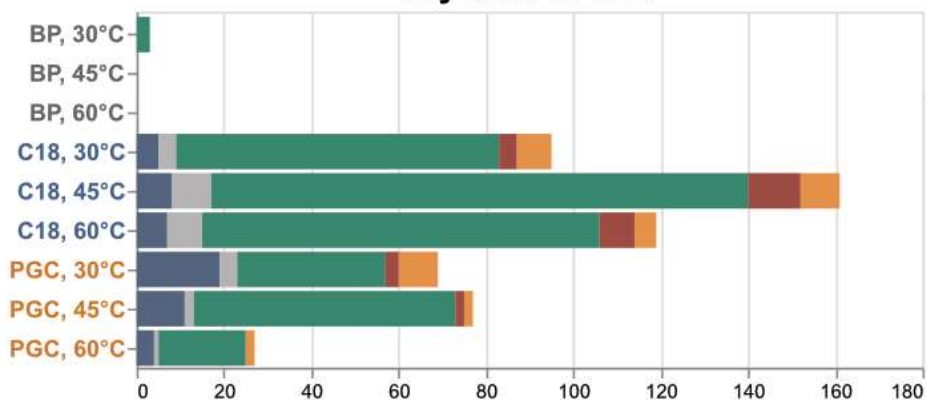
VWNSTFIEDYR + HexNAc(2)Hex(9)



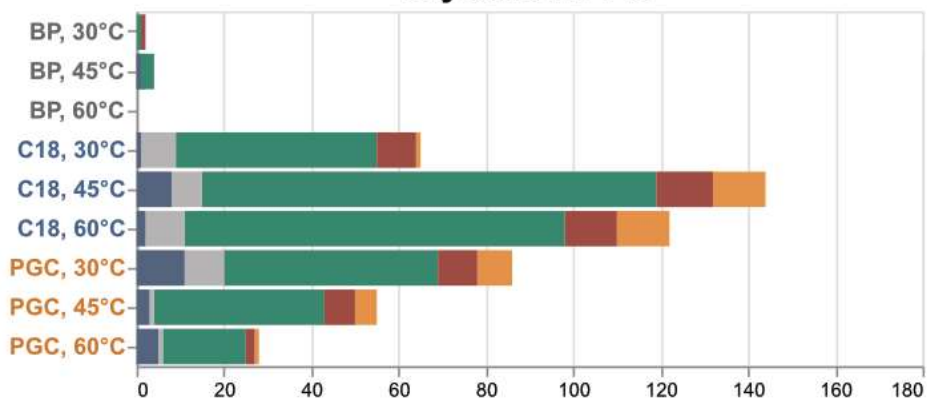
# Glycoproteome Profiles



**Glycans in NT1**



**Glycans in T10**



# Conclusion

1. Tandem RPLC and PGC analysis provide complementary access to the human proteome
2. PGC demonstrates distinct peptide- and glycan-level differences in identified glycopeptides
3. Incorporation of PGC stationary phase is a facile avenue towards structural elucidation
4. PGC separations may provide advantages in investigative, targeted glycoproteomics applications

# Acknowledgments



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