

Comparative Glycoproteomics Analysis

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Contents

1. Introduction

This report details a site-specific, comparative analysis of glycopeptide data from mass spectrometry experiments. The analysis was performed on `psm.tsv` files generated by the FragPipe MSFragger-Glyco workflow.

The primary protein of interest is **VP8_SA11**. The goal is to compare glycosylation patterns across multiple experimental conditions, as defined by the input files.

Parameters for this analysis:

- **Protein of Interest:** VP8_SA11
 - **Signal Peptide Length (to subtract):** 19
 - **Input Files:** `psm_withEndoE.tsv`, `psm_withoutEndo.tsv`
-

2. Data Loading and Preprocessing

The `psm.tsv` files were loaded and combined. The data was then filtered for the protein of interest. **Crucially, to correctly identify unoccupied sites, PSMs are grouped by their peptide backbone. Glycosite information is propagated from glycosylated peptides to their non-glycosylated counterparts. Only then are peptides lacking glycan information correctly labeled as “Unoccupied”.**

```
# Function to load and preprocess a single PSM file
load_and_prep_psm <- function(file_path) {
  read_tsv(file_path, show_col_types = FALSE) %>%
    # Use the filename (without extension) as the sample name
    mutate(sample = tools::file_path_sans_ext(basename(file_path))) %>%
    # Select the relevant columns, ensuring 'sample' and 'Peptide' are retained
    select(sample, Peptide, Protein, `Best Positions`, `Protein Start`, `Total Glycan Composition`) %>%
    # Rename columns for easier use
    rename_with(~str_replace_all(., " ", "_") %>% tolower())
}

# Load all files and combine them
all_psms_raw <- map_dfr(params$psm_files, load_and_prep_psm)

# Process the combined data
```

```

gpsm_data <- all_psms_raw %>%
  # Filter for the target protein
  filter(protein == params$protein_name) %>%
  # Calculate initial glycosite position (will be NA for non-glyco peptides)
  mutate(
    glycosite = as.numeric(str_extract(best_positions, "\\d+")) + protein_start - params$signal_peptide
  ) %>%
  # *** FIX: Correctly identify Unoccupied peptides ***
  # Group by the peptide backbone to find non-glycosylated versions of glycopeptides
  group_by(peptide, sample) %>%
  # Propagate the glycosite information from the glycosylated PSM to the non-glycosylated one
  fill(glycosite, .direction = "downup") %>%
  ungroup() %>%
  # Now that glycosites are filled, filter out any peptides that are never associated with a site
  filter(!is.na(glycosite)) %>%
  # Now, we can safely label the remaining NAs as Unoccupied
  mutate(total_glycan_composition = replace_na(total_glycan_composition, "Unoccupied % 0.0")) %>%
  # Extract glycan composition and mass
  mutate(
    glycan = str_trim(str_extract(total_glycan_composition, ".*(?=%)")),
    glycan_mass = as.numeric(str_extract(total_glycan_composition, "(?<=%)[\\d\\.]+"))
  ) %>%
  # Handle cases where mass extraction fails or is zero for unoccupied
  mutate(glycan_mass = if_else(is.na(glycan_mass) | glycan == "Unoccupied", 0.0, glycan_mass))

cat("Data loaded and preprocessed.\n")

```

```
## Data loaded and preprocessed.
```

```
cat("Total PSMS for", params$protein_name, ":", nrow(gpsm_data), "\n")
```

```
## Total PSMS for VP8_SA11 : 318
```

Glycoforms are defined as unique combinations of glycan structures at specific glycosites. The `total_glycan_composition` column contains the glycan structure and its mass, which is used to identify and categorize glycoforms.

Glycoform subcategories are defined based on the monosaccharide composition of the glycan structures. The categorization is done using a set of rules that classify glycans into broader categories (e.g., High Mannose, Hybrid, Complex) and specific subcategories (e.g., M5, M6, E, H).

3. Glycoform Categorization

Each identified glycan was classified into a broader category and a more specific subcategory based on its monosaccharide composition. This allows for both high-level and detailed comparisons of glycan types.

```

# Function to categorize glycoforms and subcategories based on composition string
categorize_glycoform <- function(glycan_str) {

```

```

# Helper to extract counts, returns 0 if pattern not found
get_count <- function(pattern) {
  match <- str_match(glycan_str, pattern)
  if (is.na(match[1, 2])) 0 else as.numeric(match[1, 2])
}

hexnac <- get_count("HexNAc\\((\\d+)\\)")
h_hex <- get_count("Hex\\((\\d+)\\)")
fuc <- get_count("Fuc\\((\\d+)\\)") + get_count("dHex\\((\\d+)\\)") # Combine Fuc and dHex
neuac <- get_count("NeuAc\\((\\d+)\\)")

# Apply categorization rules
category <- case_when(
  str_detect(glycan_str, "Unoccupied") ~ "Unoccupied",
  hexnac == 1 & h_hex == 0 & neuac == 0 ~ "EndoE Truncated",
  hexnac == 2 & h_hex >= 5 ~ "High Mannose",
  hexnac == 2 & h_hex >= 2 & h_hex < 5 & fuc == 0 ~ "Hybrid",
  hexnac == 2 & h_hex >= 2 & h_hex < 5 & fuc >= 1 ~ "Hybrid (Fucosylated)",
  (hexnac >= 3 & h_hex >= 2) | (hexnac >= 2 & h_hex >= 3) | neuac >= 1 ~ "Complex",
  TRUE ~ "Other" # Default case
)

# Apply subcategory rules
subcategory <- case_when(
  category == "Unoccupied" ~ "U0",
  category == "EndoE Truncated" & fuc == 0 ~ "E",
  category == "EndoE Truncated" & fuc == 1 ~ "E F1",
  category == "High Mannose" & h_hex == 5 ~ "M5",
  category == "High Mannose" & h_hex == 6 ~ "M6",
  category == "High Mannose" & h_hex == 7 ~ "M7",
  category == "High Mannose" & h_hex == 8 ~ "M8",
  category == "High Mannose" & h_hex == 9 ~ "M9",
  category == "High Mannose" & h_hex == 10 ~ "M10",
  category == "Hybrid" ~ "H",
  category == "Hybrid (Fucosylated)" ~ "FH",
  category == "Other" ~ "O",
  TRUE ~ NA_character_
)

return(tibble(glycoform_category = category, glycoform_subcategory = subcategory))
}

# Apply the categorization to the data
gpsm_data <- gpsm_data %>%
  mutate(purrr::map_df(total_glycan_composition, categorize_glycoform))

# Define a consistent order for categories for all plots
category_order <- c('Unoccupied', 'EndoE Truncated', 'Hybrid', 'Hybrid (Fucosylated)',
  'High Mannose',
  'Complex', 'Other')

# Define a consistent order for subcategories
subcategory_order <- c('U0', 'E', 'E F1', 'H', 'FH',

```

```

      'M5', 'M6', 'M7', 'M8', 'M9', 'M10', 'O')

# Filter the order to only include categories present in the data
category_order_filtered <- intersect(category_order, unique(gpsm_data$glycoform_category))

# Create a consistent color map using a new palette
num_colors <- length(category_order_filtered)
color_palette <- brewer.pal(max(3, num_colors), name = "Spectral")
category_colors <- setNames(color_palette[1:num_colors], category_order_filtered)

# Display a summary table of category counts
gpsm_data %>%
  # Convert to factor with the specified level order
  mutate(glycoform_category = factor(glycoform_category, levels = category_order)) %>%
  # Count the occurrences
  count(sample, glycoform_category, .drop = FALSE) %>%
  # Pivot to wide format
  pivot_wider(names_from = sample, values_from = n, values_fill = 0) %>%
  # Arrange the final table according to the specified order
  arrange(glycoform_category) %>%
  knitr::kable(caption = "PSM Counts per Glycoform Category")

```

Table 1: PSM Counts per Glycoform Category

glycoform_category	psm_withEndoE	psm_withoutEndoE
Unoccupied	46	17
EndoE Truncated	35	3
Hybrid	1	17
Hybrid (Fucosylated)	1	65
High Mannose	32	75
Complex	0	7
Other	19	0

4. Comparative Analysis of Glycosite Occupancy and Diversity

Occupancy Heatmaps The following heatmaps show the percentage of glycoforms at each site for each sample. This provides a high-level overview of glycan diversity and site occupancy. Darker colors indicate higher relative abundance. The grid now shows all categories and sites, even those with 0% abundance, for consistent comparison.

```

# Calculate percentage for heatmaps and other plots
plot_data <- gpsm_data %>%
  count(sample, glycosite, glycoform_category, glycoform_subcategory, name = "psm_count") %>%
  group_by(sample, glycosite) %>%
  mutate(percentage = psm_count / sum(psm_count) * 100) %>%
  ungroup()

```

```

# Get all unique sites across all samples to ensure they are all plotted
all_sites_in_data <- sort(unique(gpsm_data$glycosite))

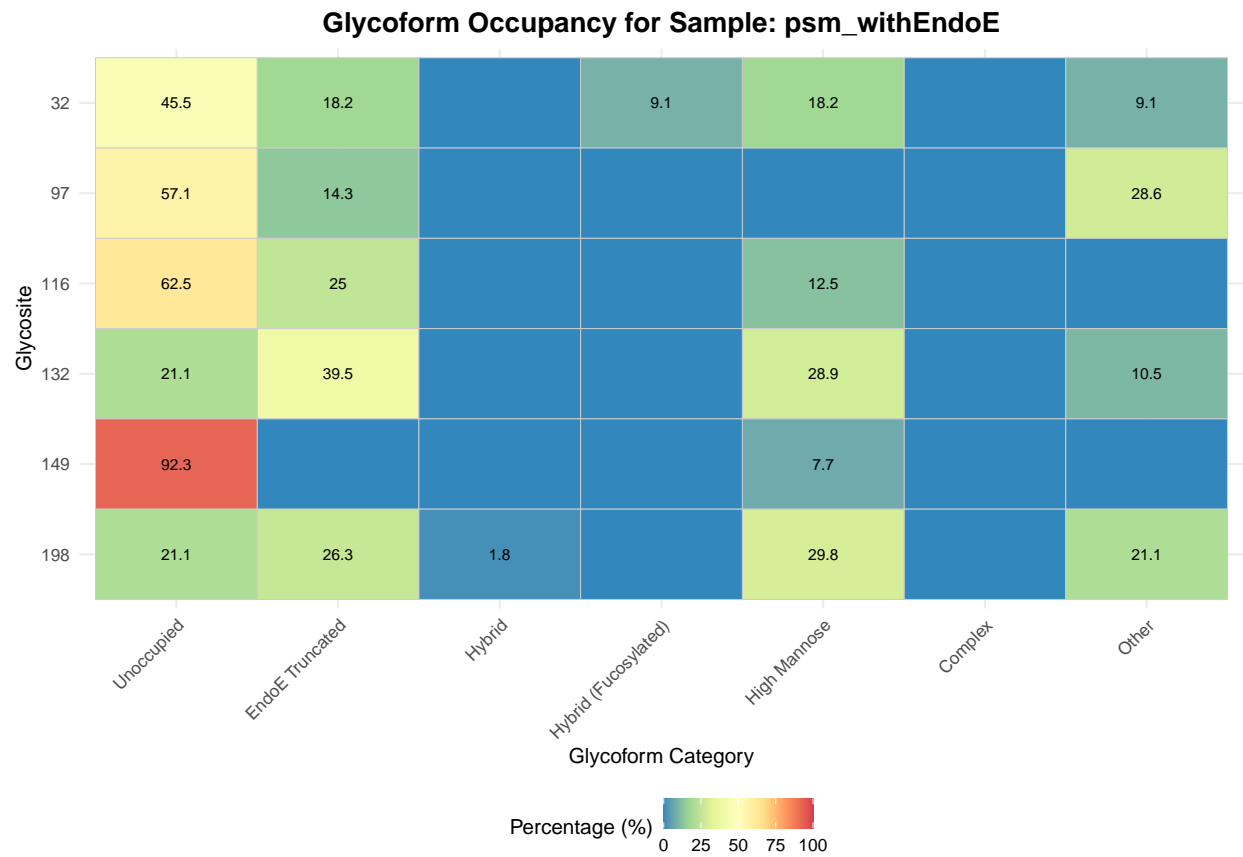
# Generate a heatmap for each sample
for (s in unique(plot_data$sample)) {

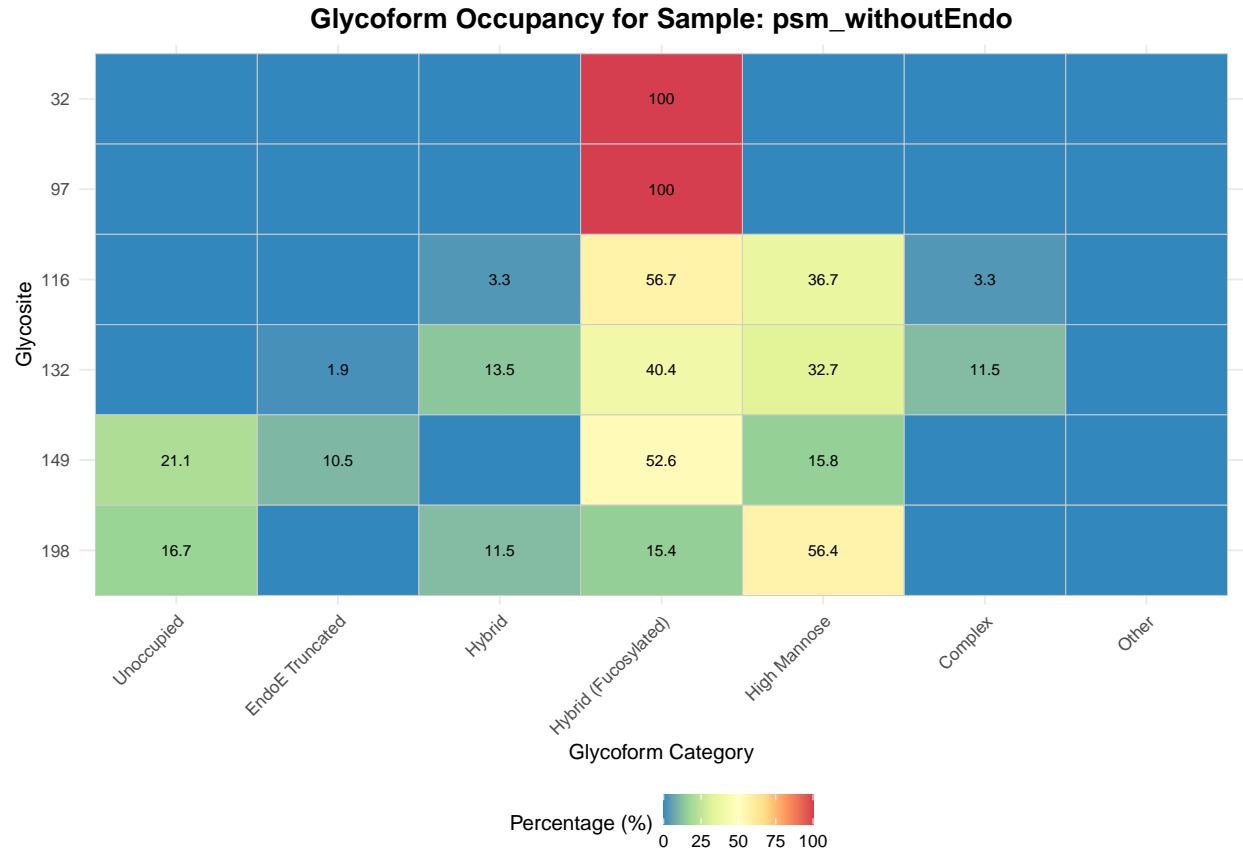
  # Aggregate data for the main category heatmap
  heatmap_cat_data <- plot_data %>%
    filter(sample == s) %>%
    group_by(sample, glycosite, glycoform_category) %>%
    summarise(percentage = sum(percentage), .groups = 'drop') %>%
    ungroup() %>%
    tidyr::complete(glycosite = all_sites_in_data,
                     glycoform_category = category_order_filtered,
                     fill = list(percentage = 0, sample = s))

  p <- heatmap_cat_data %>%
    ggplot(aes(x = glycoform_category, y = as.factor(glycosite), fill = percentage)) +
    geom_tile(color = "gray80") +
    geom_text(data = . %>% filter(percentage > 0), aes(label = round(percentage, 1)), color = "black", size = 8) +
    scale_fill_distiller(palette = "Spectral", name = "Percentage (%)", limits = c(0, 100)) +
    # Use limits to enforce order and presence of all categories/sites
    scale_x_discrete(limits = category_order_filtered, drop = FALSE, guide = guide_axis(angle = 45)) +
    scale_y_discrete(limits = rev(as.character(all_sites_in_data)), drop = FALSE) +
    labs(
      title = paste("Glycoform Occupancy for Sample:", s),
      x = "Glycoform Category",
      y = "Glycosite"
    )

  print(p)
}

```





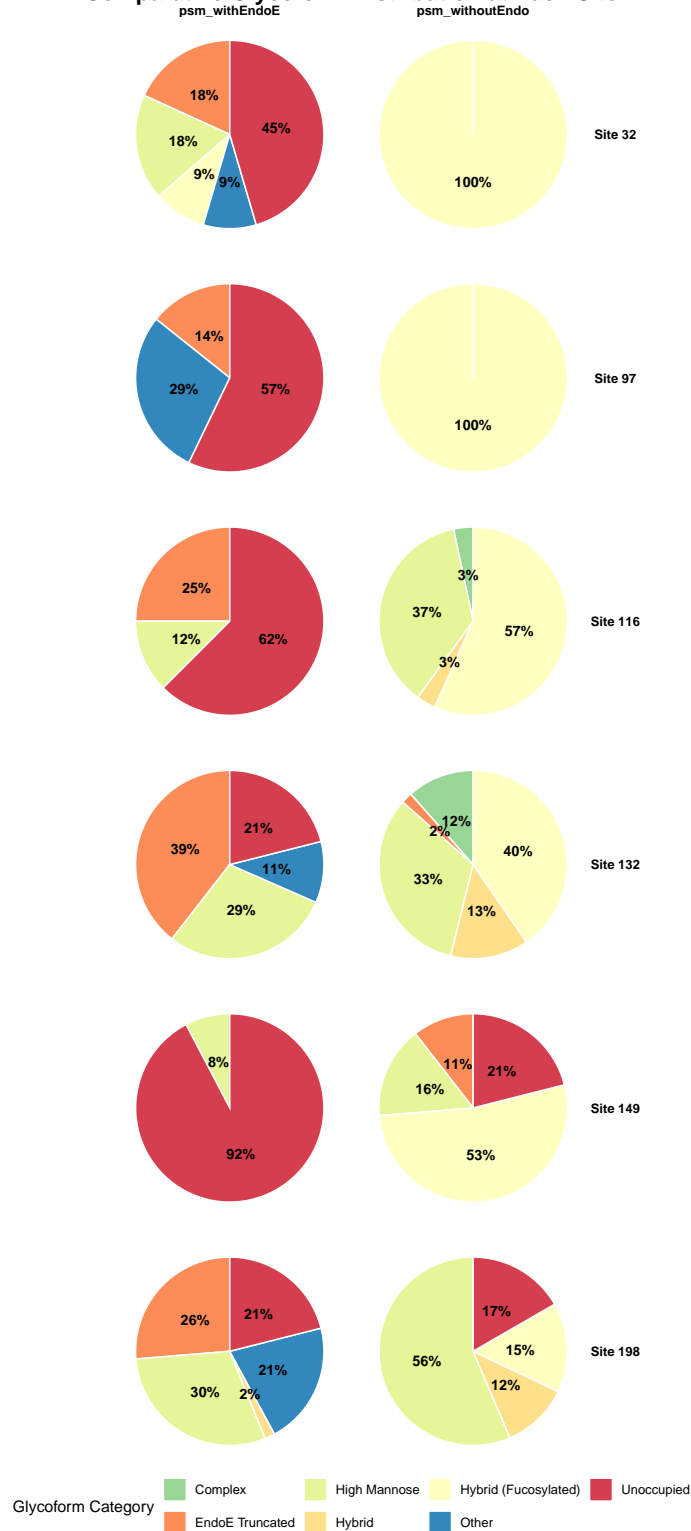
Comparative Pie Charts per Site To compare the relative abundance of glycoform categories more directly, the following plots show a pie chart for each sample at each glycosite. Labels are placed to avoid overlap for better readability.

```
# Aggregate data for pie charts
pie_plot_data <- plot_data %>%
  group_by(sample, glycosite, glycoform_category) %>%
  summarise(percentage = sum(percentage), .groups = 'drop') %>%
  filter(percentage > 1)

ggplot(pie_plot_data, aes(x = 1, y = percentage, fill = glycoform_category)) +
  geom_col(width = 1, color = "white") +
  geom_text(aes(label = paste0(round(percentage), "%")),
    position = position_stack(vjust = 0.5),
    color = "black",
    size = 3.5,
    fontface = "bold") +
  coord_polar("y", start = 0) +
  facet_grid(glycosite ~ sample, labeller = labeller(glycosite =
    function(x) paste("Site", x))) +
  scale_fill_manual(values = category_colors, name = "Glycoform Category") +
  labs(
    title = "Comparative Glycoform Distribution at Each Site"
  ) +
  theme_void() +
```

```
theme(  
  plot.title = element_text(face = "bold", hjust = 0.5, size = 16),  
  strip.text = element_text(face = "bold"),  
  legend.position = "bottom"  
)
```


Comparative Glycoform Distribution at Each Site



Venn Diagram of Unique Glycopeptides The Venn diagram below illustrates the overlap of unique glycopeptides between the two sample conditions. A glycopeptide is defined as a unique combination of a peptide backbone and its attached glycan. This helps to visualize the number of shared and condition-specific

glycopeptides.

```
# Create a unique identifier for each glycopeptide (peptide + glycan)
# We filter out "Unoccupied" as it does not represent a glycopeptide.
venn_data <- gpsm_data %>%
  filter(glycoform_category != "Unoccupied") %>%
  mutate(glycopeptide_id = paste(peptide, glycan, sep = "_"))

# Get unique glycopeptides for the 'withEndoE' sample
with_endo_e_peptides <- venn_data %>%
  filter(sample == "psm_withEndoE") %>%
  distinct(glycopeptide_id) %>%
  pull(glycopeptide_id)

# Get unique glycopeptides for the 'withoutEndo' sample
without_endo_peptides <- venn_data %>%
  filter(sample == "psm_withoutEndo") %>%
  distinct(glycopeptide_id) %>%
  pull(glycopeptide_id)

# Create a list for the Venn diagram function
# The names of the list elements will be the labels on the diagram
venn_list <- list(
  `With EndoE` = with_endo_e_peptides,
  `Without EndoE` = without_endo_peptides
)

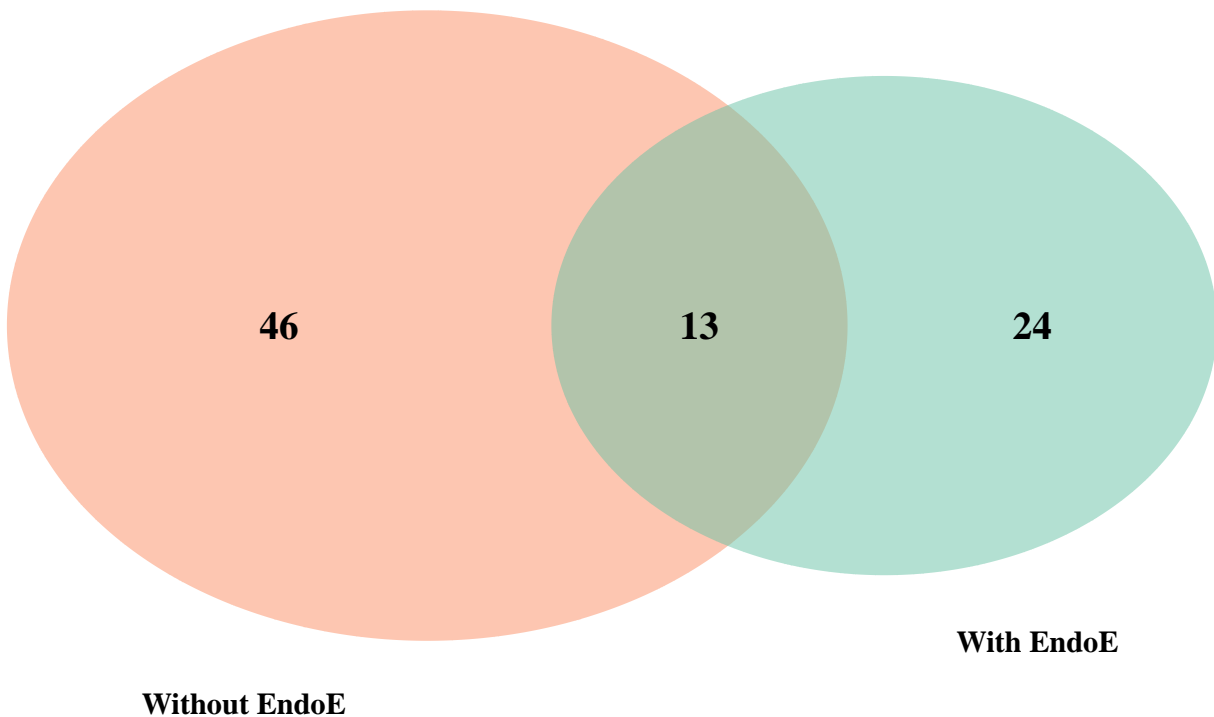
# Disable the log file generation that VennDiagram creates by default
futile.logger::flog.threshold(futile.logger::ERROR, name = "VennDiagramLogger")
```

NULL

```
# Generate the Venn diagram. The plot is drawn directly to the output device.
grid.newpage()
venn.plot <- venn.diagram(
  x = venn_list,
  filename = NULL, # This ensures it plots to the R device instead of a file
  output = TRUE,
  imagetype = "png",
  # Main title
  main = "Comparison of Unique Glycopeptides",
  main.cex = 1.5,
  main.fontface = "bold",
  # Circles
  lwd = 2,
  lty = 'blank',
  fill = c("#66C2A5", "#FC8D62"), # FIX: Provide a vector of 2 colors
  # Numbers inside circles
  cex = 1.5,
  fontface = "bold",
  # Set names (Category names)
  cat.cex = 1.2,
  cat.fontface = "bold",
```

```
cat.default.pos = "outer",
cat.dist = c(0.055, 0.055),
cat.pos = c(-20, 20)
)
grid.draw(venn.plot)
```

Comparison of Unique Glycopeptides



5. Site-Specific Microheterogeneity Analysis

The following plots provide a more detailed, site-by-site view of the specific glycan structures and categories identified, allowing for a deep dive into the microheterogeneity at each location.

Category-Level PSM Counts This plot shows the absolute number of PSMs for each glycoform **category** at each site. This is useful for comparing raw counts rather than percentages. The bars are set to a fixed width for easier comparison across facets.

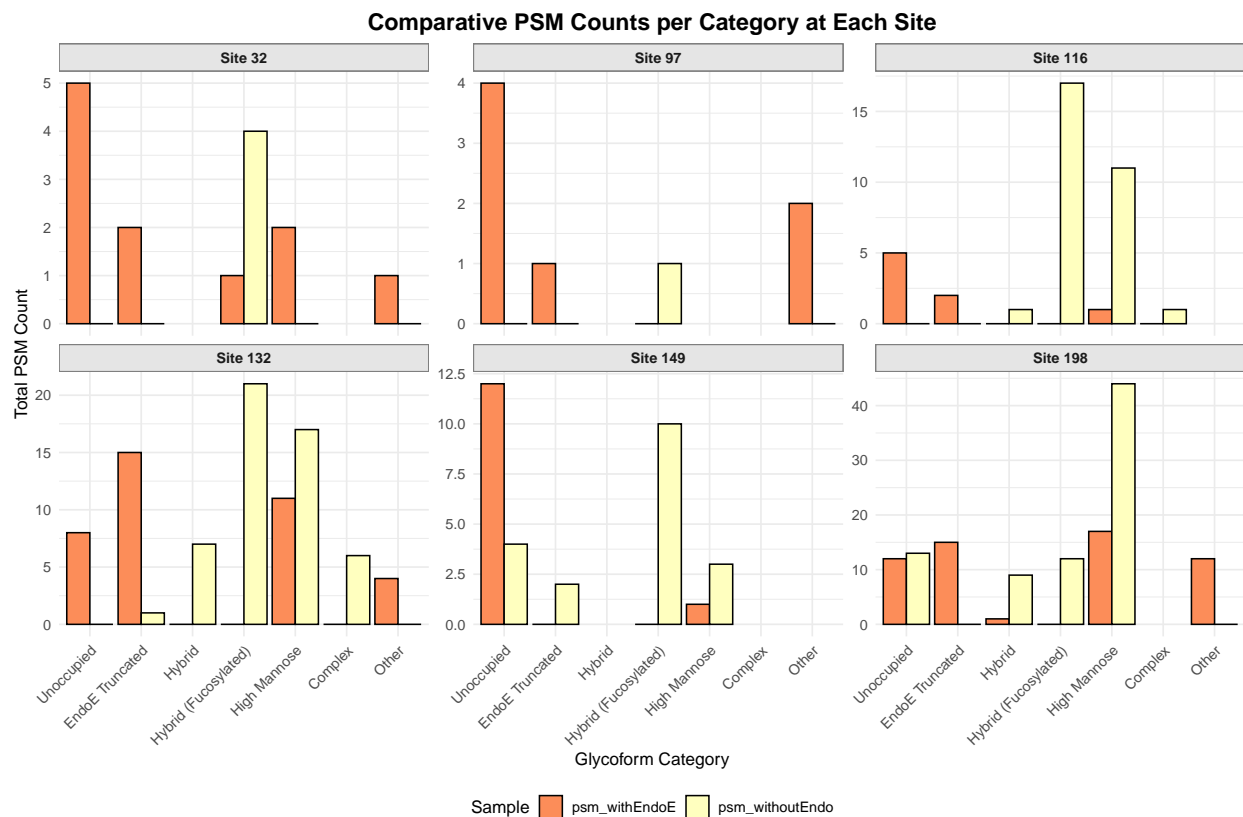
```
# Aggregate data to the category level
category_plot_data <- plot_data %>%
  group_by(sample, glycosite, glycoform_category) %>%
  summarise(psm_count = sum(psm_count), .groups = 'drop') %>%
```

```

ungroup() %>%
# Ensure all categories and samples are present for correct bar alignment
tidyr::complete(nesting(glycosite, glycoform_category), sample, fill = list(psm_count = 0))

ggplot(category_plot_data, aes(x = glycoform_category, y = psm_count, fill = sample)) +
# Use position_dodge(preserve = "total") to keep bar widths consistent
geom_col(position = position_dodge(preserve = "total"), color = "black", linewidth = 0.5) +
facet_wrap(~glycosite, ncol = 3, scales = "free_y", labeller = labeller(glycosite =
  function(x) paste("Site", x))) +
scale_fill_brewer(palette = "Spectral", name = "Sample") +
# Enforce the new category order on the x-axis
scale_x_discrete(limits = category_order) +
labs(
  title = "Comparative PSM Counts per Category at Each Site",
  x = "Glycoform Category",
  y = "Total PSM Count"
) +
theme(axis.text.x = element_text(angle = 45, hjust = 1))

```



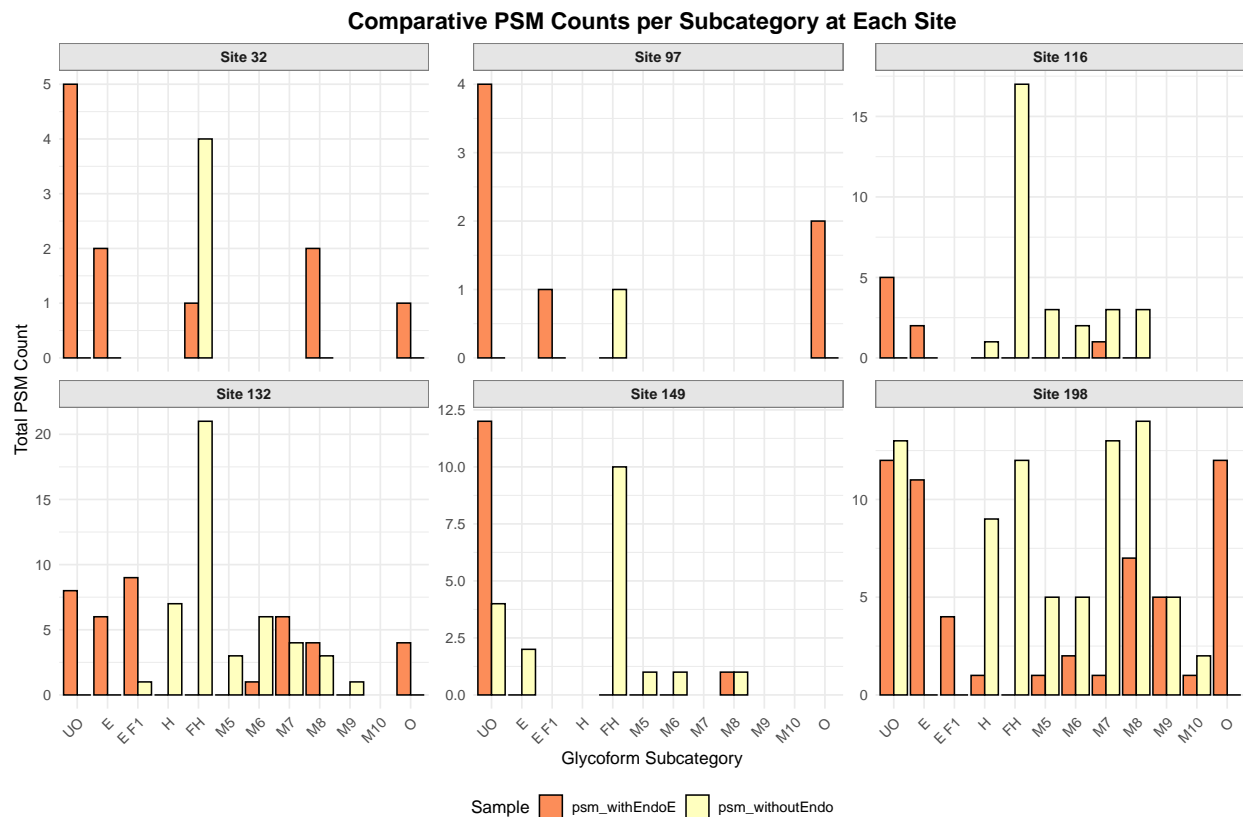
Subcategory-Level PSM Counts This plot shows the absolute number of PSMs for each glycoform subcategory at each site. This is useful for comparing the abundance of specific glycan structures (e.g., M5 vs. M9). The bars are set to a fixed width for easier comparison across facets.

```

# Data is already prepared in 'plot_data'
subcategory_plot_data <- plot_data %>%
  filter(!is.na(glycoform_subcategory)) %>%
  ungroup() %>%
  # Ensure all subcategories and samples are present for correct bar alignment
  tidyr::complete(nesting(glycosite, glycoform_subcategory), sample, fill = list(psm_count = 0))

if(nrow(subcategory_plot_data) > 0) {
  ggplot(subcategory_plot_data, aes(x = glycoform_subcategory, y = psm_count, fill = sample)) +
    # Use position_dodge(preserve = "total") to keep bar widths consistent
    geom_col(position = position_dodge(preserve = "total"), color = "black", linewidth = 0.5) +
    facet_wrap(~glycosite, ncol = 3, scales = "free_y", labeller = labeller(glycosite =
      function(x) paste("Site", x))) +
    scale_fill_brewer(palette = "Spectral", name = "Sample") +
    # Enforce the new subcategory order on the x-axis
    scale_x_discrete(limits = subcategory_order) +
    labs(
      title = "Comparative PSM Counts per Subcategory at Each Site",
      x = "Glycoform Subcategory",
      y = "Total PSM Count"
    ) +
    theme(axis.text.x = element_text(angle = 45, hjust = 1))
} else {
  cat("No subcategory data available to plot.")
}

```



6. Conclusion

This report provides a comprehensive, comparative analysis of glycopeptide data. The visualizations highlight key differences in site occupancy, glycoform diversity, and specific glycan abundance between the analyzed samples.

Appendix: Processed PSM Data Table

The following table contains the relevant processed data for all PSMs used in this analysis. You can search, sort, and filter the table to explore the data.

Table 2: Summary of Processed PSMs

Sample	Peptide	Total Glycan Glycosite Composition	Glycoform Category	Glycoform Subcategory
psm_withEndoE	FDLSDEIQEIGSTKSQNV	BNPGLNHexNAc(1) % 203.0794	EndoE	E
			Truncated	
psm_withEndoE	FDLSDEIQEIGSTKSQNV	BNPGLNUnoccupied % 0.0	Unoccupied	UO
psm_withEndoE	FDLSDEIQEIGSTKSQNV	BNPGLNUnoccupied % 0.0	Unoccupied	UO
psm_withEndoE	FDLSDEIQEIGSTKSQNV	BNPGLNUnoccupied % 0.0	Unoccupied	UO
psm_withEndoE	FDLSDEIQEIGSTKSQNV	BNPGLNUnoccupied % 0.0	Unoccupied	UO
psm_withEndoE	FDLSDEIQEIGSTKSQNV	BNPGLNUnoccupied % 0.0	Unoccupied	UO
psm_withEndoE	FDLSDEIQEIGSTKSQNV	BNPGLNHexNAc(2)Hex(8) %	High Mannose	M8
		1702.5814		
psm_withEndoE	FDLSDEIQEIGSTKSQNV	BNPGLNHexNAc(2)Hex(8) %	High Mannose	M8
		1702.5814		
psm_withEndoE	FDLSDEIQEIGSTKSQNV	BNPGLNHexNAc(2)Hex(2)Fuc(1) % 876.3223	Hybrid (Fucosylated)	FH
psm_withEndoE	FDLSDEIQEIGSTKSQNV	BNPGLNHexNAc(1)Fuc(1) %	Other	O
		365.1322		
psm_withEndoE	FDLSDEIQEIGSTKSQNV	BNPGLNHexNAc(1)Fuc(1) % 203.0794	EndoE	E
			Truncated	
psm_withoutHyd	FDLSDEIQEIGSTKSQNV	BNPGLNHexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutHyd	FDLSDEIQEIGSTKSQNV	BNPGLNHexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutHyd	FDLSDEIQEIGSTKSQNV	BNPGLNHexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutHyd	FDLSDEIQEIGSTKSQNV	BNPGLNHexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withEndoE	MLLAPTPGVVIVEGTNNT	DRWHexNAc(1)Fuc(1) %	EndoE	E F1
		349.1373	Truncated	
psm_withEndoE	MLLAPTPGVVIVEGTNNT	DRWHexNAc(1)Hex(1) %	Other	O
		365.1322		
psm_withEndoE	MLLAPTPGVVIVEGTNNT	DRWUnoccupied % 0.0	Unoccupied	UO
psm_withEndoE	MLLAPTPGVVIVEGTNNT	DRWHexNAc(1)Hex(1) %	Other	O
		365.1322		
psm_withEndoE	MLLAPTPGVVIVEGTNNT	DRWUnoccupied % 0.0	Unoccupied	UO
psm_withEndoE	MLLAPTPGVVIVEGTNNT	DRWUnoccupied % 0.0	Unoccupied	UO
psm_withEndoE	MLLAPTPGVVIVEGTNNT	DRWUnoccupied % 0.0	Unoccupied	UO

Sample	Peptide	Glycosite	Total Glycan Composition	Glycoform Category	Glycoform Subcategory
psm_without	LAETPTPGVIVEGTNNTDRW97		HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withEndo	LAETILIEPNVQSENRTY	116	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7
psm_withEndo	LAETILIEPNVQSENRTY	116	HexNAc(1) % 203.0794	EndoE Truncated	E
psm_withEndo	LAETILIEPNVQSENRTY	116	HexNAc(1) % 203.0794	EndoE Truncated	E
psm_withEndo	LAETILIEPNVQSENRTY	116	Unoccupied % 0.0	Unoccupied	UO
psm_withEndo	LAETILIEPNVQSENRTY	116	Unoccupied % 0.0	Unoccupied	UO
psm_withEndo	LAETILIEPNVQSENRTY	116	Unoccupied % 0.0	Unoccupied	UO
psm_withEndo	LAETILIEPNVQSENRTY	116	Unoccupied % 0.0	Unoccupied	UO
psm_withEndo	LAETILIEPNVQSENRTY	116	Unoccupied % 0.0	Unoccupied	UO
psm_without	LEPNVQSENRTY	116	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7
psm_without	LEPNVQSENRTY	116	HexNAc(3)Hex(3)Fuc(1) % 1241.4545	Complex	NA
psm_without	LEPNVQSENRTY	116	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_without	LEPNVQSENRTY	116	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_without	LEPNVQSENRTY	116	HexNAc(2)Hex(2)Fuc(1) % 876.3223	Hybrid (Fucosylated)	FH
psm_without	LEPNVQSENRTY	116	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_without	LEPNVQSENRTY	116	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_without	LAETILIEPNVQSENRTY	116	HexNAc(2)Hex(5) % 1216.4229	High Mannose	M5
psm_without	LAETILIEPNVQSENRTY	116	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_without	LEPNVQSENRTYTIF	116	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7
psm_without	LEPNVQSENRTYTIF	116	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_without	LEPNVQSENRTYTIF	116	HexNAc(2)Hex(5) % 1216.4229	High Mannose	M5
psm_without	LEPNVQSENRTYTIF	116	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_without	LEPNVQSENRTYTIF	116	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_without	LEPNVQSENRTYTIF	116	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_without	LEPNVQSENRTYTIF	116	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_without	LAETILIEPNVQSENRTY	116	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_without	LAETILIEPNVQSENRTY	116	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_without	LAETILIEPNVQSENRTY	116	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7

Sample	Peptide	Glycosite	Total Glycan Composition	Glycoform Category	Glycoform Subcategory
psm_withoutEnAB	ELIEPNVQSENRTY	116	HexNAc(2)Hex(6) % 1378.4757	High Mannose	M6
psm_withoutEnAB	ELIEPNVQSENRTY	116	HexNAc(2)Hex(6) % 1378.4757	High Mannose	M6
psm_withoutEnAB	ELIEPNVQSENRTY	116	HexNAc(2)Hex(5) % 1216.4229	High Mannose	M5
psm_withoutEnAB	ELIEPNVQSENRTY	116	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutEnAB	ELIEPNVQSENRTY	116	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutEnAB	ELIEPNVQSENRTY	116	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutEnAB	ELIEPNVQSENRTY	116	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutEnAB	ELIEPNVQSENRTY	116	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutEnAB	ELIEPNVQSENRTY	116	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutEnAB	ELIEPNVQSENRTY	116	HexNAc(2)Hex(3) % 892.3172	Hybrid	H
psm_withoutEnAB	ELIEPNVQSENRTY	116	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withEndoB	FFGIQEQLTVSNTSQDQW32	32	HexNAc(1)Fuc(1) % 349.1373	EndoE Truncated	E F1
psm_withEndoB	FFGIQEQLTVSNTSQDQW32	32	Unoccupied % 0.0	Unoccupied	UO
psm_withEndoB	FFGIQEQLTVSNTSQDQW32	32	HexNAc(1)Hex(1) % 365.1322	Other	O
psm_withEndoB	FFGIQEQLTVSNTSQDQW32	32	HexNAc(1) % 203.0794	EndoE Truncated	E
psm_withEndoB	FFGIQEQLTVSNTSQDQW32	32	HexNAc(1)Hex(1) % 365.1322	Other	O
psm_withEndoB	FFGIQEQLTVSNTSQDQW32	32	HexNAc(1) % 203.0794	EndoE Truncated	E
psm_withEndoB	FFGIQEQLTVSNTSQDQW32	32	HexNAc(1)Hex(1) % 365.1322	Other	O
psm_withEndoB	FFGIQEQLTVSNTSQDQW32	32	HexNAc(1) % 203.0794	EndoE Truncated	E
psm_withEndoB	FFGIQEQLTVSNTSQDQW32	32	HexNAc(1) % 203.0794	EndoE Truncated	E
psm_withEndoB	FFGIQEQLTVSNTSQDQW32	32	Unoccupied % 0.0	Unoccupied	UO
psm_withEndoB	FFGIQEQLTVSNTSQDQW32	32	Unoccupied % 0.0	Unoccupied	UO
psm_withEndoB	FFSNTSQDQW	132	HexNAc(1)Fuc(1) % 349.1373	EndoE Truncated	E F1
psm_withEndoB	GGQEQLTVSNTSQDQW	132	Hex(1) % 162.0528	Other	O
psm_withEndoB	GGQEQLTVSNTSQDQW	132	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_withEndoB	GGQEQLTVSNTSQDQW	132	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_withEndoB	GGQEQLTVSNTSQDQW	132	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_withEndoB	GGQEQLTVSNTSQDQW	132	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7

Sample	Peptide	Glycosite	Total Glycan Composition	Glycoform Category	Glycoform Subcategory
psm_withEndo	GHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7
psm_withEndo	GHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7
psm_withEndo	GHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7
psm_withEndo	GHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7
psm_withEndo	GHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(6) % 1378.4757	High Mannose	M6
psm_withEndo	GHQEQLTVSNTSQDQW	132	HexNAc(1)Fuc(1) % 349.1373	EndoE Truncated	E F1
psm_withEndo	GHQEQLTVSNTSQDQW	132	HexNAc(1) % 203.0794	EndoE Truncated	E
psm_withEndo	GHQEQLTVSNTSQDQW	132	Unoccupied % 0.0	Unoccupied	UO
psm_withEndo	GHQEQLTVSNTSQDQW	132	HexNAc(1)Fuc(1) % 349.1373	EndoE Truncated	E F1
psm_withEndo	GHQEQLTVSNTSQDQW	132	HexNAc(1) % 203.0794	EndoE Truncated	E
psm_withEndo	GHQEQLTVSNTSQDQW	132	Unoccupied % 0.0	Unoccupied	UO
psm_withEndo	GHQEQLTVSNTSQDQW	132	HexNAc(1)Fuc(1) % 349.1373	EndoE Truncated	E F1
psm_withEndo	GHQEQLTVSNTSQDQW	132	HexNAc(1)Fuc(1) % 349.1373	EndoE Truncated	E F1
psm_withEndo	GHQEQLTVSNTSQDQW	132	HexNAc(1)Fuc(1) % 349.1373	EndoE Truncated	E F1
psm_withEndo	GHQEQLTVSNTSQDQW	132	HexNAc(1)Fuc(1) % 349.1373	EndoE Truncated	E F1
psm_withEndo	GHQEQLTVSNTSQDQW	132	Unoccupied % 0.0	Unoccupied	UO
psm_withEndo	GHQEQLTVSNTSQDQW	132	HexNAc(1)Fuc(1) % 349.1373	EndoE Truncated	E F1
psm_withEndo	GHQEQLTVSNTSQDQW	132	Unoccupied % 0.0	Unoccupied	UO
psm_withEndo	GHQEQLTVSNTSQDQW	132	Unoccupied % 0.0	Unoccupied	UO
psm_withEndo	BHFGIQEQLTVSNTSQDQW	32	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_withEndo	BHFGIQEQLTVSNTSQDQW	32	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7
psm_withoutEndo	HYVNTSQDQW	132	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutEndo	CHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(4) % 1054.3701	Hybrid	H
psm_withoutEndo	CHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(4) % 1054.3701	Hybrid	H
psm_withoutEndo	CHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(4) % 1054.3701	Hybrid	H
psm_withoutEndo	CHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(9) % 1864.6342	High Mannose	M9
psm_withoutEndo	CHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_withoutEndo	CHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8

Sample	Peptide	Glycosite	Total Glycan Composition	Glycoform Category	Glycoform Subcategory
psm_without	EQQLTVSNTSQDQW	132	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_without	EQQLTVSNTSQDQW	132	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7
psm_without	EQQLTVSNTSQDQW	132	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7
psm_without	EQQLTVSNTSQDQW	132	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7
psm_without	EQQLTVSNTSQDQW	132	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7
psm_without	EQQLTVSNTSQDQW	132	HexNAc(2)Hex(6) % 1378.4757	High Mannose	M6
psm_without	EQQLTVSNTSQDQW	132	HexNAc(2)Hex(6) % 1378.4757	High Mannose	M6
psm_without	EQQLTVSNTSQDQW	132	HexNAc(2)Hex(6) % 1378.4757	High Mannose	M6
psm_without	EQQLTVSNTSQDQW	132	HexNAc(2)Hex(6) % 1378.4757	High Mannose	M6
psm_without	EQQLTVSNTSQDQW	132	HexNAc(2)Hex(6) % 1378.4757	High Mannose	M6
psm_without	EQQLTVSNTSQDQW	132	HexNAc(2)Hex(6) % 1378.4757	High Mannose	M6
psm_without	EQQLTVSNTSQDQW	132	HexNAc(2)Hex(5) % 1216.4229	High Mannose	M5
psm_without	EQQLTVSNTSQDQW	132	HexNAc(2)Hex(5) % 1216.4229	High Mannose	M5
psm_without	EQQLTVSNTSQDQW	132	HexNAc(2)Hex(5) % 1216.4229	High Mannose	M5
psm_without	EQQLTVSNTSQDQW	132	HexNAc(3)Hex(3)Fuc(1) % 1241.4545	Complex	NA
psm_without	EQQLTVSNTSQDQW	132	HexNAc(3)Hex(3)Fuc(1) % 1241.4545	Complex	NA
psm_without	EQQLTVSNTSQDQW	132	HexNAc(3)Hex(3)Fuc(1) % 1241.4545	Complex	NA
psm_without	EQQLTVSNTSQDQW	132	HexNAc(3)Hex(3)Fuc(1) % 1241.4545	Complex	NA
psm_without	EQQLTVSNTSQDQW	132	HexNAc(3)Hex(3)Fuc(1) % 1241.4545	Complex	NA
psm_without	EQQLTVSNTSQDQW	132	HexNAc(3)Hex(3)Fuc(1) % 1241.4545	Complex	NA
psm_without	EQQLTVSNTSQDQW	132	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_without	EQQLTVSNTSQDQW	132	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_without	EQQLTVSNTSQDQW	132	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_without	EQQLTVSNTSQDQW	132	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_without	EQQLTVSNTSQDQW	132	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_without	EQQLTVSNTSQDQW	132	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH

Sample	Peptide	Glycosite	Total Glycan Composition	Glycoform Category	Glycoform Subcategory
psm_withoutEnD	CHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutEnD	CHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutEnD	CHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutEnD	CHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutEnD	CHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutEnD	CHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutEnD	CHQEQLTVSNTSQDQW	132	HexNAc(1)Fuc(1) % 349.1373	EndoE Truncated	E F1
psm_withoutEnD	CHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutEnD	CHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutEnD	CHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(4) % 1054.3701	Hybrid	H
psm_withoutEnD	CHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(2)Fuc(1) % 876.3223	Hybrid (Fucosylated)	FH
psm_withoutEnD	CHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(3) % 892.3172	Hybrid	H
psm_withoutEnD	CHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(2)Fuc(1) % 876.3223	Hybrid (Fucosylated)	FH
psm_withoutEnD	CHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutEnD	CHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutEnD	CHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(2)Fuc(1) % 876.3223	Hybrid (Fucosylated)	FH
psm_withoutEnD	CHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(4) % 1054.3701	Hybrid	H
psm_withoutEnD	CHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(3) % 892.3172	Hybrid	H
psm_withoutEnD	CHQEQLTVSNTSQDQW	132	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withEndo	KEIDVVKTTANGSIGQY	149	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_withEndo	KEIDVVKTTANGSIGQY	149	Unoccupied % 0.0	Unoccupied	UO
psm_withEndo	KEIDVVKTTANGSIGQY	149	Unoccupied % 0.0	Unoccupied	UO
psm_withEndo	KEIDVVKTTANGSIGQY	149	Unoccupied % 0.0	Unoccupied	UO
psm_withEndo	KEIDVVKTTANGSIGQY	149	Unoccupied % 0.0	Unoccupied	UO
psm_withEndo	KEIDVVKTTANGSIGQY	149	Unoccupied % 0.0	Unoccupied	UO
psm_withEndo	KEIDVVKTTANGSIGQY	149	Unoccupied % 0.0	Unoccupied	UO
psm_withEndo	KEIDVVKTTANGSIGQY	149	Unoccupied % 0.0	Unoccupied	UO
psm_withEndo	KEIDVVKTTANGSIGQY	149	Unoccupied % 0.0	Unoccupied	UO
psm_withEndo	KEIDVVKTTANGSIGQY	149	Unoccupied % 0.0	Unoccupied	UO
psm_withEndo	KEIDVVKTTANGSIGQY	149	Unoccupied % 0.0	Unoccupied	UO
psm_withEndo	KEIDVVKTTANGSIGQY	149	Unoccupied % 0.0	Unoccupied	UO

Sample	Peptide	Glycosite	Total Glycan Composition	Glycoform Category	Glycoform Subcategory
psm_withEndo	KEIDVVKTTANGSIGQY	149	Unoccupied % 0.0	Unoccupied	UO
psm_withoutEndo	EDVVKTTANGSIGQY	149	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutEndo	EDVVKTTANGSIGQY	149	HexNAc(1) % 203.0794	EndoE Truncated	E
psm_withoutEndo	EDVVKTTANGSIGQY	149	Unoccupied % 0.0	Unoccupied	UO
psm_withoutEndo	EDVVKTTANGSIGQY	149	Unoccupied % 0.0	Unoccupied	UO
psm_withoutEndo	EDVVKTTANGSIGQY	149	Unoccupied % 0.0	Unoccupied	UO
psm_withoutEndo	KEIDVVKTTANGSIGQY	149	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_withoutEndo	KEIDVVKTTANGSIGQY	149	HexNAc(2)Hex(6) % 1378.4757	High Mannose	M6
psm_withoutEndo	KEIDVVKTTANGSIGQY	149	HexNAc(2)Hex(5) % 1216.4229	High Mannose	M5
psm_withoutEndo	KEIDVVKTTANGSIGQY	149	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutEndo	KEIDVVKTTANGSIGQY	149	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutEndo	KEIDVVKTTANGSIGQY	149	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutEndo	KEIDVVKTTANGSIGQY	149	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutEndo	KEIDVVKTTANGSIGQY	149	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutEndo	KEIDVVKTTANGSIGQY	149	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutEndo	KEIDVVKTTANGSIGQY	149	HexNAc(1) % 203.0794	EndoE Truncated	E
psm_withoutEndo	KEIDVVKTTANGSIGQY	149	Unoccupied % 0.0	Unoccupied	UO
psm_withoutEndo	KEIDVVKTTANGSIGQYGP49	149	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutEndo	KEIDVVKTTANGSIGQYGP49	149	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withoutEndo	KEIDVVKTTANGSIGQYGP49	149	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_withEndo	DEVNMTAFCDFY	198	HexNAc(1)Hex(1) % 365.1322	Other	O
psm_withEndo	SETNYDSVNMTAFCDF	198	Unoccupied % 0.0	Unoccupied	UO
psm_withEndo	SETNYDSVNMTAFCDF	198	Unoccupied % 0.0	Unoccupied	UO
psm_withEndo	SETNYDSVNMTAFCDF	198	HexNAc(1)Hex(1) % 365.1322	Other	O
psm_withEndo	DEVNMTAFCDFY	198	Unoccupied % 0.0	Unoccupied	UO
psm_withEndo	DEVNMTAFCDFY	198	Unoccupied % 0.0	Unoccupied	UO
psm_withEndo	SETNYDSVNMTAF	198	HexNAc(1)Fuc(1) % 349.1373	EndoE Truncated	E F1
psm_withEndo	SETNYDSVNMTAF	198	HexNAc(1) % 203.0794	EndoE Truncated	E
psm_withEndo	SETNYDSVNMTAF	198	HexNAc(1) % 203.0794	EndoE Truncated	E
psm_withEndo	SETNYDSVNMTAF	198	Unoccupied % 0.0	Unoccupied	UO
psm_withEndo	SETNYDSVNMTAF	198	Unoccupied % 0.0	Unoccupied	UO

Sample	Peptide	Glycosite	Total Glycan Composition	Glycoform Category	Glycoform Subcategory
psm_withEndo	SETNYDSVNMTAFCDF	198	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_withEndo	SETNYDSVNMTAFCDF	198	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7
psm_withEndo	SETNYDSVNMTAF	198	HexNAc(1) % 203.0794	EndoE Truncated	E
psm_withEndo	SETNYDSVNMTAFCDF	198	HexNAc(1) % 203.0794	EndoE Truncated	E
psm_withEndo	SETNYDSVNMTAFCDF	198	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_withEndo	SETNYDSVNMTAFCDF	198	HexNAc(2)Hex(6) % 1378.4757	High Mannose	M6
psm_withEndo	SETNYDSVNMTAFCDF	198	HexNAc(2)Hex(6) % 1378.4757	High Mannose	M6
psm_withEndo	SETNYDSVNMTAFCDF	198	HexNAc(1)Hex(1) % 365.1322	Other	O
psm_withEndo	SETNYDSVNMTAFCDF	198	HexNAc(2)Hex(5) % 1216.4229	High Mannose	M5
psm_withEndo	SETNYDSVNMTAFCDF	198	HexNAc(2)Hex(9) % 1864.6342	High Mannose	M9
psm_withEndo	SETNYDSVNMTAFCDF	198	HexNAc(2)Hex(3) % 892.3172	Hybrid	H
psm_withEndo	SETNYDSVNMTAFCDF	198	HexNAc(1)Hex(1) % 365.1322	Other	O
psm_withEndo	SETNYDSVNMTAFCDF	198	HexNAc(1) % 203.0794	EndoE Truncated	E
psm_withEndo	SETNYDSVNMTAF	198	Unoccupied % 0.0	Unoccupied	UO
psm_withEndo	SETNYDSVNMTAFCDF	198	HexNAc(1)Hex(1) % 365.1322	Other	O
psm_withEndo	SETNYDSVNMTAFCDF	198	Unoccupied % 0.0	Unoccupied	UO
psm_withEndo	SETNYDSVNMTAFCDF	198	Unoccupied % 0.0	Unoccupied	UO
psm_withEndo	SETNYDSVNMTAFCDF	198	HexNAc(1)Hex(1) % 365.1322	Other	O
psm_withEndo	SETNYDSVNMTAFCDF	198	HexNAc(1)Hex(1) % 365.1322	Other	O
psm_withEndo	DEVNMTAFCDFY	198	HexNAc(1)Fuc(1) % 349.1373	EndoE Truncated	E F1
psm_withEndo	DEVNMTAFCDFY	198	HexNAc(1) % 203.0794	EndoE Truncated	E
psm_withEndo	SETNYDSVNMTAFCDF	198	HexNAc(1)Fuc(1) % 349.1373	EndoE Truncated	E F1
psm_withEndo	SETNYDSVNMTAFCDF	198	HexNAc(1)Hex(1) % 365.1322	Other	O
psm_withEndo	SETNYDSVNMTAFCDF	198	HexNAc(1)Hex(1) % 365.1322	Other	O
psm_withEndo	SETNYDSVNMTAFCDF	198	HexNAc(1)Hex(1) % 365.1322	Other	O
psm_withEndo	DEVNMTAFCDFY	198	HexNAc(1) % 203.0794	EndoE Truncated	E
psm_withEndo	SETNYDSVNMTAFCDF	198	HexNAc(1)Hex(1) % 365.1322	Other	O

Sample	Peptide	Glycosite	Total Glycan Composition	Glycoform Category	Glycoform Subcategory
psm_withEndoB	DEVNMTAFCDFY	198	HexNAc(1) % 203.0794	EndoE	E
psm_withEndoB	DEVNMTAFCDFY	198	Unoccupied % 0.0	Truncated	
psm_withEndoB	DEVNMTAFCDFY	198	Unoccupied % 0.0	Unoccupied	UO
psm_withEndoB	SETNYDSVNMTAFCDF	198	HexNAc(1)Fuc(1) % 349.1373	Unoccupied	UO
psm_withEndoB	SETNYDSVNMTAFCDF	198	HexNAc(1) % 203.0794	EndoE	E F1
psm_withEndoB	SETNYDSVNMTAFCDF	198	HexNAc(2)Hex(10) % 2026.6870	Truncated	
psm_withEndoB	SETNYDSVNMTAFCDF	198	HexNAc(2)Hex(9) % 1864.6342	EndoE	E
psm_withEndoB	SETNYDSVNMTAFCDF	198	HexNAc(2)Hex(9) % 1864.6342	High Mannose	M10
psm_withEndoB	SETNYDSVNMTAFCDF	198	HexNAc(2)Hex(9) % 1864.6342	High Mannose	M9
psm_withEndoB	SETNYDSVNMTAFCDF	198	HexNAc(2)Hex(9) % 1864.6342	High Mannose	M9
psm_withEndoB	SETNYDSVNMTAFCDF	198	HexNAc(2)Hex(9) % 1864.6342	High Mannose	M9
psm_withEndoB	SETNYDSVNMTAFCDF	198	HexNAc(2)Hex(9) % 1864.6342	High Mannose	M9
psm_withEndoB	SETNYDSVNMTAFCDF	198	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M9
psm_withEndoB	SETNYDSVNMTAFCDF	198	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_withEndoB	SETNYDSVNMTAFCDF	198	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_withEndoB	SETNYDSVNMTAFCDF	198	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_withEndoB	SETNYDSVNMTAFCDF	198	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_withEndoB	SETNYDSVNMTAFCDF	198	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_withEndoB	SETNYDSVNMTAFCDF	198	HexNAc(1) % 203.0794	EndoE	E
psm_withEndoB	SETNYDSVNMTAFCDF	198	HexNAc(1) % 203.0794	Truncated	
psm_withEndoB	DEVNMTAFCDFY	198	Unoccupied % 0.0	EndoE	E
psm_withEndoB	SETNYDSVNMTAFCDF	198	HexNAc(1)Hex(1) % 365.1322	Truncated	
psm_withoutEndoB	DEVNMTAF	198	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Unoccupied	UO
psm_withoutEndoB	SETNYDSVNMTAF	198	HexNAc(2)Hex(9) % 1864.6342	Other	O
psm_withoutEndoB	SETNYDSVNMTAF	198	HexNAc(2)Hex(9) % 1864.6342	Hybrid (Fucosylated)	FH
psm_withoutEndoB	SETNYDSVNMTAF	198	HexNAc(2)Hex(9) % 1864.6342	High Mannose	M9
psm_withoutEndoB	SETNYDSVNMTAF	198	HexNAc(2)Hex(9) % 1864.6342	High Mannose	M9
psm_withoutEndoB	SETNYDSVNMTAF	198	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M9
psm_withoutEndoB	SETNYDSVNMTAF	198	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_withoutEndoB	SETNYDSVNMTAF	198	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_withoutEndoB	SETNYDSVNMTAF	198	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M8
psm_withoutEndoB	SETNYDSVNMTAF	198	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7
psm_withoutEndoB	SETNYDSVNMTAF	198	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7
psm_withoutEndoB	SETNYDSVNMTAF	198	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7

Sample	Peptide	Glycosite	Total Glycan Composition	Glycoform Category	Glycoform Subcategory
psm_without_S116	STENYDSVNMTAF	198	HexNAc(2)Hex(6) % 1378.4757	High Mannose	M6
psm_without_S116	STENYDSVNMTAF	198	HexNAc(2)Hex(5) % 1216.4229	High Mannose	M5
psm_without_S116	STENYDSVNMTAF	198	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_without_S116	STENYDSVNMTAF	198	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_without_S116	STENYDSVNMTAF	198	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_without_S116	STENYDSVNMTAF	198	HexNAc(2)Hex(3) % 892.3172	Hybrid	H
psm_without_S116	STENYDSVNMTAF	198	HexNAc(2)Hex(3) % 892.3172	Hybrid	H
psm_without_S116	STENYDSVNMTAF	198	Unoccupied % 0.0	Unoccupied	UO
psm_without_S116	STENYDSVNMTAF	198	Unoccupied % 0.0	Unoccupied	UO
psm_without_S116	STENYDSVNMTAF	198	Unoccupied % 0.0	Unoccupied	UO
psm_without_S116	STENYDSVNMTAF	198	HexNAc(2)Hex(9) % 1864.6342	High Mannose	M9
psm_without_S116	STENYDSVNMTAF	198	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_without_S116	STENYDSVNMTAF	198	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_without_S116	STENYDSVNMTAF	198	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7
psm_without_S116	STENYDSVNMTAF	198	HexNAc(2)Hex(5) % 1216.4229	High Mannose	M5
psm_without_S116	STENYDSVNMTAF	198	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_without_S116	STENYDSVNMTAF	198	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_without_S116	STENYDSVNMTAF	198	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_without_S116	STENYDSVNMTAF	198	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_without_S116	STENYDSVNMTAF	198	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_without_S116	STENYDSVNMTAF	198	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_without_S116	STENYDSVNMTAF	198	HexNAc(2)Hex(9) % 1864.6342	High Mannose	M9
psm_without_S116	STENYDSVNMTAF	198	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_without_S116	STENYDSVNMTAF	198	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_without_S116	STENYDSVNMTAF	198	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_without_S116	STENYDSVNMTAF	198	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7
psm_without_S116	STENYDSVNMTAF	198	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7
psm_without_S116	STENYDSVNMTAF	198	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7

Sample	Peptide	Glycosite	Total Glycan Composition	Glycoform Category	Glycoform Subcategory
psm_without_S116	STENNYDSVNMTAFCDF	198	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7
psm_without_S116	STENNYDSVNMTAFCDF	198	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7
psm_without_S116	STENNYDSVNMTAFCDF	198	HexNAc(2)Hex(6) % 1378.4757	High Mannose	M6
psm_without_S116	STENNYDSVNMTAFCDF	198	HexNAc(2)Hex(5) % 1216.4229	High Mannose	M5
psm_without_S116	STENNYDSVNMTAFCDF	198	HexNAc(2)Hex(4) % 1054.3701	Hybrid	H
psm_without_S116	STENNYDSVNMTAFCDF	198	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_without_S116	STENNYDSVNMTAFCDF	198	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_without_S116	STENNYDSVNMTAFCDF	198	HexNAc(2)Hex(3) % 892.3172	Hybrid	H
psm_without_S116	STENNYDSVNMTAFCDF	198	HexNAc(2)Hex(3) % 892.3172	Hybrid	H
psm_without_S116	STENNYDSVNMTAF	198	Unoccupied % 0.0	Unoccupied	UO
psm_without_S116	STENNYDSVNMTAF	198	Unoccupied % 0.0	Unoccupied	UO
psm_without_S116	STENNYDSVNMTAFCDFY	198	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_without_S116	STENNYDSVNMTAFCDFY	198	HexNAc(2)Hex(6) % 1378.4757	High Mannose	M6
psm_without_S116	STENNYDSVNMTAFCDF	198	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_without_S116	STENNYDSVNMTAFCDF	198	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_without_S116	STENNYDSVNMTAFCDFY	198	HexNAc(2)Hex(3)Fuc(1) % 1038.3751	Hybrid (Fucosylated)	FH
psm_without_S116	STENNYDSVNMTAFCDF	198	HexNAc(2)Hex(10) % 2026.6870	High Mannose	M10
psm_without_S116	STENNYDSVNMTAFCDF	198	HexNAc(2)Hex(10) % 2026.6870	High Mannose	M10
psm_without_S116	STENNYDSVNMTAFCDFY	198	HexNAc(2)Hex(3) % 892.3172	Hybrid	H
psm_without_S116	STENNYDSVNMTAFCDF	198	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_without_S116	STENNYDSVNMTAFCDF	198	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_without_S116	STENNYDSVNMTAFCDF	198	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7
psm_without_S116	STENNYDSVNMTAFCDF	198	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7
psm_without_S116	STENNYDSVNMTAFCDF	198	HexNAc(2)Hex(6) % 1378.4757	High Mannose	M6
psm_without_S116	STENNYDSVNMTAFCDF	198	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_without_S116	STENNYDSVNMTAFCDF	198	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7
psm_without_S116	STENNYDSVNMTAFCDF	198	HexNAc(2)Hex(6) % 1378.4757	High Mannose	M6

Sample	Peptide	Glycosite	Total Glycan Composition	Glycoform Category	Glycoform Subcategory
psm_without_S116	STLENYDSVNMTAFCDF	198	Unoccupied % 0.0	Unoccupied	UO
psm_without_S116	STLENYDSVNMTAFCDF	198	Unoccupied % 0.0	Unoccupied	UO
psm_without_S116	STLENYDSVNMTAFCDF	198	HexNAc(2)Hex(5) % 1216.4229	High Mannose	M5
psm_without_S116	STLENYDSVNMTAFCDF	198	HexNAc(2)Hex(4) % 1054.3701	Hybrid	H
psm_without_S116	STLENYDSVNMTAFCDF	198	Unoccupied % 0.0	Unoccupied	UO
psm_without_S116	STLENYDSVNMTAFCDF	198	HexNAc(2)Hex(3) % 892.3172	Hybrid	H
psm_without_S116	STLENYDSVNMTAFCDF	198	HexNAc(2)Hex(4) % 1054.3701	Hybrid	H
psm_without_S116	STLENYDSVNMTAFCDF	198	HexNAc(2)Hex(5) % 1216.4229	High Mannose	M5
psm_without_DSV	DSVNMTAFCDFY	198	Unoccupied % 0.0	Unoccupied	UO
psm_without_DSV	DSVNMTAFCDFY	198	Unoccupied % 0.0	Unoccupied	UO
psm_without_DSV	DSVNMTAFCDFY	198	Unoccupied % 0.0	Unoccupied	UO
psm_without_DSV	DSVNMTAFCDFY	198	Unoccupied % 0.0	Unoccupied	UO
psm_without_DSV	DSVNMTAFCDFY	198	Unoccupied % 0.0	Unoccupied	UO
psm_without_S116	STLENYDSVNMTAFCDF	198	HexNAc(2)Hex(9) % 1864.6342	High Mannose	M9
psm_without_S116	STLENYDSVNMTAFCDF	198	HexNAc(2)Hex(8) % 1702.5814	High Mannose	M8
psm_without_S116	STLENYDSVNMTAFCDF	198	HexNAc(2)Hex(7) % 1540.5285	High Mannose	M7