

What's new in Bruker ProteoScape Package 2025b: GlycoScape

Bruker ProteoScape Package

- Bruker ProteoScape Package includes:
 - HP Z8 workstation with 2x GPU cards
 - Ethernet switch
 - Bruker ProteoScape application
 - Including Spectronaut Core module
 - TIMSrescore, TIMS DIANN, TIMSquant etc.
 - Optional module: BPS Novor
 - GlycoScape application
 - Myriad workflow

ProteoScape Package

Bruker ProteoScape™

- Spectronaut 19 module
- Run & Done
- Acquisition Control
- TIMSrescore
- TIMS DIANN
- TIMSquant
- BPS Novor

GlycoScape™

- Run & Done
- Acquisition Control
- Myriad workflow

BRUKER
GlycoScape™



What's new in Bruker ProteoScape 2025b

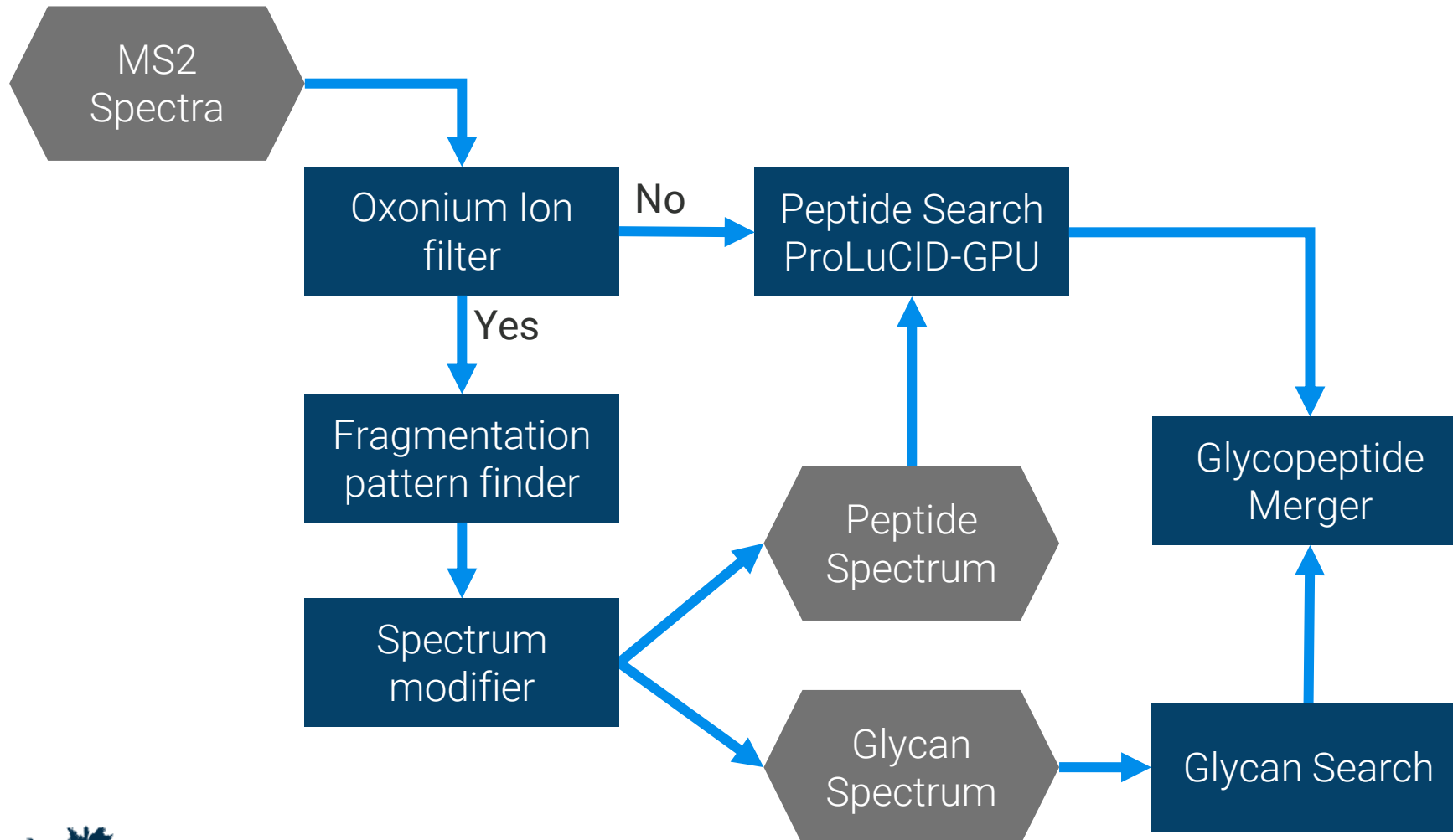
- GlycoScape utilizing the Myriad workflow for glycopeptide analysis
- Reminder of what's new in 2025:
 - Spectronaut module updated to v19.0
 - Includes diagonal-PASEF support
 - Improved deep learning models for increased identification
 - TIMSrescore workflow
 - AI/ML models for increased identification
 - Dedicated quantitation workflow
 - UI/UX improvements
 - Most columns are sortable
 - First search functionality within table (case sensitive)
 - Others ...
 - Robustness and stability improvements



GLYCOPEPTIDE ANALYSIS AT THE SPEED OF PASEF

GlycoScape™

GlycoScape: real-time glycopeptide analysis workflow



- GlycoScape utilizes the Myriad workflow originally described by Armony et al., 2023
- Each spectrum is analyzed for the presence of oxonium ions, if found then the spectrum is separated into two components
 - The peptide spectrum component is analyzed by ProLuCID-GPU
 - The glycan spectrum component is analyzed by Myriad's composition generator **without any glycan databases**

“A sister-product to Bruker’s ProteoScape, GlycoScape now opens up the analysis of glycoproteomic mass spectrometry data from the timsTOF platform for on-the-fly processing without glycan database restrictions.”



Dr. Hans Wessels
RadboudUMC



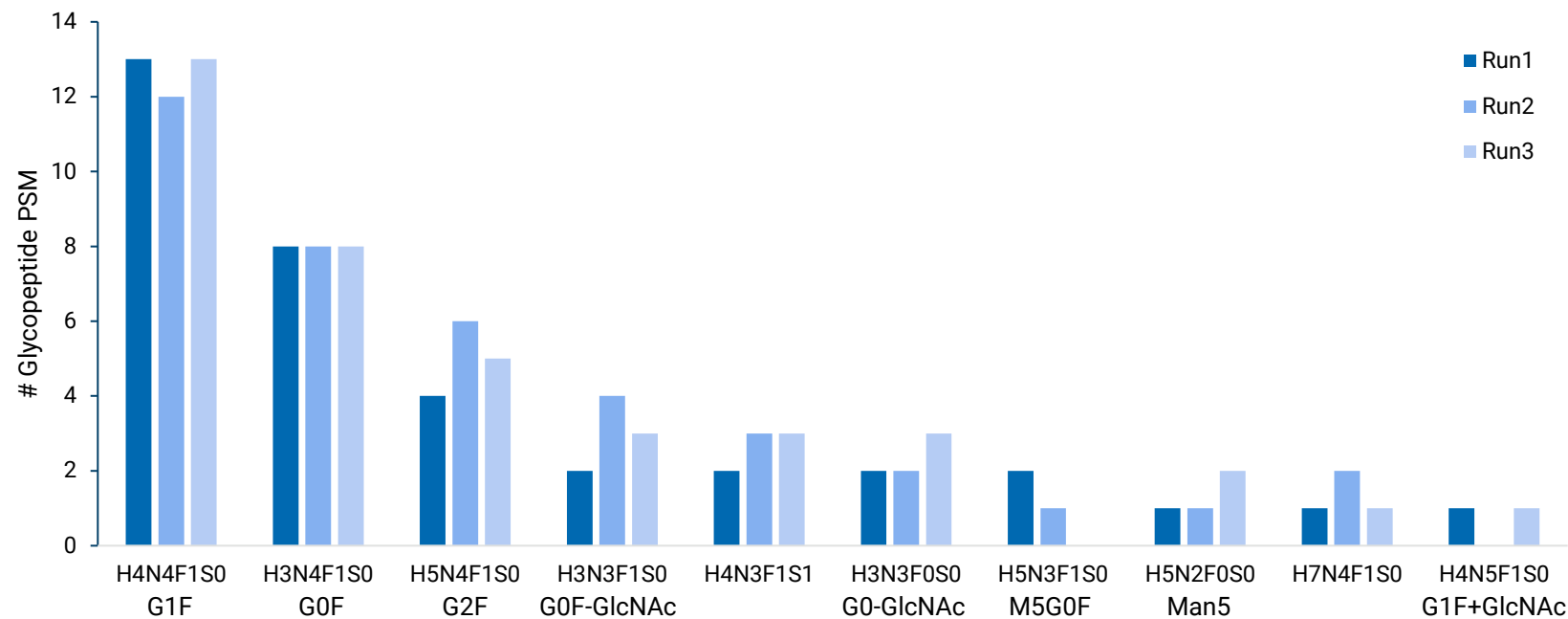
Myriad
Workflow
Publication



Glyco-PASEF
Optimization
Publication



GlycoScape: real-time identification of glycopeptides from NIST mAB reference standard



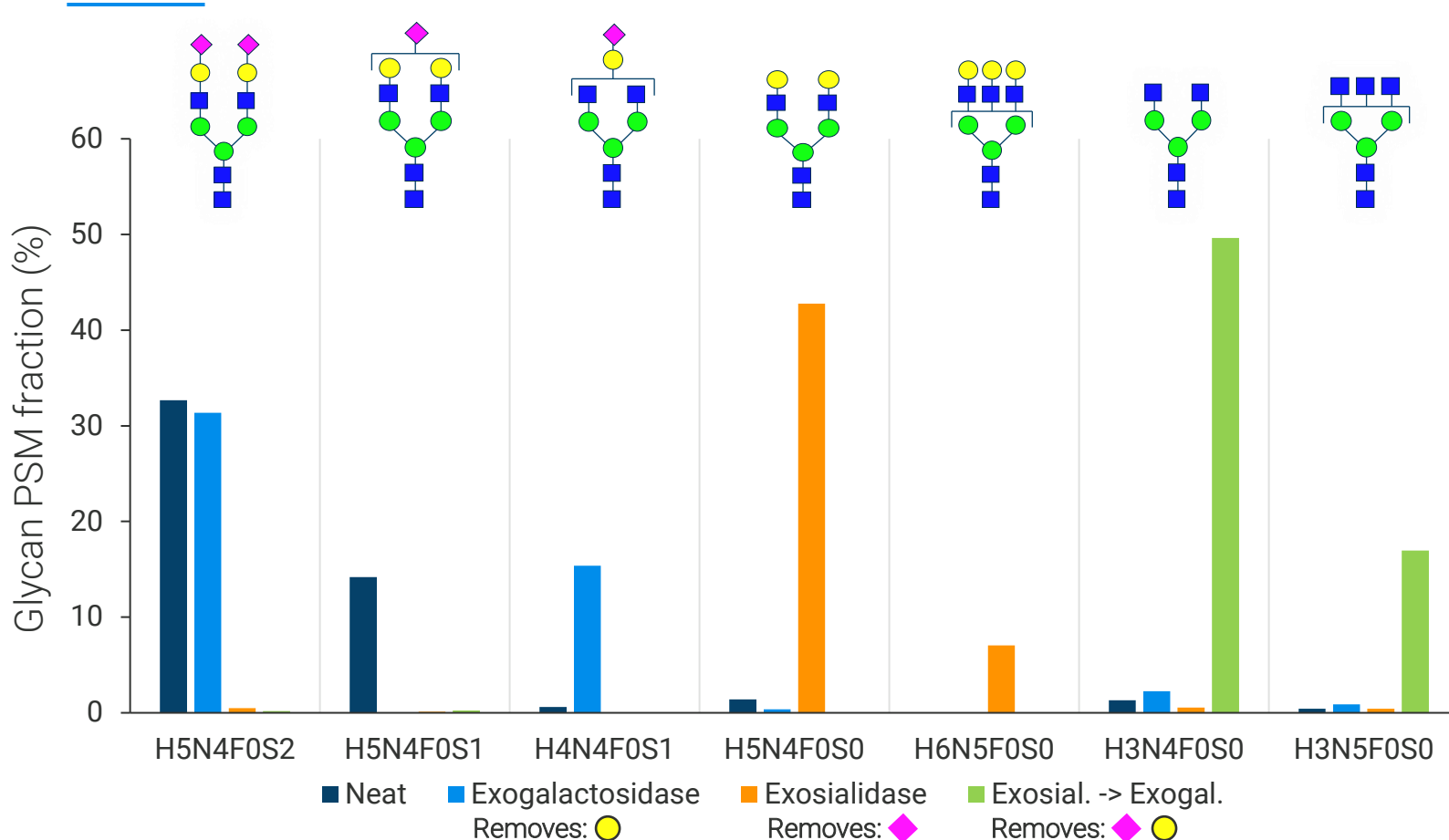
- GlycoScape, utilizing the Myriad workflow (Armony et al., 2023), identifies 12-20 glycan compositions (depending on acquisition method) on the IgG heavy-chain of the NIST mAB reference standard, in line with the interlaboratory study by Leoz et al., 2020
- Shown above, top 10 most abundant glycan compositions identified

- 50ng Trypsin digested NIST mAB analyzed with 35min nLC gradient on timsTOF Pro2
- With GlycoScape:
 - Identify glycopeptides
 - In real-time
 - With results available seconds after acquisition ends

Data provided by:
 Ho-Tak Lau and Richard Rogers
 Umoja Biopharma, Seattle, WA USA
 Acquisition methods based on:
<https://doi.org/10.1021/acs.analchem.3c05874>

<https://doi.org/10.3390/ijms24097869>
<https://doi.org/10.1074/mcp.RA119.001677>

GlycoScape shows great specificity for the identified glycan compositions

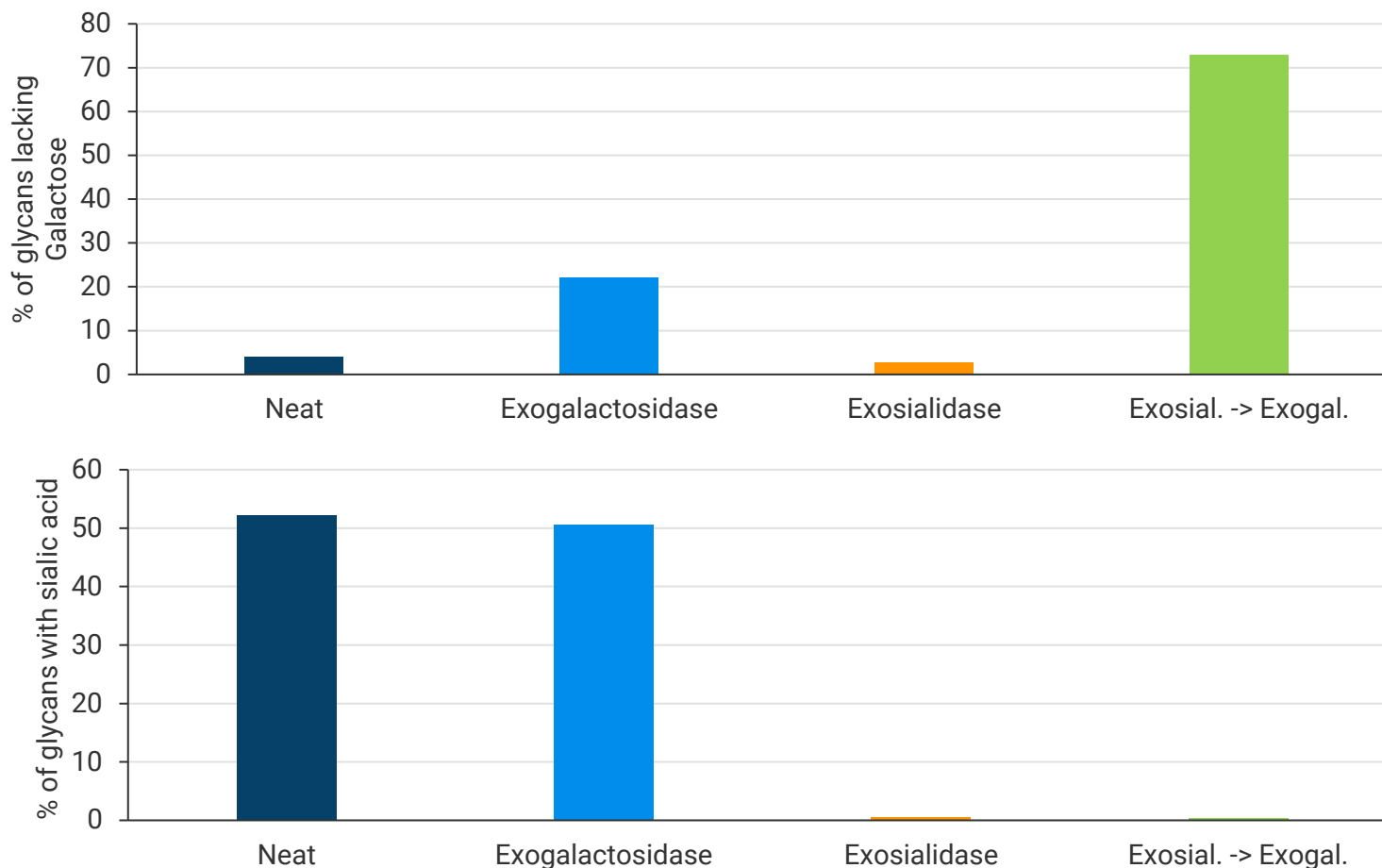


For simplicity, the average of 2 replicates is shown for each condition.

Data provided by: Fokje Zijlstra, Gad Armony, Alain van Gool, Dirk Lefeber and Hans Wessels. RadboudUMC, the Netherlands

- In HILIC enriched Human plasma samples:
 - Treatment with Exogalactosidase shows only the unprotected Galactose residues are removed
 - Treatment with Exosialidase shows only sialic acids residues are removed
 - Sequential treatment of Exosialidase followed by Exogalactosidase shows de-protection and removal of Galactose residues.

GlycoScape shows great specificity for the identified glycan compositions

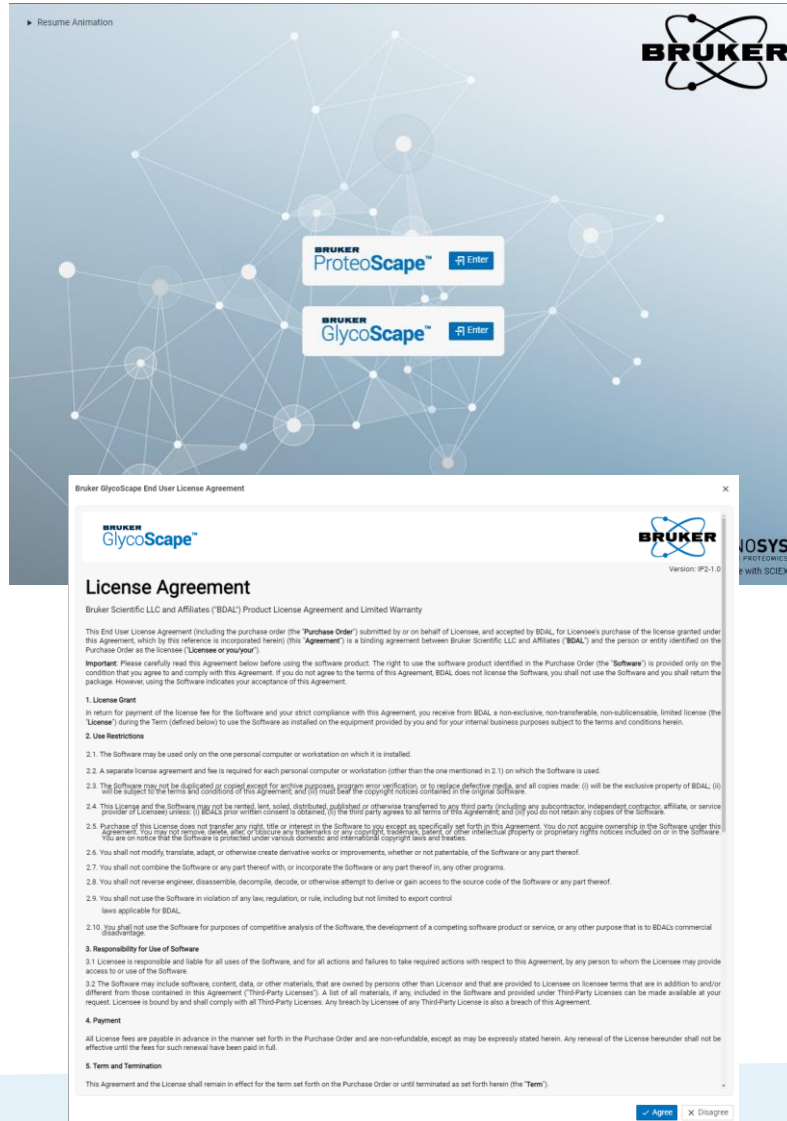


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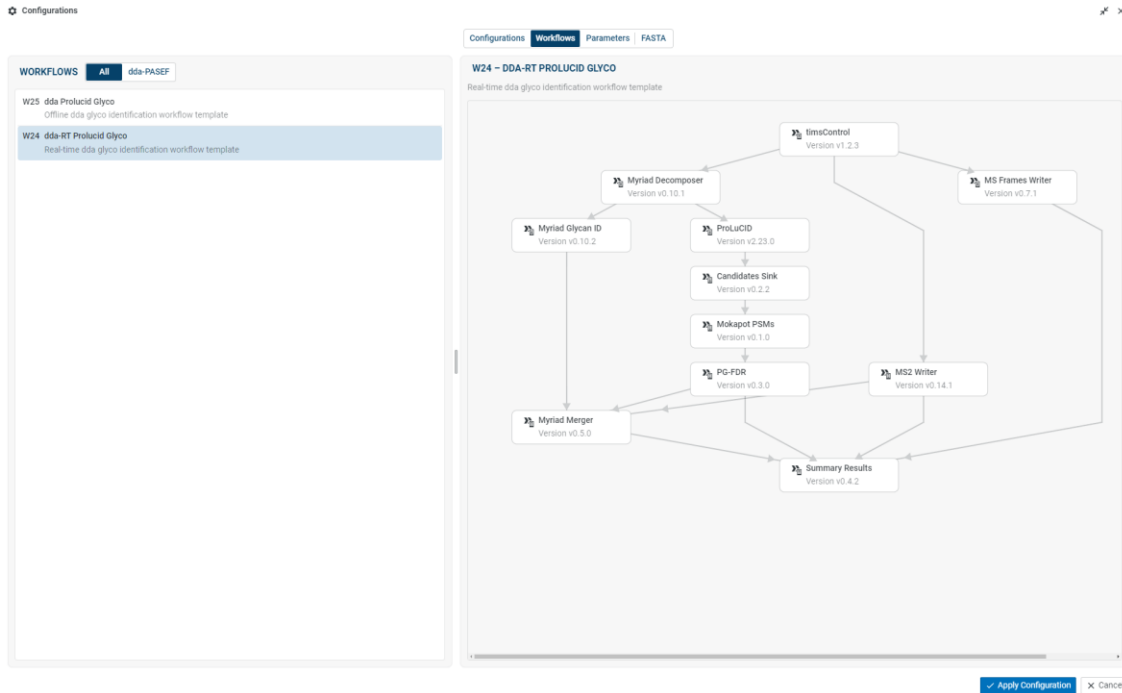
Using GlycoScape

Open the GlycoScape Application



- Login as usual, then the idle screen will present the choice of application to enter
- Choose GlycoScape
 - On first use, EULA will be presented for acceptance.

Create a configuration for real-time or offline re-analysis



- Default parameters should work for human derived samples

Myriad – GlycanID Parameters

Configurations

WORKFLOW TASKS

- timsControl
timsTOF acquisition
- MS Frames Writer
MS1 raw data sink for timsTOF acquisition
- MS2 Writer
MS2 raw data sink for timsTOF acquisition
- Myriad Decomposer
decompose glycopeptide spectra into peptide-and glycan- spectra
- ProLuCID
Peptide search engine
- Myriad Glycan ID
Glycan ID - Generates glycan-moiety compositions
- Candidates Sink
Candidates sink
- Mokapot PSMs
Select PSMs from candidates using the mokapot library
- PG-FDR
BPS Engine for Protein Group FDR
- Myriad Merger
Merge peptide and glycan identifications
- Summary Results
Summary results engine for glyco DDA-ID

PARAMETERS

P9 - NEW PARAMETERS

Configurations | Workflows | Parameters | FASTA

P9 - NEW PARAMETERS Edit

Composition Generator

Sugar building blocks

5	Sugar Name	Mass	One letter code	Min. sugar number	Max. sugar number	Use this building block?
1	Hex	162.05282	H	0	12	yes
2	HexNAc	203.07937	N	1	7	yes
3	dHex	146.05791	F	0	2	yes
4	NeuAc	291.09542	S	0	4	yes
5	NeuGc	307.0903	G	0	4	no

Glycan mass tolerance 20.0 ppm

Composition Ranker

Fragment ion mass tolerance 20.0 ppm

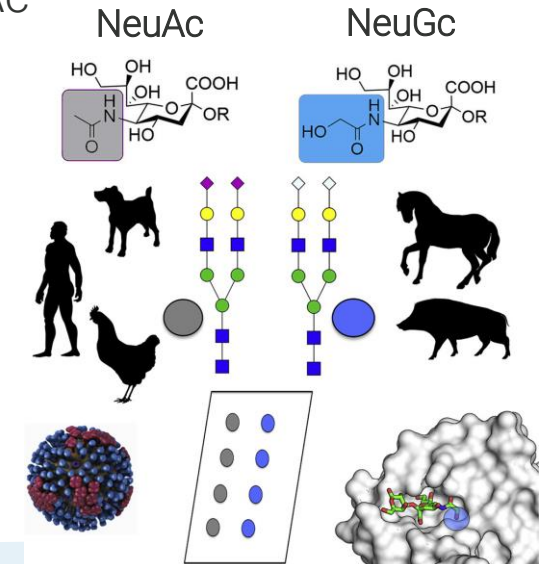
Minimum fragment ion intensity 0.01 relative

maximum isotopic offset 2

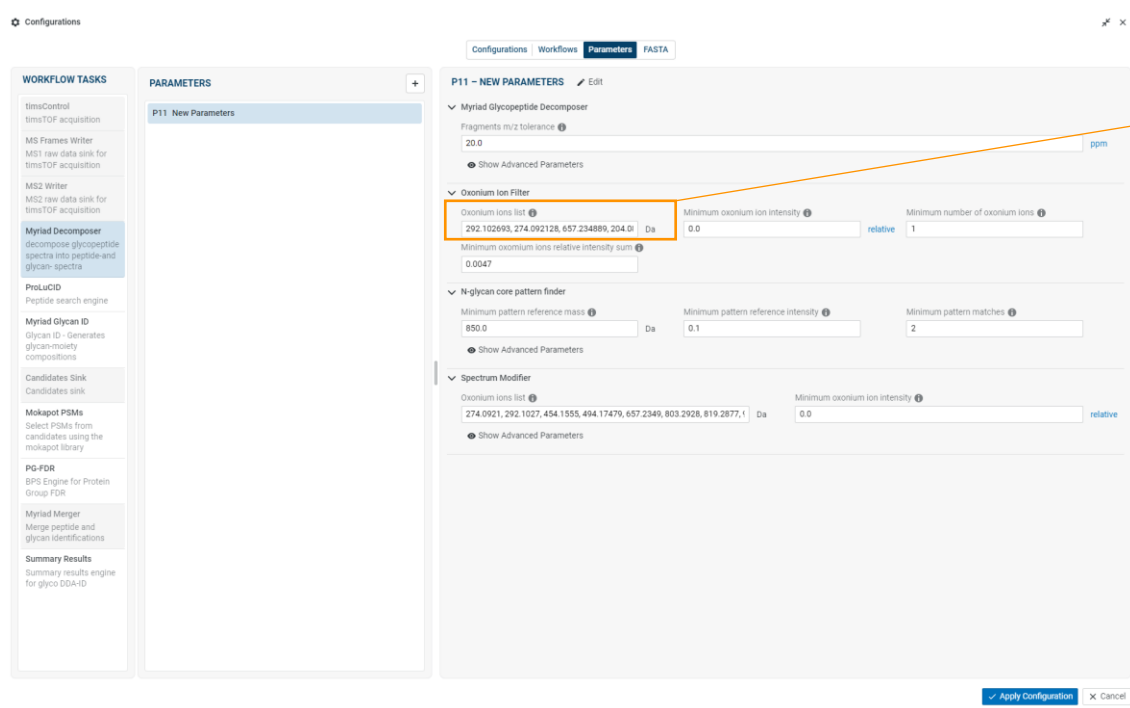
Show Advanced Parameters

Apply Configuration Cancel

- Currently limited to the 5 sugar building blocks shown
- Typical human samples utilize NeuAc but some cancer tissues utilize NeuGc
- Most other species utilize NeuGc and not NeuAc

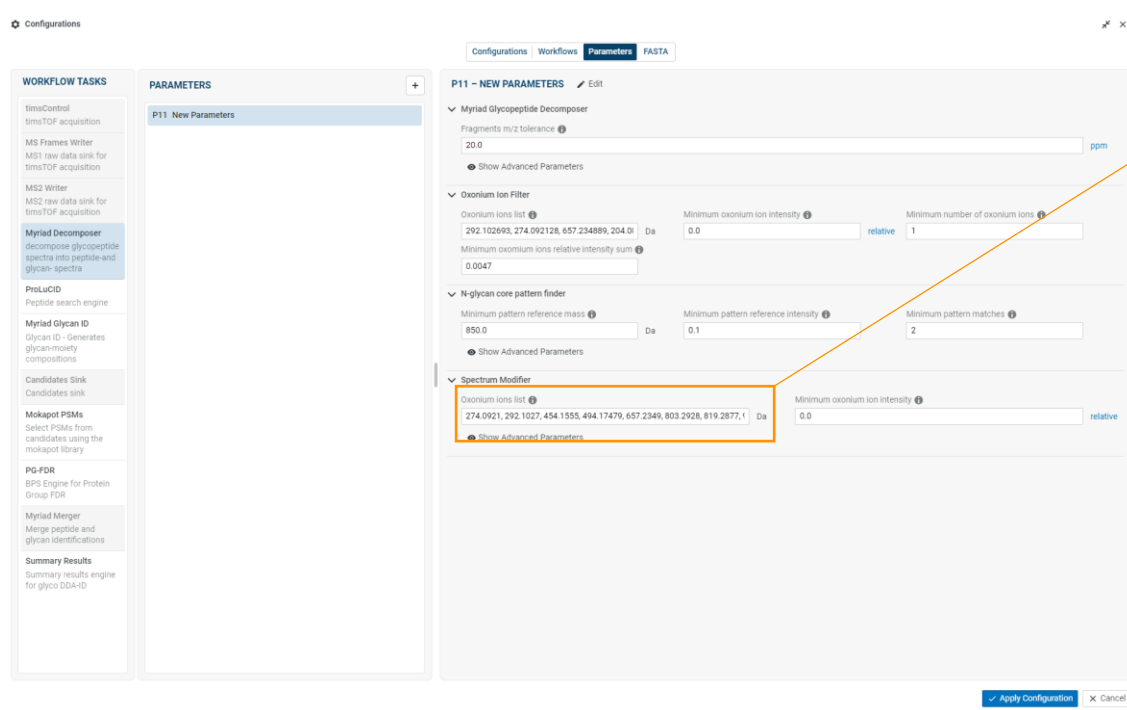


Myriad Decomposer – Oxonium Ion Filter



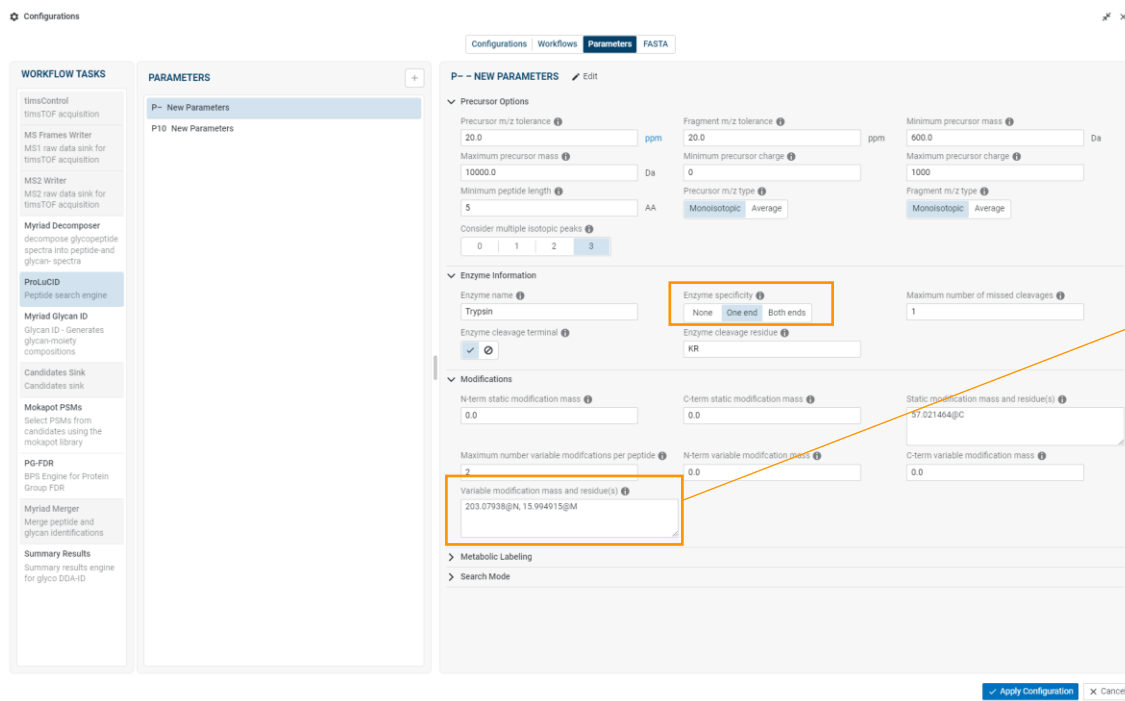
- If NeuGc is selected in the GlycanID, then the default Oxonium Ion Filter and Oxonium ions list needs to be modified:
- Oxonium Ion filter:
 - Ions considered: S, S-H₂O, HNS, N, HN, HNF
 - Default NeuAc: 292.102693, 274.092128, 657.234889, 204.0867, 366.139472, 512.19793
 - NeuGc: 308.0976, 290.087, 673.2298, 204.0867, 366.139472, 512.19793
 - NeuAc & NeuGc: 292.102693, 274.092128, 657.234889, 308.0976, 290.087, 673.2298, 204.0867, 366.139472, 512.19793

Myriad Decomposer – Oxonium Ion list



- If NeuGc is selected in the GlycanID, then the default Oxonium Ion Filter and Oxonium ions list needs to be modified:
- Oxonium Ion List:
 - Ions considered: S-H2O, S, HS, NS, HNS, HNFS, H2NS, H2NFS, F, H, N, HF, H2, NF, HN, N2, H3, HNF, H2N, N2F, HN2, H4, H2NF, H3N, N2F2, HN2F, H2N2, H5, H3NF, HN2F2, H2N2F, H3N2, H6, H2N2F2, H3N2F, H3N3, H7, H3N2F2, H3N3F, H8, H3N4, H3N3F2, H3N4F, H9, H3N4F2, H10, H11, H12
 - Default NeuAc: 274.0921, 292.1027, 454.1555, 494.17479, 657.2349, 803.2928, 819.2877, 965.3456, 147.0652, 163.0601,
 - NeuGc: 290.0870, 308.0976, 470.1504, 510.16969, 673.2298, 819.2877, 835.2826, 981.3405, 147.0652, 163.0601,
 - NeuAc & NeuGc : 274.0921, 292.1027, 454.1555, 494.17479, 657.2349, 803.2928, 819.2877, 965.3456, 290.0870, 308.0976, 470.1504, 510.16969, 673.2298, 819.2877, 835.2826, 981.3405, 147.0652, 163.0601,

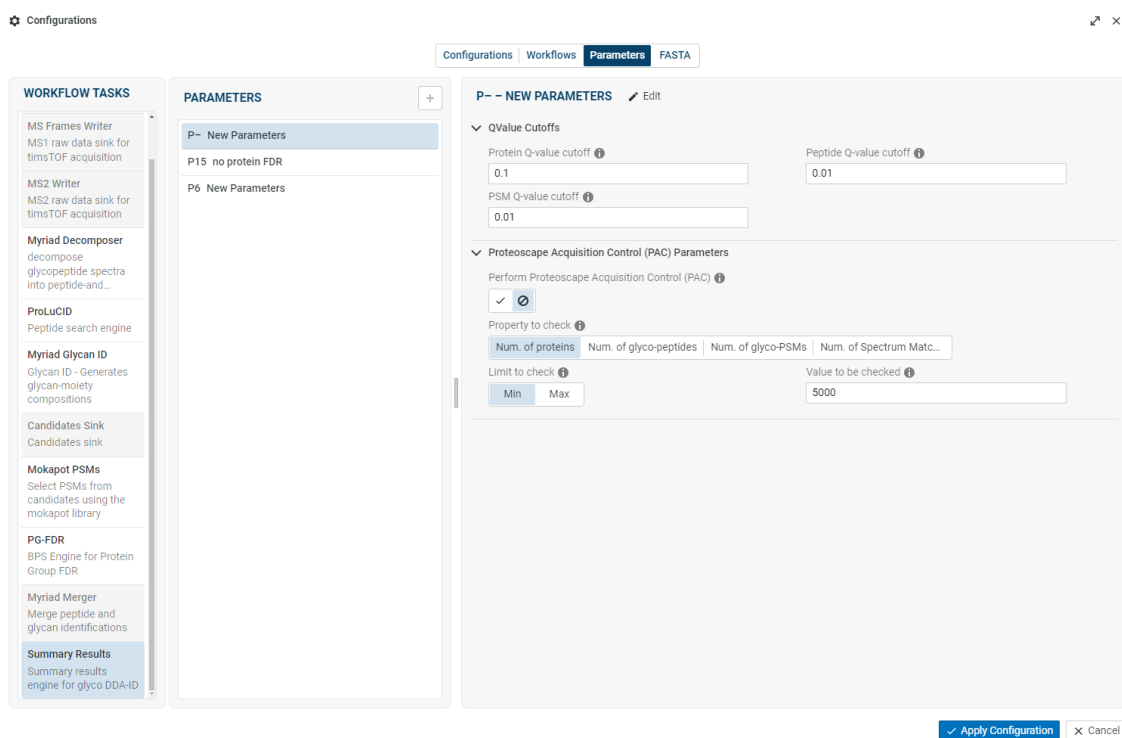
ProluCID



The screenshot displays the 'Parameters' configuration window for a ProluCID search. The 'Enzyme Information' section is highlighted with an orange box, showing 'Enzyme name' set to 'Trypsin' and 'Enzyme specificity' set to 'One end'. The 'Enzyme cleavage terminal' is set to 'KR'. The 'Modifications' section is also highlighted with an orange box, showing a 'Variable modification mass and residue(s)' set to '203.07938@N, 15.994915@M'. The 'FASTA' tab is selected at the top of the configuration window.

- By default, it semi-tryptic searches are recommended. Typically, this is done in conjunction with a smaller FASTA file (secreted proteins only) or some such, if not a longer than acquisition search is likely.
- Variable modification of by N-Acetylhexosamine on Asparagine must be specified for the Myriad workflow to function correctly = [203.07938@N](#)

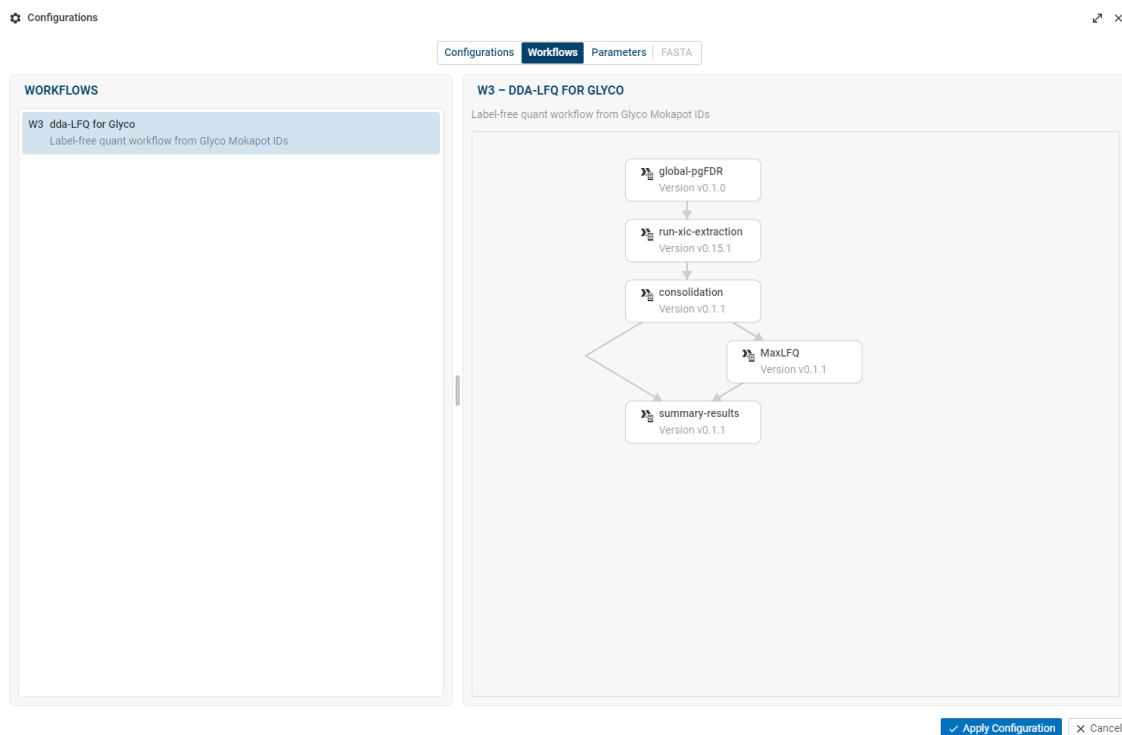
Summary results



The screenshot displays the Bruker software configuration interface. On the left, a 'WORKFLOW TASKS' sidebar lists various modules including MS Frames Writer, MS2 Writer, Myriad Decomposer, ProLuCID, Myriad Glycan ID, Candidates Sink, Mokapot PSMs, PG-FDR, and Myriad Merger. The 'Summary Results' task is highlighted. The main area shows the 'PARAMETERS' section for 'NEW PARAMETERS', with tabs for 'Configurations', 'Workflows', 'Parameters', and 'FASTA'. The 'QValue Cutoffs' section is expanded, showing 'Protein Q-value cutoff' set to 0.1 and 'Peptide Q-value cutoff' set to 0.01. The 'Proteomics Acquisition Control (PAC) Parameters' section is also expanded, showing 'Perform Proteomics Acquisition Control (PAC)' checked, 'Property to check' set to 'Num. of proteins', and 'Limit to check' set to 'Min' with a 'Value to be checked' of 5000. At the bottom, there are 'Apply Configuration' and 'Cancel' buttons.

- Often times when a small database is utilized for protein identification, it's desirable to set the Protein Q-value cutoff in the Summary Results to a value greater than 0.01. By default, results up to 0.1 are shown.
- For very small FASTA files, such as NIST mAB with only contaminant proteins, the Summary Results protein Q-value filter can be set 1 so that visual elements can be utilized in GlycoScape

Quant with GlycoScape



- After single run analysis, >2 samples can be selected for quantitation
 - Global FDR is calculated across selected samples
 - Then XIC extracted for all (glyco)peptides above user specified q-value
 - maxLFQ based protein quantitation is provided
-
- Currently missing match-between-runs type functionality ... only quantified precursors identified in the run (no transfer between runs)

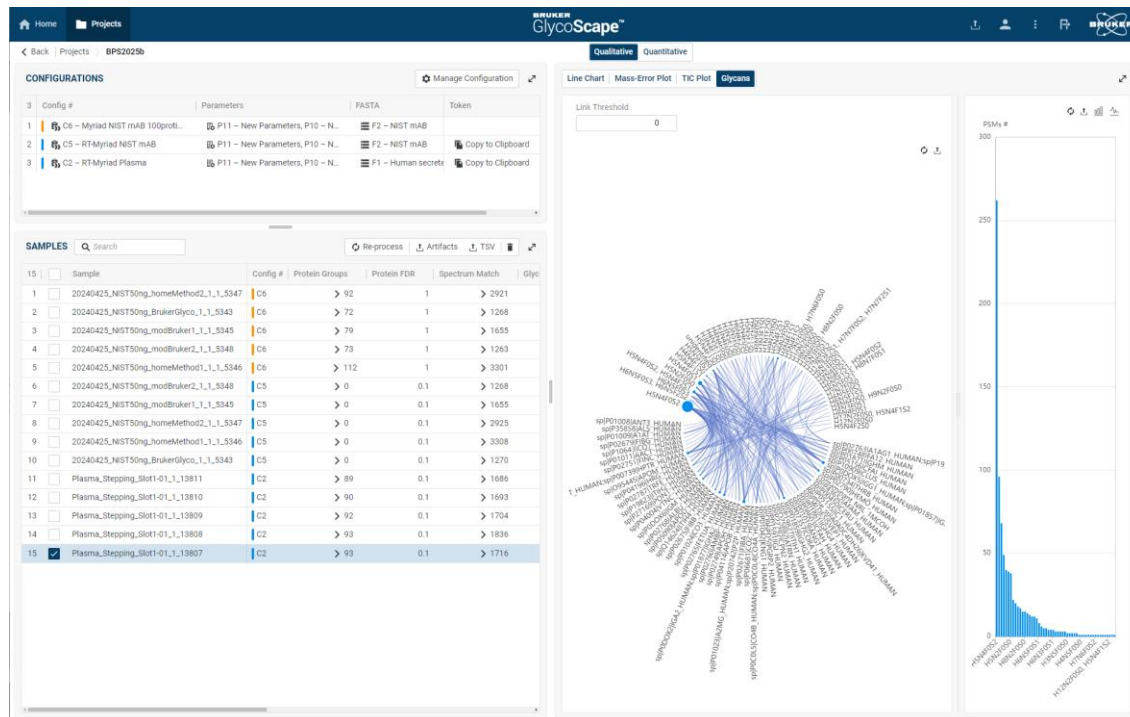
GlycoScape Specific Views

Mass Error Plots



- Glycan and Peptide mass errors are plotted independently

Chord Diagrams – Sample view



- From Samples view, a chord diagram can be accessed for each sample (only one sample can be shown at a time)
 - Diagram shows all identified glycan compositions and which protein groups they were found on
 - Node size = PSM counts
- Additional, bar graph of counts of each Glycan composition

Protein View

The screenshot shows the Proteomics software interface. On the left, a table lists proteins with columns for Protein Name, Protein Group Q Value, Stripped Peptides, Peptides, PSMs, Protein Group Score, and Proteins. The top protein is `1 qpp02571F8A_HUMAN`. On the right, the 'Protein Coverage & PTM' panel shows the protein sequence with glycosylation motifs underlined in yellow. The sequence is: `M N S L G A V I A L L I R G Q L F A V D G C N V D T I A D D G C K P P E I A N G`. The underlined motifs are: `Y E H S V Y T C E R N Y E L A T E G D G V T I L D R K G I N K A V G D H E P`, `E C R A D D G C K P F F I A H G Y V E S V R T C C R N Y T L A T E G D G V Y T`, `L N N E K C H I H A V G D K L F E C A V C G P F F A F P V O R I L G D H E D`, `A R G S F P P Q A L M Y R H N L T G A T L I N G W L L T A K L P L F R S E E`, `R E V Y V H V E R V P I C L F P E D I A E Y S R V G V T S G R R H A F P F T D`, `R E Y V N L P V A D D G C I I H Y E G S T V P E K E T F F R P V G Q P I L N E`, and `H T P C A G M K Y Q E D T C Y G D A G A P A V D E E D T N Y A T S L P F D`. Below the sequence is a bar chart showing the number of PSMs for various PTMs.

- Any potential glycosylation motifs are underlined in the sequence
- Chord diagram for glycan compositions mapping to peptides is accessible

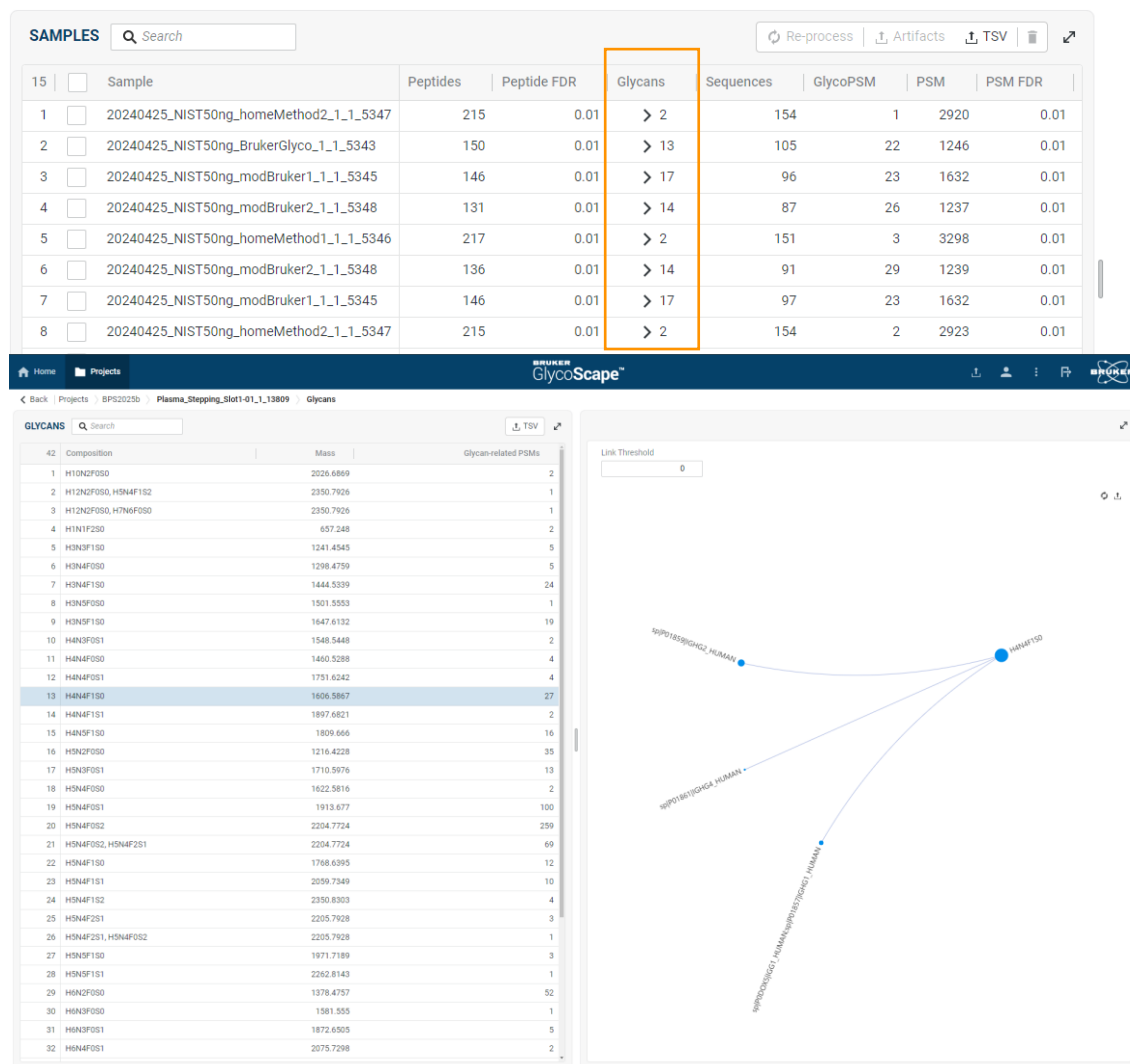
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PSM View

- PSM View
 - Top show peptide candidate
 - Bottom show glycan candidate compositions
 - Can choose candidate to be viewed if more than one is possible

The screenshot displays the Bruker GlycoScape interface. On the left, a table lists various peptides with columns for MS2 ID, Peptide Sequence, Glycan Composition, Glycosylation Motif, XCorr Score, and Mokapot PSM value. The peptide **IEK.VV.LHPN(203.07938)YSQVDIGLIK.LKQ** is highlighted. On the right, a detailed view of this peptide is shown, including its sequence **VV.LHPNYSQVDIGLIK**, glycan composition **H5N4F0S1**, and mass spectrometry data such as m/z: 927.9253, 1/K0: 0.91, and RT: 23.47 min. The interface also shows a list of top and bottom candidates for the peptide.

Glycan View



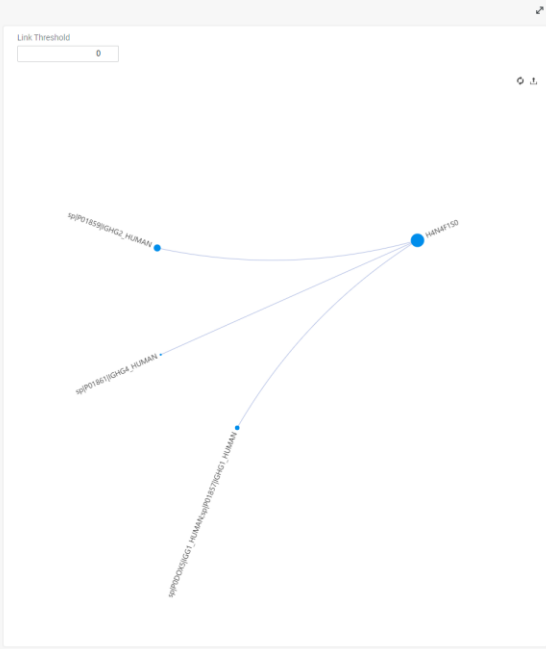
SAMPLES Re-process Artifacts TSV

15	Sample	Peptides	Peptide FDR	Glycans	Sequences	GlycoPSM	PSM	PSM FDR
1	20240425_NIST50ng_homeMethod2_1_1_5347	215	0.01	> 2	154	1	2920	0.01
2	20240425_NIST50ng_BrukerGlyco_1_1_5343	150	0.01	> 13	105	22	1246	0.01
3	20240425_NIST50ng_modBruker1_1_1_5345	146	0.01	> 17	96	23	1632	0.01
4	20240425_NIST50ng_modBruker2_1_1_5348	131	0.01	> 14	87	26	1237	0.01
5	20240425_NIST50ng_homeMethod1_1_1_5346	217	0.01	> 2	151	3	3298	0.01
6	20240425_NIST50ng_modBruker2_1_1_5348	136	0.01	> 14	91	29	1239	0.01
7	20240425_NIST50ng_modBruker1_1_1_5345	146	0.01	> 17	97	23	1632	0.01
8	20240425_NIST50ng_homeMethod2_1_1_5347	215	0.01	> 2	154	2	2923	0.01

GLYCANS TSV

42	Composition	Mass	Glycan-related PSMs
1	H10N2F050	2026.6869	2
2	H12N2F050, H5N4F1S2	2350.7926	1
3	H12N2F050, H7N6F050	2350.7926	1
4	H1N1F230	657.248	2
5	H3N3F130	1241.4543	5
6	H3N4F030	1298.4759	5
7	H3N4F130	1444.5339	24
8	H3N5F030	1501.5553	1
9	H3N5F130	1647.6132	19
10	H4N3F031	1548.5448	2
11	H4N4F030	1460.5288	4
12	H4N4F031	1751.6242	4
13	H4N4F130	1606.5867	27
14	H4N4F131	1897.6821	2
15	H4N5F130	1809.666	16
16	H5N2F030	1216.4228	35
17	H5N3F031	1710.5976	13
18	H5N4F030	1622.5816	2
19	H5N4F031	1913.677	100
20	H5N4F032	2204.7724	259
21	H5N4F032, H5N4F2S1	2204.7724	69
22	H5N4F130	1768.6895	12
23	H5N4F131	2059.7349	10
24	H5N4F132	2350.8303	4
25	H5N4F231	2205.7928	3
26	H5N4F231, H5N4F032	2205.7928	1
27	H5N5F130	1971.7189	3
28	H5N5F131	2262.8143	1
29	H6N2F030	1378.4757	52
30	H6N3F030	1581.555	1
31	H6N3F031	1872.6505	5
32	H6N4F031	2075.7298	2

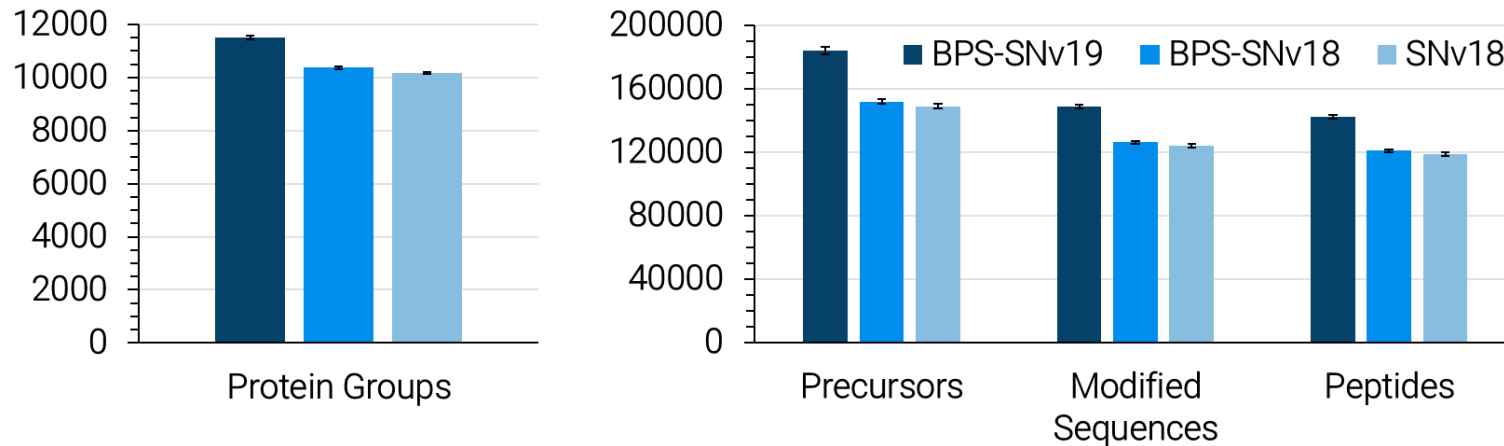
Link Threshold



- Glycan view can be accessed from the sample table for each sample
- Provides chord diagrams for each glycan composition

Spectronaut 19 module in BPS

Increased identifications with Spectronaut 19 module in Bruker ProteoScape



A three species mix of human, E.Coli and Yeast analyzed with a 45min active LC gradient on timsTOF Pro 2 was re-analyzed in BPS using the directDIA workflow.

Reminder: The Spectronaut module in BPS uses directDIA+ (Fast) by default, where the Spectronaut standalone uses directDIA+(Deep) by default. For comparison, be sure to use the same settings. In the examples above, directDIA+(Fast) was utilized.

- On average a 13% gain in identifications can be observed between SN18 and SN19
- New deep-learning models are the largest contributors.
 - DeepCCS
 - DeepFrag
 - DeepiRT
 - DeepQuant

diagonal-PASEF support in BPS with SN v19

- BPS 2025 now supports the analysis of diagonal-PASEF data, including synchro-PASEF and midia-PASEF, with the Spectronaut v19 module's directDIA workflow

midiaPASEF maximizes information content in data-independent acquisition proteomics

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2023/01/30

MCP TECHNOLOGICAL INNOVATION AND RESOURCES

Synchro-PASEF Allows Precursor-Specific Fragment Ion Extraction and Interference Removal in Data-Independent Acquisition

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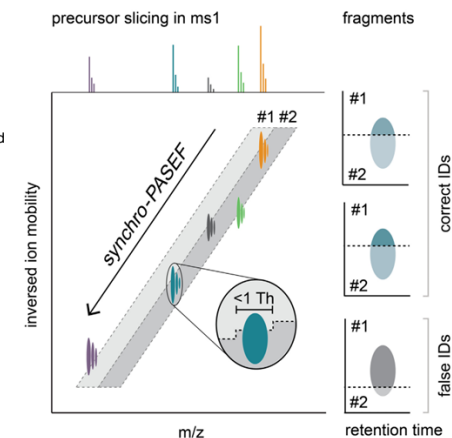
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In Brief

The novel scan mode synchro-PASEF efficiently follows the natural shape of the precursor cloud in the m/z and the trapped ion mobility space. This manifests in short cycle times and high sampling frequency of the eluting peptides and fragment signal amplification. Additionally, the seamlessly movement of the quadrupole nearly universally slices the precursor in the ion mobility dimension. The slicing position adds tremendous specificity, allowing deconvolution of the fragment space to 'pure fragmentation spectra' reminiscent of data-dependent acquisition spectra.

Graphical Abstract



Highlights

- Synchro-PASEF is a highly efficient scan mode for MS-based proteomics.
- It allows very fast cycle times, amplifying the fragment signal three-fold.
- Fragments are directly linked to precursors *via* precursor slicing.
- Precursor slicing enables deconvolution to pure fragmentation spectra.
- Synchro-PASEF unites the benefits of data-dependent and data-independent acquisition.

Abstract

dent acquisition (DIA) approaches provide comprehensive records of all detectable present ions. Here we introduce midiaPASEF, a novel DIA scan mode using mobility-coding of overlapping quadrupole windows to optimally cover the ion population in mass to charge plane. Using overlapping ion mobility-encoded quadrupole windows, midiaPASEF maximizes information content in DIA acquisitions which enables the determination of the mass of each fragment ion with a precision of less than 2 Th. The Snakemake-based MIDIAID pipeline enables fully automated processing of midiaPASEF files and exports highly specific DDA-like MSMS files suitable for *de novo* sequencing and can be searched directly with established tools like FragPipe and Mascot. midiaPASEF acquisition identifies over 40 unique peptides per precursor. midiaPASEF provides powerful library-free DIA analyses including phosphopeptidome and immunopep-

midiaPASEF, DIA, DDA, PASEF, Scan Mode, scanning quadrupole, TOF

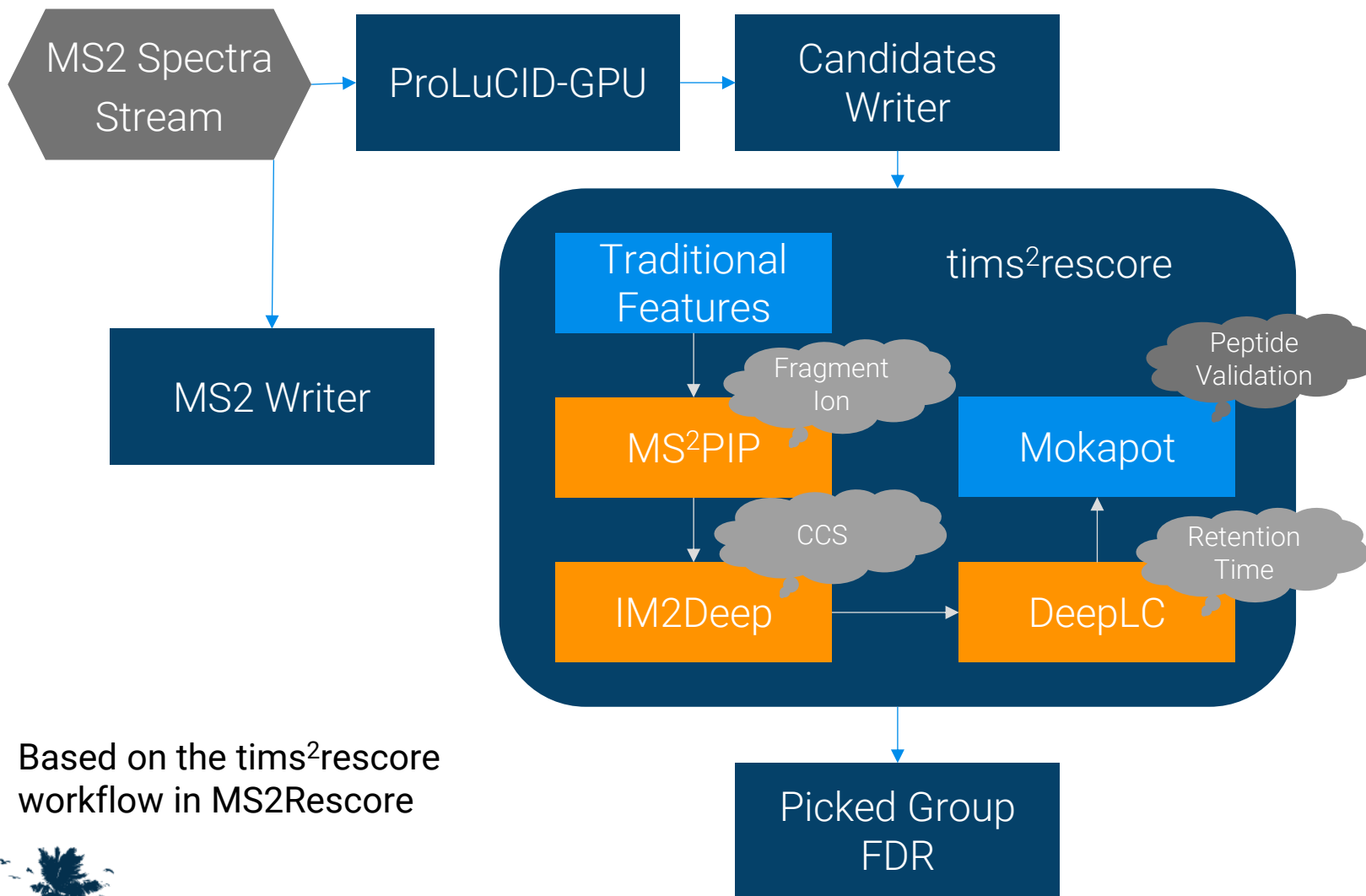
MiDIA-PASEF <https://doi.org/10.1101/2023.01.30.526204>

synchro-PASEF <https://doi.org/10.1016/j.mcpro.2022.100489>

2023, Mol Cell Proteomics 22(2), 100489
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TIMSrescore

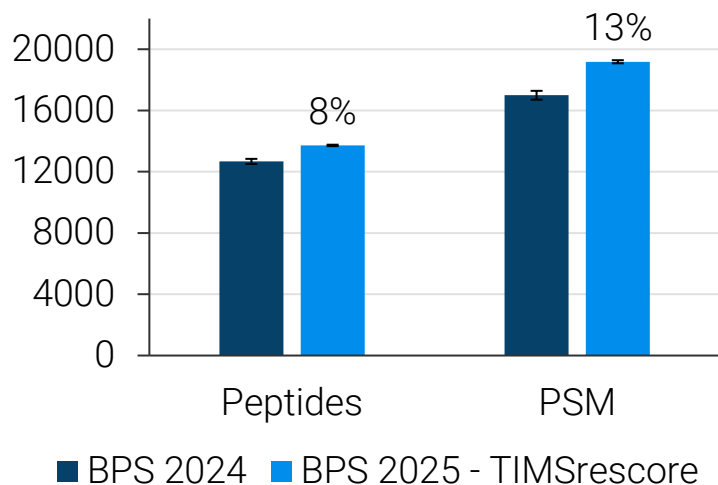
The TIMSrescore workflow



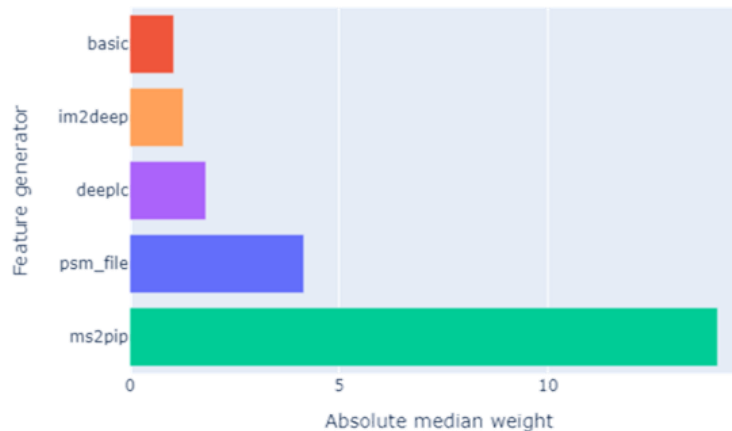
Based on the tims²rescore workflow in MS2Rescore

- The TIMSrescore workflow:
 - Identify peptides with database search
 - For each peptide compare:
 - Predicted fragment ion intensity
 - Predicted CCS
 - Predicted retention time
 - Validate peptides based on all these extended metrics
 - Create protein groups from validated peptides

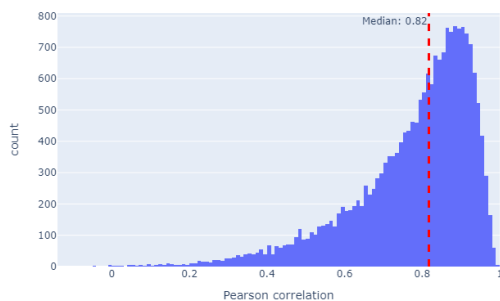
TIMSrescore increases confident identifications



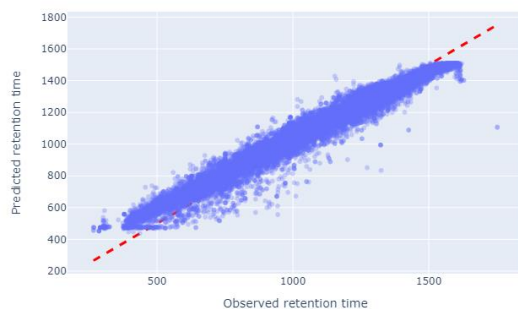
Absolute median weights, summed by feature generator



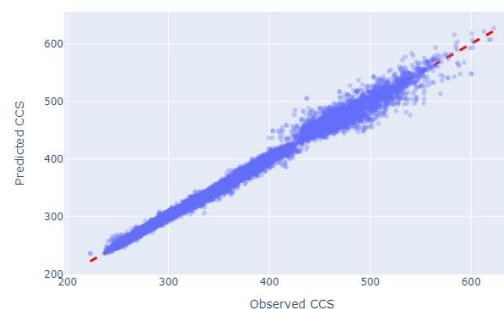
- In this HeLa Elastase digested triplicate measurement:
 - Peptides increased 8%
 - PSMs increased 13%
- Primary contribution for the gain was the timsTOF optimized fragment ion intensity prediction by ms²pip



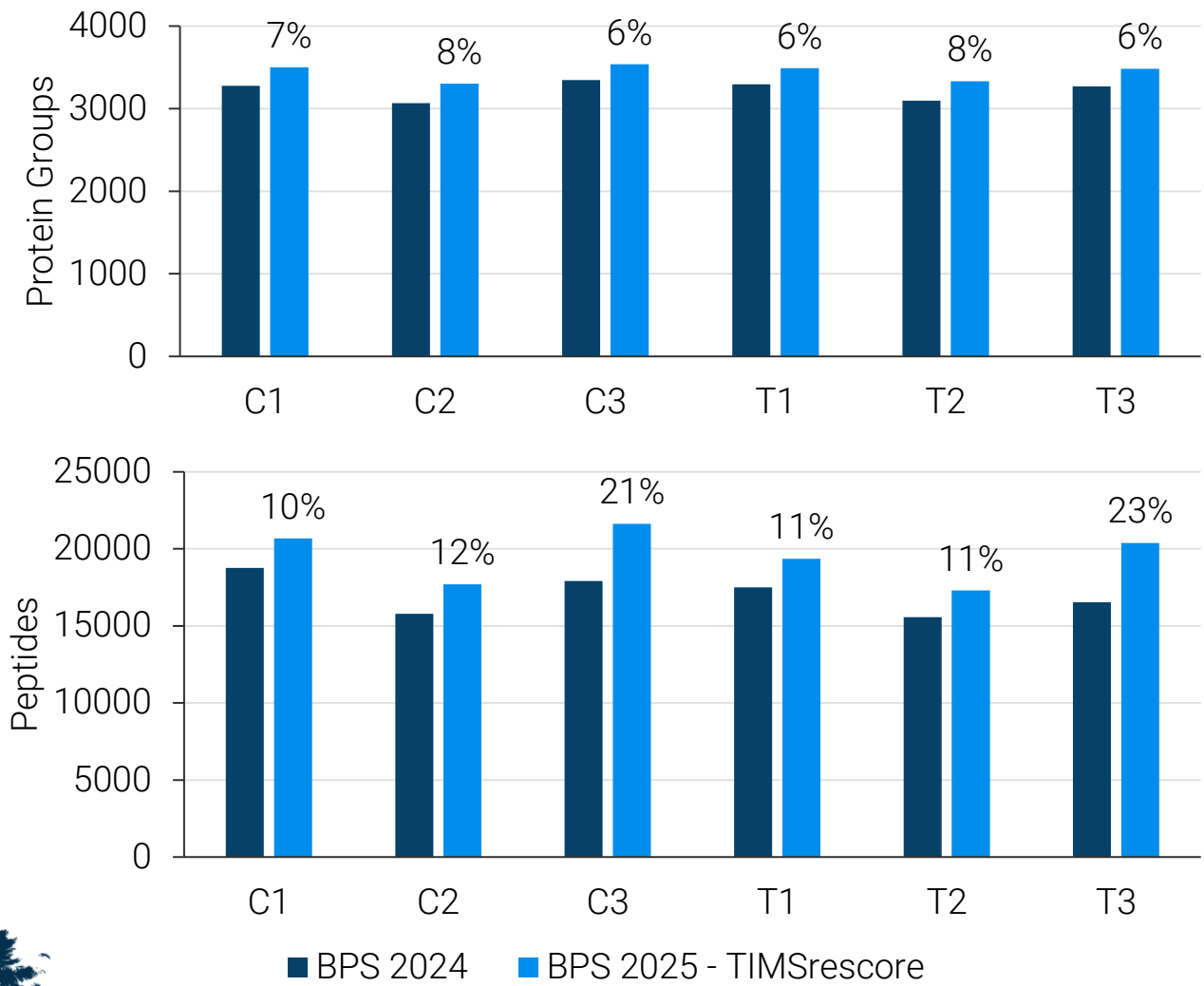
Predicted vs. observed retention times



Predicted vs. observed CCS

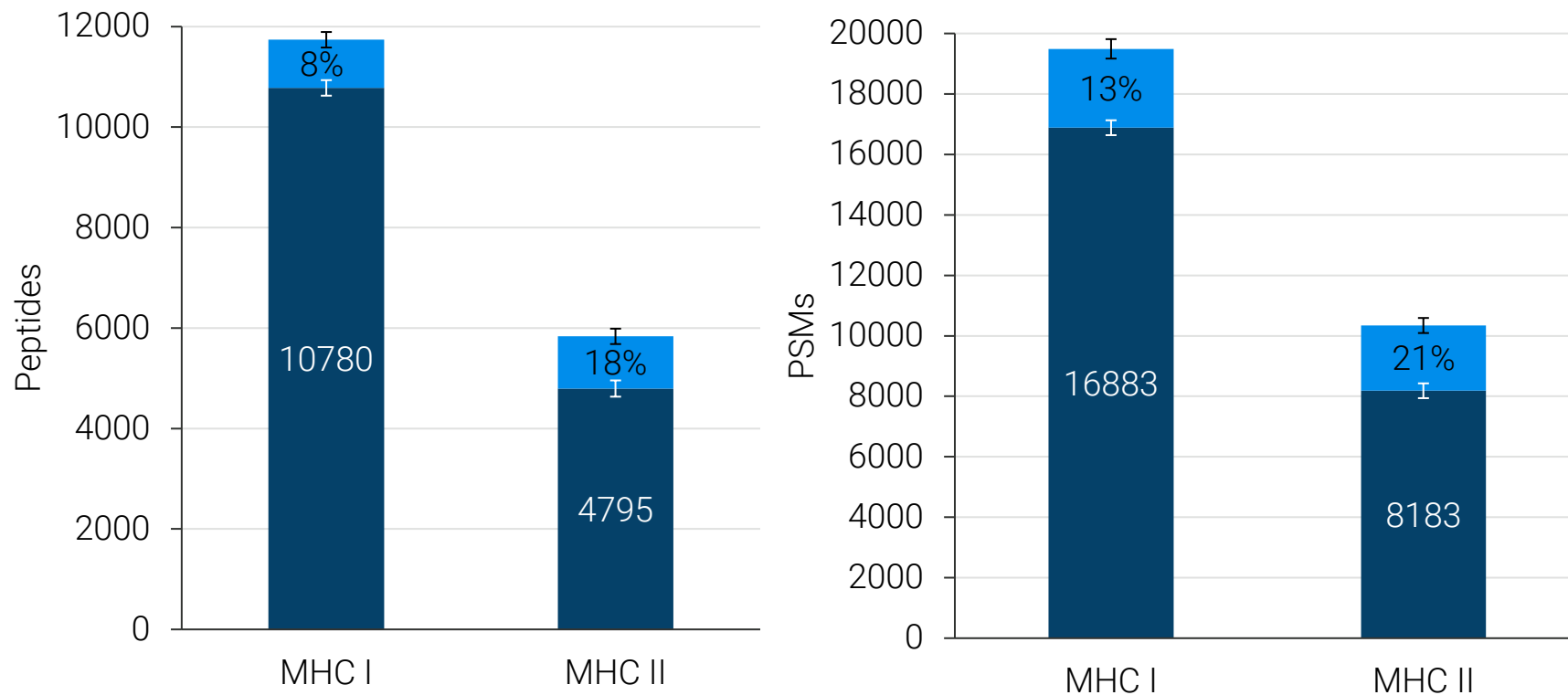


TIMSrescore increases confident identifications for phosphorylation enriched data

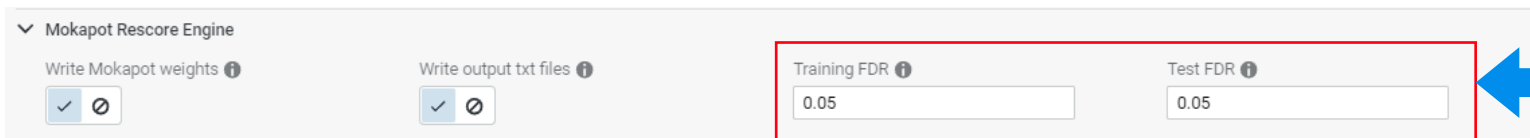


- Phospho-enriched dataset shows:
 - Protein groups increased ~7%
 - Peptides increased ~15%
- TIMSrescore consistently increases phosphorylated peptides and protein groups

TIMSrescore increases confident identifications for immunoproteomics data



■ BPS 2024 ■ BPS 2025 - TIMSrescore



- TIMSrescore increased confident MHC-I peptides by 8% and MHC-II peptides by 18%.
- timsTOF optimized fragmentation ion intensities and CCS predictions were largest contributors

For large search spaces, such as immunopeptidomics it is necessary to adjust the Training and Test FDR to be less stringent (0.01 -> 0.05)

Raw data from: Hoenisch Gravel, N. et al. TOFIMS mass spectrometry-based immunopeptidomics refines tumor antigen identification. *Nat Commun* 14, 7472 (2023)

UI/UX improvements

UI/UX improvements in BPS 2025

- Samples, Proteins and peptides tables have a case sensitive search bar
- Samples, Proteins and peptides tables can be sorted by user desired columns
- Columns in protein and peptide tables have been rearranged to provided most queried information to the front
- All Tables have row number and top right shown total # rows in the table.

← Back | Projects > DIA HYE SN19 - 60min Gradients Qualitative Quantitative

CONFIGURATIONS Manage Configuration

Config #	Parameters	FASTA	Spectral Library	Token
1	C137 - New Configuration	P109 - Semi-Nterm	F9 - HYE Uniprot	
2	C135 - Copy of C134 - SN19 19...	P106 - Phospho Biotin Deami-NQ	F14 - HYE Uniprot Isoforms iRT	
3	C134 - SN19 190624 glygly	P105 - GlyGly	F14 - HYE Uniprot Isoforms iRT	
4	C104 - New Configuration	P80 - New Parameters, P79 - N...	F12 - New Fasta	Copy to Clipboard
5	C75 - SN19 HYE	P66 - directDIA Fast, P63 - New...	F1 - HYE Uniprot	Copy to Clipboard

SAMPLES Re-process + Generate Spec Lib Artifacts TSV

Search

Sample	Config #	Protein Groups	Protein FDR	Peptides	Peptide FDR	Sequences	Precursors	Precursors FDR	PSM	PSM FDR
1	G9215	C137 > 8872	0.01	> 85683	0	83155	100309	0.01	0	0
2	G9196	C75 > 9529	0.01	> 100805	0	97302	121004	0.01	0	0
3	G9212	C75 > 9724	0.01	> 100832	0	97163	121202	0.01	0	0
4	G9203	C75 > 9771	0.01	> 102287	0	98645	123340	0.01	0	0
5	G9206	C75 > 9953	0.01	> 105424	0	102031	126905	0.01	0	0
6	G9192	C75 > 9979	0.01	> 107156	0	103798	127481	0.01	0	0
7	G9189	C75 > 10004	0.01	> 104433	0	100641	121757	0.01	0	0
8	G9199	C75 > 10016	0.01	> 107827	0	104401	129651	0.01	0	0
9	G9185	C75 > 10081	0.01	> 106502	0	103087	126001	0.01	0	0
10	G9182	C75 > 10268	0.01	> 108502	0	104478	126571	0.01	0	0
11	G9215	C75 > 10270	0.01	> 105009	0	101549	125560	0.01	0	0

UI/UX improvements in BPS 2025

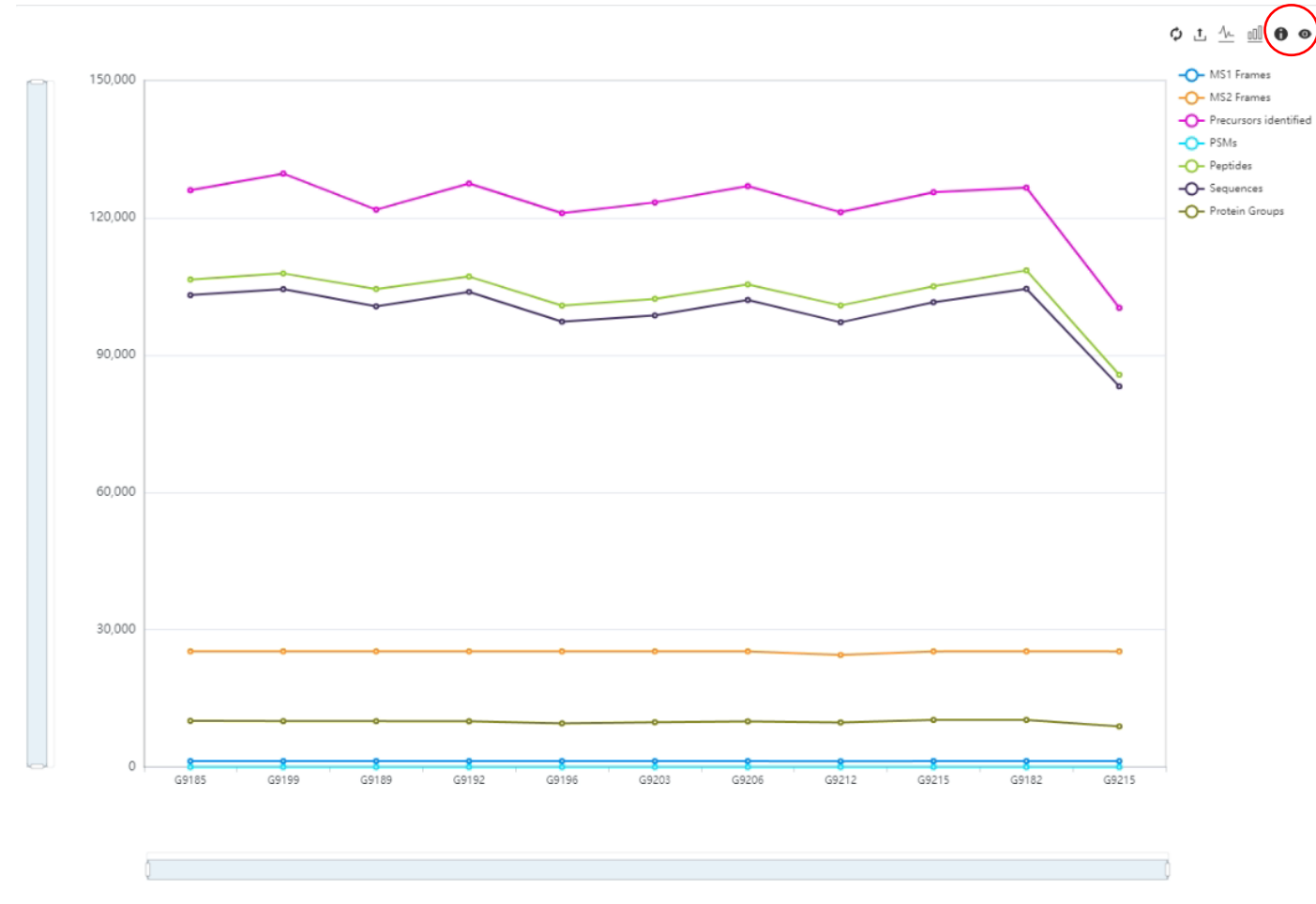
- Clicking on protein coverage maps, jumps to peptide view
- Peptide view table simplified by showing modification in the peptide sequence
- Prolucid ppm mass error corrected for amplitude and isotope mismatches

The screenshot displays the ProteoScape interface with three main panels:

- PROTEINS Table:** A table listing proteins with columns for Majority Protein Name, Number Stripped Peptides, Number Peptides, Number PSMs, Protein Group Q Value, Protein Group Score, and Protein Name. Row 4 (sp|P07237|PDIA1_HUMAN) is highlighted.
- PROTEIN COVERAGE & PTM MAP:** A sequence alignment view for PDIA1_HUMAN. A red circle highlights a peptide sequence: **KENLLDFIK**. A tooltip shows modifications: L226, 4-NFEGEVTKENLLDFIK, and 2-ENLLDFIK.
- PEPTIDES Table:** A table for the peptide **ENLLDFIK** with columns for MS2 ID, Peptide Sequence, mokapot_psm_qvalue, mokapot_peptide_qvalue, x_corr_score, Precursor MZ, charge, RT, look0, and Protein Group Name. Row 1 (91849) is highlighted.
- Bottom Candidate Panel:** Shows mass spectrometry data for the peptide **ENLLDFIK** (m/z: 496.2770, RT: 33.63 min, z: 2+). It includes a mass spectrum plot and a fragmentation diagram.

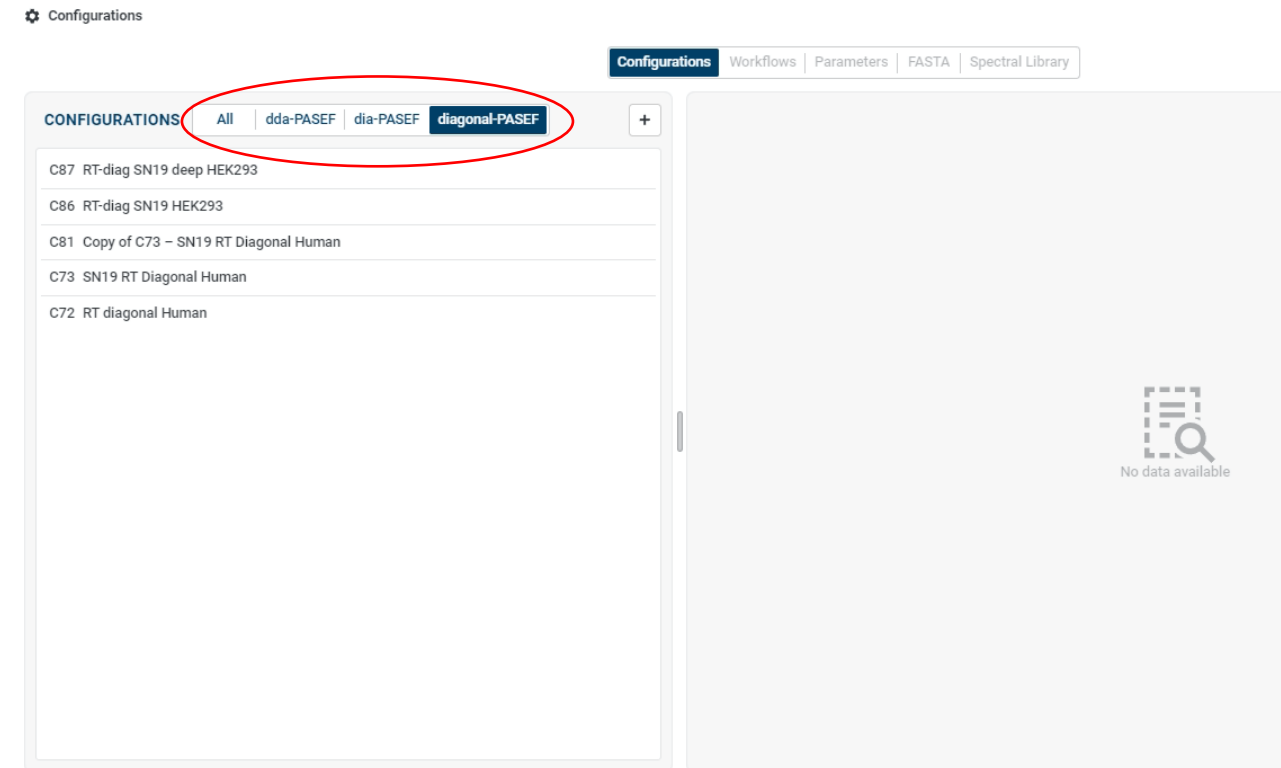
UI/UX improvements in BPS 2025

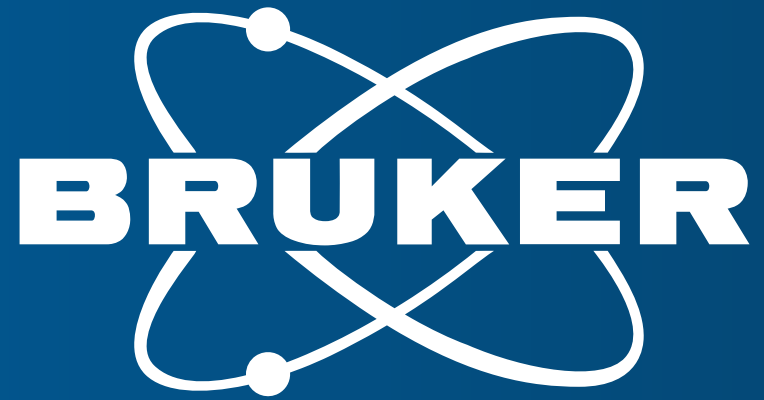
- Updates to most graph type visualizations
 - Legends always on the right-hand side
 - Show\hide legends and x-axis labels
 - Zoom bars for both axis



UI/UX improvements in BPS 2025

- Scan mode-based filtering of configurations and workflows





Innovation with Integrity