

Automation and HTP MS to Accelerate Biotherapeutics Discovery

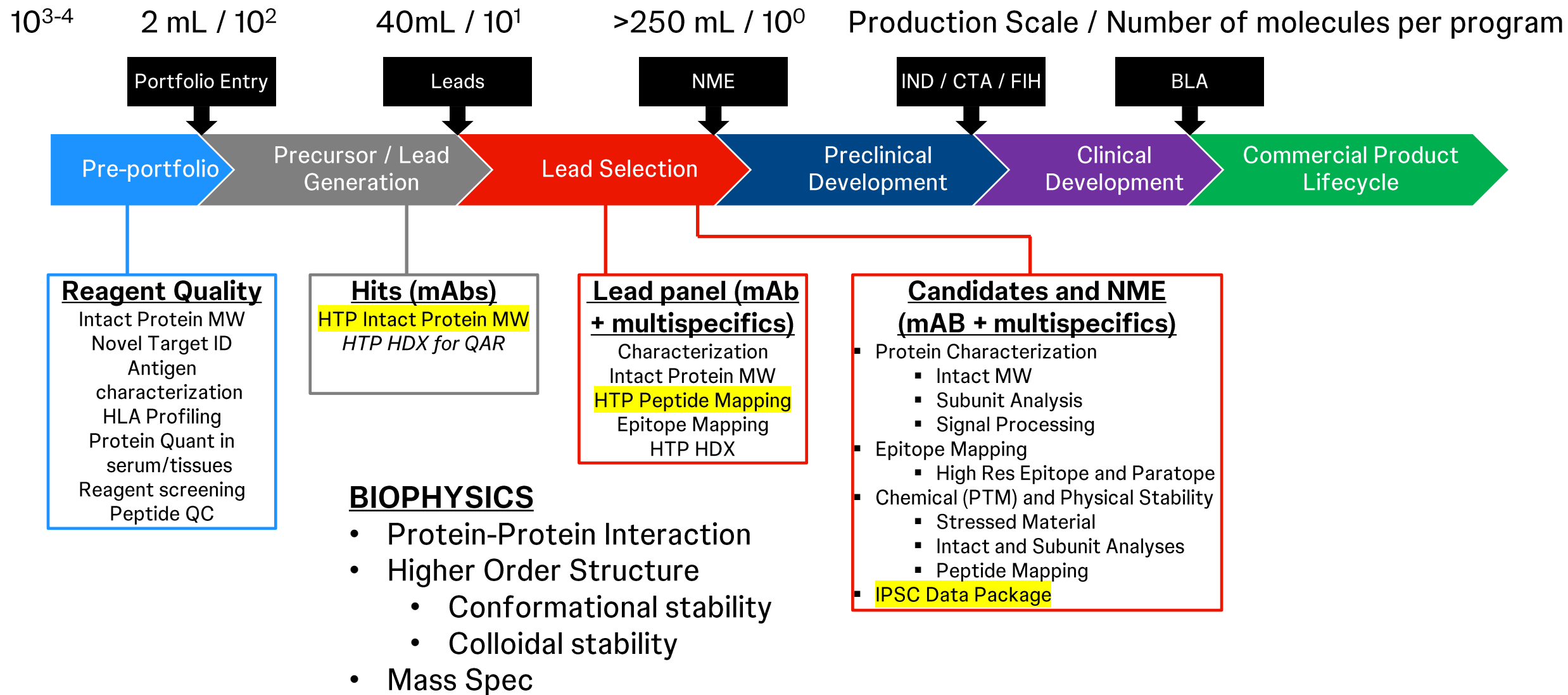
Steven C Pomerantz

Biophysics and Molecular Attributes

Biologics Discovery

Therapeutics Discovery

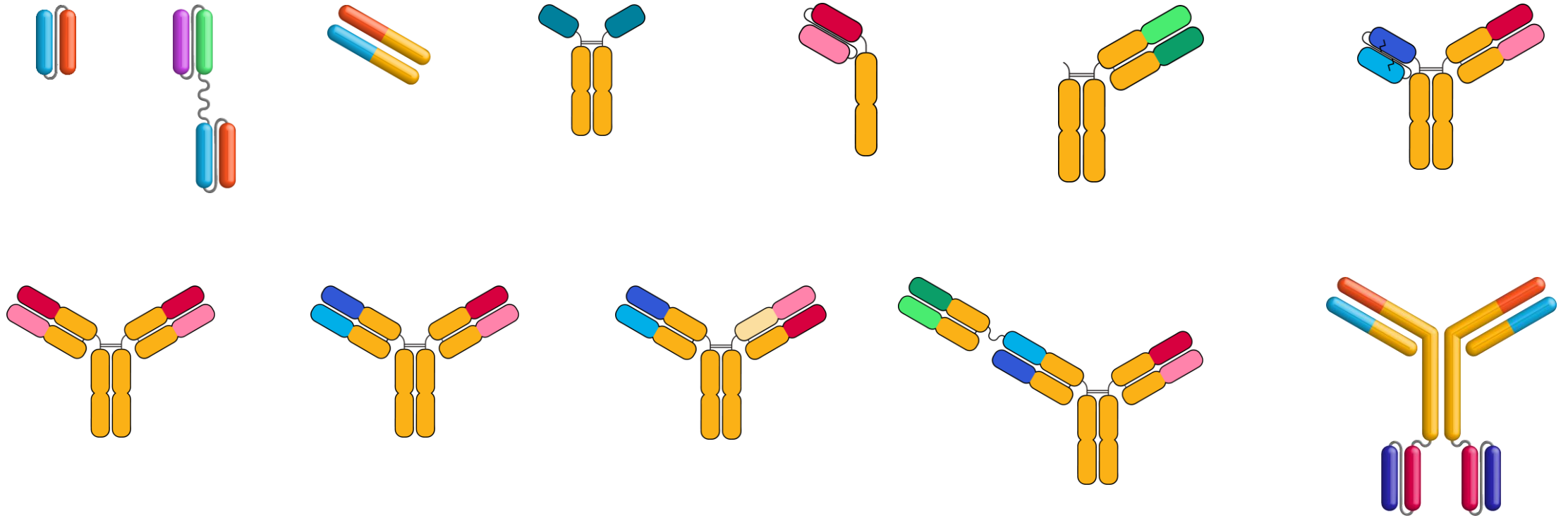
Biophysics MS Touchpoints in Product Lifecycle



Format Diversity

Antibody configurations with any combination of Fc, scFv, spFv, Fab, VHH, fusion partner, etc and 1-6 chains

365



Multiplexed Automated IMW for IPSC Panels

Import Protein Configuration from Biologics - Settings

Get Sequences

Add Metadata

Parse File Name

Logging

Display

☒ Parse File Name

Metadata Order: Request, Batch_ID, Condition, Glycosylation, Reduction

Delimiter: ,

☒ Parse Glycosylation from File Name

Glycosylation Name in Metadata Order: Glycosylation

Degly Name in File Name: Degly

Non-degly Name in File Name: Non-degly

Missing Information: Non-degly

Glycosylation Metadata Column to Report: Glycosylation

Degly Name to Report: Degly

Non-degly Name to Report: Non-degly

☒ Parse Reduction from File Name

Reduction Name in Metadata Order: Reduction

Reduced in File Name: Reduced

Non-reduced Name in File Name: Non-reduced

Reduction Metadata Column to Report: Reduction

Reduced Name to Report: Reduced

Non-reduced Name to Report: Non-reduced

☒ Parse Condition from File Name

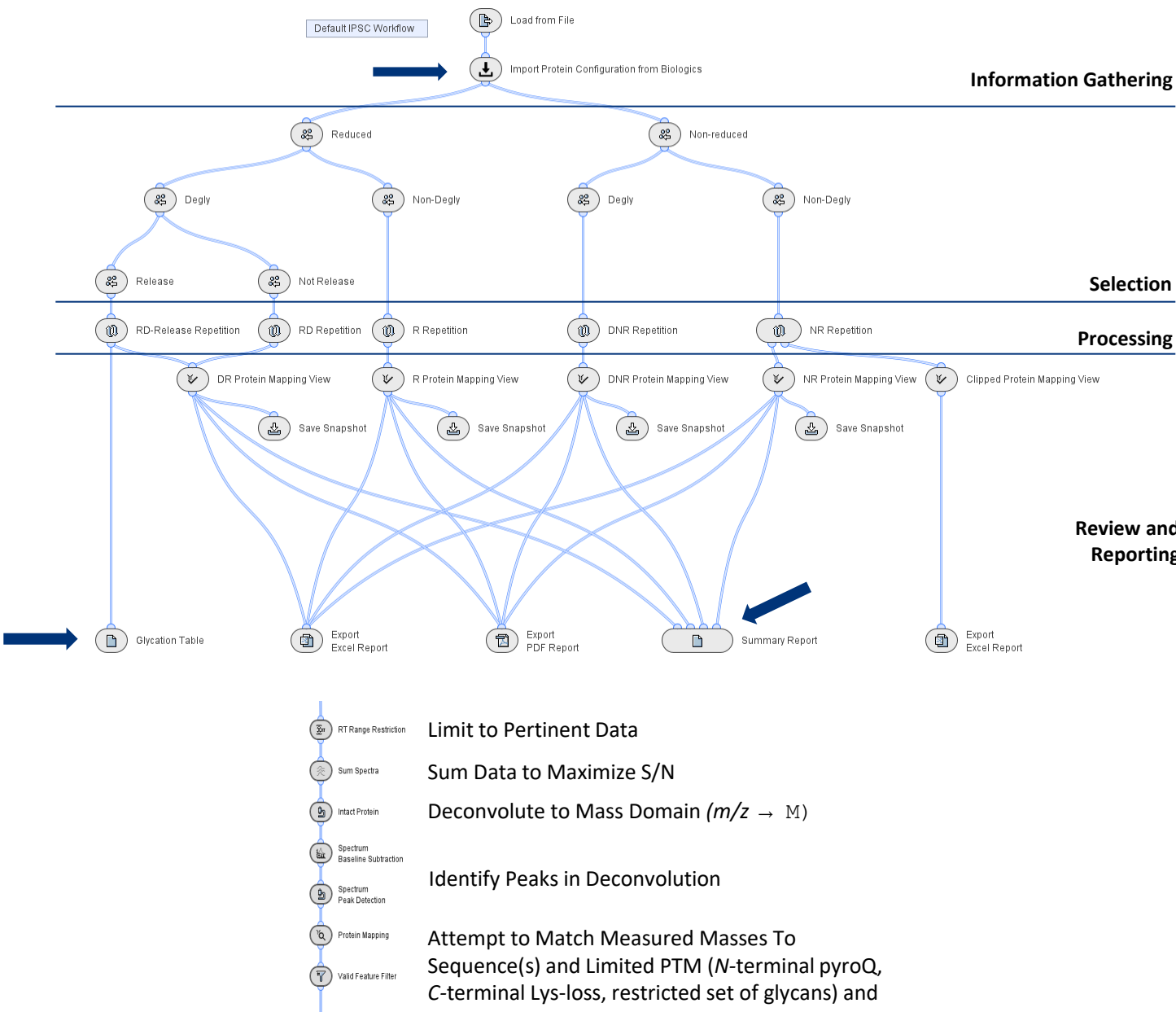
Condition Name in Metadata Order: Condition

Condition Library File: IPSC_Default_Conditions...

OK

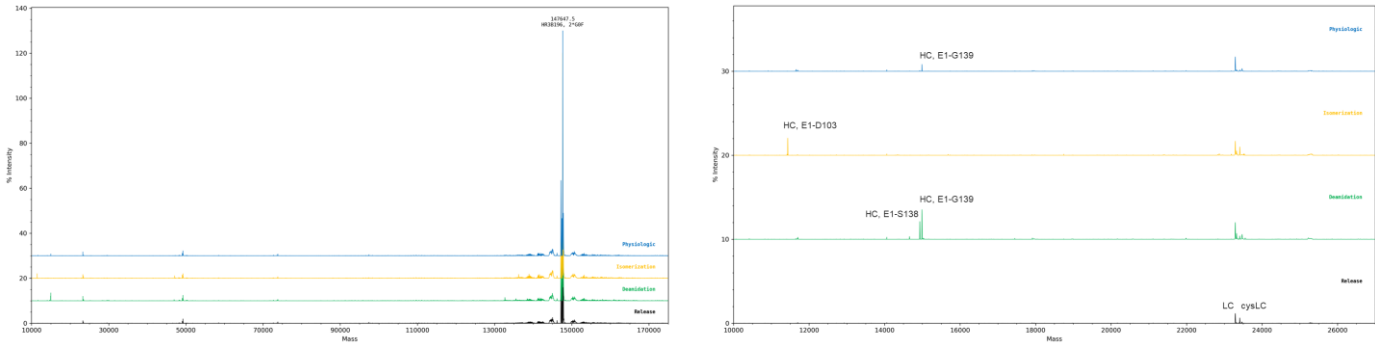
Cancel

Apply



Automated IPSC Data Package for Candidate Selection

MAB509		NR Mass			Degly NR Mass			Reduced						Degly & Reduced						Clipping (site & estimated quantity)	Oxidation (Chain and # of oxidation)
		Measured [Da]	Delta [Da]	Delta [ppm]	Measured [Da]	Delta [Da]	Delta [ppm]	Measured HC1 [Da]	Delta [Da]	Delta [ppm]	Measured LC1 [Da]	Delta [Da]	Delta [ppm]	Measured HC1 [Da]	Delta [Da]	Delta [ppm]	Measured LC1 [Da]	Delta [Da]	Delta [ppm]		
MAB509.003	Release	202157.2	2.0	9.9	199268.5	4.0	20.1	77642.2	-0.6	-7.7	23458.9	0.0	0.0	76198.4	0.9	11.8	23458.7	-0.2	-8.5		
MAB509.021	Physiologic	202157.2	2.0	9.9	199268.5	4.0	20.1	77643.7	0.9	11.6	23458.9	0.0	0.0	76199.8	2.3	30.2	23458.4	-0.5	-21.3		
MAB509.019	Thermal	202160.2	5.0	24.7	199261.1	-3.4	-17.1	77643.5	0.7	9.0	23458.6	-0.3	-12.8	76198.9	1.4	18.4	23458.8	-0.1	-4.3		
MAB509.016	Deamidation	202160.7	5.5	27.2	199260.7	-3.8	-19.1	77643.1	0.3	3.9	23459.2	0.3	12.8	76199.2	1.7	22.3	23458.2	-0.7	-29.8	HC pQ1-G140	
MAB509.017	Isomerization	202159.5	4.3	21.3	199268.6	4.1	20.6	77642.5	-0.3	-3.9	23458.7	-0.2	-8.5	76199.0	1.5	19.7	23458.5	-0.4	-17.1		
MAB509.018	Chem Ox	202275.5	120.3	595.1	199387.5	122.0	612.2	77704.5	61.7	794.6	23458.7	-0.2	-8.5	76261.3	63.8	837.3	23459.2	0.3	12.8		4 per HC
MAB509.020	PBS 4C	202156.9	1.7	8.4	199269.1	4.6	23.1	77643.3	0.5	6.4	23458.4	-0.5	-21.3	76199.1	1.6	21.0	23459.0	0.1	4.3		

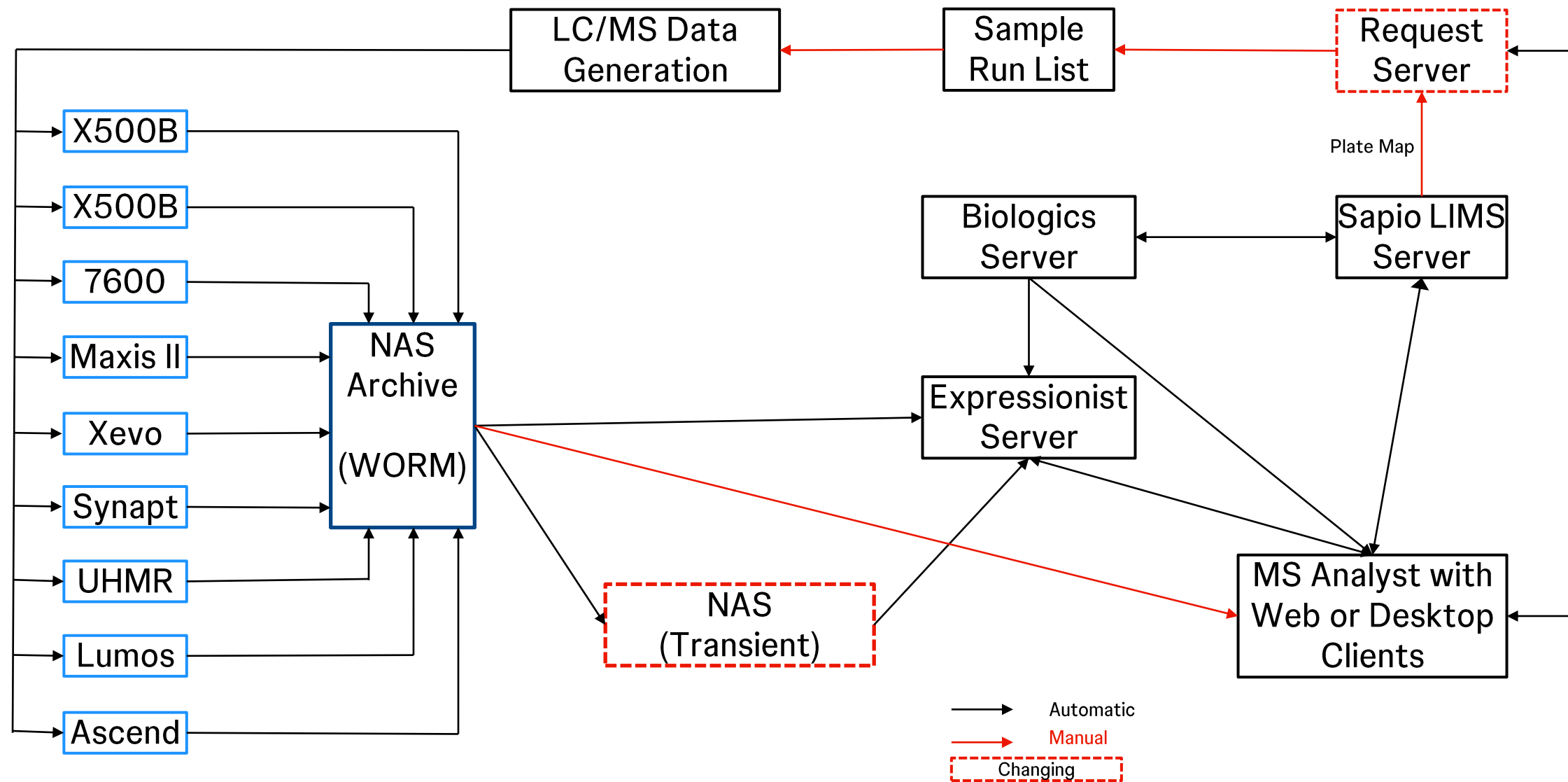


	Variable Region N-linked Glycans (in-silico)	O-linked Glycans	Glycation (% Relative Abundance)				Unpaired Cysteine	Signal Peptide Processing
			HC1	HC2	LC1	LC2		
MAB001	None predicted or observed	None observed	3.1		2.7		None predicted or observed	No clipping or elongation observed
MAB002	None predicted or observed	None observed	1.6		3.1		None predicted or observed	No clipping or elongation observed
MAB003	None predicted or observed	None observed	3.5				None predicted or observed	No clipping or elongation observed
MAB004	None predicted or observed	None observed	3.3	3.2		3.3	None predicted or observed	No clipping or elongation observed
MAB005	None predicted or observed	None observed	6.1				None predicted or observed	No clipping or elongation observed
MAB006	None predicted or observed	None observed	2.5		3.3		None predicted or observed	No clipping or elongation observed
MAB007	None predicted or observed	None observed	1.3		4.1		None predicted or observed	No clipping or elongation observed



- To demonstrate the universality of the platform, a set of 56 data files representing the diverse set of seven molecules shown at left in two conditions and four sample preparations was completely processed in 25:06, independent of data review by analyst.
- The single longest step was the data file load which took 7:44 and includes the translation of the vendor specific data types into the Genedata internal representation.
- The various processing activities took anywhere from 10-50 sec, depending on the complexity of the underlying data set and the allowed glycan and PTM repertoire.
- Creation of the Summary report, including the tabular data compilation and the 14 associated graphs took 48.9 seconds.
- It is estimated that an experienced analyst would have taken 1-2 days to fully process, analyze, interpret, generate graphics and compile the complete report.

Equipment and Data Flows



HTP File Naming Conventions

Date-Instrument-Request-Molecular name-PPB-Labware-Well-Condition-Enzyme
20250201-SQTOF4-BPR952-JNJB123-PPB000196297-L0000000000-C1-REL-Try

← Intact Mass → *Pep Map*

IMW Condition

Non-reduced	NR
Reduced	R
Deglycosylated Non-reduced	DNR
Deglycosylated Reduced	DR

Stress Condition

Release	REL
PBS 4°C control	P4C
Acetate 4°C control	A4C
Histidine 4°C control	H4C
Thermal stress	THS
High pH	DEM
Isomerization	ISO
Chemical Oxidation	CEO
Metal Oxidation	MEO
Physiological stress	PHY

Enzymes

Trypsin	Try
Chymotrypsin	Chy
Proalanase	PrA
Lys-C	LysC
AspN	AspN
GluC	GluC

HTP Peptide Mapping

Developability PTM Stress Package

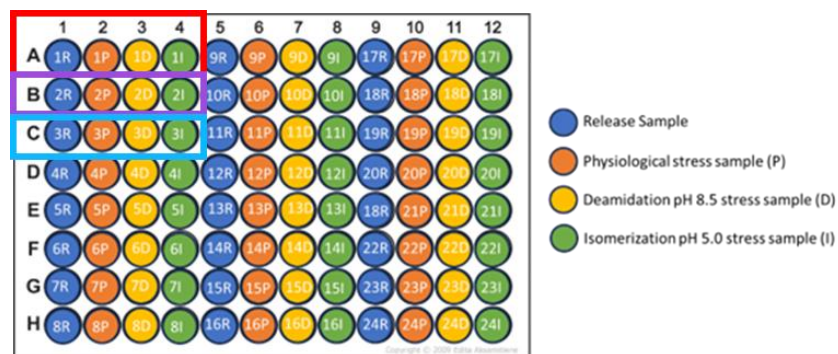
(1-2 molecules, 2 digests)

- ~ 9 Stress conditions

HTP PTM Stress Package

(≤ 24 molecules, 1 digest)

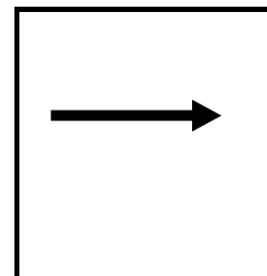
- ~ 4 Stress conditions



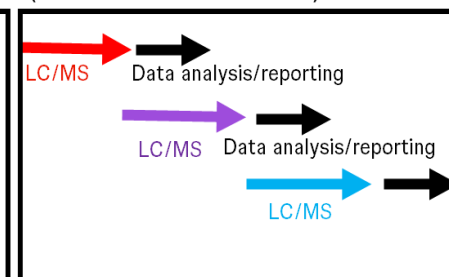
GOALS

- Move de-risking further upstream
- Build database for in silico PTM risk assessment
 - Does multi-specific partner alter PTM risk ?

Sample processing
(~5hrs)



LC/MS analysis and data reporting
(2-4hrs/set of molecule)

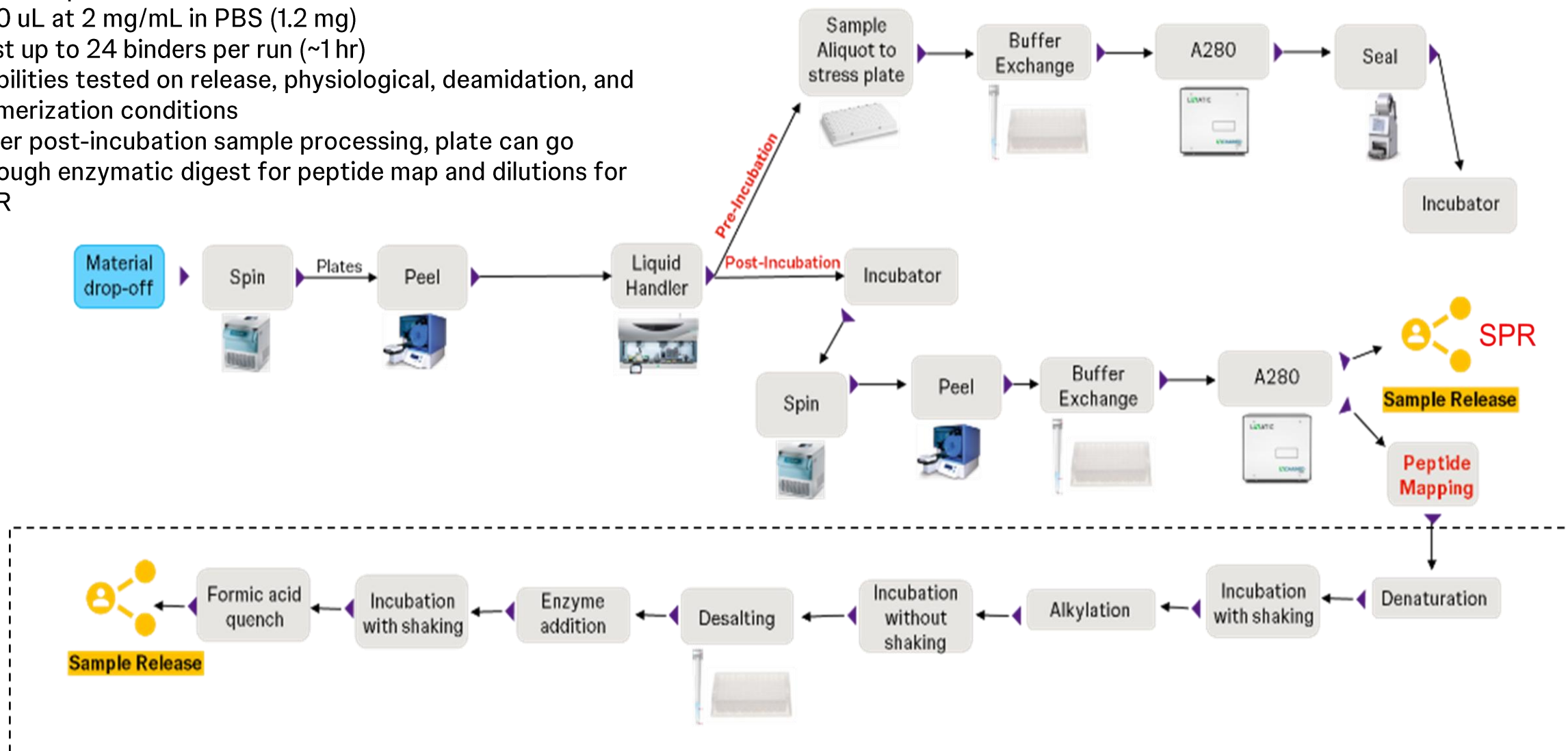


GDB data
archiving

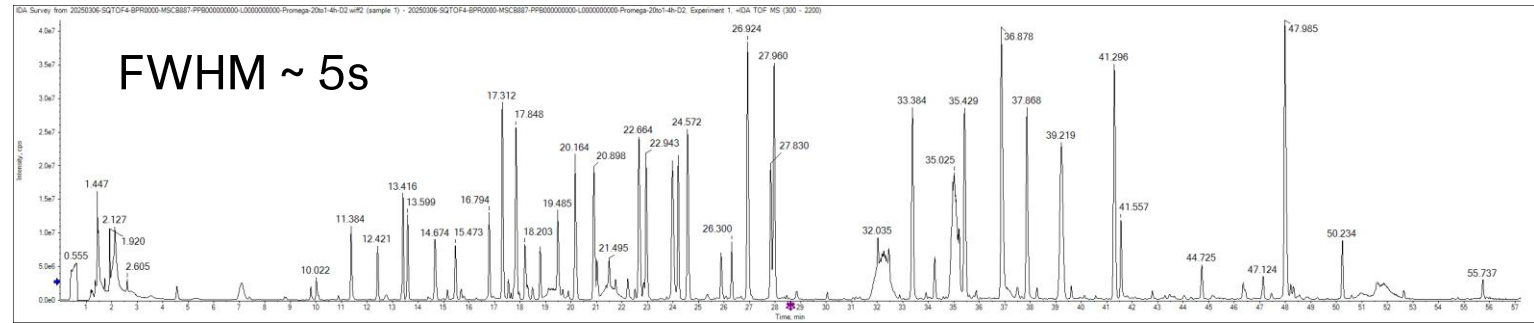
Automated PTM Sample Prep

Sample Requirements:

- ✓ 600 μ L at 2 mg/mL in PBS (1.2 mg)
- ✓ Test up to 24 binders per run (~1 hr)
- ✓ Liabilities tested on release, physiological, deamidation, and isomerization conditions
- ✓ After post-incubation sample processing, plate can go through enzymatic digest for peptide map and dilutions for SPR



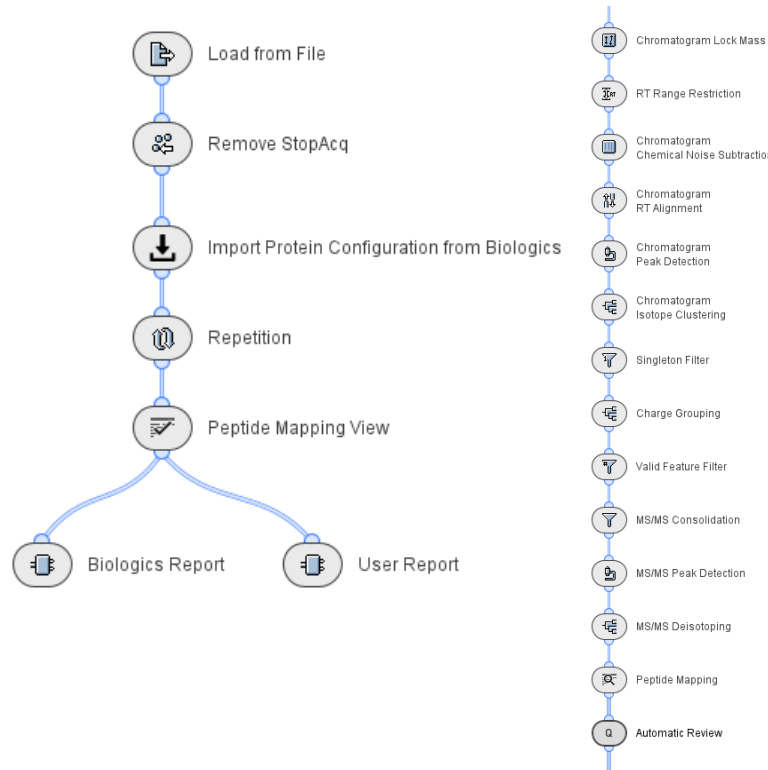
HTP Peptide Mapping – Data Generation and Processing



Thermo Ascend



Sciex 7600 with Optiflow



Need ExD capability to distinguish Asp / isoAsp ($c/z \pm 57$)

Require near baseline chromatographic separation for accurate quantitation

Library of N/D/isoD mutants being validated as tool for testing limits of LC compression

Trastuzumab HTP Peptide Mapping – Database Upload

Analyzed Entity Name	Measurement Type	Grouping Criterion	Genbank Label	Chain	Region	Modifications	CDR Sequence	Modified Residue	% Modified	Comment
PPB000000000	Peptide Mapping	VH,HCDR1,Deamidated,N28	VH	MSCB887 Heavy Chain	HCDR1	Deamidated	GFNIKDTY	N28	0.05	
PPB000000000	Peptide Mapping	VH,HCDR1,Isomerization,D31	VH	MSCB887 Heavy Chain	HCDR1	Isomerization	GFNIKDTY	D31	0	Not Detected
PPB000000000	Peptide Mapping	VH,HCDR2,Deamidated,N55	VH	MSCB887 Heavy Chain	HCDR2	Deamidated	IYPTNGYT	N55	3.29	
PPB000000000	Peptide Mapping	VH,HCDR3,Isomerization,D102/D108	VH	MSCB887 Heavy Chain	HCDR3	Isomerization	SRWGGDGFYAMDY	D102/D108	5.27	
PPB000000000	Peptide Mapping	VH,HCDR3,Oxidation,M107	VH	MSCB887 Heavy Chain	HCDR3	Oxidation	SRWGGDGFYAMDY	M107	1.72	
PPB000000000	Peptide Mapping	C region,Fc,Isomerization,D252	C region	MSCB887 Heavy Chain	Fc	Isomerization	DTLMISR	D252	0.03	
PPB000000000	Peptide Mapping	C region,Fc,Oxidation,M255	C region	MSCB887 Heavy Chain	Fc	Oxidation	DTLMISR	M255	1.63	
PPB000000000	Peptide Mapping	C region,Fc,Deamidated,N387	C region	MSCB887 Heavy Chain	Fc	Deamidated	GFYPSDIAVEWESNGQPENNYK	N387	2.08	
PPB000000000	Peptide Mapping	C region,Fc,Deamidated,N392	C region	MSCB887 Heavy Chain	Fc	Deamidated	GFYPSDIAVEWESNGQPENNYK	N392	0.97	
PPB000000000	Peptide Mapping	VL,LCDR1,Deamidated,N30	VL	MSCB887 Light Chain	LCDR1	Deamidated	QDVNTA	N30	4.85	
PPB000000000	Peptide Mapping	VL,LCDR1,Isomerization,D28	VL	MSCB887 Light Chain	LCDR1	Isomerization	QDVNTA	D28	0	Not Detected
PPB000000000	Peptide Mapping	VH,HCDR1,Deamidated,N28	VH	MSCB887 Heavy Chain	HCDR1	Deamidated	GFNIKDTY	N28	0.06	
PPB000000000	Peptide Mapping	VH,HCDR1,Isomerization,D31	VH	MSCB887 Heavy Chain	HCDR1	Isomerization	GFNIKDTY	D31	0	Not Detected
PPB000000000	Peptide Mapping	VH,HCDR2,Deamidated,N55	VH	MSCB887 Heavy Chain	HCDR2	Deamidated	IYPTNGYT	N55	3.67	
PPB000000000	Peptide Mapping	VH,HCDR3,Isomerization,D102/D108	VH	MSCB887 Heavy Chain	HCDR3	Isomerization	SRWGGDGFYAMDY	D102/D108	17.9	
PPB000000000	Peptide Mapping	VH,HCDR3,Oxidation,M107	VH	MSCB887 Heavy Chain	HCDR3	Oxidation	SRWGGDGFYAMDY	M107	1.81	
PPB000000000	Peptide Mapping	C region,Fc,Isomerization,D252	C region	MSCB887 Heavy Chain	Fc	Isomerization	DTLMISR	D252	0.03	
PPB000000000	Peptide Mapping	C region,Fc,Oxidation,M255	C region	MSCB887 Heavy Chain	Fc	Oxidation	DTLMISR	M255	2.92	
PPB000000000	Peptide Mapping	C region,Fc,Deamidated,N387	C region	MSCB887 Heavy Chain	Fc	Deamidated	GFYPSDIAVEWESNGQPENNYK	N387	2.17	
PPB000000000	Peptide Mapping	C region,Fc,Deamidated,N392	C region	MSCB887 Heavy Chain	Fc	Deamidated	GFYPSDIAVEWESNGQPENNYK	N392	2.35	
PPB000000000	Peptide Mapping	VL,LCDR1,Deamidated,N30	VL	MSCB887 Light Chain	LCDR1	Deamidated	QDVNTA	N30	21.37	
PPB000000000	Peptide Mapping	VL,LCDR1,Isomerization,D28	VL	MSCB887 Light Chain	LCDR1	Isomerization	QDVNTA	D28	0	Not Detected
PPB000000000	Peptide Mapping	VH,HCDR1,Deamidated,N28	VH	MSCB887 Heavy Chain	HCDR1	Deamidated	GFNIKDTY	N28	0.06	
PPB000000000	Peptide Mapping	VH,HCDR1,Isomerization,D31	VH	MSCB887 Heavy Chain	HCDR1	Isomerization	GFNIKDTY	D31	0	Not Detected
PPB000000000	Peptide Mapping	VH,HCDR2,Deamidated,N55	VH	MSCB887 Heavy Chain	HCDR2	Deamidated	IYPTNGYT	N55	4.02	
PPB000000000	Peptide Mapping	VH,HCDR3,Isomerization,D102/D108	VH	MSCB887 Heavy Chain	HCDR3	Isomerization	SRWGGDGFYAMDY	D102/D108	16.36	
PPB000000000	Peptide Mapping	VH,HCDR3,Oxidation,M107	VH	MSCB887 Heavy Chain	HCDR3	Oxidation	SRWGGDGFYAMDY	M107	1.93	
PPB000000000	Peptide Mapping	C region,Fc,Isomerization,D252	C region	MSCB887 Heavy Chain	Fc	Isomerization	DTLMISR	D252	0.03	
PPB000000000	Peptide Mapping	C region,Fc,Oxidation,M255	C region	MSCB887 Heavy Chain	Fc	Oxidation	DTLMISR	M255	2.34	
PPB000000000	Peptide Mapping	C region,Fc,Deamidated,N387	C region	MSCB887 Heavy Chain	Fc	Deamidated	GFYPSDIAVEWESNGQPENNYK	N387	2.3	
PPB000000000	Peptide Mapping	C region,Fc,Deamidated,N392	C region	MSCB887 Heavy Chain	Fc	Deamidated	GFYPSDIAVEWESNGQPENNYK	N392	5.05	
PPB000000000	Peptide Mapping	VL,LCDR1,Deamidated,N30	VL	MSCB887 Light Chain	LCDR1	Deamidated	QDVNTA	N30	32.41	
PPB000000000	Peptide Mapping	VL,LCDR1,Isomerization,D28	VL	MSCB887 Light Chain	LCDR1	Isomerization	QDVNTA	D28	0	Not Detected
PPB000000000	Peptide Mapping	VH,HCDR1,Deamidated,N28	VH	MSCB887 Heavy Chain	HCDR1	Deamidated	GFNIKDTY	N28	0.05	
PPB000000000	Peptide Mapping	VH,HCDR1,Isomerization,D31	VH	MSCB887 Heavy Chain	HCDR1	Isomerization	GFNIKDTY	D31	0	Not Detected
PPB000000000	Peptide Mapping	VH,HCDR2,Deamidated,N55	VH	MSCB887 Heavy Chain	HCDR2	Deamidated	IYPTNGYT	N55	3.41	
PPB000000000	Peptide Mapping	VH,HCDR3,Isomerization,D102/D108	VH	MSCB887 Heavy Chain	HCDR3	Isomerization	SRWGGDGFYAMDY	D102/D108	13.53	
PPB000000000	Peptide Mapping	VH,HCDR3,Oxidation,M107	VH	MSCB887 Heavy Chain	HCDR3	Oxidation	SRWGGDGFYAMDY	M107	2.04	
PPB000000000	Peptide Mapping	C region,Fc,Isomerization,D252	C region	MSCB887 Heavy Chain	Fc	Isomerization	DTLMISR	D252	0.02	
PPB000000000	Peptide Mapping	C region,Fc,Oxidation,M255	C region	MSCB887 Heavy Chain	Fc	Oxidation	DTLMISR	M255	2.3	
PPB000000000	Peptide Mapping	C region,Fc,Deamidated,N387	C region	MSCB887 Heavy Chain	Fc	Deamidated	GFYPSDIAVEWESNGQPENNYK	N387	2.19	
PPB000000000	Peptide Mapping	C region,Fc,Deamidated,N392	C region	MSCB887 Heavy Chain	Fc	Deamidated	GFYPSDIAVEWESNGQPENNYK	N392	1.14	

Trastuzumab HTP Peptide Mapping – User Report

Molecule	Genbank Label	Chain	Region	PTM Type	Motif	Modification	CDR Sequence	4 Samples (N=1)			
								Release [%]	Physiologic [%]	Deamidation [%]	Isomerization [%]
MSCB887	VH	MSCB887 Heavy Chain	HCDR1	Deamidated	N28	VH,HCDR1,Deamidated,N28	GF N IKDTY	0.10	0.12	0.22	0.17
MSCB887	VH	MSCB887 Heavy Chain	HCDR1	Isomerization	D31	VH,HCDR1,Isomerization,D31	GFNIK D TY	ND	0.01	0.04	0.01
MSCB887	VH	MSCB887 Heavy Chain	HCDR2	Deamidated	N55	VH,HCDR2,Deamidated,N55	IYPT N GYT	1.47	1.93	3.11	1.47
MSCB887	VH	MSCB887 Heavy Chain	HFW3	Isomerization	D73	VH,HFW3,Isomerization,D73	RYADSVKGRFTIS A DTSKNTAYLQMNSLRAEDTAVYYC	2.85	2.97	3.76	5.14
MSCB887	VH	MSCB887 Heavy Chain	HCDR3	Isomerization	D102/D108	VH,HCDR3,Isomerization,D102/D108	SRWGG D GFY A MDY	2.57	22.82	5.48	8.74
MSCB887	VH	MSCB887 Heavy Chain	HCDR3	Oxidation	M107	VH,HCDR3,Oxidation,M107	SRWGGDGFY A MDY	2.32	3.08	1.69	1.70
MSCB887	C region	MSCB887 Heavy Chain	Fc	Isomerization	D252	C region,Fc,Isomerization,D252	D TL M ISR	ND	ND	ND	ND
MSCB887	C region	MSCB887 Heavy Chain	Fc	Oxidation	M255	C region,Fc,Oxidation,M255	DTL M ISR	4.07	1.81	3.21	1.83
MSCB887	C region	MSCB887 Heavy Chain	Fc	Deamidated	N387	C region,Fc,Deamidated,N387	GFYPSDIAVEWES N GQPEN N YK	0.67	0.71	1.03	0.34
MSCB887	C region	MSCB887 Heavy Chain	Fc	Deamidated	N392	C region,Fc,Deamidated,N392	GFYPSDIAVEWES N GQPEN N YK	0.30	1.53	7.08	0.14
MSCB887	VL	MSCB887 Light Chain	LCDR1	Deamidated	N30	VL,LCDR1,Deamidated,N30	QDV N TA	6.52	34.79	64.79	11.94
MSCB887	VL	MSCB887 Light Chain	LCDR1	Isomerization	D28	VL,LCDR1,Isomerization,D28	Q D VNTA	ND	ND	ND	ND

Consolidated summary of the Biologics upload report

Covers all stress conditions encountered

Can be used for full Developability package

When multiple PTM in same peptide, can report separately or combined

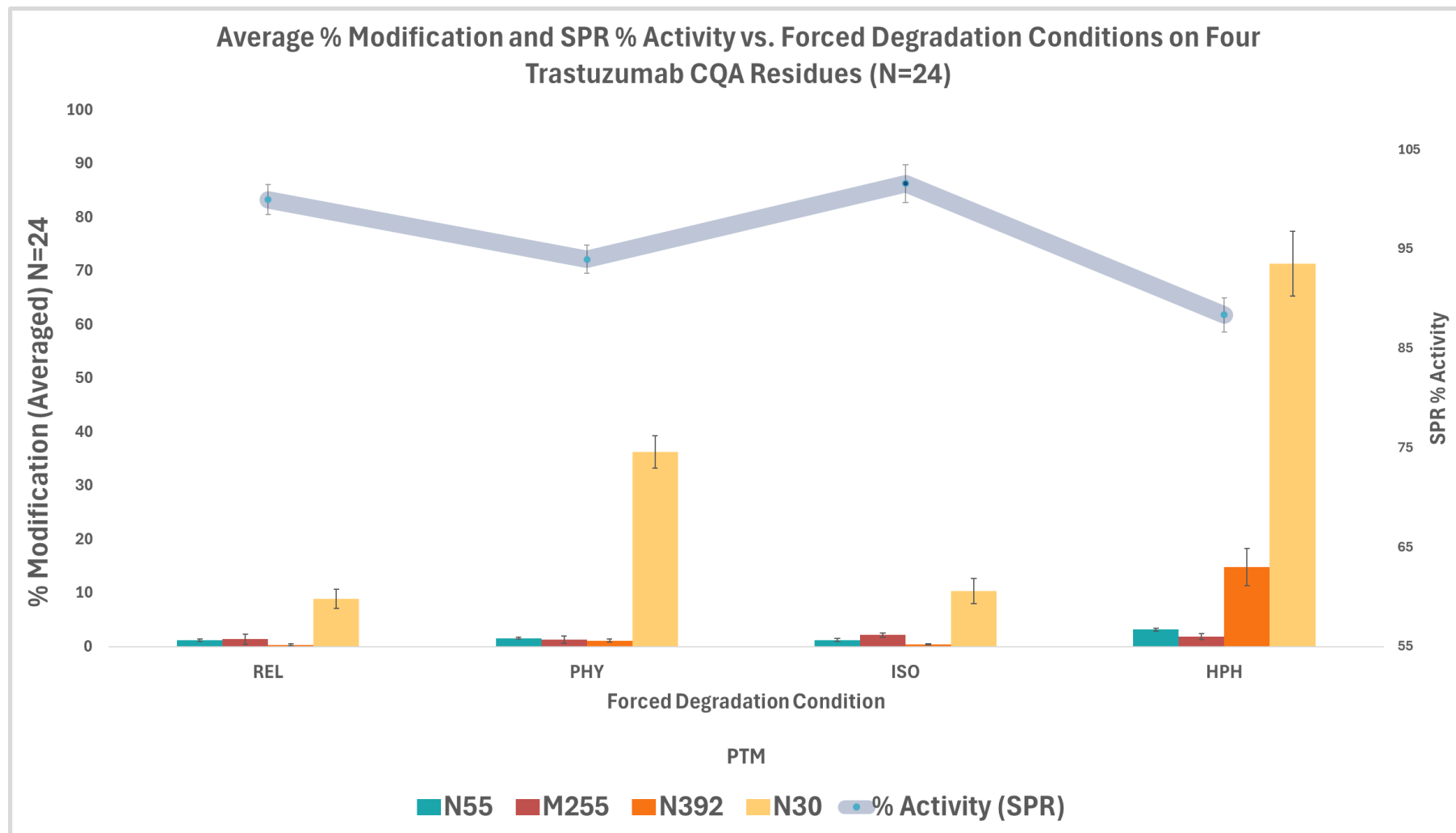
Note automatic highlights for elevated responses (5-10%, >10%)

From file upload to final report - 00:10:55 (hh:mm:ss) = 2.7 min/sample

~80% of time spent on Chem Noise Subtraction and RT Alignment

HTP Peptide Mapping – Correlation to Function

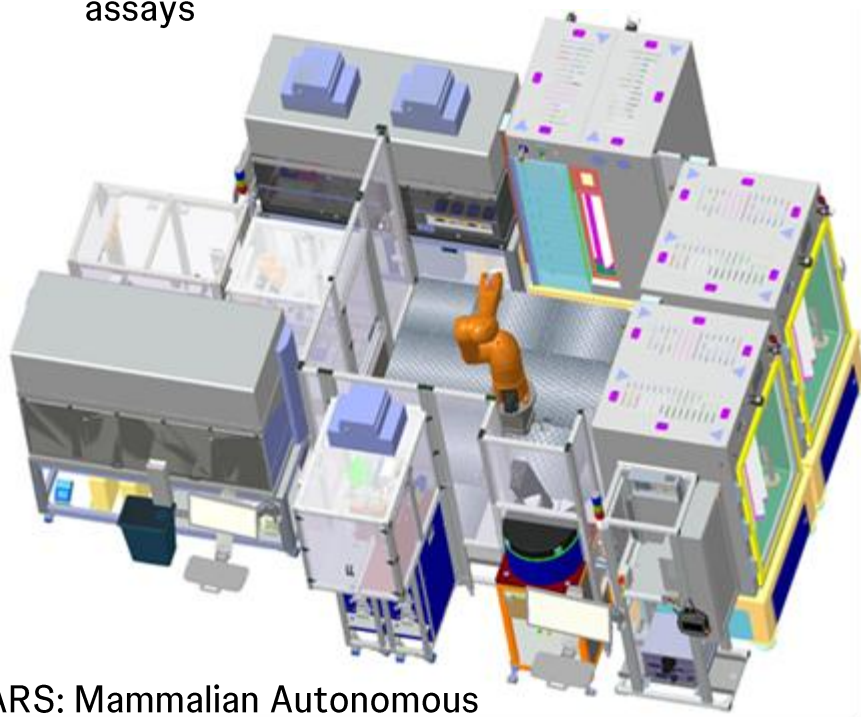
- Repeatability demonstrated across 24 replicates for PTM & SPR
- Modification quantification agrees with literature
- SPR and PTM data correlation trends well



HTP Intact Mass Analysis

Rationale

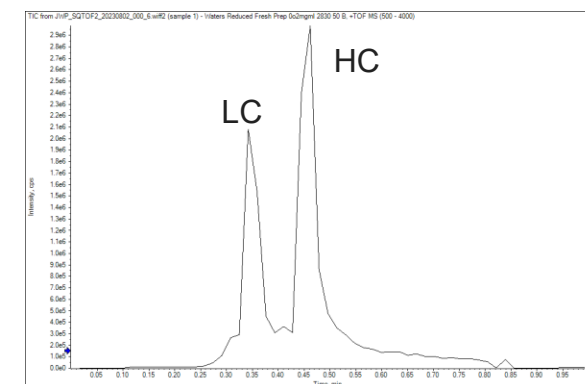
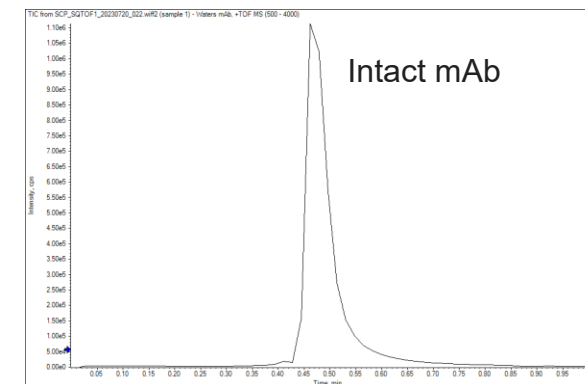
- Recently installed protein production system (MARS) capable of producing hundreds of molecules/day
- Need 100% quality assurance inspection to ensure reliable results for downstream assays



MARS: Mammalian Autonomous Robo-expression System

Data Generation

- 2 identical LC/MS systems consisting of:
 - Sciex X500B
 - Agilent 1290 Infinity II LC with 14 plate capacity
 - Typical reverse phase buffers (H₂O, ACN, 0.1% formic)
- High flow rate and temperature, very short columns
- 60 second cycle time
 - Including gradient elution and re-equilibration
 - Can resolve LC and HC



HTP Intact Mass Analysis

Category	Decision Tree Rules	Risk
Pass	Expected protein is observed with 100% RIA No other major impurities, cross-contamination or mispaired species (<15% RIA)	None
Pass with Comments	Expected protein is observed (100% RIA or less) but other undesired species of known identity are detected. Half antibody with > 15% RIA, or Parental homodimer present in a bispecific species with >15% RIA, or Significant unprocessed C-terminal Lys, or Atypical glycosylation: G0F/G0F is not most abundant glycan, high mannose, O-Link, Sialylation	Low-Medium
Conditional Pass	Expected protein is observed (100% RIA or less) but unknown species are detected (>15%). Possibility of clipping and/or contamination but protein correctly expressed	Medium-high
Fail	No expected protein is observed (> 75 ppm mass error)	High
N/A	Sample was submitted at low protein concentration/volume; Poor mass spectrum	N/A

Expected protein < 100%, Incomplete chains assembly > 15%	▼
C-term Lys > 15%	▲
Expected protein < 100%	
Afucosylation > 15%	
High Mannose > 15%	
Incomplete chains assembly > 15%	
Homodimer > 15%	
Potential cystenialation > 15%	
Unknown (contamination) > 15%	
Potential additional glycosylation > 15%	
Poor spectrum	
Atypical Glycosylation	
Potential O-glycans > 15%	▼
Based on SCIEX OS data	
Potential desGK > 15%	
Aglycosylated > 15%	
Half antibody > 15%	
Based on rerun data	
Based on reduced MS results	
Clipping(s) > 15%	
Mis-paired chain > 15%	▼

HTP Intact Mass Reporting – Summary Table

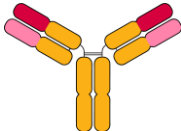
ELN	ELN Link	Name	File Name	PPB Number	TPP Number	Molecule Name	Plate Label	Well	Refiner	Calc. Mass	Obs. Mass	Glycoform	Global Rel. Int.	Local Rel. Int.	Delta [Da]	Delta [ppm]	Result conditional	Link	Comment
		PPB000278436		PPB000278436	TPP000327934	MAB38	L0000012485	D05	148792.7	148799.5	2*G0F	100	100	100	6.8	45.7	Pass	Link	
		PPB000278437		PPB000278437	TPP000327935	MAB50	L0000012485	E05	148456.3	148461.2	2*G0F	100	100	100	4.9	32.9	Pass	Link	
		PPB000278438		PPB000278438	TPP000327937	MAB42	L0000012485	D09	149301.4	149307.4	2*G0F	100	100	100	6.1	40.6	Pass	Link	
		PPB000278439		PPB000278439	TPP000327938	MAB54	L0000012485	E09	147859.6	147864.1	2*G0F	100	100	100	4.5	30.7	Pass	Link	
		PPB000278440		PPB000278440	TPP000327939	MAB05	L0000012485	A06	148446.2	148450.1	2*G0F	100	100	100	3.9	25.9	Pass	Link	
		PPB000278441		PPB000278441	TPP000327940	MAB16	L0000012485	B06	148109.8	148114.5	2*G0F	100	100	100	4.7	31.9	Pass	Link	
		PPB000278442		PPB000278442	TPP000327941	MAB88	L0000012485	H09	149342.4	149347.0	2*G0F	100	100	100	4.6	30.9	Pass with Comments	Link	High Mannose > 15.0%
		PPB000278443		PPB000278443	TPP000327942	MAB09	L0000012485	A10	148954.8	148958.2	2*G0F	100	100	100	3.4	22.6	Pass	Link	
		PPB000278444		PPB000278444	TPP000327943	MAB51	L0000012485	E06	146433.3	146437.1	2*G0F	100	100	100	3.8	26.2	Pass	Link	
		PPB000278445		PPB000278445	TPP000327944	MAB63	L0000012485	F06	147019.9	147023.1	2*G0F	100	100	100	3.2	22.0	Pass	Link	
		PPB000278446		PPB000278446	TPP000327945	MAB74	L0000012485	G06	146683.5	146688.1	2*G0F	100	100	100	4.6	31.7	Pass	Link	
		PPB000278447		PPB000278447	TPP000327946	MAB55	L0000012485	E10	147916.1	147920.0	2*G0F	100	100	100	3.9	26.5	Pass	Link	
		PPB000278448		PPB000278448	TPP000327947	MAB06	L0000012485	A07	147528.5	147532.1	2*G0F	100	100	100	3.6	24.5	Pass	Link	
		PPB000278449		PPB000278449	TPP000327948	MAB78	L0000012485	G10	146825.5	146829.2	2*G0F	100	100	100	3.7	24.9	Pass	Link	
		PPB000278450		PPB000278450	TPP000327949	MAB89	L0000012485	H10	147412.2	147415.2	2*G0F	100	100	100	3.1	20.9	Pass	Link	
		PPB000278451		PPB000278451	TPP000327950	MAB40	L0000012485	D07	147075.7	147079.4	2*G0F	100	100	100	3.7	25.0	Pass	Link	
		PPB000278452		PPB000278452	TPP000327952	MAB64	L0000012485	F07	147920.8	147924.4	2*G0F	100	100	100	3.6	24.2	Pass	Link	
		PPB000278453		PPB000278453	TPP000327953	MAB44	L0000012485	D11	147845.8	147848.4	2*G0F	100	100	100	2.6	17.7	Pass	Link	
		PPB000278454		PPB000278454	TPP000327954	MAB56	L0000012485	E11	148432.4	148435.8	2*G0F	100	100	100	3.5	23.3	Pass	Link	
		PPB000278455		PPB000278455	TPP000327956	MAB18	L0000012485	B08	149328.6	149331.5	2*G0F	100	100	100	2.9	19.5	Pass	Link	
		PPB000278456		PPB000278456	TPP000327958	MAB41	L0000012485	D08	148103.2	148106.5	2*G0F	100	100	100	3.4	22.8	Pass	Link	
		PPB000278457		PPB000278457	TPP000327960	MAB33	L0000012485	C12	148353.3	148357.9	2*G0F	100	100	100	4.6	30.9	Pass	Link	
		PPB000278458		PPB000278458	TPP000327961	MAB45	L0000012485	D12	149586.0	149590.2	2*G0F	100	100	100	4.2	28.0	Pass with Comments	Link	High Mannose > 15.0%
		PPB000278459		PPB000278459	TPP000327962	MAB87	L0000012485	H08	149198.4	149200.9	2*G0F	100	100	100	2.5	16.7	Pass	Link	
		PPB000278460		PPB000278460	TPP000327934	MAB08	L0000012485	A09	148792.7	148798.9	2*G0F	100	100	100	6.1	41.2	Pass	Link	
		PPB000278461		PPB000278461	TPP000327936	MAB30	L0000012485	C09	149688.9	149695.2	2*G0F	100	100	100	6.3	41.9	Pass	Link	
		PPB000278462		PPB000278462	TPP000327937	MAB73	L0000012485	G05	149301.4	149307.5	2*G0F	100	100	100	6.2	41.3	Pass	Link	
		PPB000278463		PPB000278463	TPP000327938	MAB84	L0000012485	H05	147859.6	147864.2	2*G0F	100	100	100	4.6	30.9	Pass	Link	
		PPB000278464		PPB000278464	TPP000327939	MAB66	L0000012485	F09	148446.2	148450.0	2*G0F	100	100	100	3.8	25.6	Pass	Link	
		PPB000278465		PPB000278465	TPP000327940	MAB77	L0000012485	G09	148109.8	148114.5	2*G0F	100	100	100	4.8	32.1	Pass	Link	
		PPB000278466		PPB000278466	TPP000327942	MAB39	L0000012485	D06	148954.8	148958.2	2*G0F	100	100	100	3.4	22.7	Pass	Link	
		PPB000278467		PPB000278467	TPP000327943	MAB20	L0000012485	B10	146433.3	146436.5	2*G0F	100	100	100	3.2	22.2	Pass	Link	
		PPB000278468		PPB000278468	TPP000327944	MAB31	L0000012485	C10	147019.9	147023.1	2*G0F	100	100	100	3.2	22.0	Pass	Link	
		PPB000278469		PPB000278469	TPP000327945	MAB43	L0000012485	D10	146683.5	146688.1	2*G0F	100	100	100	4.6	31.5	Pass	Link	
		PPB000278470		PPB000278470	TPP000327946	MAB85	L0000012485	H06	147916.1	147919.9	2*G0F	100	100	100	3.8	25.4	Pass	Link	
		PPB000278471		PPB000278471	TPP000327947	MAB67	L0000012485	F10	147528.5	147532.3	2*G0F	100	100	100	3.8	25.8	Pass	Link	
		PPB000278472		PPB000278472	TPP000327948	MAB17	L0000012485	B07	146825.5	146829.2	2*G0F	100	100	100	3.7	25.0	Pass	Link	
		PPB000278473		PPB000278473	TPP000327949	MAB28	L0000012485	C07	147412.2	147415.0	2*G0F	100	100	100	2.9	19.7	Conditional Pass	Link	Unknown (contamination) > 15.0%
		PPB000278474		PPB000278474	TPP000327951	MAB52	L0000012485	E07	148308.4	148311.6	2*G0F	100	100	100	3.3	22.0	Pass	Link	
		PPB000278475		PPB000278475	TPP000327952	MAB32	L0000012485	C11	147920.8	147924.5	2*G0F	100	100	100	3.7	24.9	Pass	Link	
		PPB000278476		PPB000278476	TPP000327953	MAB75	L0000012485	G07	147845.8	147848.9	2*G0F	100	100	100	3.1	20.8	Pass	Link	
		PPB000278477		PPB000278477	TPP000327955	MAB07	L0000012485	A08	148096.0	148098.5	2*G0F	100	100	100	2.5	17.1	Pass	Link	
		PPB000278478		PPB000278478	TPP000327957	MAB29	L0000012485	C08	148941.0	148944.8	2*G0F	100	100	100	3.8	25.6	Pass	Link	
		PPB000278479		PPB000278479	TPP000327958	MAB11	L0000012485	A12	148103.2	148106.6	2*G0F	100	100	100	3.5	23.4	Pass	Link	
		PPB000278480		PPB000278480	TPP000327959	MAB22	L0000012485	B12	148689.8	148692.7	2*G0F	100	100	100	2.9	19.6	Pass	Link	
		PPB000278481		PPB000278481	TPP000327960	MAB65	L0000012485	F08	148353.3	148358.1	2*G0F	100	100	100	4.8	32.2	Pass	Link	
		PPB000278482		PPB000278482	TPP000327961	MAB76	L0000012485	G08	149586.0	149589.7	2*G0F	100	100	100	3.7	24.7	Pass	Link	
		PPB000278483		PPB000278483	TPP000327962	MAB57	L0000012485	E12	149198.4	149201.5	2*G0F	100	100	100	3.1	21.1	Pass	Link	

Result Summary	Count	Percent
Pass	74	82.2
Pass with Comments	9	10.0
Conditional Pass	7	7.8
Fail		
N/A		
Total	90	100



Chains

1



2



3



3



4

HTP IMW Reporting – Glycoform Profiling

Details relative abundances of the most common glycoform combinations

G0F/G0F

G0F/G1F

G1F/G1F

G2F/G1F

G2F/G2F

G0F/G0F-N

G0F/G0

G0F/M5

G0F/-

G0/G0

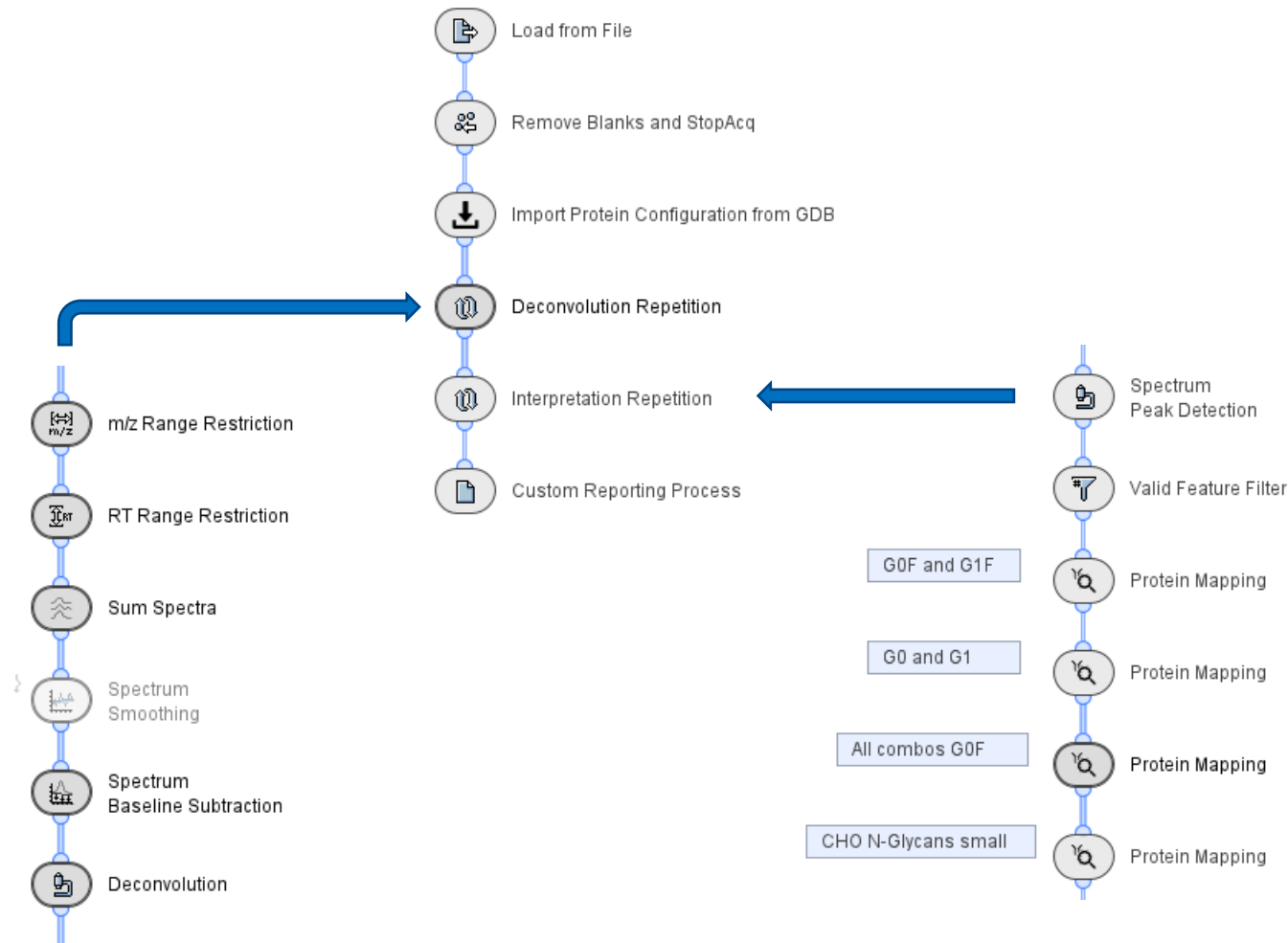
M5/M5

ELN	ELN Link	Name	File Name	Plate Label	PPB Number	TPP Number	Molecule Name	Well	2*G0F	G0F + G1F	2*G1F	G1F + G2F	2*G2F	G0F + G0F-N	2*G0	G0 + G0F	2*M5	G0F + M5	G0F
		PPB000278436		L0000012485	PPB000278436	TPP000327934	MAB38	D05	100	27.4	8.9			15.9					3.2
		PPB000278437		L0000012485	PPB000278437	TPP000327935	MAB50	E05	100	29	11			16.1					3.6
		PPB000278438		L0000012485	PPB000278438	TPP000327937	MAB42	D09	100	27.6	8.2			11.6					2.8
		PPB000278439		L0000012485	PPB000278439	TPP000327938	MAB54	E09	100	29.6	10.3			14.8					3.6
		PPB000278440		L0000012485	PPB000278440	TPP000327939	MAB05	A06	100	28.7	8.9			15.2					3.3
		PPB000278441		L0000012485	PPB000278441	TPP000327940	MAB16	B06	100	29.9	10.8	1.2		17.2					4.2
		PPB000278442		L0000012485	PPB000278442	TPP000327941	MAB88	H09	100	27.8	9.2					4.5			2.9
		PPB000278443		L0000012485	PPB000278443	TPP000327942	MAB09	A10	100	29.4	10.1	1.1		14.4					3.1
		PPB000278444		L0000012485	PPB000278444	TPP000327943	MAB51	E06	100	26.6	8.8			12.1					2.2
		PPB000278445		L0000012485	PPB000278445	TPP000327944	MAB63	F06	100	25.5	8			12.4					2.3
		PPB000278446		L0000012485	PPB000278446	TPP000327945	MAB74	G06	100	25	9.7			16.4					2.8
		PPB000278447		L0000012485	PPB000278447	TPP000327946	MAB55	E10	100	26.3	8.5			15.6		3.8			2.1
		PPB000278448		L0000012485	PPB000278448	TPP000327947	MAB06	A07	100	26.2	8.8			12.1					2.2
		PPB000278449		L0000012485	PPB000278449	TPP000327948	MAB78	G10	100	27.1	9.8	1.1		9.3					1.9
		PPB000278450		L0000012485	PPB000278450	TPP000327949	MAB89	H10	100	25.1	7.7			10.6					2
		PPB000278451		L0000012485	PPB000278451	TPP000327950	MAB40	D07	100	26.6	10.5	1.2		12.2					2.5
		PPB000278452		L0000012485	PPB000278452	TPP000327952	MAB64	F07	100	28	9			8					1.9
		PPB000278453		L0000012485	PPB000278453	TPP000327953	MAB44	D11	100	29.3	10.5			14.6	2.9				3.6
		PPB000278454		L0000012485	PPB000278454	TPP000327954	MAB56	E11	100	26.1	8.4			17.9					3.4
		PPB000278455		L0000012485	PPB000278455	TPP000327956	MAB18	B08	100	25	8.7					6.3			2.5
		PPB000278456		L0000012485	PPB000278456	TPP000327958	MAB41	D08	100	34.6	13.9	2		9.7	5.4				3.3
		PPB000278457		L0000012485	PPB000278457	TPP000327960	MAB33	C12	100	39.4	15.8	2.5		9.7	2.8				3.3
		PPB000278458		L0000012485	PPB000278458	TPP000327961	MAB45	D12	100	30	11.1	1.1		13.2					2.8
		PPB000278459		L0000012485	PPB000278459	TPP000327962	MAB87	H08	100	33.1	12.3	1.8		9.2	3.7				2.8
		PPB000278460		L0000012485	PPB000278460	TPP000327934	MAB08	A09	100	26.4	8.6			15.9					3
		PPB000278461		L0000012485	PPB000278461	TPP000327936	MAB30	C09	100	25.8	8.4			19.6					2.3
		PPB000278462		L0000012485	PPB000278462	TPP000327937	MAB73	G05	100	28.9	9.7			11.8					2.8
		PPB000278463		L0000012485	PPB000278463	TPP000327938	MAB84	H05	100	29.5	10			15.3					3.9
		PPB000278464		L0000012485	PPB000278464	TPP000327939	MAB66	F09	100	29.5	9.5			14					3.2
		PPB000278465		L0000012485	PPB000278465	TPP000327940	MAB77	G09	100	26.9	9.8			18.5					3.7
		PPB000278466		L0000012485	PPB000278466	TPP000327942	MAB39	D06	100	28.1	9.5			14.5					3.4
		PPB000278467		L0000012485	PPB000278467	TPP000327943	MAB20	B10	100	24.6	8.4			12.2					2.2
		PPB000278468		L0000012485	PPB000278468	TPP000327944	MAB31	C10	100	24.1	7.7			13.2					2.1
		PPB000278469		L0000012485	PPB000278469	TPP000327945	MAB43	D10	100	26.5	10.3			15.4					2.5
		PPB000278470		L0000012485	PPB000278470	TPP000327946	MAB85	H06	100	24.4	8.4			15.5					2.1
		PPB000278471		L0000012485	PPB000278471	TPP000327947	MAB67	F10	100	29.4	10.5			10.6					1.9
		PPB000278472		L0000012485	PPB000278472	TPP000327948	MAB17	B07	100	26.5	9.7			9					2.2
		PPB000278473		L0000012485	PPB000278473	TPP000327949	MAB28	C07	100	27.2	8.3			10.1					2.2
		PPB000278474		L0000012485	PPB000278474	TPP000327951	MAB52	E07	100	23.9	8.2			12.6			3.5		1.6
		PPB000278475		L0000012485	PPB000278475	TPP000327952	MAB32	C11	100	26.4	9			10.5	3.1				2.9
		PPB000278476		L0000012485	PPB000278476	TPP000327953	MAB75	G07	100	28.6	10.3			15.4	3.1				3.5
		PPB000278477		L0000012485	PPB000278477	TPP000327955	MAB07	A08	100	25.4	8.8			21.7					3.8
		PPB000278478		L0000012485	PPB000278478	TPP000327957	MAB29	C08	100	28.1	9.2			13.6	4.5				3.2
		PPB000278479		L0000012485	PPB000278479	TPP000327958	MAB11	A12	100	32.2	12.7	1.4		9.9	5				3.2
		PPB000278480		L0000012485	PPB000278480	TPP000327959	MAB22	B12	100	33.3	12.4	1.6		8.9	4.5				3.2
		PPB000278481		L0000012485	PPB000278481	TPP000327960	MAB65	F08	100	34	14.2	2.2		11	2.7				3.5
		PPB000278482		L0000012485	PPB000278482	TPP000327961	MAB76	G08	100	30.8	10.9			13					2.6
		PPB000278483		L0000012485	PPB000278483	TPP000327962	MAB57	E12	100	34.9	13.3	2.2		8.6	4				2.9
		PPB000278484		L0000012485	PPB000278484	TPP000164111	MAB01	A01	100	26.5	9.5	1.1		8.7					2
		PPB000278485		L0000012485	PPB000278485	TPP000236011	MAB69	G01	100	24.8	6.5			14.9					
		PPB000278486		L0000012485	PPB000278486	TPP000249384	MAB47	E02	100	29	10	1.1		13.9					
		PPB000278487		L0000012485	PPB000278487	TPP000249611	MAB24	C02	100	34	10.8		7.9	15.8					
		PPB000278490		L0000012485	PPB000278490	TPP000327935	MAB19	B09	100	24.9	8.9			17.8					3.2

HTP IMW Reporting - Graphics

Name	File Name	Pub Number	Structure	Label	Well
TPP0000261186, A1, NR	mAb13	MSR000007	A1		
Full Range Deconvoluted Spectrum Zoomed Range Deconvoluted Spectrum Input Spectrum TIC Spectrum					
TPP000010507, A2, NR	mAb01	MSR000007	A2		
Full Range Deconvoluted Spectrum Zoomed Range Deconvoluted Spectrum Input Spectrum TIC Spectrum					
TPP000010507, A3, NR	mAb01	MSR000007	A3		
Full Range Deconvoluted Spectrum Zoomed Range Deconvoluted Spectrum Input Spectrum TIC Spectrum					
TPP000173087, A4, NR	mAb07	MSR000007	A4		
Full Range Deconvoluted Spectrum Zoomed Range Deconvoluted Spectrum Input Spectrum TIC Spectrum					
TPP000236011, A5, NR	mAb08	MSR000007	A5		
Full Range Deconvoluted Spectrum Zoomed Range Deconvoluted Spectrum Input Spectrum TIC Spectrum					
TPP000249611, B1, NR	mAb11	MSR000007	B1		
Full Range Deconvoluted Spectrum Zoomed Range Deconvoluted Spectrum Input Spectrum TIC Spectrum					

HTP Workflow and Performance Metrics



Activity	Time for 90 Samples
Load from File	3:58
GDB Import	2:51
Deconvolution	6:31
Interpretation	0:29
Reporting	3:28
Total	17:17
	~11.5 sec/sample

HTP Productivity Benefits

HTP IMW Data Processing and Reporting

Manual Interpretation, Report Generation and Result Formatting = 10 min (perfect case for rockstar analyst)

3200 samples/month x 10 min/sample = 32000 minutes = 22.22 days/month (@24/7) = 3-4 FTE just for HTP

3200 samples/month x ~11 sec/sample = 587 minutes = ~9.8 hrs

HTP Peptide Mapping Data Processing and Reporting

Manual Interpretation, Report Generation and Result Formatting = 30 min (perfect case for rockstar analyst)

384 samples/month x 30 min/sample = 11520 minutes = 8 days/month (@24/7) = 1-2 FTE just for HTP

384 samples/month x 2.7 min/sample = 1048 minutes = 0.73 days/month

2 robot licenses (~\$30-40K) vs 4-6 FTE (~\$400-900K or more)

Acknowledgments

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