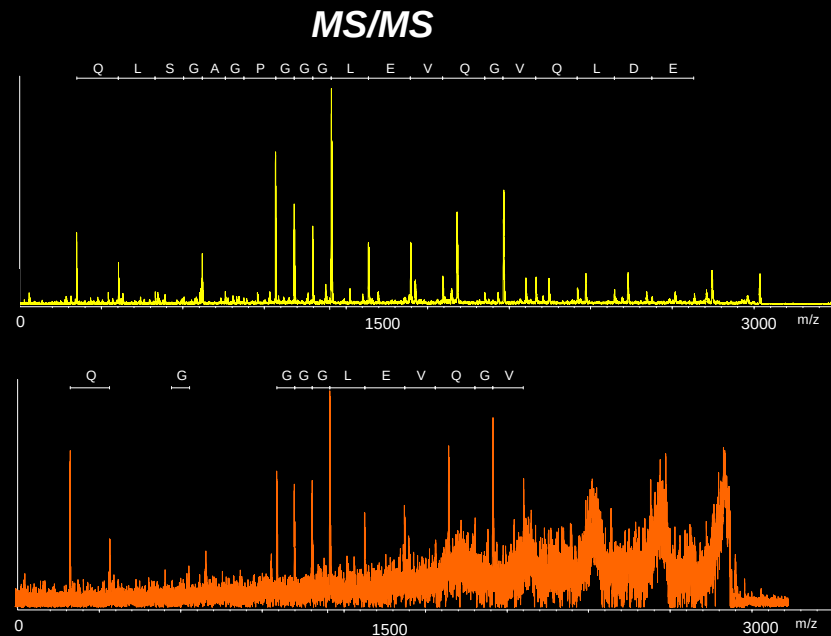
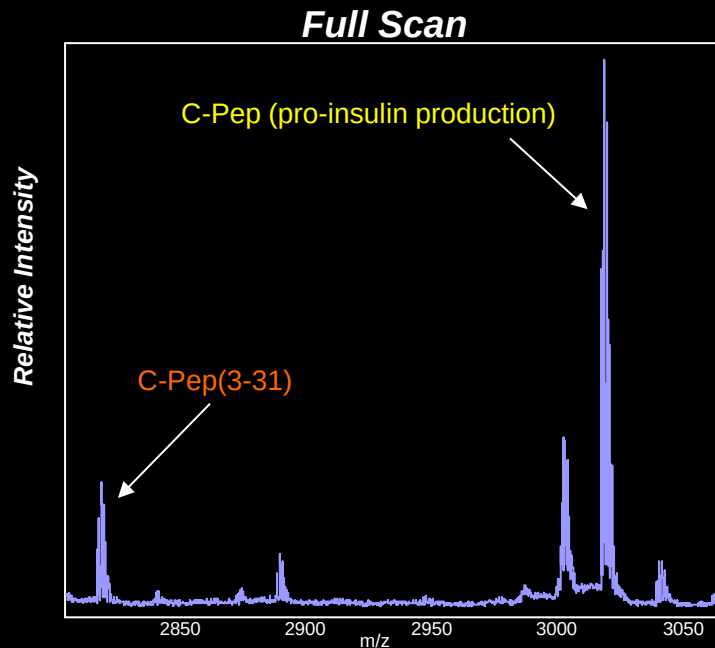


Combines Induction, Deduction & Direct Analysis for Exact Definition of Analyte.

➤ Example: C-Peptide

- FDA-Approved Test System for Abnormal Insulin Secretion (21CFR862.1135)
 - Sequence 0: EAEDLQVGQVELGGGPGAGSLQPLALEGSLQ (Epitope)
 - Sequence 1: EAEDLQVGQVELGGGPGAGSLQPLALEGSLQ (Confirm Epitope & C-Pep)
 - Sequence 2: EAEDLQVGQVELGGGPGAGSLQPLALEGSLQ (Discover Variant)



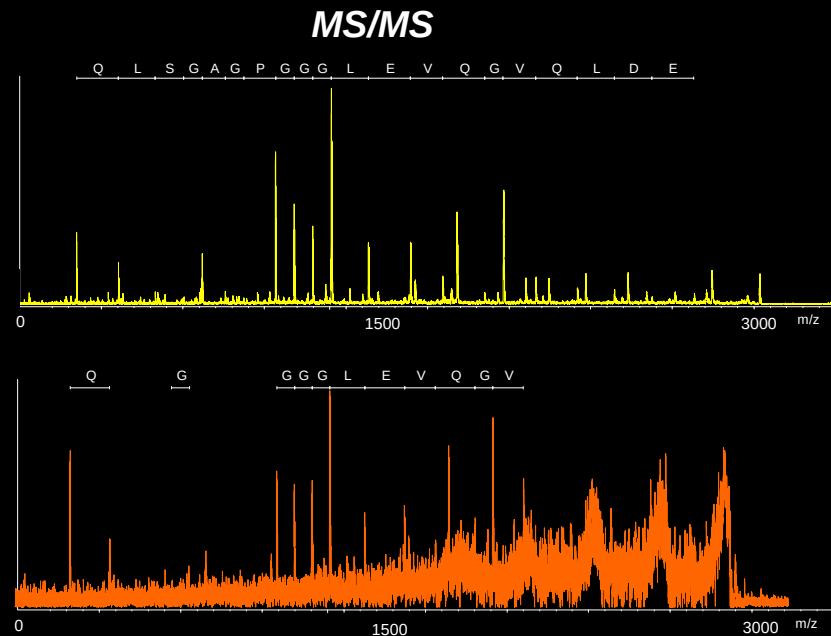
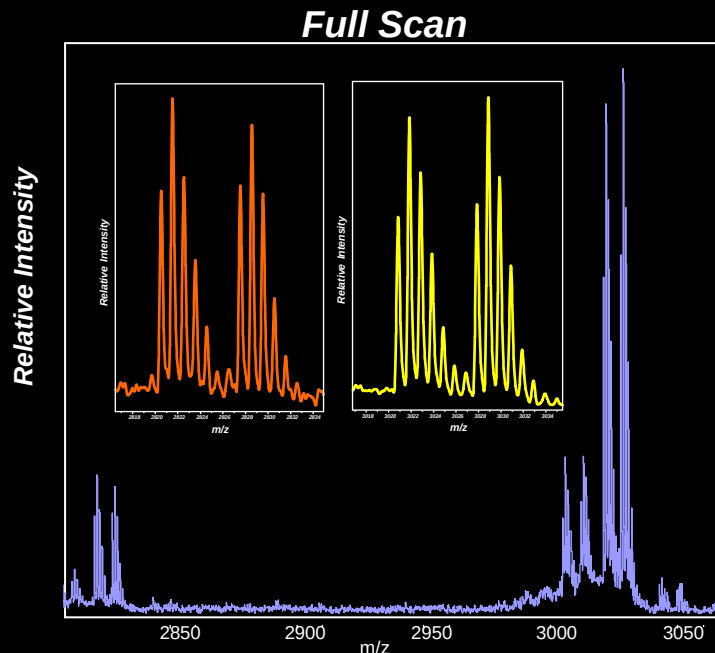
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 - Sequence 2: EAEDLQVGQVELGGPGAGSLQPLALEGSLQ (Discover Variant)

➤ Quantification:

- Heavy isotopes
 - Added to biological samples and carried through entire MSIA process



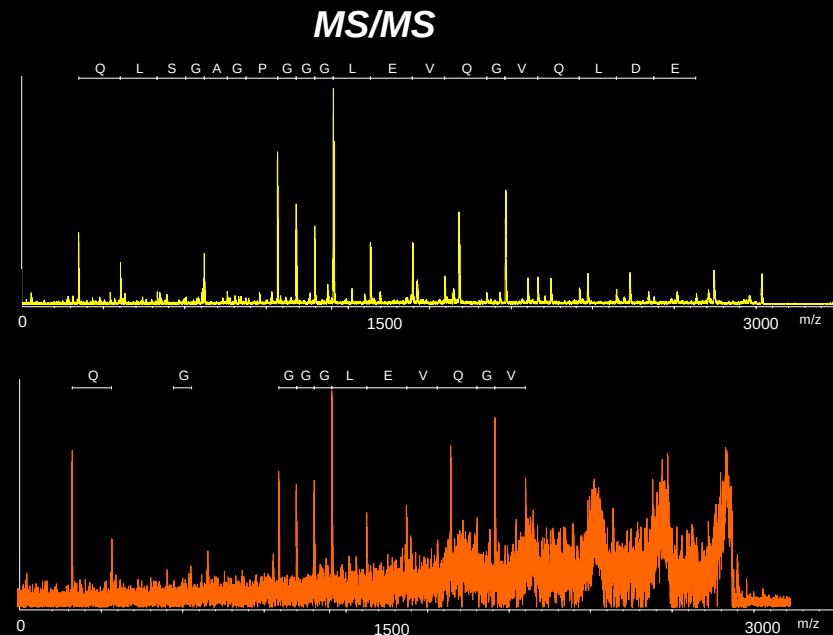
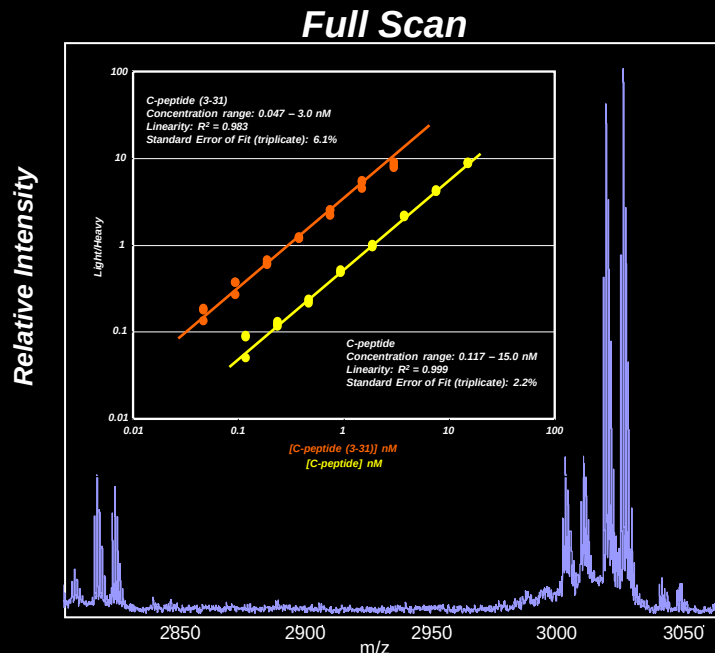
Combines Induction, Deduction & Direct Analysis for Exact Definition of Analyte.

➤ Example: C-Peptide

- FDA-Approved Test System for Abnormal Insulin Secretion (21CFR862.1135)
- Sequence 0: EAEDLQVGQVELGGGPGAGSLQPLALEGSLQ (Epitope)
- Sequence 1: EAEDLQVGQVELGGGPGAGSLQPLALEGSLQ (Confirm Epitope & C-Pep)
- Sequence 2: EAEDLQVGQVELGGGPGAGSLQPLALEGSLQ (Discover Variant)

➤ Quantification:

- Heavy isotopes
 - Added to biological samples and carried through entire MSIA process
- Working curves generated simultaneously for both species
 - Linear Dynamic Range > 100; Std. Error < 6%; LOD's < 50 pM



Combines Induction, Deduction & Direct Analysis for Exact Definition of Analyte.

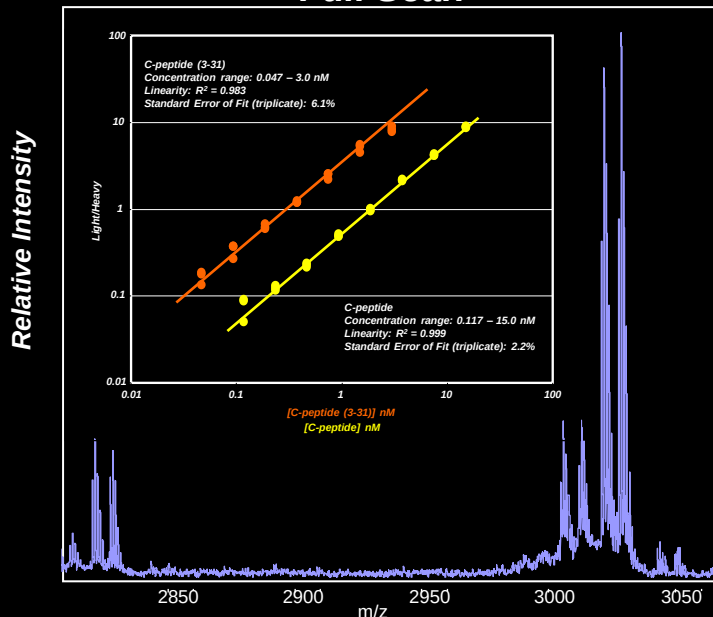
➤ Example: C-Peptide

- FDA-Approved Test System for Abnormal Insulin Secretion (21CFR862.1135)
 - Sequence 0: EAEDLQVGQVELGGGPGAGSLQPLALEGSLQ (*Epitope*)
 - Sequence 1: EAEDLQVGQVELGGGPGAGSLQPLALEGSLQ (Confirm Epitope & C-Pep)
 - Sequence 2: EAEDLQVGQVELGGGPGAGSLQPLALEGSLQ (Discover Variant)

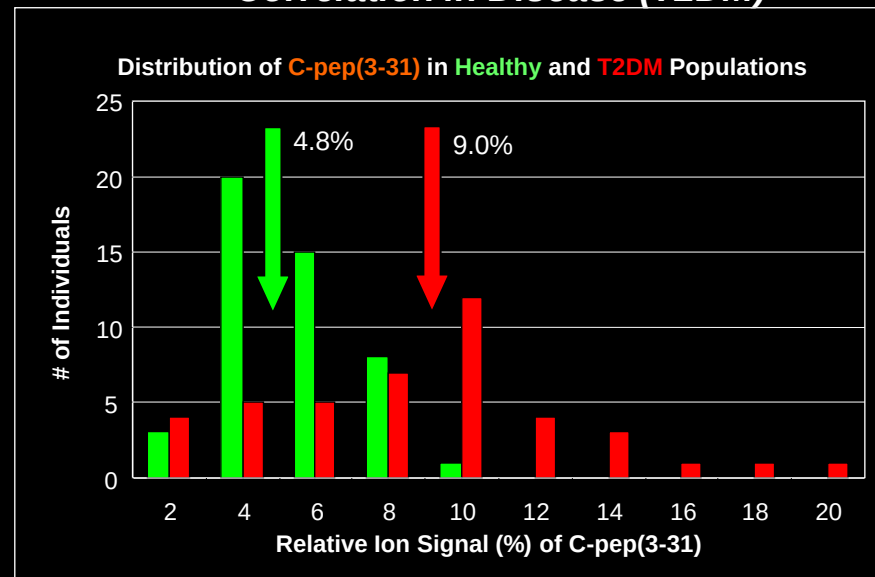
➤ Implications in T2DM:

- DPP-IV Motif – Target of T2DM DPP-IV Inhibitor Therapy (*Vildagliptin* (e.g., *Galvus*))
 - Variant Specific to Drug Target – Emphasizes the Stoichiometry between Variants
- Quantitative Contribution of Variant can result in 100% Error in C-Peptide Determination
 - Population and/or Disease-Based Microheterogeneity

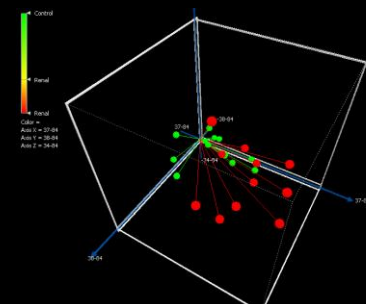
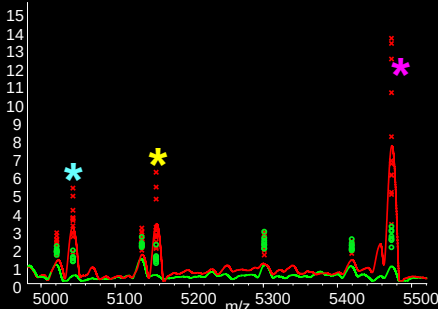
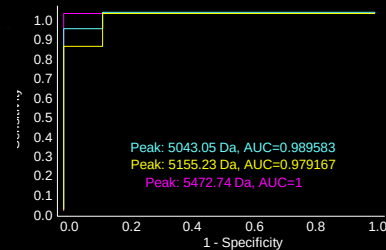
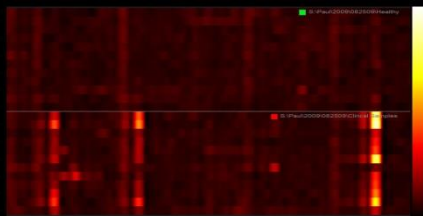
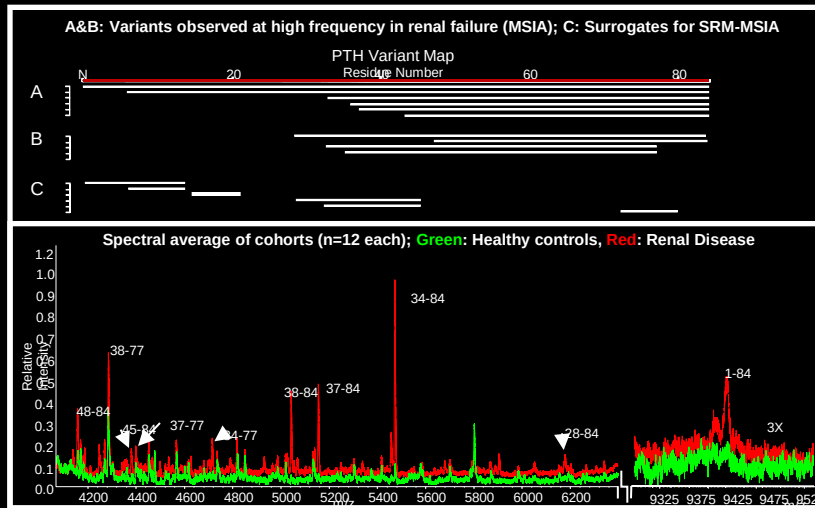
Full Scan



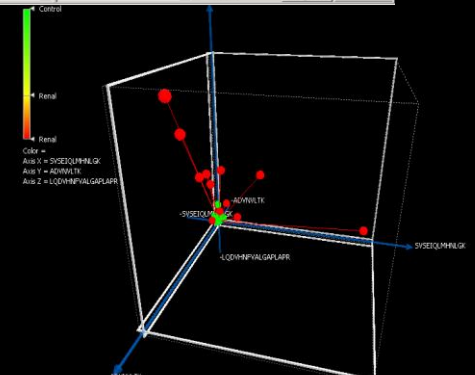
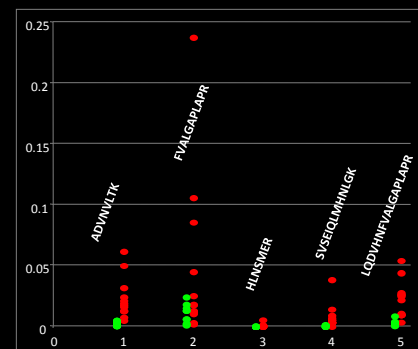
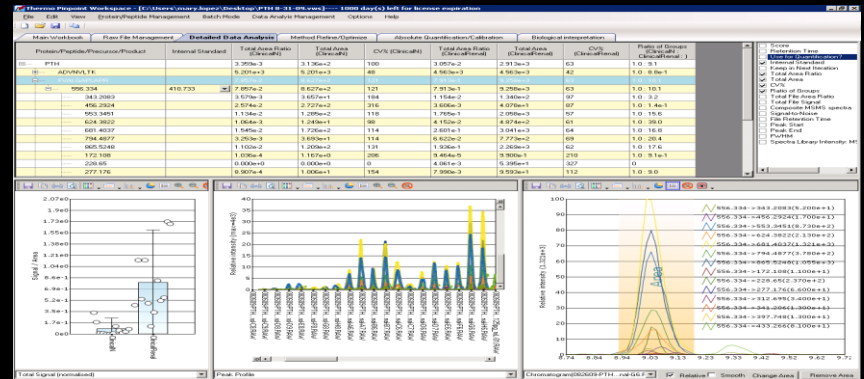
Correlation in Disease (T2DM)



MALDI-TOFMS



ESI-SRM (Triple Quad)



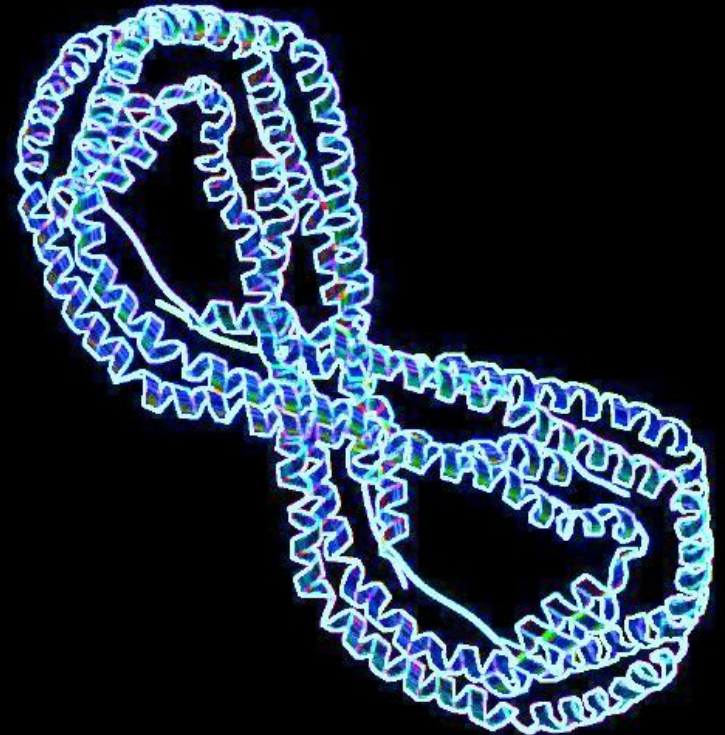
- > 10 Variants (Known & Discovered)
- Conversion to ESI-SRM-MSIA
 - Single Antibody/Post-extraction Digestion
 - 6 Variants; 32 SRM Transitions; > 50% Coverage
 - LOD < 10 pg/mL; LOQ 16 pg/mL; SE ~ 7%
- Conversion to MALDI-MRM-MSIA
 - Bioreactive Plates
 - Full-scan & Tandem TOFMS

Apolipoprotein A1

DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLG PVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLD
DFQKKWQEE MEL YRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDEL RQLAARLEALKENG GARLA EYHAKATEHLSTL
SEKAKPALEDLRQG LLPVLESFKVSFLSALEEYTKKLNTQ

➤ **Full-length Functional Form**

- MW = 28,080
- Reference: 106 – 220 mg/dL
- HDL Protein
 - Cholesterol Transport
 - Ratio relative to other Apolipoproteins
- Diseases
 - Heart diseases
 - Atherosclerosis
 - Tangiers
- Modified forms cause or created by disease
 - Oxidative Stress
 - Defense Mechanisms (Milano)
 - Environmental Effects
 - Hyperglycemia

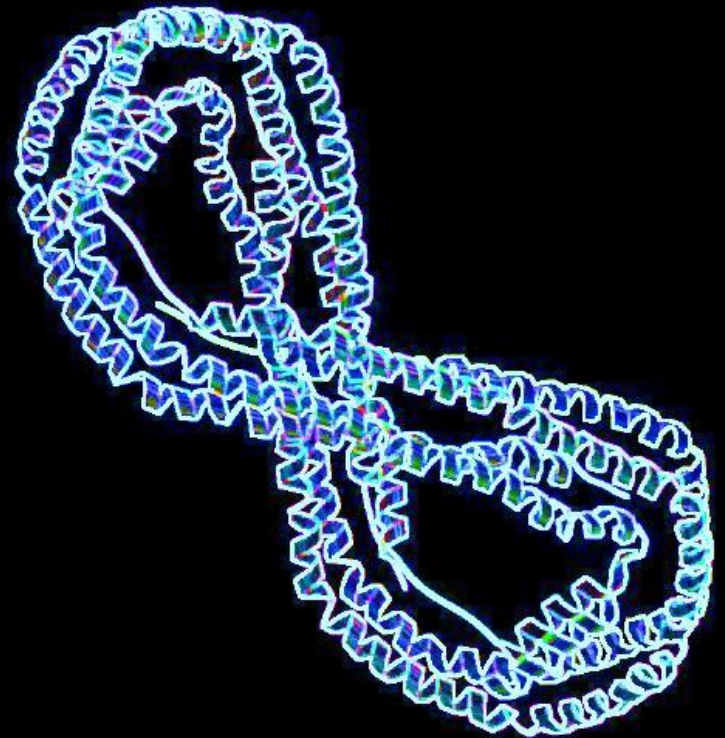
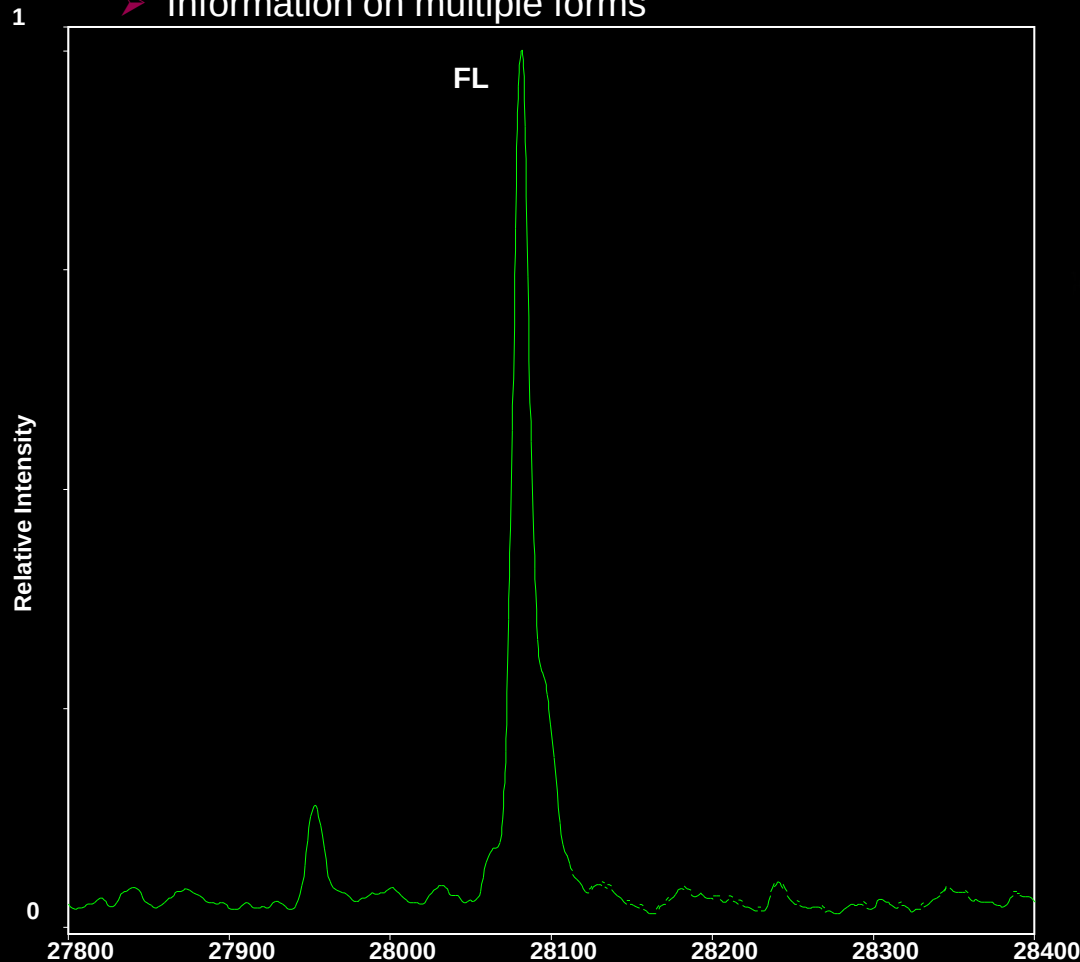


Apolipoprotein A1

DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLD
DFQKKWQEE/MELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELQRRLAARLEALKENG GARLA EYHAKATEHLSTL
SEKAKPALEDLRQGILLPVLESFKVSFLSALEEYTKLNTQ

➤ **Full-length (Direct)**

➤ Information on multiple forms

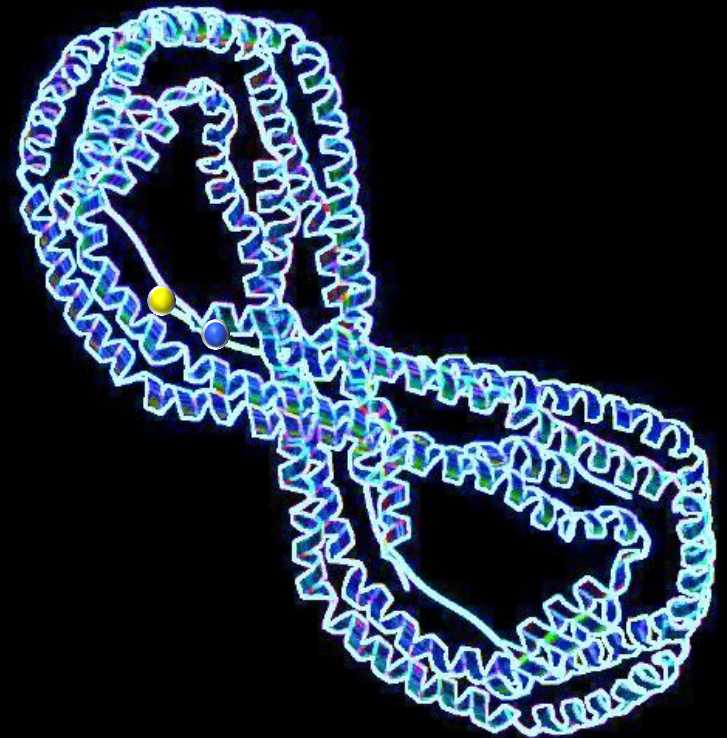
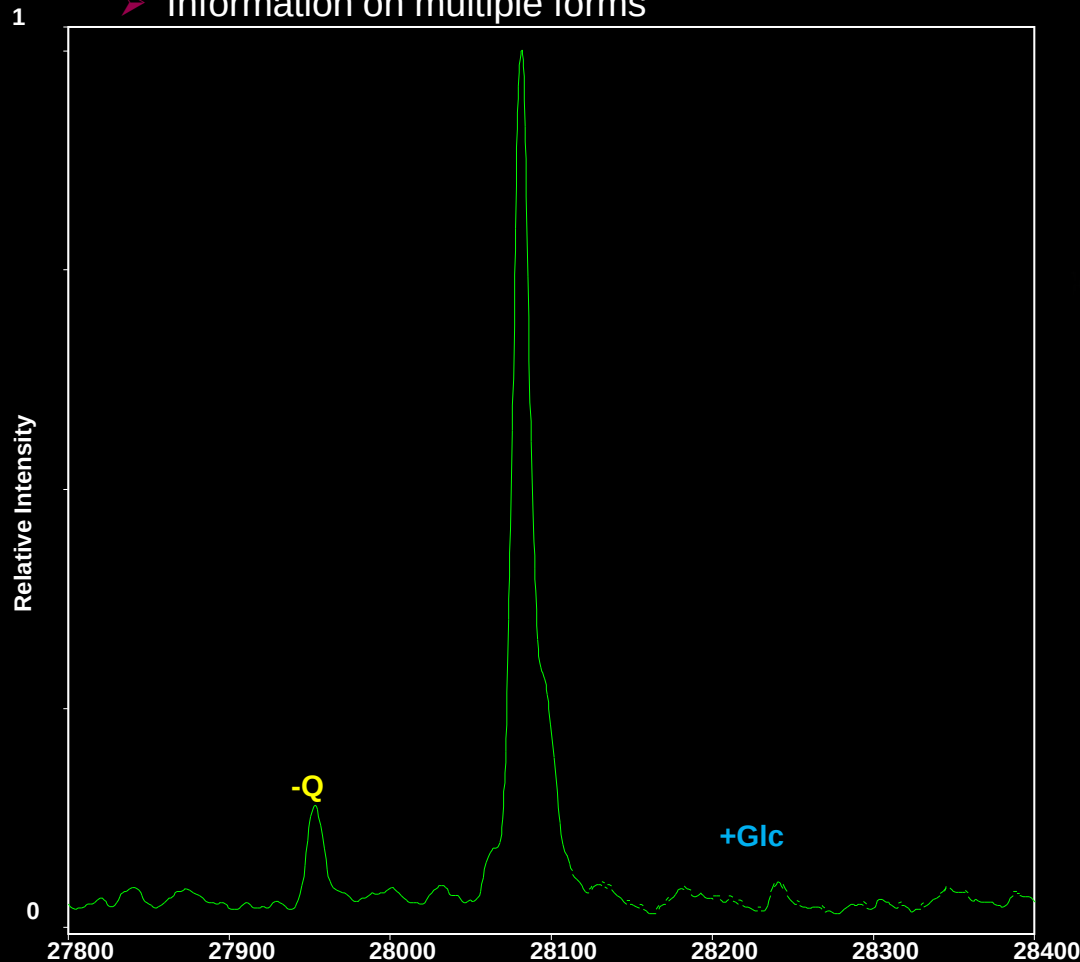


Apolipoprotein A1

DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLD
DFQKKWQEE~~M~~ELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDEL~~R~~QLAARLEALKENG~~G~~ARLAEYHAKATEHLSTL
SEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTK~~KLNT~~~~Q~~

➤ **Full-length (Direct)**

➤ Information on multiple forms



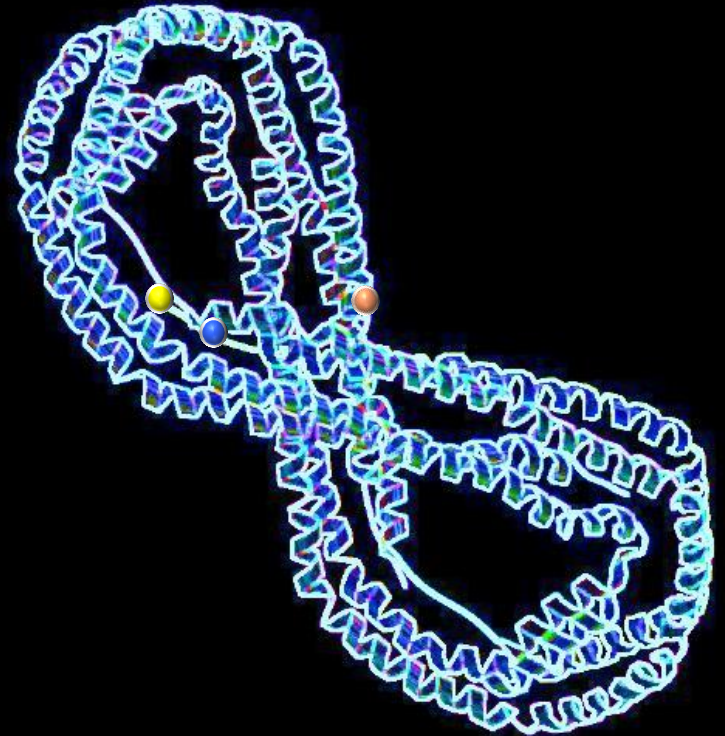
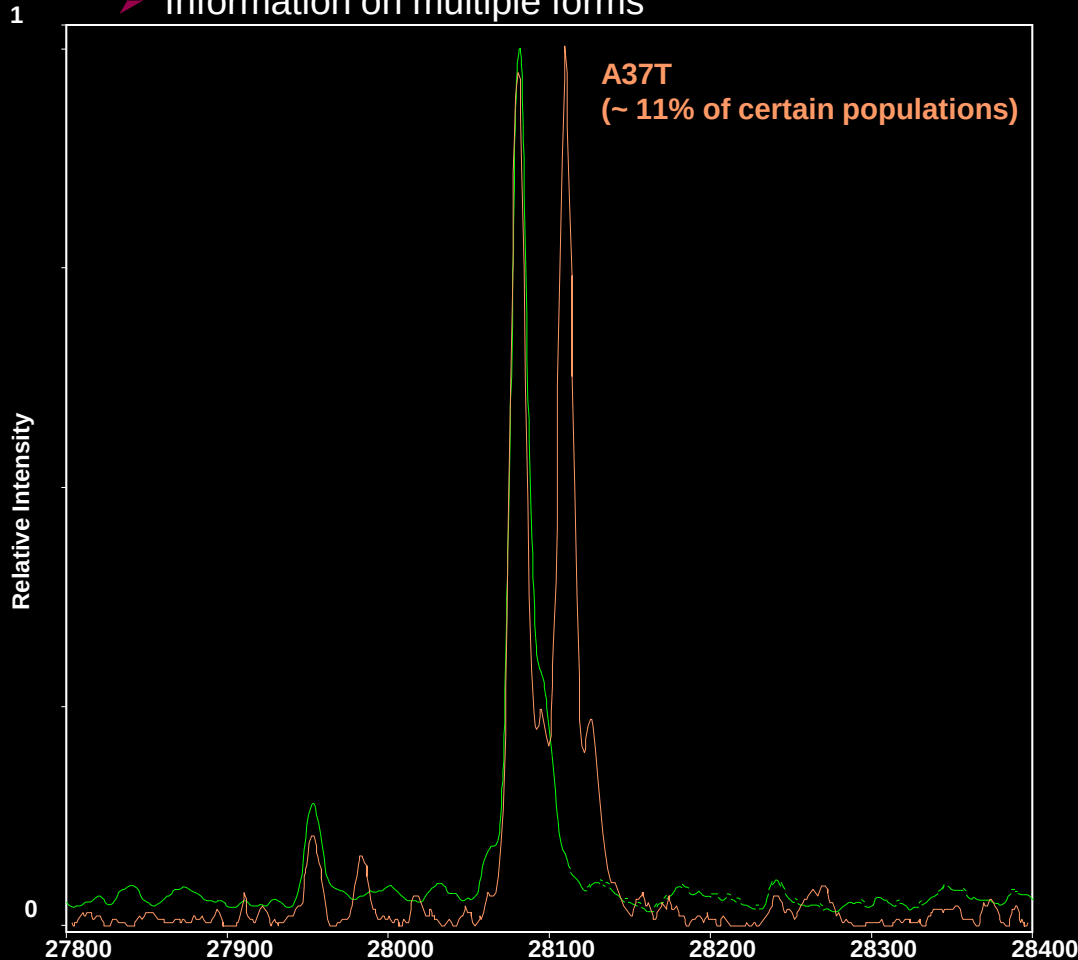
Apolipoprotein A1 (Full-length + PTM's + Point Mutations)

Apolipoprotein A1

DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLD
DFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELQRRLAARLEALKENGGARLAEYHAKATEHLSTL
SEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKLNTQ

➤ Full-length (Direct)

➤ Information on multiple forms



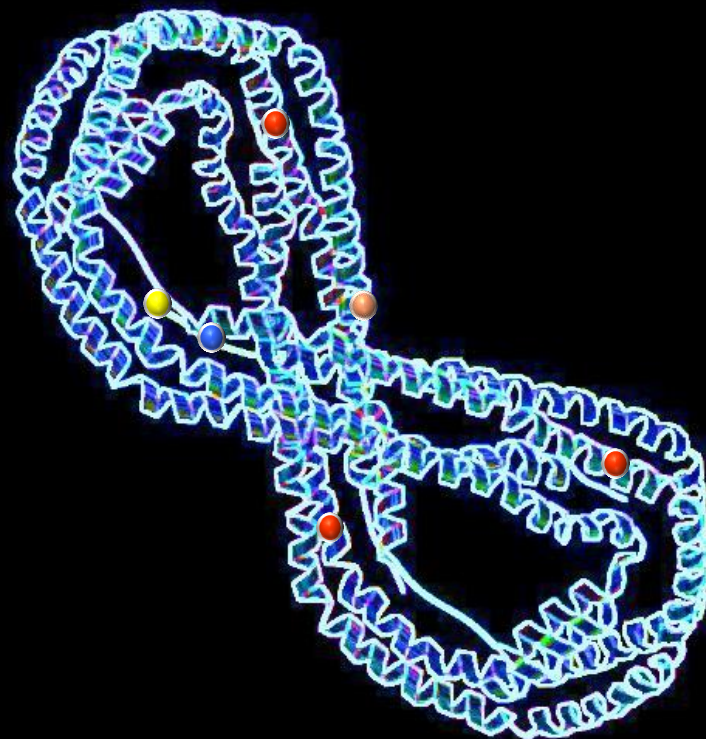
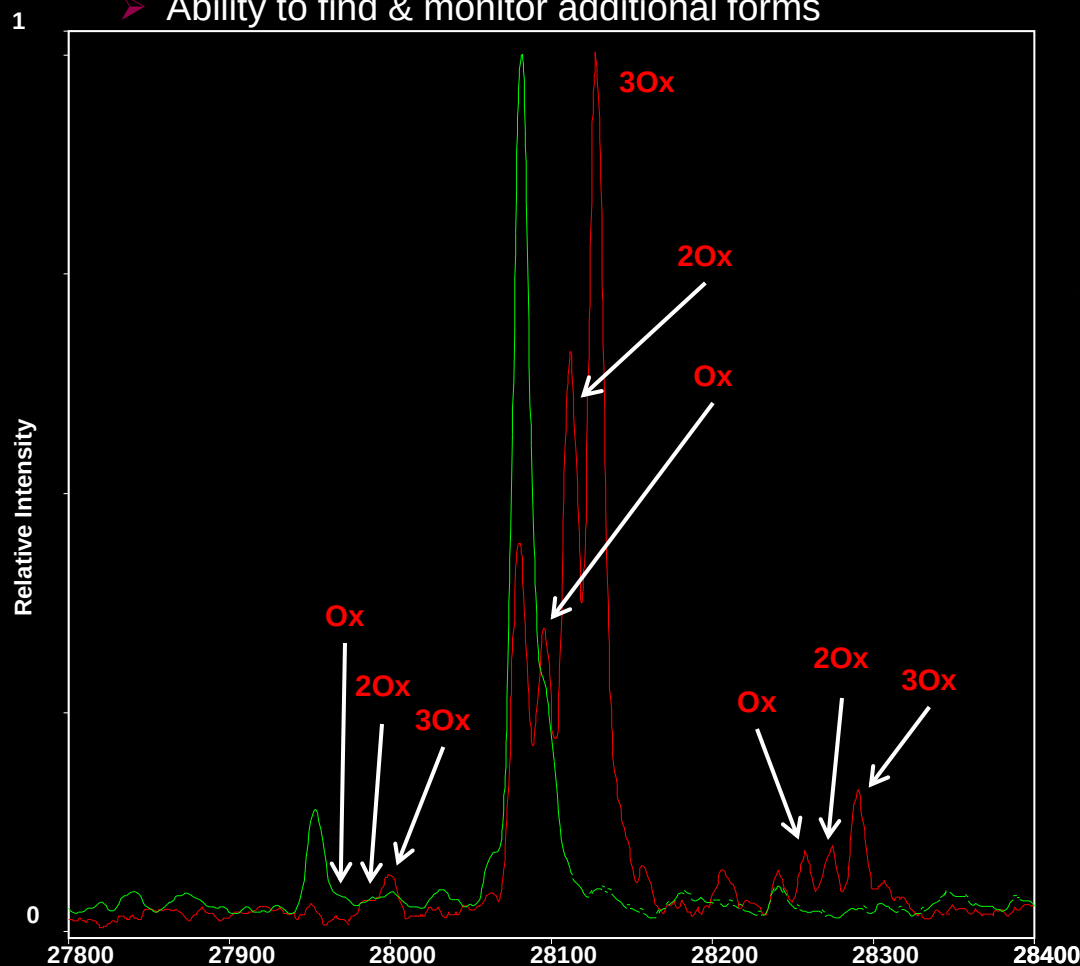
Apolipoprotein A1 (Full-length + PTM's + Point Mutations)

Apolipoprotein A1

DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGRLRQEMSKDLEEVKAKVQPYLD
DFQKKWQEE MELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEE MRDRARAHVDALRTHLAPYSDELQRRLAARLEALKENG GARLA EYHAKATEHLSTL
SEKAKPALEDLRQG LLPVLESFKVSFLSALEEYTK LNTQ

➤ Full-length (Direct)

- Ability to find & monitor additional forms

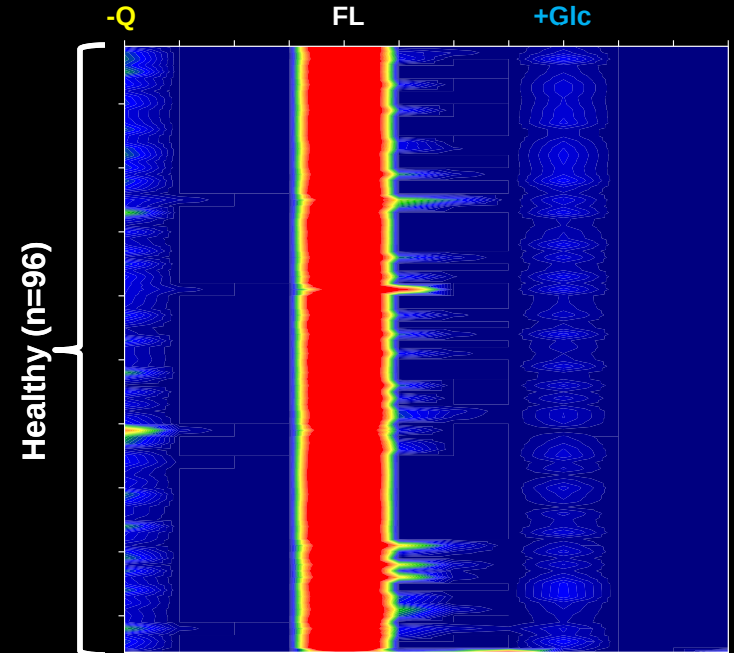
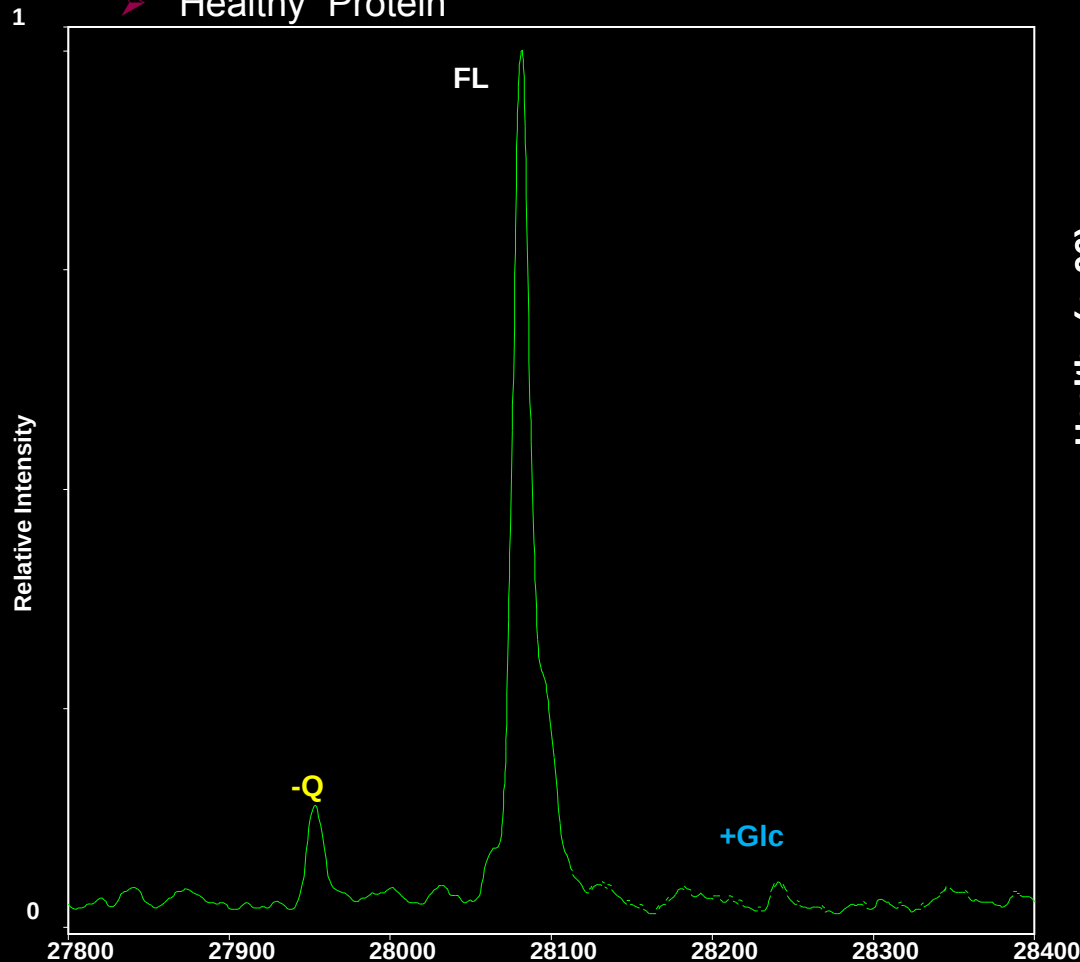


Apolipoprotein A1

DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGRLRQEMSKDLEEVKAKVQPYLD
DFQKKWQEE MELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEE MRDRARAHVDALRTHLAPYSDEL RQRLAARLEALKENG GARLA EYHAKATEHLSTL
SEKAKPALEDLRQG LLPVLESFKVSFLSALEEYTK LNT Q

➤ Full-length (Direct)

➤ “Healthy” Protein

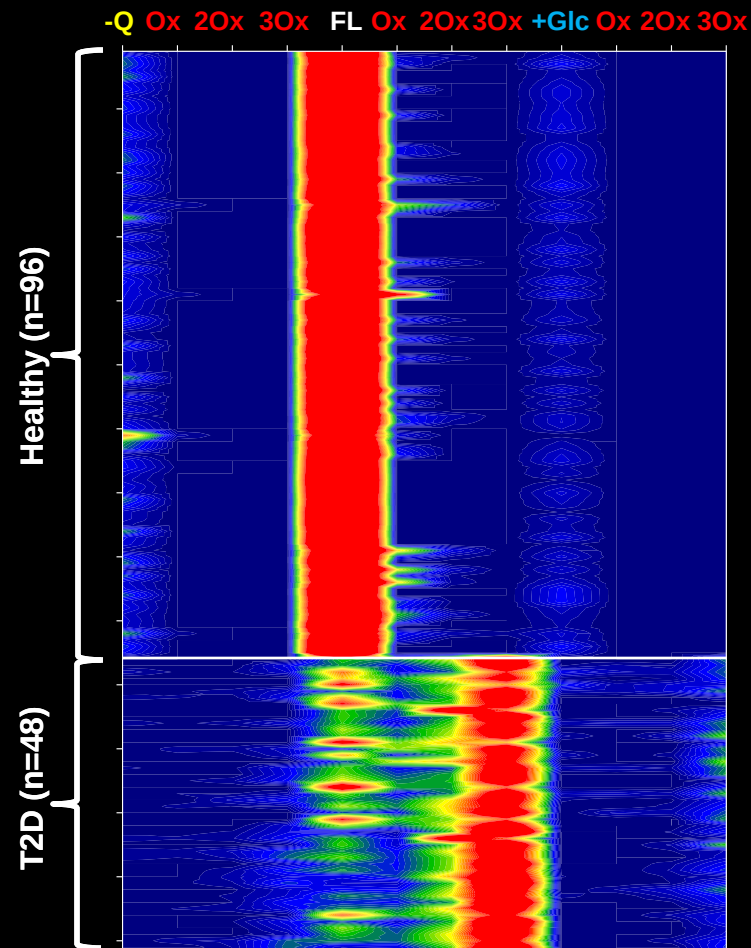
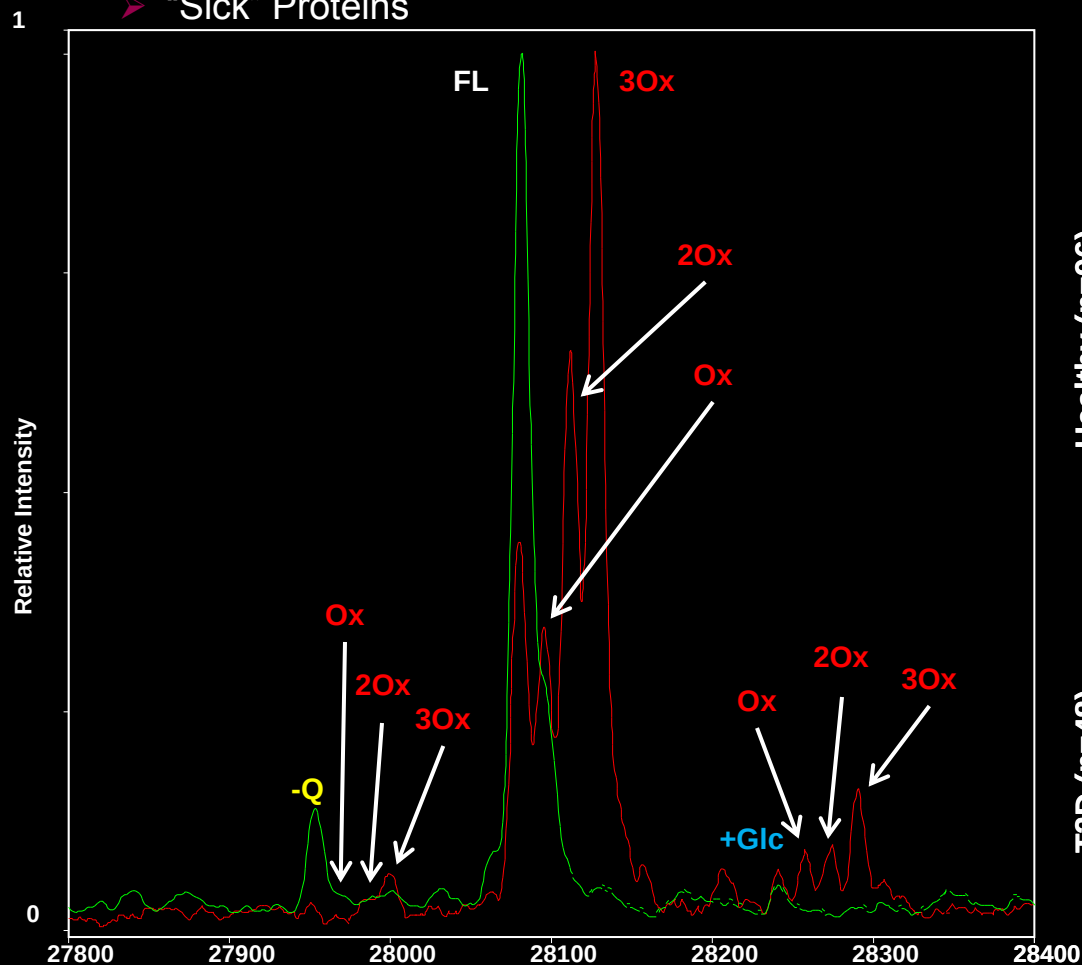


Apolipoprotein A1

DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGRLRQEMSKDLEEVKAKVQPYLD
DFQKKWQEE**M**ELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEE**M**RDRARAHVDALRTHLAPYSDELQRQLAARLEALKENGGARLAEYHAKATEHLSTL
SEKAKPALEDLRQGILLPVLESFKVSFLSALEEYTK**L**NT**Q**

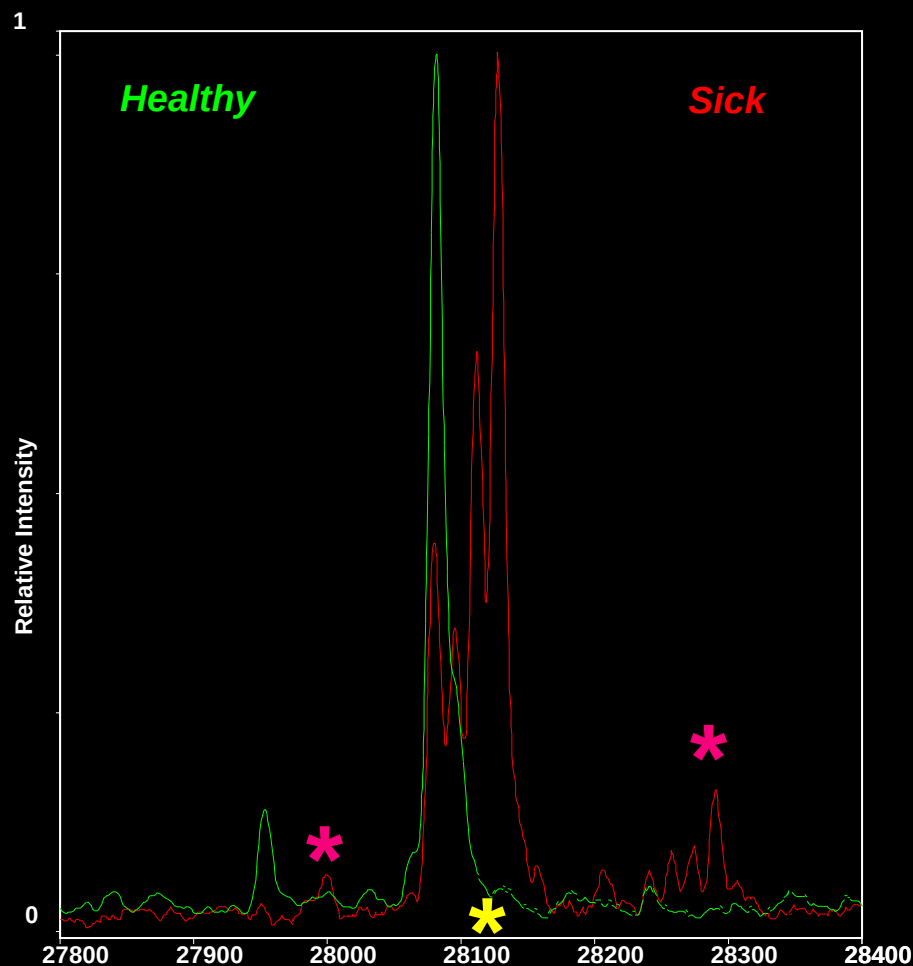
➤ **Full-length (Direct)**

➤ "Sick" Proteins



Apolipoprotein A1

DEPPQSPWDRVKDLATVYVDVLKDSGRDYSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGRLRQEMSKDLEEVKAKVQPYLD
DFQKKWQEE**M**ELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEE**M**RDRARAHVDALRTHLAPYSDELQRQLAARLEALKENGGARLAEYHAKATEHLSTL
SEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTK**L**NT**Q**



➤ **“Sick Proteins”**

- “Multiplexed” Apo A1 Assay
 - Posttranslational Modifications
 - 12 Evident & Resolvable Forms
- Stoichiometry is Important
 - Ratio of Individual PTM to Total
 - Present LOD ~ 1%
- Data Captured by **Surrogate Assays**
 - Difficult to design to capture multiple PTM’s
 - * Four PTM’s contained in ~ 150 AA
- Anticipate Additional Low Level Variants
 - * Apo A1 with Five PTM’s
 - Estimated at:
 - ~ 250 ppm (~ 5 ug/mL) in T2D
 - << in Healthy

➤ Expanded Cohort (> 200 Patients)

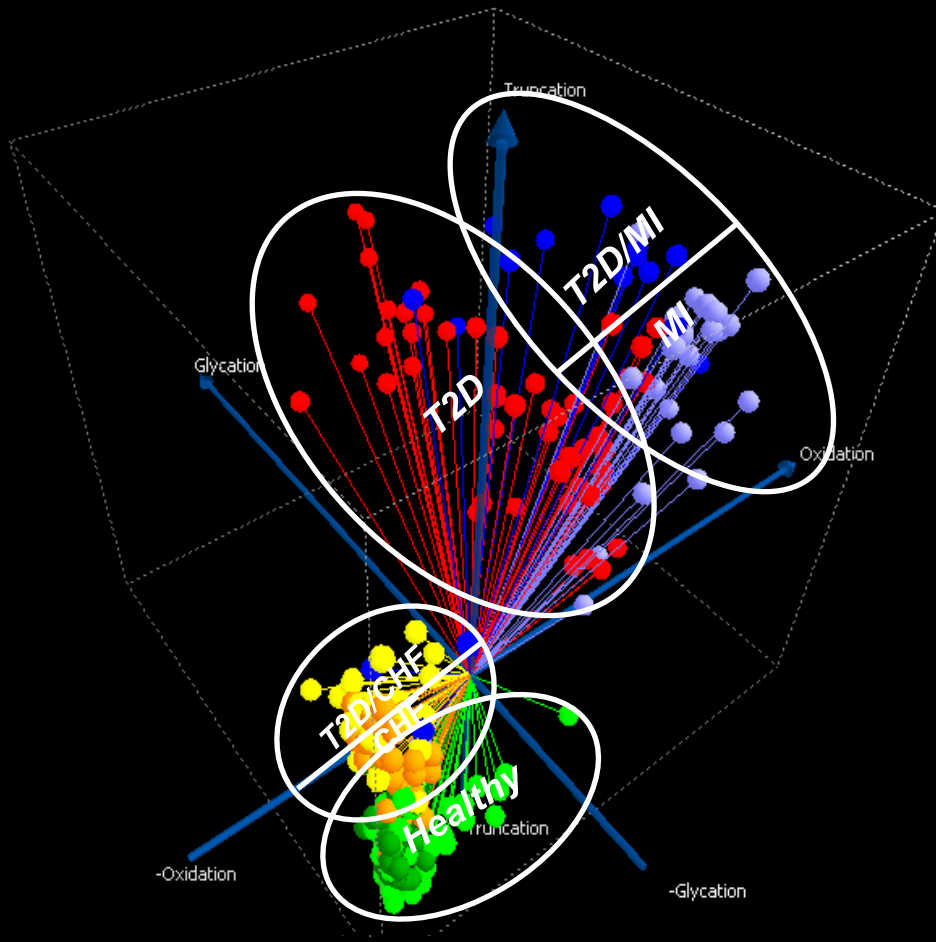
- **Healthy; T2D; T2D/MI; T2D/CHF; MI; CHF**
- **Scouting Cohorts 20 – 50 Individuals/sub-type**
- **13 Targets (> 2700 Assays Performed in Total)**
- **139 Molecular Variants found in Population (~30,000 Data Points)**
- **Principal Component Analysis & Biologically Supervised**

Target	Conc (g/L)	Variants*	Category
Alb	40	7	FL, cys, glc, cysgly
Apo A1	2	12	FL, glc, (3)ox, trunc
Apo C1	5×10^{-2}	4	FL, trunc, ox
b2m	5×10^{-3}	4	FL, ox, glc, dk58
C-peptide	9×10^{-7}	6	FL, PM, (2)trunc
CysC	1×10^{-3}	7	FL, OH-Pro, (2)trunc, (3)glc
GcG	2×10^{-1}	40	4 Allelic, glc, (3)glycos
Hemoglobin	-	8	(2)FL, HbS, glc
Insulin	5×10^{-8}	6	FL, trunc, Novolog, (3)Lantus
RANTES	3×10^{-6}	21	FL, trunc, glyc, glycos, ox
RBP	1.5×10^{-2}	4	FL, trunc
SAP	4×10^{-2}	4	FL, glycos, trunc
TTR	2×10^{-1}	16	FL, (3)PM, cys, cysgly, sulf

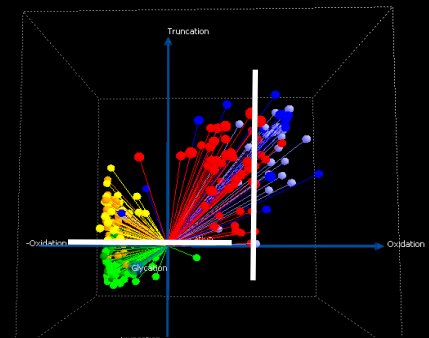
3-Dimensional View of T2DM/CVD: Biologically Supervised

- Mixed Cohorts of Healthy – to – T2DM – to – CVD Outcome
 - 213 Individuals (Healthy, T2DM, CHF, MI)
 - 7 Assays per Individual (~ 1400 Assays)
 - 21 Determinates with Biological Supervision

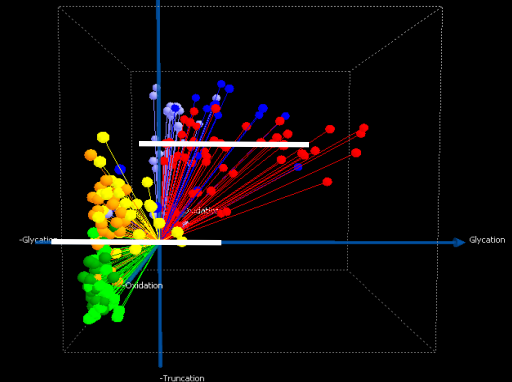
T2D Poor CTRL
 Healthy (Serum)
 Healthy
 CHF T2D
 CHF MI T2D
 CHF MI
 CHF MI
 CHF
 Color =
 Axis X = Glycation
 Axis Y = Oxidation
 Axis Z = Truncation



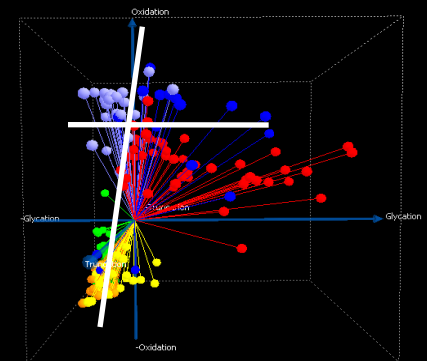
T2D Poor CTRL
 Healthy (Serum)
 Healthy
 CHF T2D
 CHF MI T2D
 CHF MI
 CHF MI
 CHF
 Color =
 Axis X = Oxidation
 Axis Y = Glycation
 Axis Z = Truncation

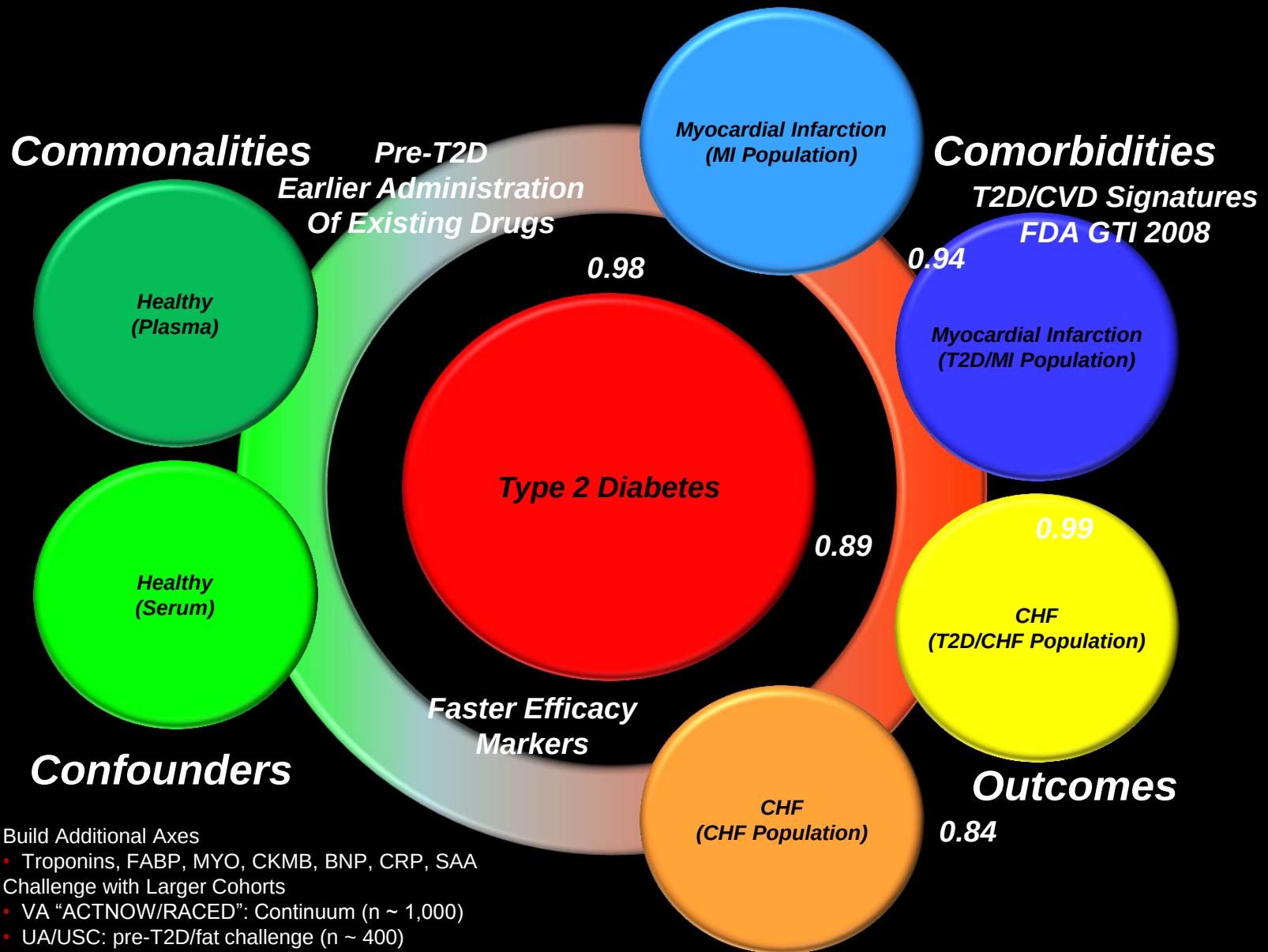


T2D Poor CTRL
 Healthy (Serum)
 Healthy
 CHF T2D
 CHF MI T2D
 CHF MI
 CHF MI
 CHF
 Color =
 Axis X = Oxidation
 Axis Y = Glycation
 Axis Z = Truncation



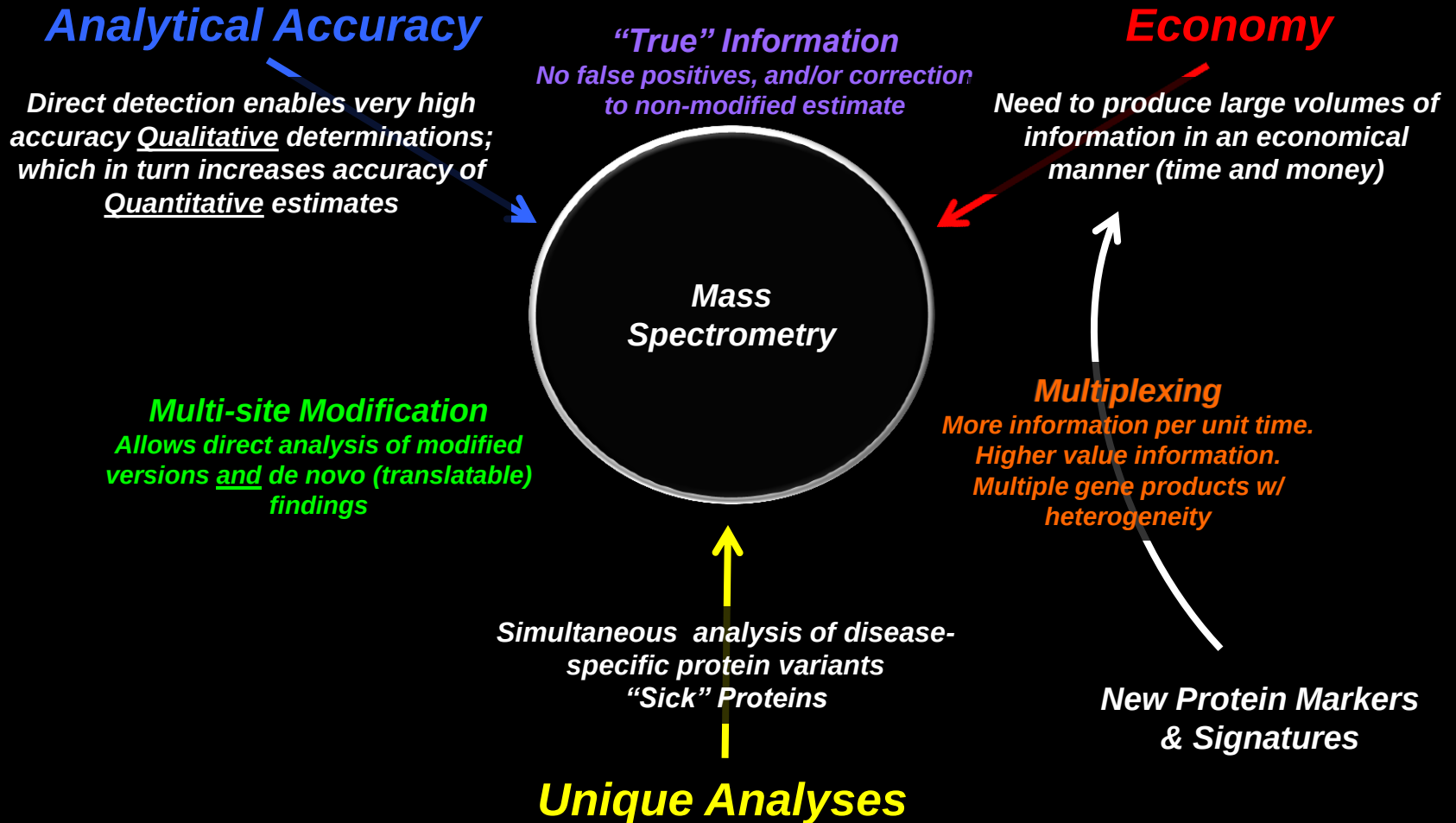
T2D Poor CTRL
 Healthy (Serum)
 Healthy
 CHF T2D
 CHF MI T2D
 CHF MI
 CHF MI
 CHF
 Color =
 Axis X = Oxidation
 Axis Y = Glycation
 Axis Z = Truncation



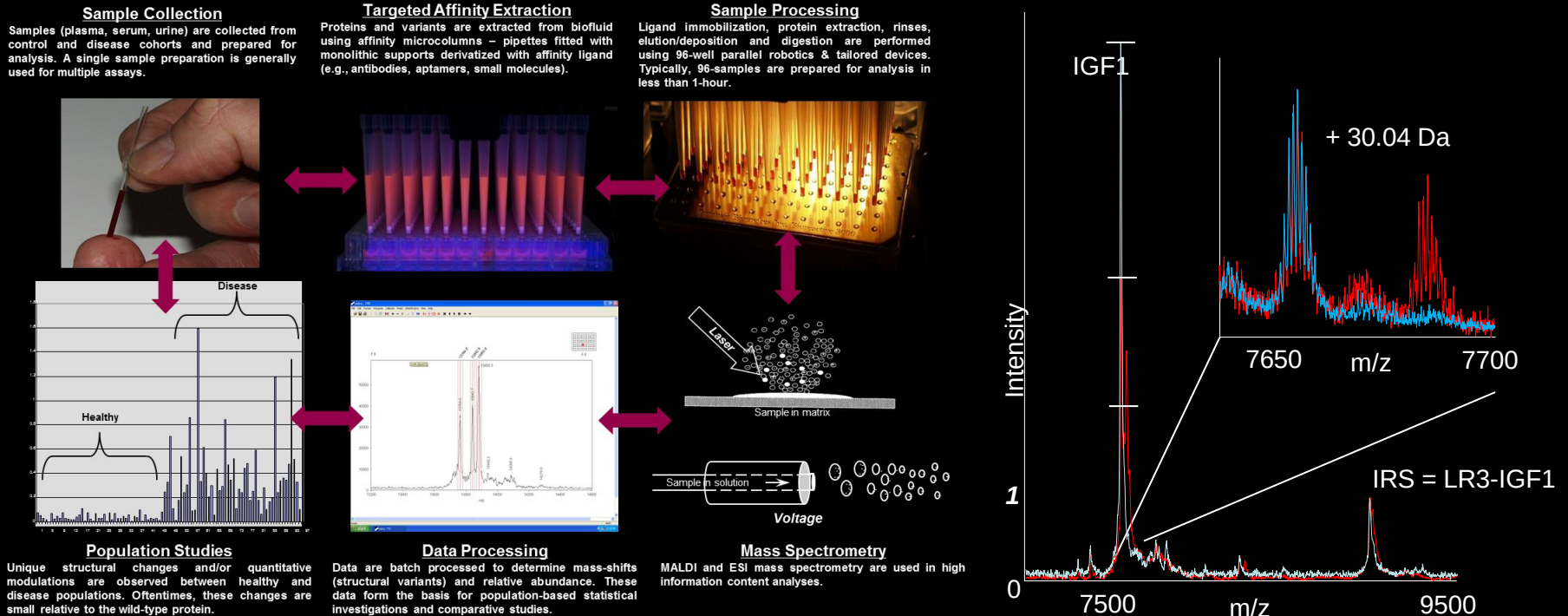


- Build Additional Axes
 - Troponins, FABP, MYO, CKMB, BNP, CRP, SAA
- Challenge with Larger Cohorts
 - VA "ACTNOW/RACED": Continuum (n ~ 1,000)
 - UA/USC: pre-T2D/fat challenge (n ~ 400)
 - SingHealth: T2D/CVD /MI(ER) (n ~ 700)
 - Pfizer "ASCOT": Longitudinal converters (n ~ 400)

Randy's Unified Thoughts on Mass Spectrometry-Based Diagnostics



- **IGF1 (1,056 Samples (T2D/CVD) + 96 Calibration Samples) – 24 hours**
 - Diagnosing growth disorders, adult growth hormone deficiency & acromegaly/gigantism
 - Monitoring of recombinant human growth hormone treatment: FDA-approved treatment of IGFD (Increlex)
 - CPT Code 84305 – \$64.24 Gross



- **IGF1 MSIA**
 - Standard Error of Working Curves = 13.078 % (n=12; inter-curve (manual processing))
 - Dynamic Range > 300 (667 pM – 210 nM) (observed in samples 3.46 – 92.5 nM)
 - LOD < 500 pM; LOQ = 667 pM (40 uL plasma; Sample re-use for more assays, e.g., IGF2)
- **Quantification of wt-IGF-1 and Variant Detection/Correction**
 - Point Mutations observed in ~ 1% of samples
 - e.g., Ala-Thr (dm = 30.03 Da)

Next-Generation Clinical Mass Spectrometry Platform (CMSP)

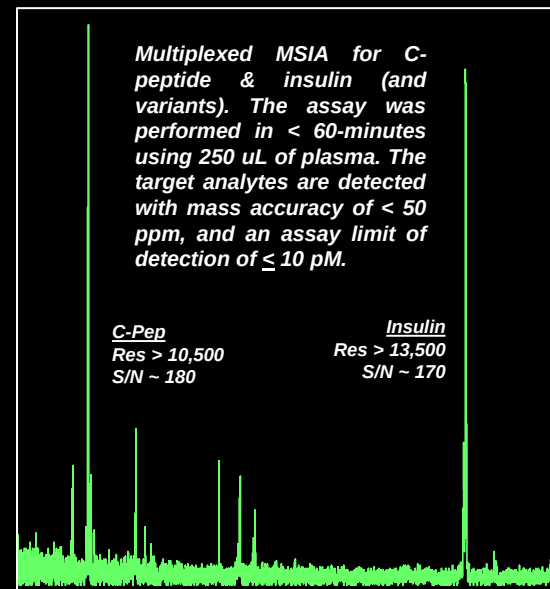
Current Technical Specifications For CMSP (from SimulToF Systems prototypes)		
Category	Metric	Notes
Throughput	Up to 3,000 analyses/day	Sample handling limits
Sample Consumption	0.1 – 2 mL biofluid	Total sample for multiple assays
Cost (platform)	\$100,000 - 300,000	Cost on par with current non-MS platforms
Cost (assay)	< \$15/data point	Cost of assay materials multiplexed preferred
User Interface	Graphic	Software paired w/assays
Ease of Use	Minimum User	Alpha prototype
Data Output	Numeric and graphic	Software paired w/assays
Size & Utilities	Benchtop (< 3 x 3 x 4 ft. d/w/h) 99/384/1584-well format/ 120V	Unobtrusive, operating on common utilities
Data Acquisition	Automated	< 10-seconds/sample (10-50k laser shots)
Cost (platform)	\$150,000 - 200,000	Depends on final specifications
Resolution/Accuracy /Range	> 20,000/ ~ 5 ppm/ 500 – 150,000 Da	Exceeds research-grade instruments
Limit of Detection	Low pM Sub-femtomole	Exceeds research-grade instruments
Preliminary Candidates for Assay Development		
Target*	Uses/Known Variants**	Price (\$)**
GIP	B-cell stimulation / truncated forms (e.g., GIP(3-42))	280.00
Glucagon	Glucagonomas, hyper- or hypoglycemia / truncated forms	175.00
C-peptide	Hypoglycemia, insulinoma, islet cell transplant / C-pep(3-31)	125.00
Insulin	Insulinoma/ exogenous forms (e.g., insulin glargine, aspart)	112.00
Angiotensin I	Renin activity / AngII precursor	175.00
Angiotensin II	Hypertension / vasoconstriction / AngIII precursor	300.00
IGF-1	Growth disorders/ Point mutations	172.00
PTH	Hypercalcemia, renal failure / PTH-(1-84) vs PTH-(7-84)	200.00
FGF-23	AD hypophosphatemic rickets / splice variants	194.00
ACTH	Hypocortisolism / truncated (e.g., ACTH(1-11), ACTH(1-34))	230.00
* Gastro Inhibitory Peptide (GIP); Insulin-like Growth Factor 1 (IGF-1), Parathyroid Hormone (PTH), Fibroblast Growth Factor 23 (FGF-23), Adrenocorticotrophic Hormone (ACTH).		
** From literature search, not meant to be exhaustive.		
*** Fees charged for service (Mayo Medical Laboratories), unit cost are ~10-15% of these values.		



Multiplexed MSIA for C-peptide & insulin (and variants). The assay was performed in < 60-minutes using 250 uL of plasma. The target analytes are detected with mass accuracy of < 50 ppm, and an assay limit of detection of ≤ 10 pM.

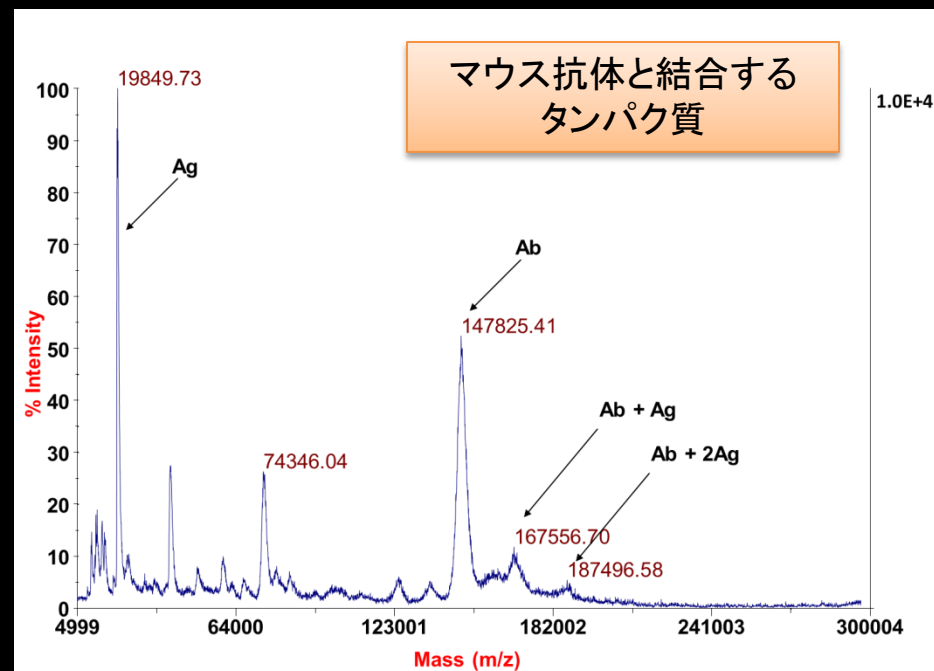
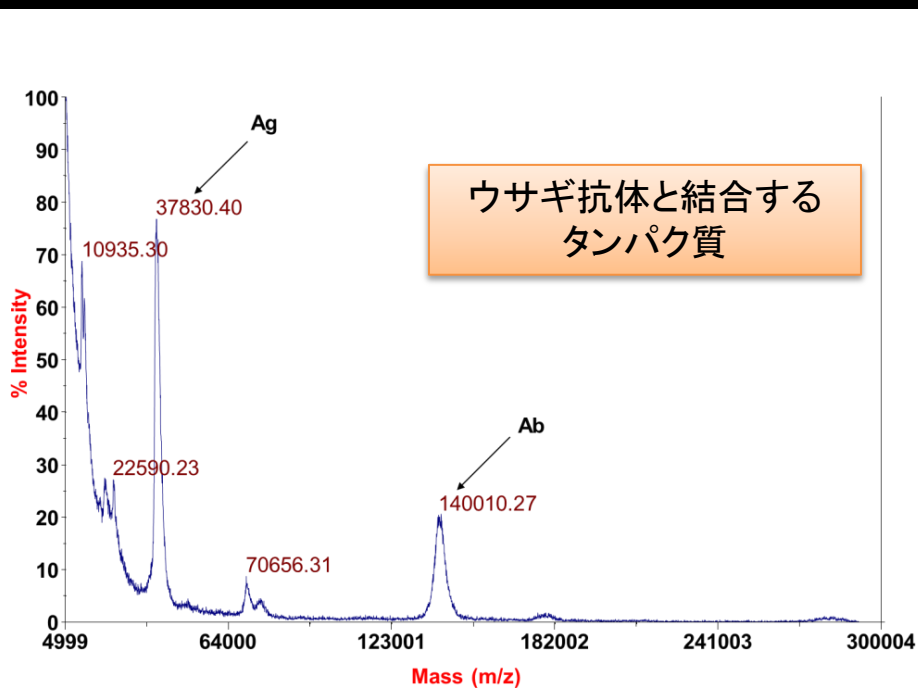
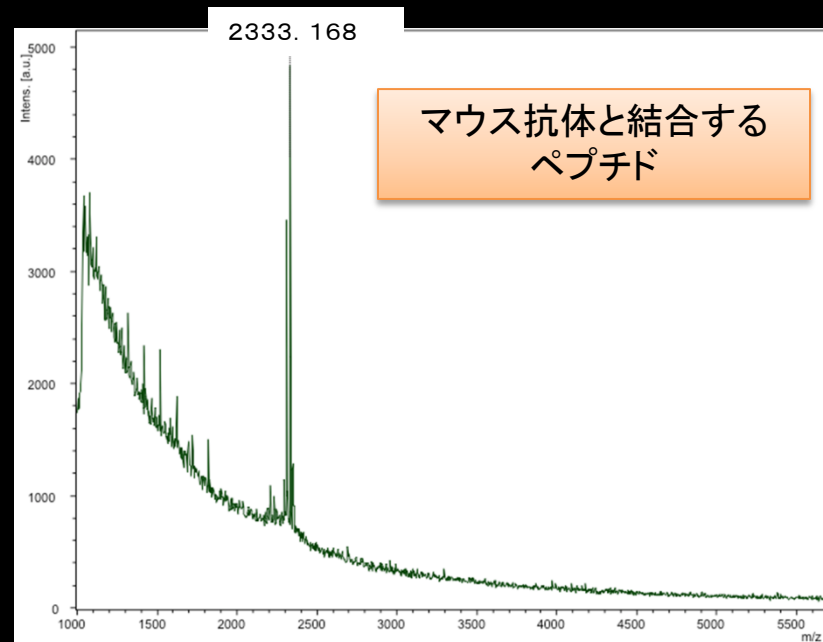
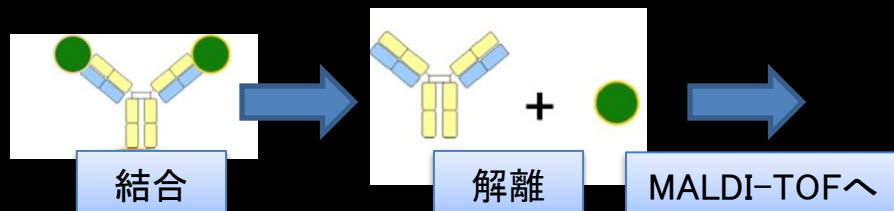
C-Pep
Res > 10,500
S/N ~ 180

Insulin
Res > 13,500
S/N ~ 170



SkiPro

細胞培養液をアナライトで、TOF-MSへ



マルチ親イオン MS-MS

superposition of 2 peptide
spectra

1296.7 green

1042.3 red

