

# MASS SPECTROMETRY ACHIEVING PROMINENCE IN CLINICAL MEDICINE



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# SYNOPSIS



- ❖ Technological transfer in laboratory medicine
- ❖ Principles of modern mass spectrometry
- ❖ Expanding role of MS in CLINICAL medicine
  - ❖ **Chemical pathology**: TDM & TOX, Endocrinology, NB screening, **microbiology**, Clinical chemome as a new diagnostic tool and omics' era diagnostics
  - ❖ **Anatomical pathology**: molecular imaging & I-knife
- ❖ The MS role in precision medicine

# Technological Transfer in Lab Medicine



## Today:

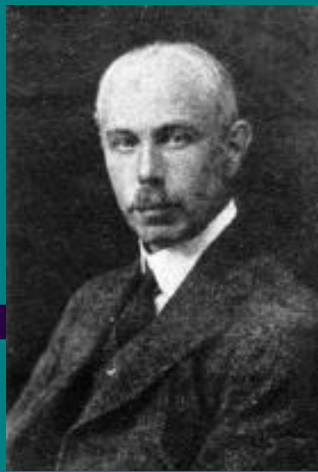
- the era of total laboratory automation
- flood of new technologies:
  - mass spectrometry
  - cell sorting platforms
  - genome assays.

## The future:

- microfluidic & in vivo assay platforms
- “omic” research turns into “omic” diagnostics
- big data analysis and patient controlled care



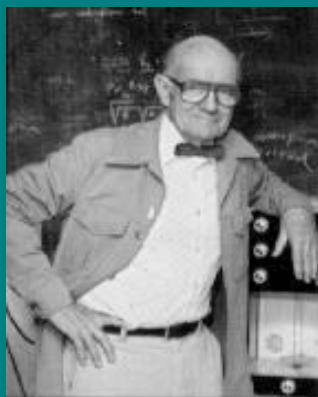
**Joseph John Thomson**  
1865-1940, Cambridge, UK  
First mass spectrometer  
Nobel Prize in Physics 1906



**Francis William Aston**  
1877-1945, Cambridge, UK  
Mass spectrometry of isotopes  
Nobel Prize in Chemistry 1922



**Wolfgang Paul**  
1913-1993, Bonn, Germany  
Q and Q Ion trap mass spectrometers  
Nobel Prize in Physics 1989



**John B Fenn**  
1917, Richmond, Virginia, USA  
Electrospray Ionization of biomolecules  
Nobel Prize in Chemistry 2002



**Koichi Tanaka**  
1959, Shimadzu Cooperation, Japan  
Matrix Assisted Laser Desorption Ionisation  
Nobel Prize in Chemistry 2002

# Clinical Chemistry's 2016 Special Issue: Clinical Mass Spectrometry—Achieving Prominence in Laboratory Medicine

Thomas M. Annesley\*

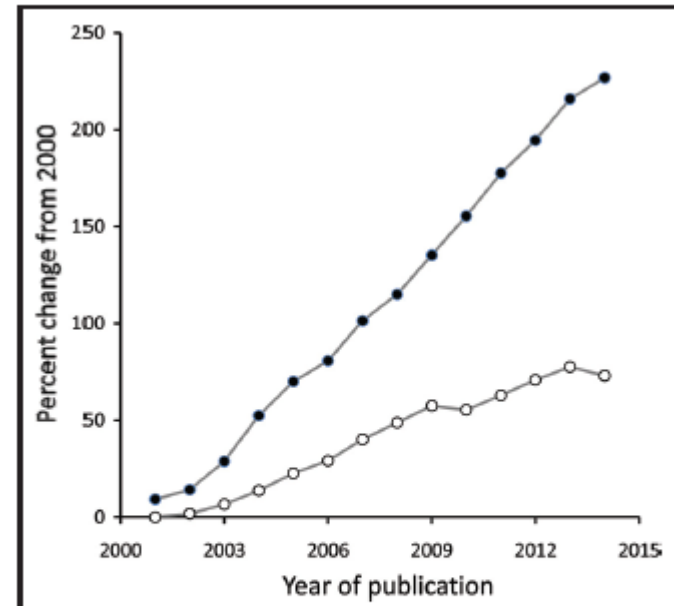
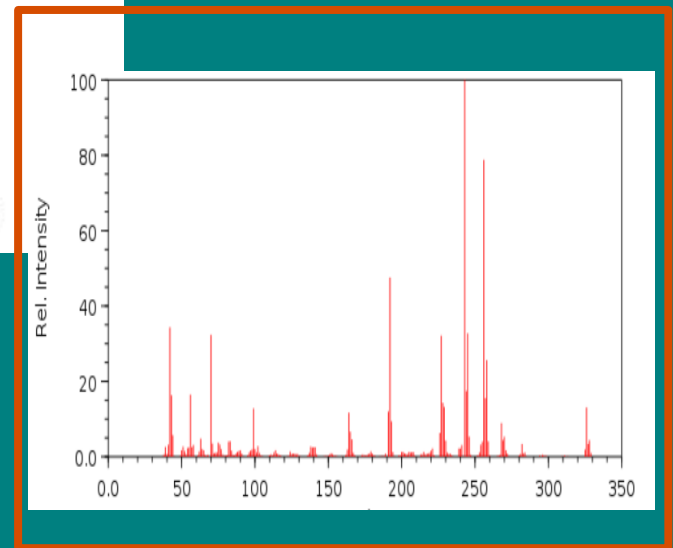
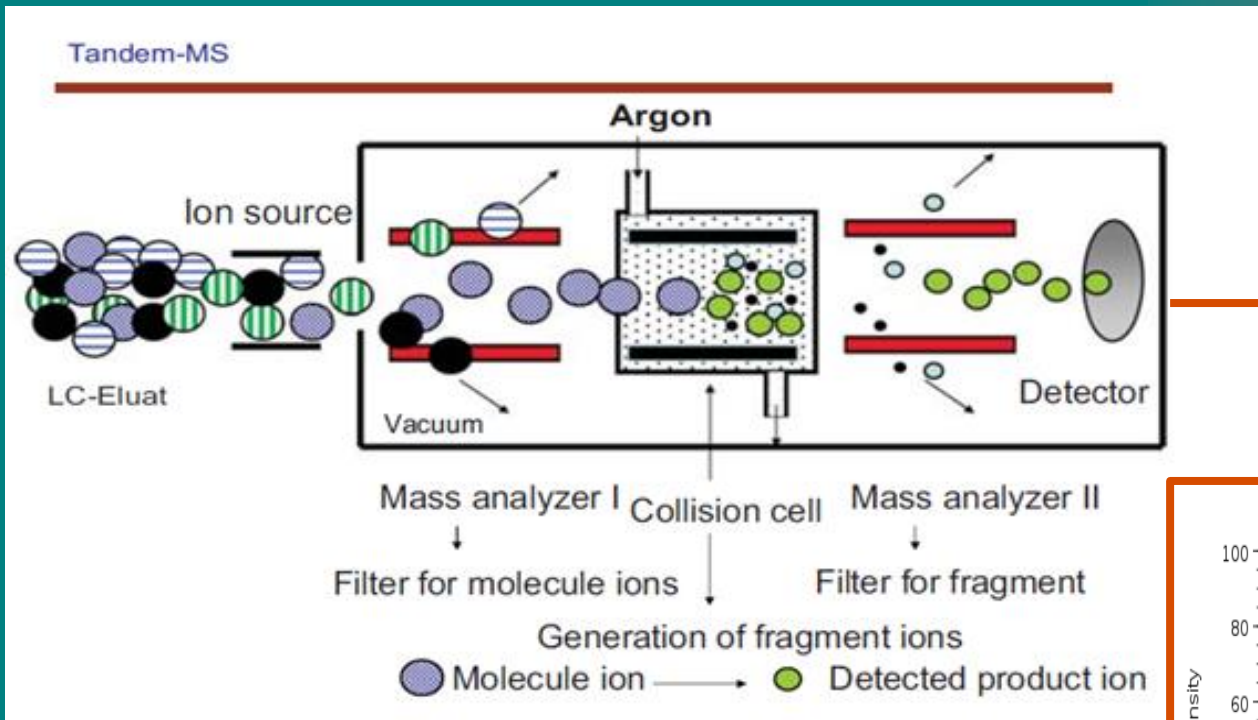


Fig. 1. Percent change in the number of publications from 2000 for the topic category "mass spectrometry" (closed circles) versus the percent change in all publications (open circles).

# Principle of LC-MS/MS (QQQ)<sub>MS</sub>



Kobold-U, Scand J Clin & Lab Invest 2012; 72 (Suppl 243):54-59, modified.

# Expanding role of mass spectrometry in the medical laboratory

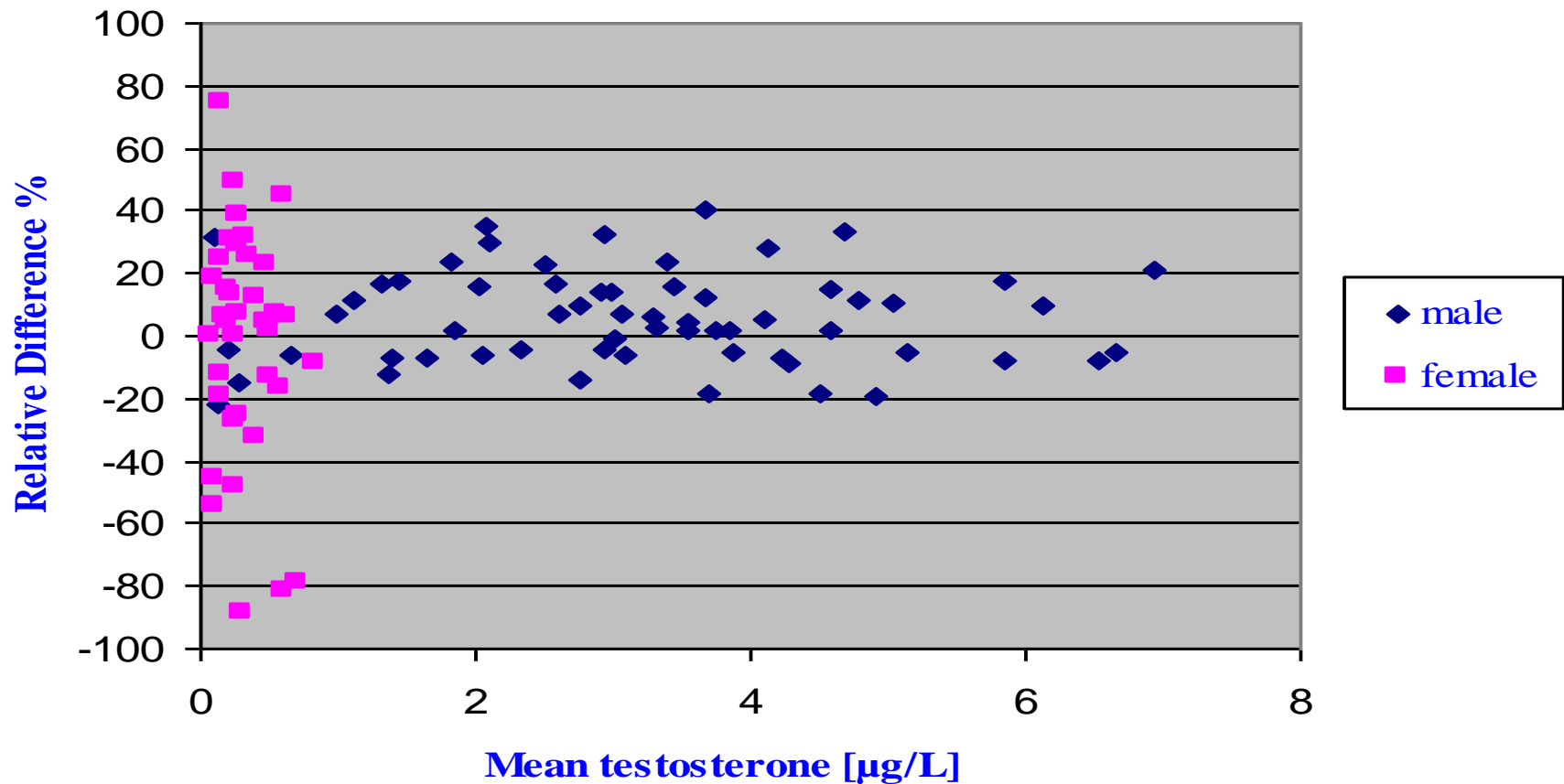
## LC-MS/MS (QQQ)

- **TDM** (immunosuppressants, antiretroviral drugs, antidepressants, antipsychotics)
- **Drugs of Abuse & Clinical Toxicology**
- **Endocrinology** (steroid profiles, FT3, FT4, free metanephrines)
- **Newborn screening** (e.g. acylcarnitines, amino acids, steroids)
- **Vitamin D status** (25-OH-D2, 25-OH-D3)
- **Peptidomics** (Angiotensins, Oxytocin, ADH, hepcidine)

## MALDI-TOF & ORBITRAP

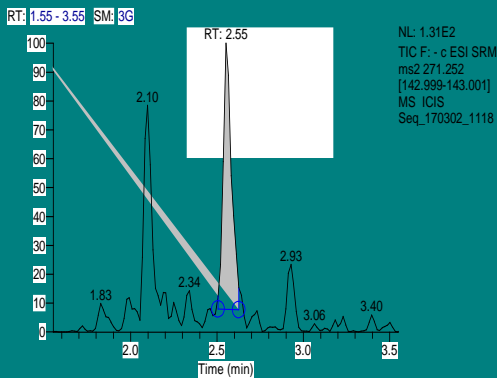
- **Proteomics** (Research, Biomarker Discovery)
- **Medical Microbiology**

# Testosterone определен с IA и LC-MS/MS

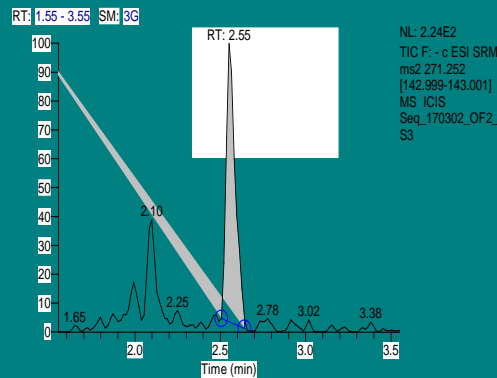




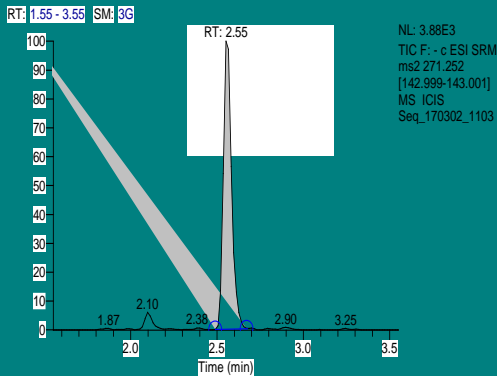
# High sensitive LC-MS/MS Analysis of Estradiol (E2) in Human Plasma



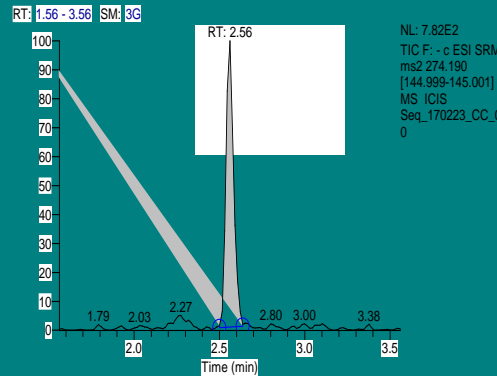
Post MP Female, E2 1.5 ng/L



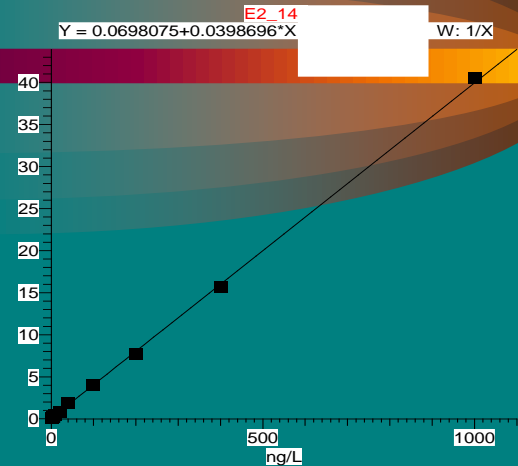
Elderly Male, E2 3.6 ng/L



Young Female, E2 152 ng/L

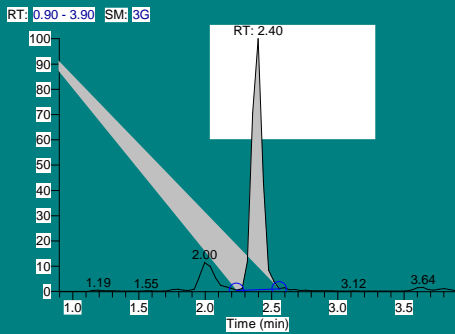


Internal Standard, d<sub>3</sub>-E2

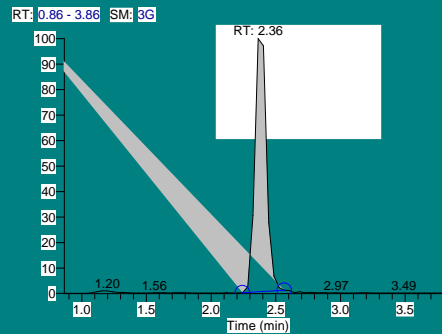


File Name	Specified Amount	Calculated Amount	% Diff
CC_00	1.000	0.934	-6.59
CC_01	2.000	2.068	3.42
CC_02	4.000	4.208	5.21
CC_03	10.000	9.857	-1.43
CC_04	20.000	18.193	-9.04
CC_05	40.000	45.714	14.28
CC_06	100.000	98.789	-1.21
CC_07	200.000	192.181	-3.91
CC_08	400.000	391.694	-2.08
CC_09	1000.000	1013.363	1.34

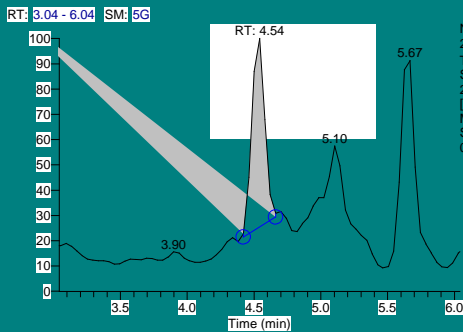
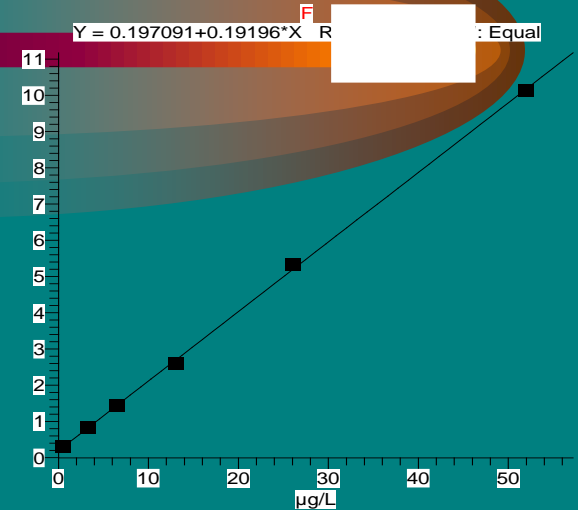
# Simultaneous LC-MS/MS Analysis of Cortisol (F) and Testosterone (T) in oral fluid



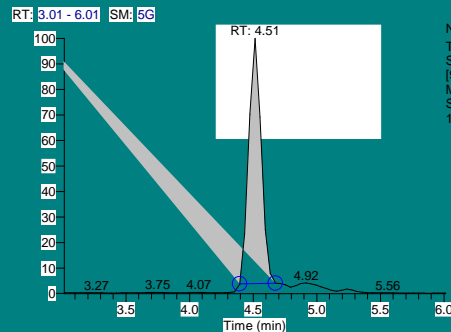
Calibration Sample01, F 2.8 µg/L



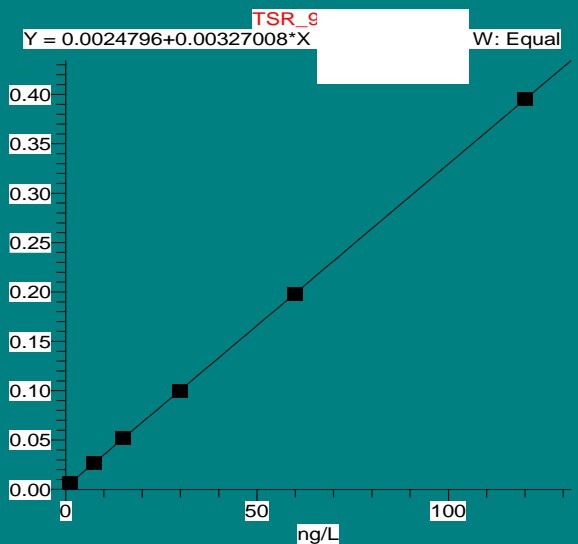
Internal Standard, d4-F



Calibration Sample01, T 6.2 ng/L



Internal Standard, d3-T



# Traditional Newborn Screening

- **Single Disease**

- **Single test**

- **Single Marker**

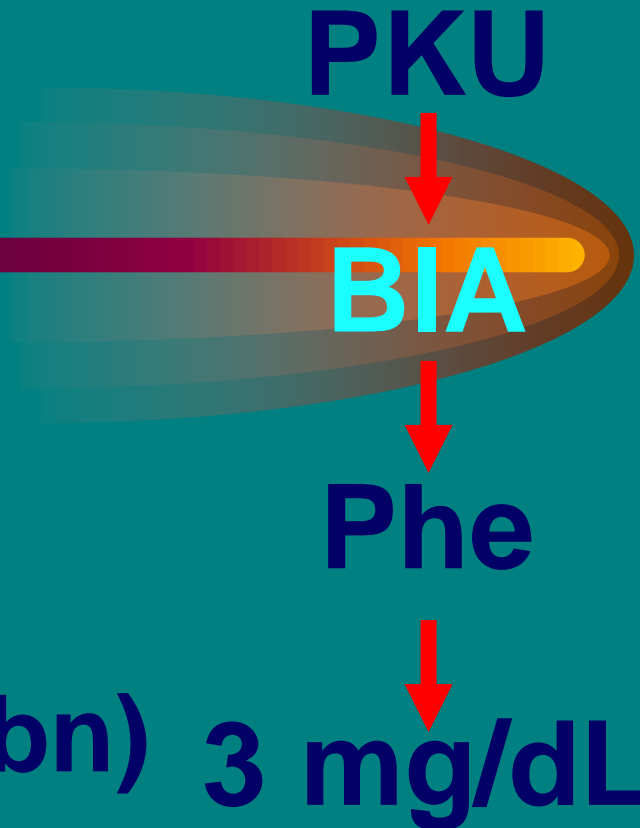
- **Single cut-off (N/Abn) 3 mg/dL**

**PKU**



**BIA**

**Phe**

**3 mg/dL**



# MS/MS Newborn Screening

- **Multiple Diseases**  $(IEM)_n$
  - **Single test**  **MS/MS**
  - **Multiple Markers**  $(AA, AC)_n$
  - **Multiple cut-offs** 0.1-1,000  $\mu\text{M}$
- 

# MS/MS Newborn Screening

> 50 ANALYTES > 30 IEM

Time < 2 min

Phenylketonuria

MSUD

Homocystinuria

Tyrosinemia type I

Argininosuccinic acidemia

Citrullinemia type I

Hyperphenylalaninemia

Tyrosinemia type II

Biopterin defects (Bios)

Tyrosinemia type III

Biopterin (Reg)

Argininemia

Hypermethioninemia

Citrullinemia type II

MCAD deficiency

VLCAD deficiency

LCHAD deficiency

TFP deficiency

Carnitine uptake

defect

Glutaric acidemia

type II

Isovaleric acidemia

Glutaric acidemia type I

Methylglutaconic acidemia

Malonic acidemia

HMG deficiency

3MCC deficiency

BKT deficiency

Multiple carboxylase deficiency

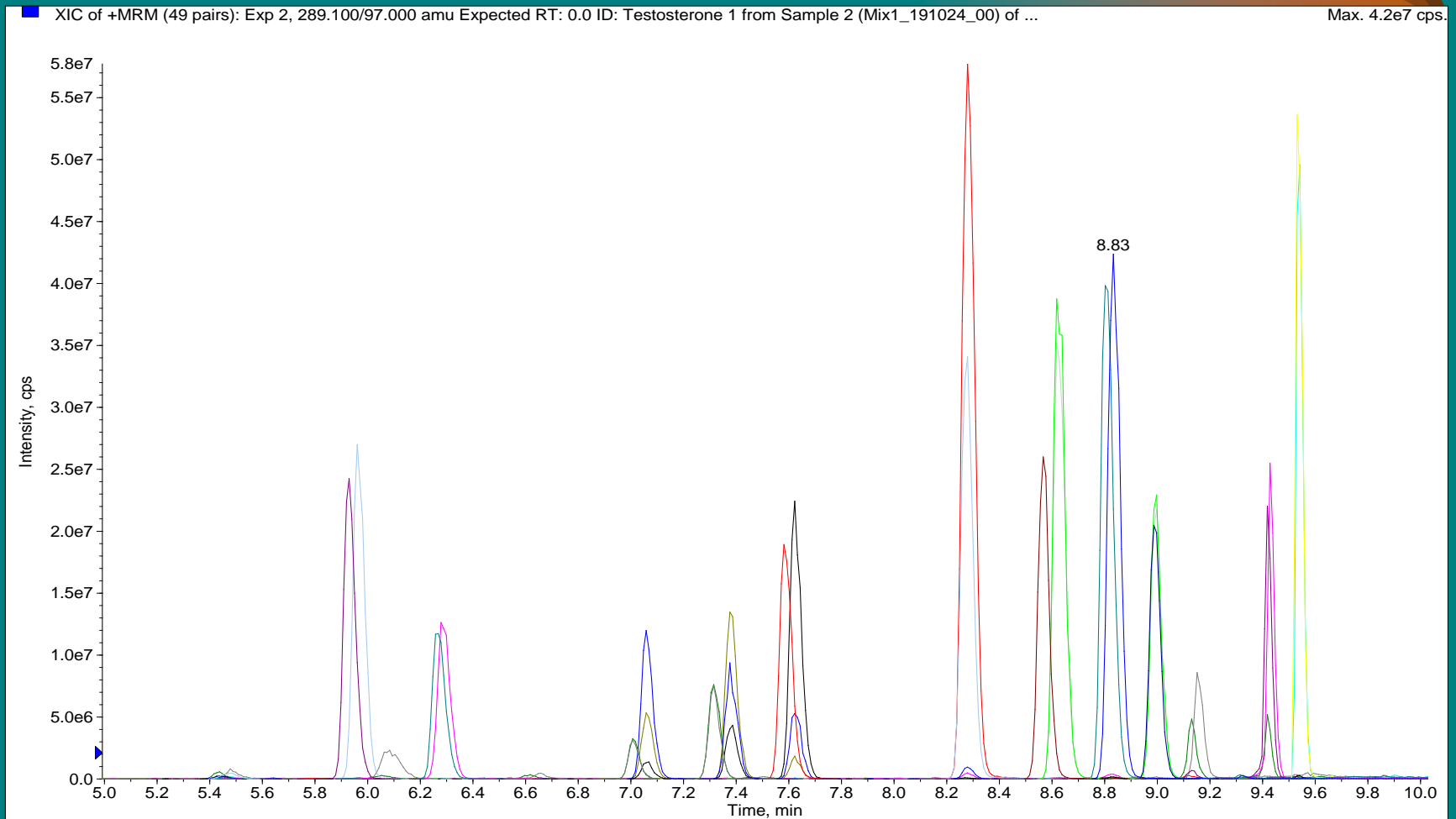
Methylmalonic acidemia (MUT)

Methylmalonic acidemia (Cbl

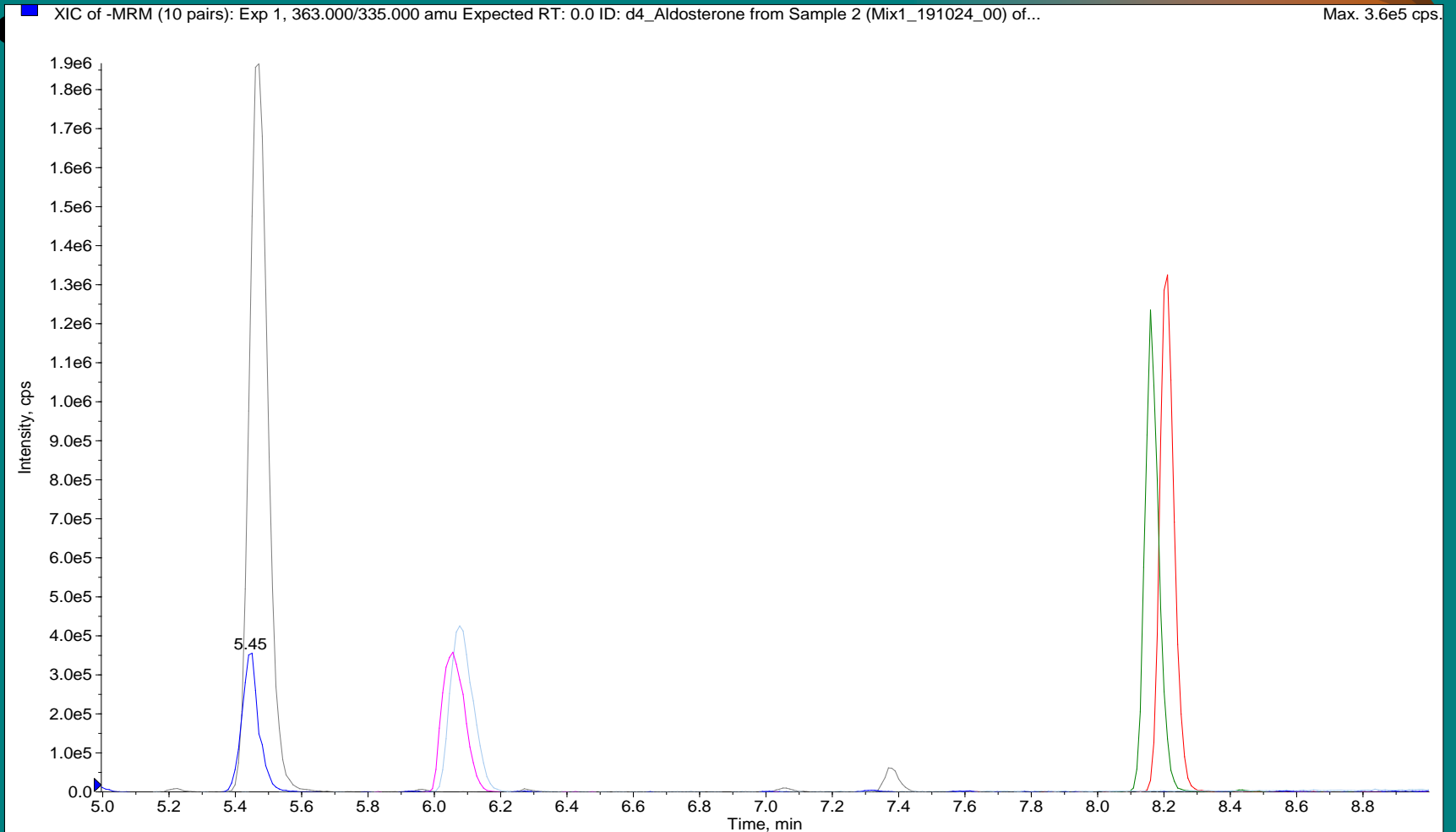
A,B)

Propionic acidemia

# Steroid profiling by LC-MS/MS



# Steroid profiling by LC-MS/MS



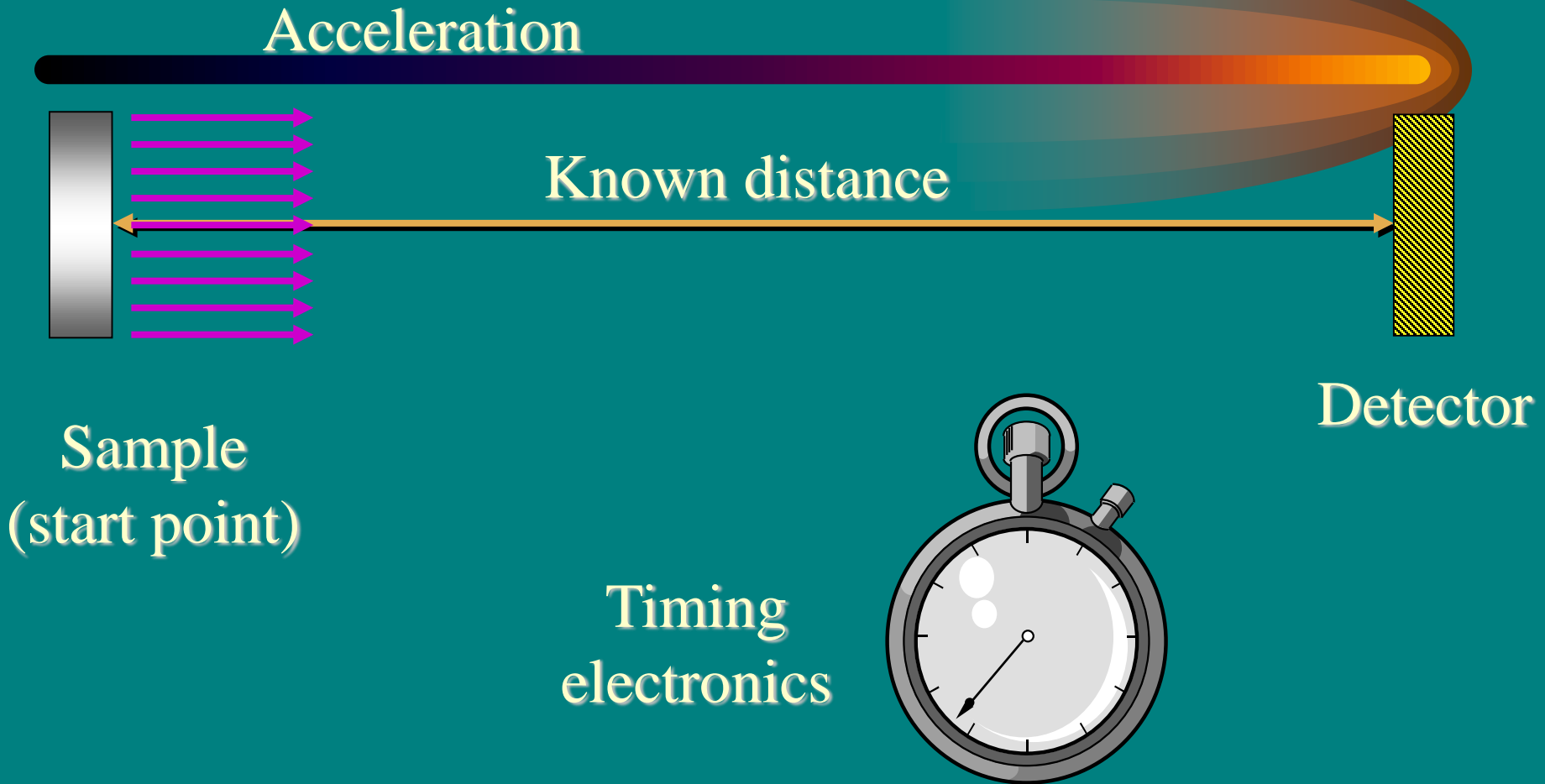
# Direct sample introduction via:



- ❖ **Matrix**
- ❖ **Assisted**
- ❖ **Lazer**
- ❖ **Desorption**
- ❖ **Ionization**



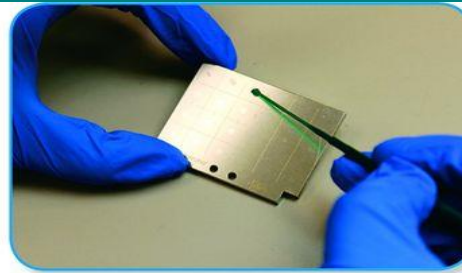
# Hardware of ToF



# MALDI-TOF MS in Medical Microbiology



- ❖ **Traditional methods require 48 – 72 h** and are restricted regarding the number of microorganisms identified
- ❖ **MALDI-TOF MS** detects highly conserved microbial proteins and peptides (mainly ribosomal) and by matching the proteomic fingerprint from the sample to a known database, differentiates thousands of individual pathogens at a species level **in a matter of minutes!**
  - ❖ **Major limitation** – cannot **yet** provide antibiotic susceptibilities
  - ❖ **Future** – identification of microbes **directly from patient samples**



**Add Formic Acid and Matrix and Dry**

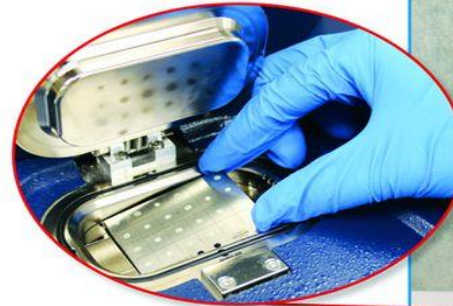


	1	2	3	4	5	6	
A	●	●	●	■	○	○	○
B	○	○	○	○	○	○	○
C	○	○	○	○	○	○	○
D	○	○	○	○	○	○	○

- Not occupied
- Prepared
- Aborted
- Measured
- Zero-line spectrum
- Measured, classified green
- Measured, classified yellow
- Measured, classified red
- Zero-line spectrum, not classified

ID	Poolion	Detected Species	Score
BTS	A1	Escherichia coli	2.375
POS CONT	A2	Candida krusei	2.308
NEG CONT	A3	no peaks found	
5902005629	A4	Candida parapsilosis	2.210

Score	Detected Species	Comment	Link
2.218	Candida parapsilosis ATCC 22019 IMA...		5480
1.859	Candida parapsilosis MY324_09 ERL		5480
1.795	Candida parapsilosis 26 PSB		5480
1.774	Candida parapsilosis DSM 4237 DSM		5480
1.711	Candida parapsilosis DSM 5794T DSM		5480
1.666	Candida parapsilosis DSM 70126 DSM		5480
1.502	Candida parapsilosis ATCC 22019 THL		5480
1.351	Cupressivus necator B479 UFL		49736
1.310	Cupressivus necator B480 UFL		49736
1.300	Candida parapsilosis DSM 70126 DSM		5480



**Mayo Clinic  
Laboratory Services Report  
MICROBIOLOGY**

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Fungal Culture, Routine FINAL 07/25/2012 14:42 MCR

**CANDIDA PARAPSILOSIS Many**  
*Identified by mass spectrometry.*

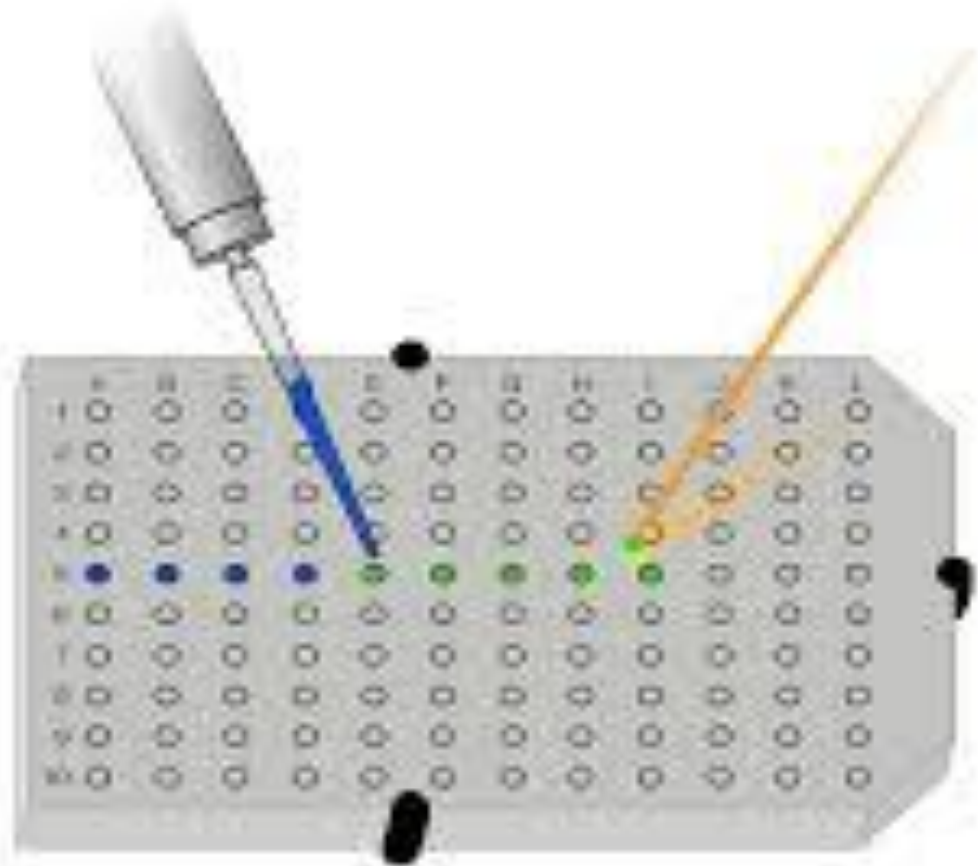
MCR Mayo Clinic Dept. of Laboratory Medicine and Pathology, 200 First Street SW, Rochester, MN 55905 Franklin R. Cockerill, M.D., Lab Director



① Sample culture



② Matrix



③ MALDI-TOF/MS  
sample plate

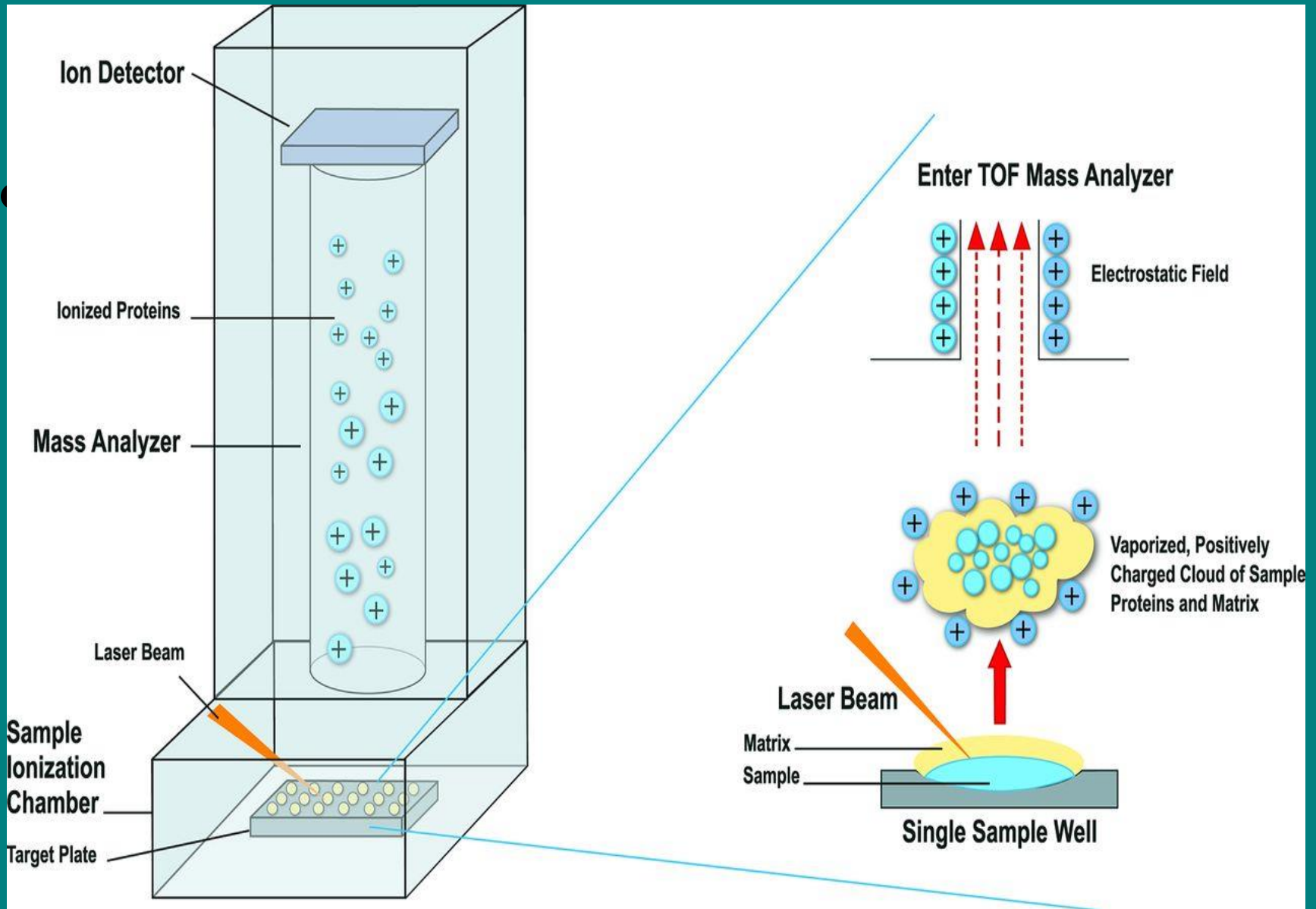
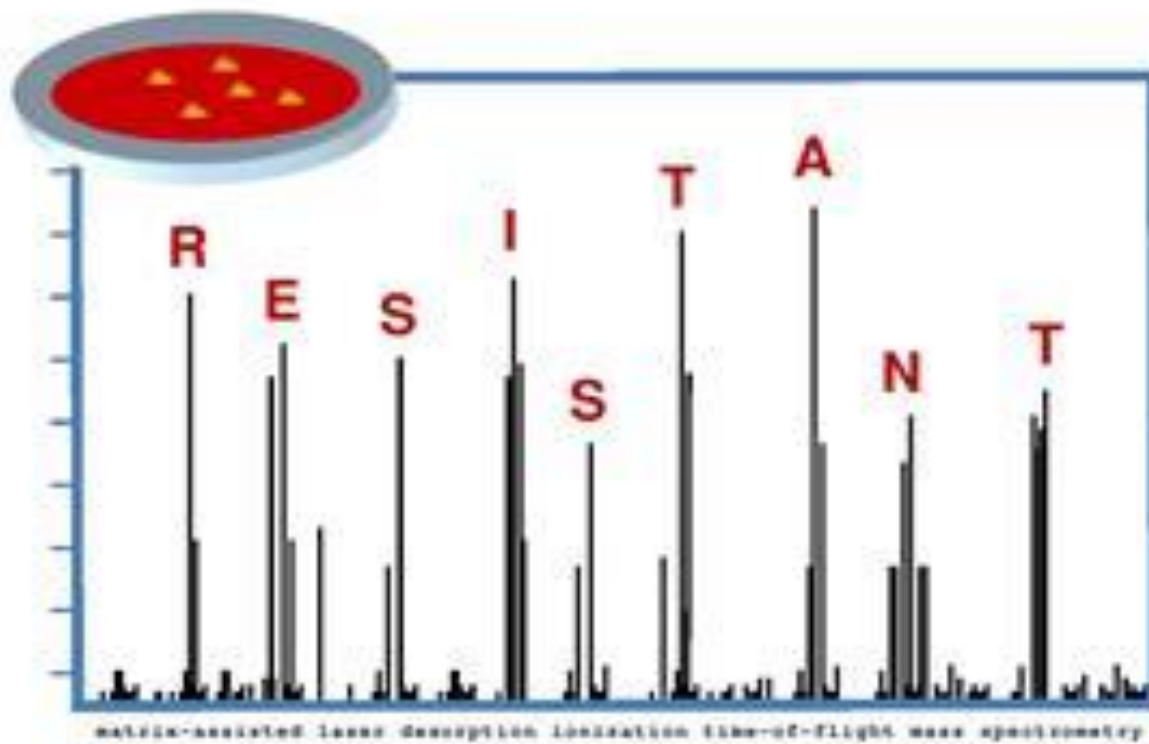


Figure Research Topic



# Orbitrap™ Mass Spectrometers



# Blood-based lipidomic biomarkers for preclinical detection of Alzheimer's disease

- ❖ **Proof-of-concept study** led by H.Federoff, MD, PhD
- ❖ By use of **MS** researchers identified a panel of lipids that **could predict the onset** of cognitive impairment **2-3 years ahead of clinical manifestation**
- ❖ In the **validation** phase they found that a **10-lipid panel predicted the progression** from normal to Alzheimer's disease with a **sensitivity of 90%** and a **specificity of 85%**, but still with **low PPV**

*Cheema A et al, AACCC 2014 Plenary & Nature Medicine, 2014*



# BUT for LC-MS/MS Problems still Exist!

- High financial investment
- Limited capability for automation
- No random access
- Special expertise required
- LDTs, limited availability of IVD certified kits
- Lack of proficiency testing schemes
- Tedious method validation
- Technical support from manufacturers
- Need for harmonization and standardization
- .....



# LC-MS/MS-Kits

## BASIC Kit A

BASIC Kit A consists of:

- Mobile Phase 1
- Mobile Phase 2
- Precipitation Reagent
- Extraction Buffer
- Dilution Buffer 1
- Dilution Buffer 2
- Rinsing Solution
- Reaction vials

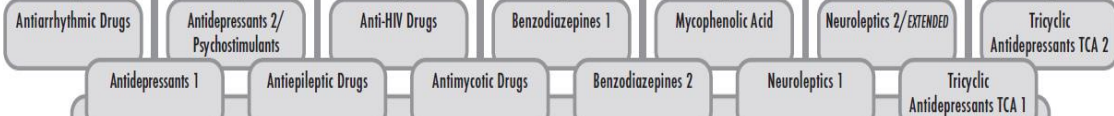
PLUS

## MasterColumn® A

Analytical column:  
equilibrated, with test chromatogram

PLUS

## Single PARAMETER Sets



Components of each PARAMETER Set:  
Multilevel Plasma Calibrator Set (3PLUS1® or 6PLUS1®)  
+ **MassCheck®** Plasma Control, Level I and Level II  
+ Internal Standard

Waters

THE SCIENCE OF WHAT'S POSSIBLE.™

MassTrak™



ClinMass® Komplettkit



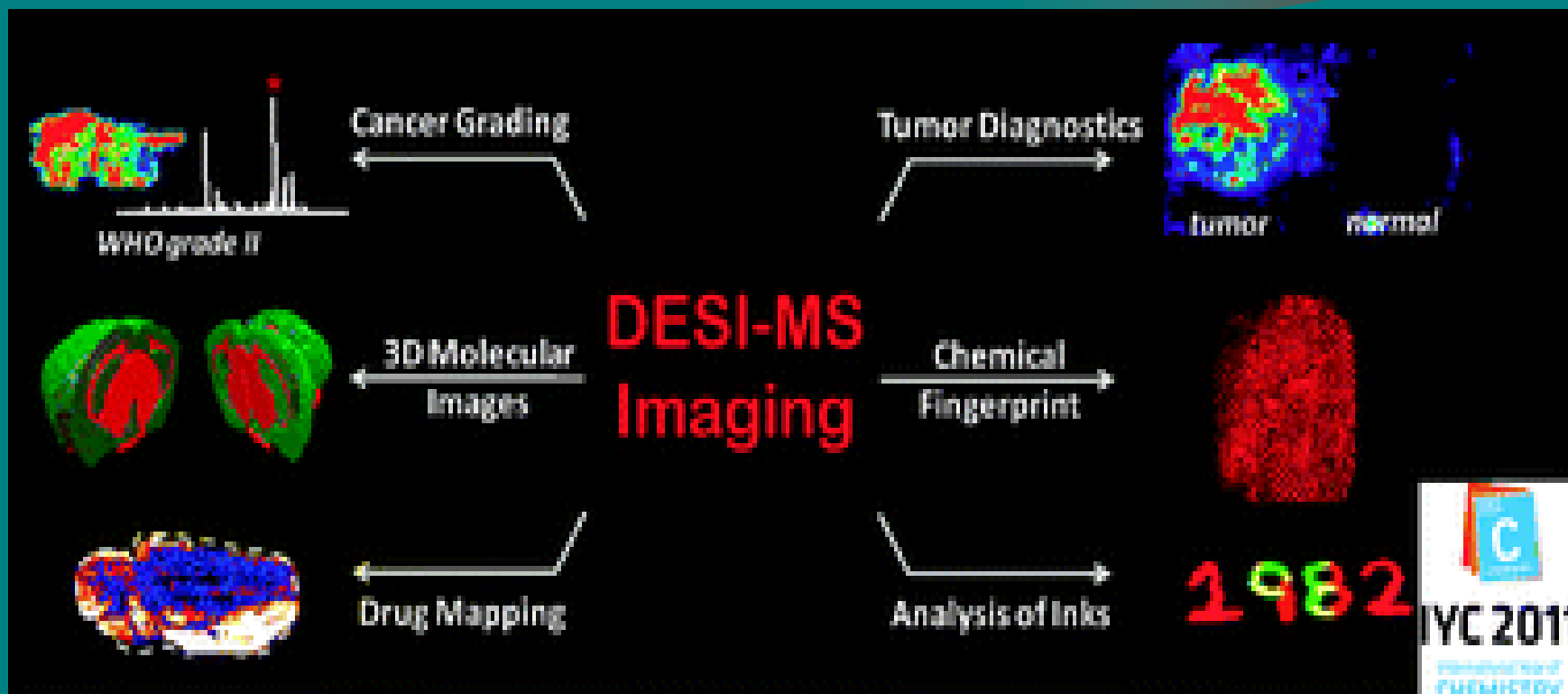
CHROMSYSTEMS

DEVELOPED BY WATERS CORP.

MassTox® Immunosuppressants  
in whole blood - ONEMinute Test



# MS IMAGING



# I-KNIFE MS IMAGING



# Precision Medicine (PM)



❖ **PM** also referred as personalized medicine employs investigation of patient's genotype and phenotype to establish individually tailored disease management

❖ **P4 medicine:**

❖ **Predictive**

❖ **Proactive**

❖ **Participatory**

❖ **Personalized**

# Genotype versus Phenotype

**Phenotype:** Variation in Organism as it Changes during Life Span



**Catherpillar**



**Butterfly**

The caterpillar and butterfly share exactly the same genome  
**BUT** show a completely different phenotype depending  
on their stage of life

GENOME: 20 000

TRANSCRIPTOME: 50 000

PROTEOME: 500 000 – 1 000 000

**METABOLOME**

5 000 0000 – 10 000 000

# Precision Medicine with MS?

MS assays provide the actual patient's phenotype with all the environmental, pharmacological and pathological variables.

The ability to perform panel profiling with simultaneous measurement of active compounds, their precursors and metabolites in a single sample enormously amplifies informative value of results with ultimate improvement of patient care.



# MAS SPECTROMETRY – MEDICAL LABORATORY ANALYSER OF THE NEAR FUTURE?

Mass spectrometry analysis of nucleic acids, proteins, low molecular metabolites provides dramatic advantages

## High throughput:

Analysis of thousands of components in a drop of blood in several minutes >> hundreds of samples in a single batch

## Absolute specificity:

Structural identification of known and unknown components >> direct analysis of PCR products!

## Extreme sensitivity:

Quantitative assays in the femtomolar range with use of microvolumes of sample

# ATHENS 2017



# CONCLUSION

- ❖ Mass spectrometry coupled to adaptive and vigilant bioinformatic pattern-recognition tools will change how disease is detected and monitored
- ❖ Thus a transfer to newer biomarkers and disease signatures will open the era of “omics” diagnostics and personal management in clinical medicine
- ❖ The result will be a nonlinear advance in our understanding of health, aging, disease, prevention, risk assessment, individualization of therapy, monitoring of relapse... *(Petricoin & Liotta, Clin Chem, 2003)*

# Thank you!

## *Questions?*

