

Detection of a multitude of (unknown) components in complex samples

Criteria for identification

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Chromatography Vs MS

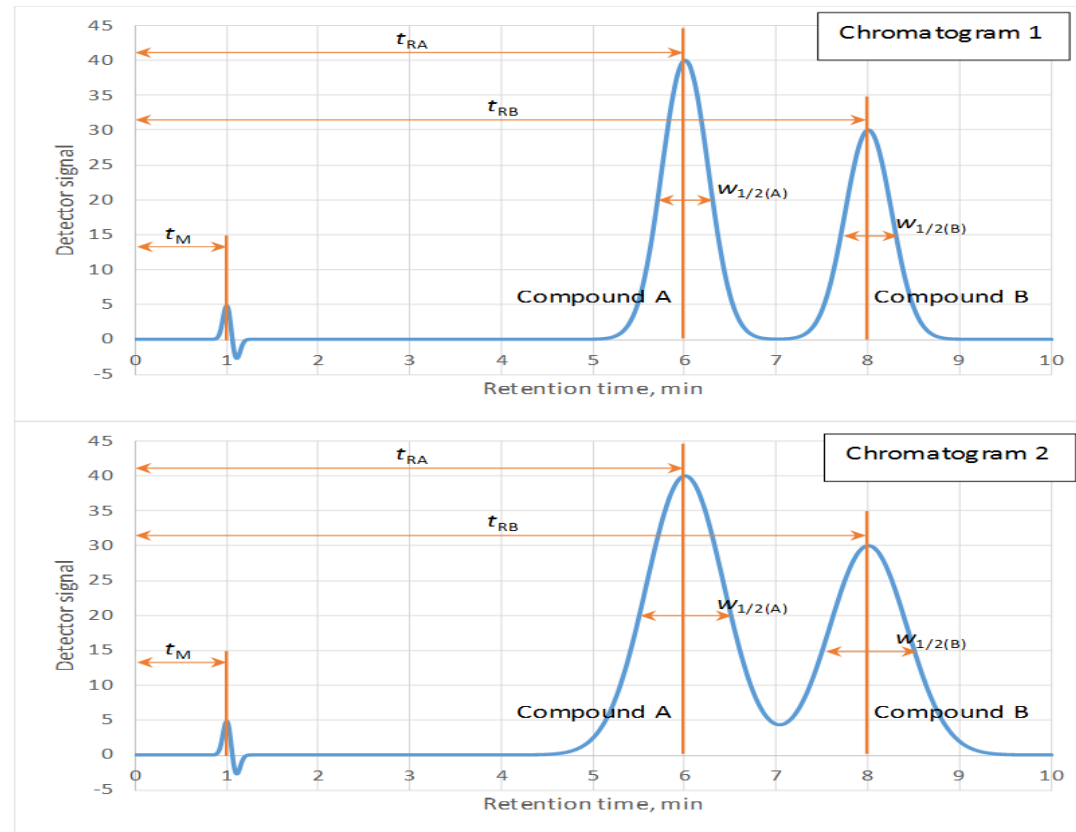
Schools of thought:

1. LC/GC is only an inlet for my mass spectrometer
2. MS is only a detector for my chromatography
3. Efficient use and understanding of both LC/GC and MS
enhances overall performance of the system



What do we want to achieve:

- Throughput
- Selectivity
- Balance



Throughput

Becomes an issue for large sample pool studies 

Increase in throughput results in:

Use of shorter columns

Reduction of selectivity

Use of shorter gradients

Reduction of sensitivity

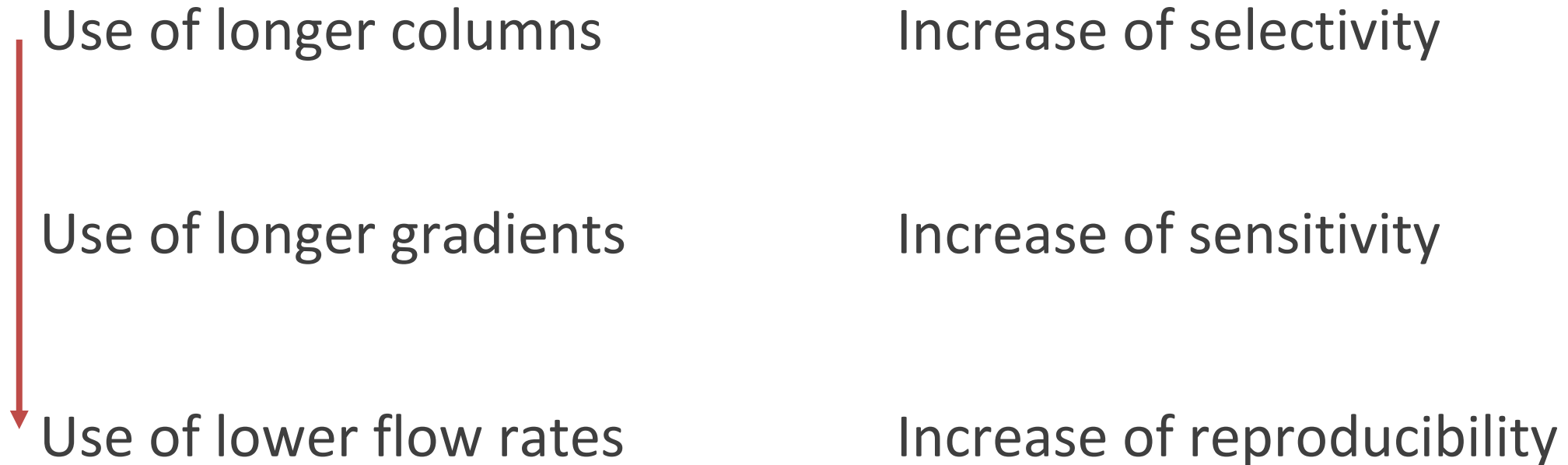
Use of higher flow rates

Reduction of reproducibility

Selectivity

Becomes an issue for complex samples 

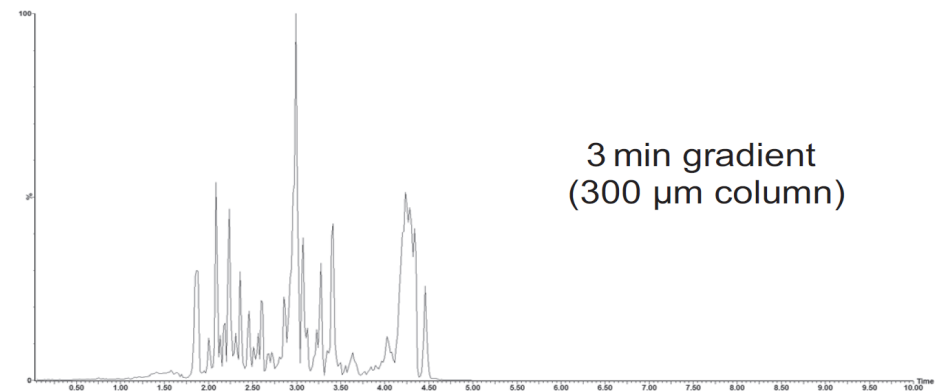
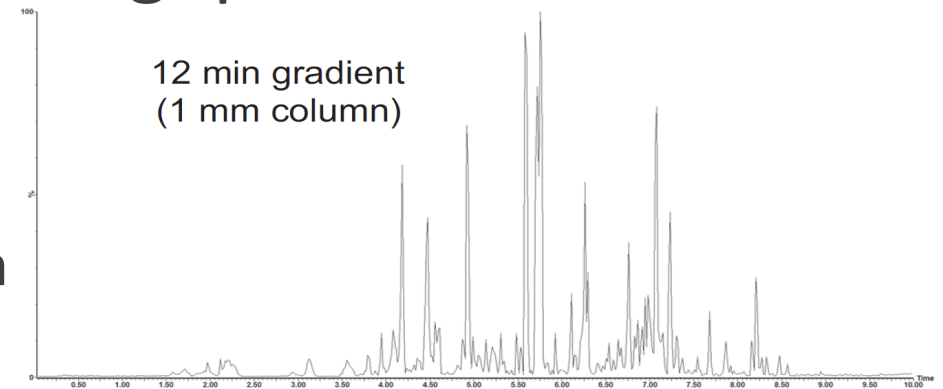
Increase in selectivity results in:



Large sample pools of high complexity

Selectivity and Throughput

- Use of narrower columns: 2.1 > 1 > 0.3 mm
- Use of shorter columns: 150 > 100 > 50 mm
- Use of columns with >2 μm particle size
- Use of columns at near pressure limit
- Use of LC at near pressure limit



Lee et al, 2017. Milford

Challenges of complex sample analysis:

1. Sample complexity
2. Narrow peaks
3. Reproducibility
4. General coelution
5. Isobaric coelution

Data acquisition strategies
Acquired data quality

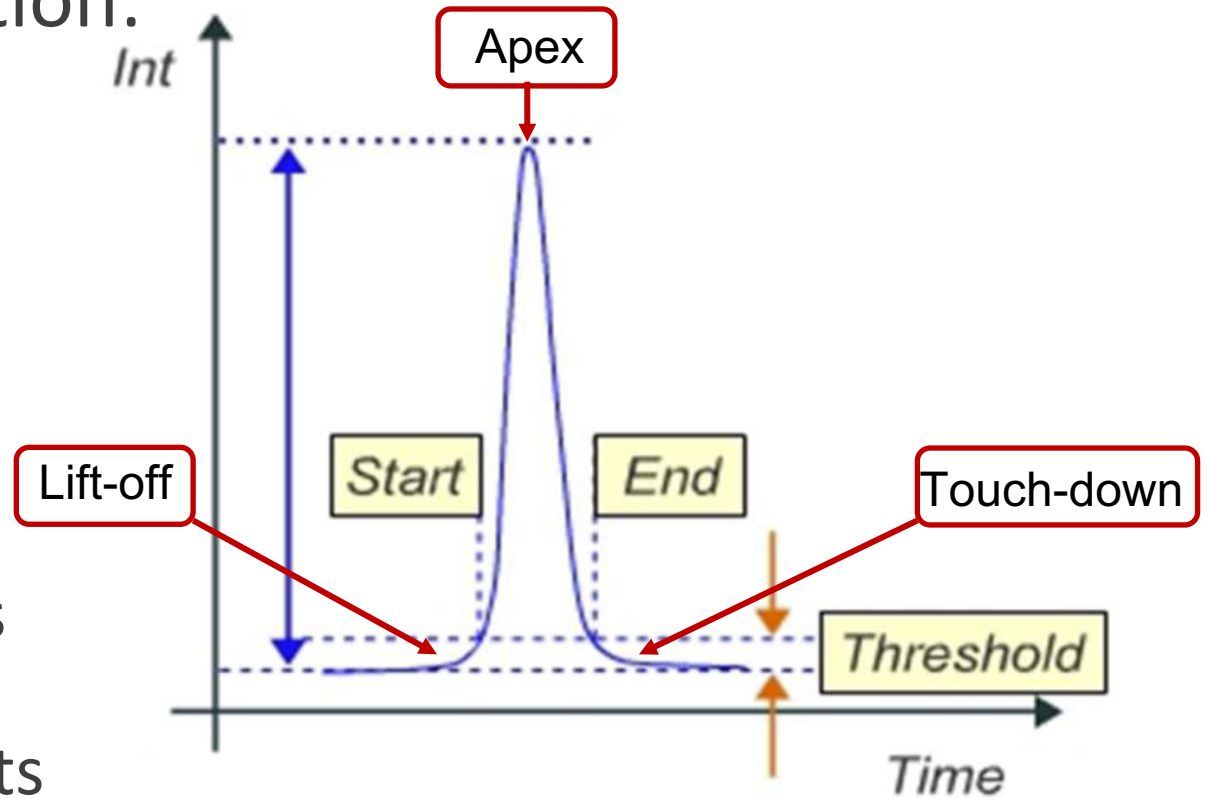
Importance of Instrumentation

Peak detection and integration:

1. Lift-off
2. Apex
3. Touch-down

Qualitative 6+ data points

Quantitative 10+ data points



Data acquisition rate becomes highly important

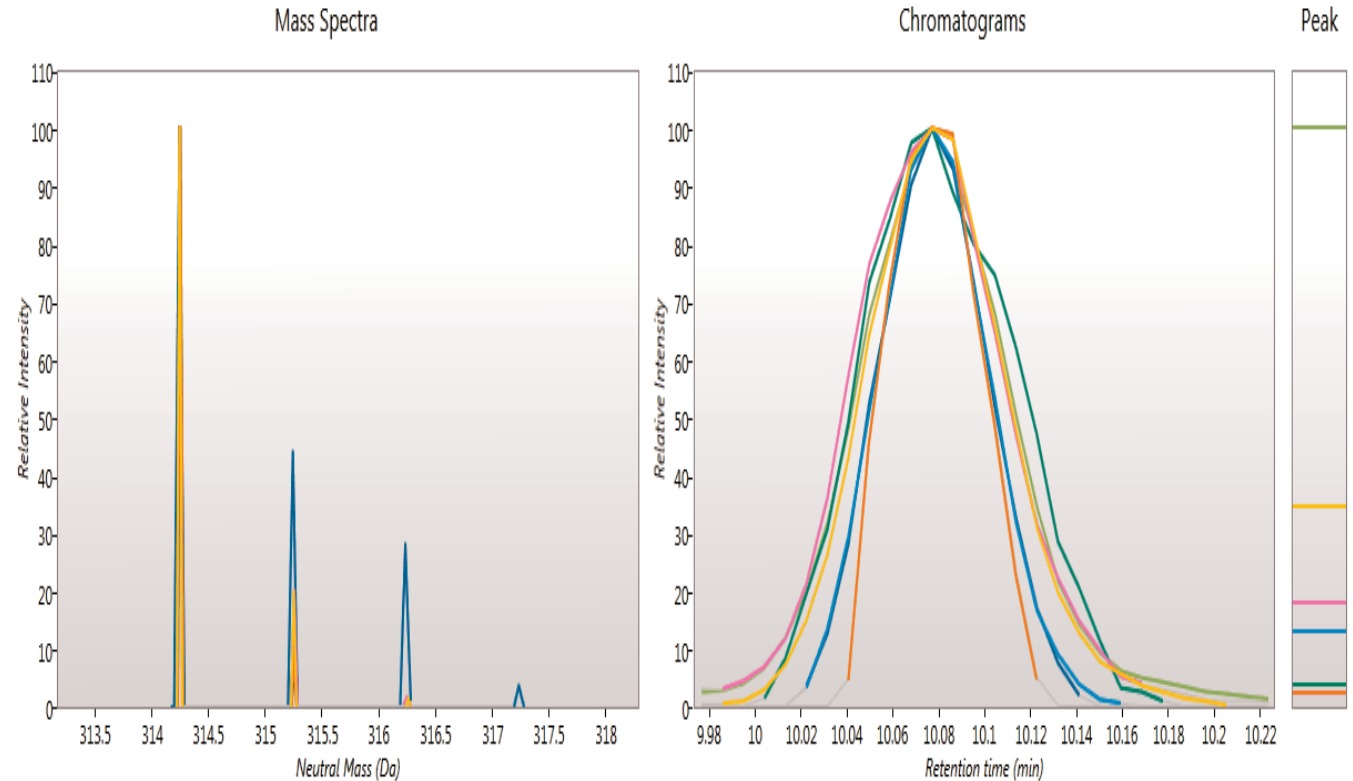
Mass accuracy

Mass resolution

Isotopic distribution

Peak deconvolution

Speed/Sensitivity



DDA

Data Dependent Acquisition

DIA

Data Independent Acquisition

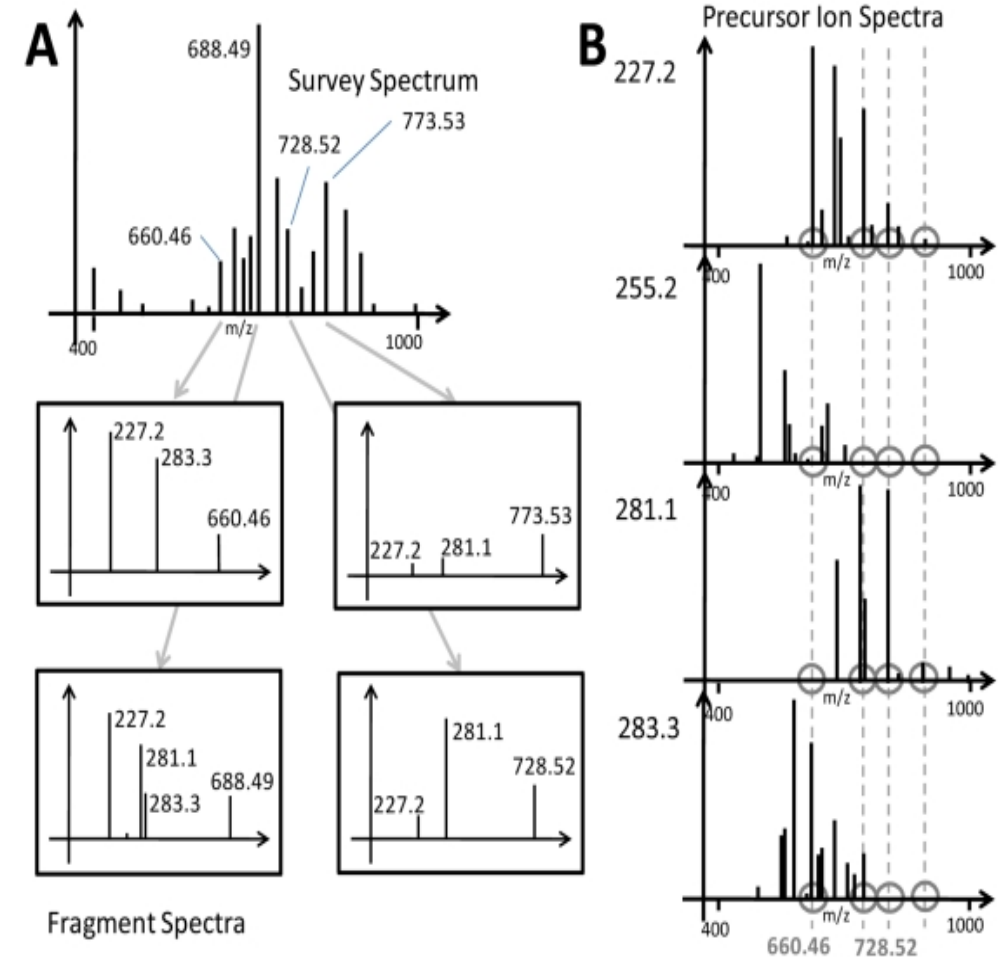
eDIA

Quadrupole-enhanced DIA

Ion mobility-enhanced DIA

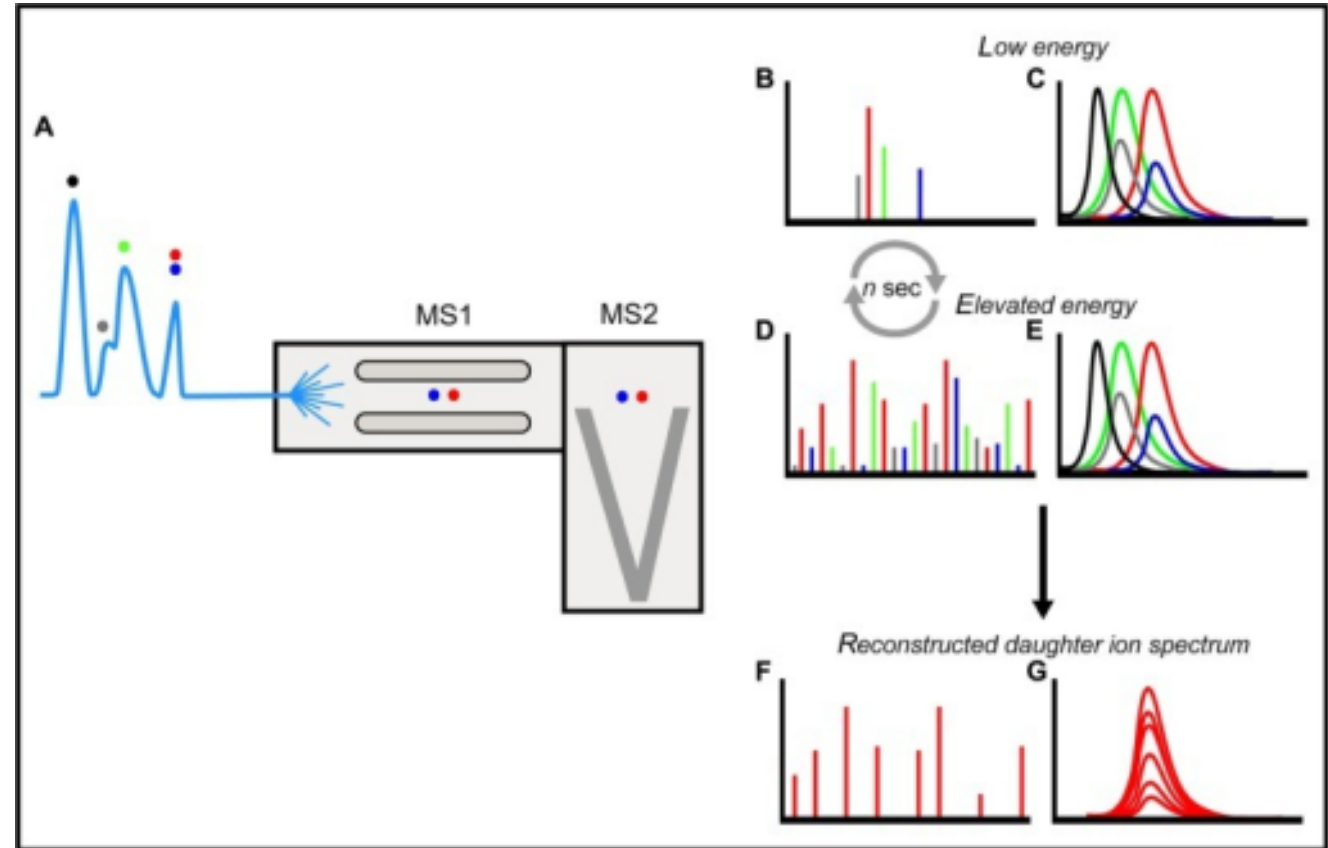
DDA

1. MS scan
2. Precursor selection
3. Precursor isolation on Q
4. Precursor fragmentation
5. Fragment scan



https://www.researchgate.net/profile/Julio_Sampaio/publication/221772729/figure/fig2/AS:202910513274881@1425389044734/The-scheme-explains-how-data-dependent-acquisition-of-full-MS-MS-spectra-DDA-driven.png

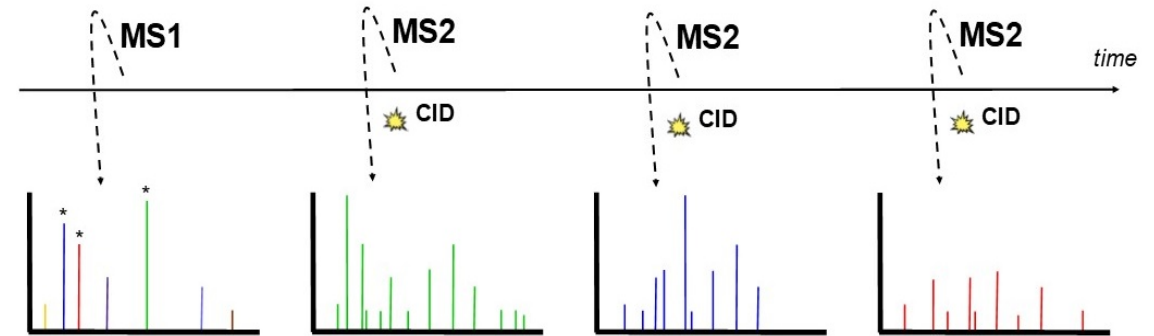
1. MS scan
2. Fragmentation
3. Fragment scan



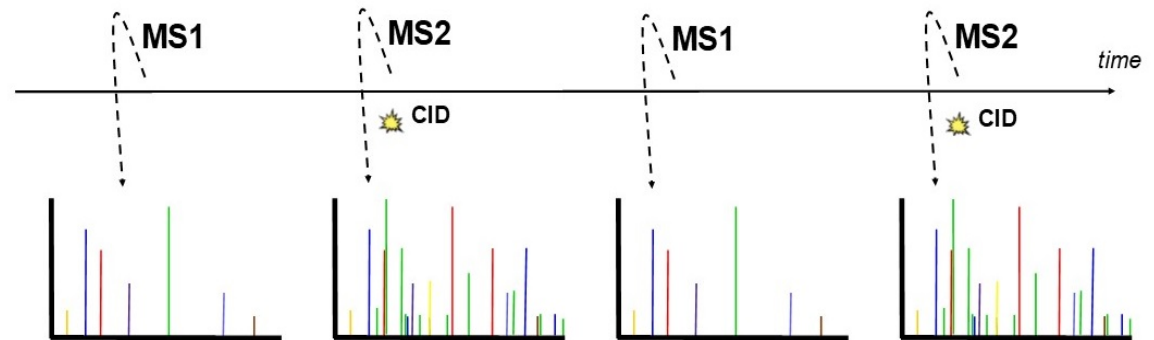
DDA vs DIA

	Pros	Cons
DDA	Higher specificity	Slow
DIA	No missed data	Lower specificity

DDA



DIA

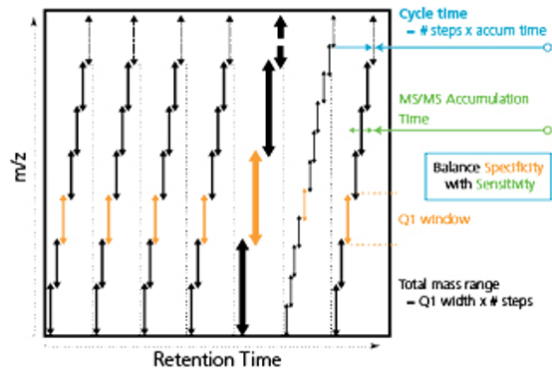


https://2.bp.blogspot.com/E6LAzAMWZFw/WtYVj6BUmKI/AAAAAAAAAC0/PmQZjuLtzaoqd0iiNv1SAmfcYHFMI_3QCEwYBhgL/s1600/dda-vs-dia.jpg

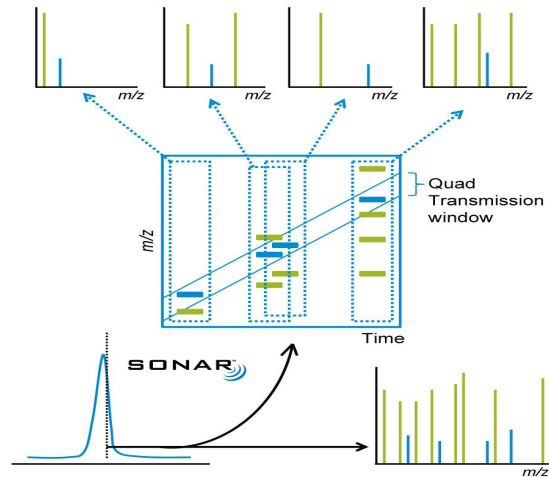
Enhanced-DIA

Quadrupole-eDIA

SWATH



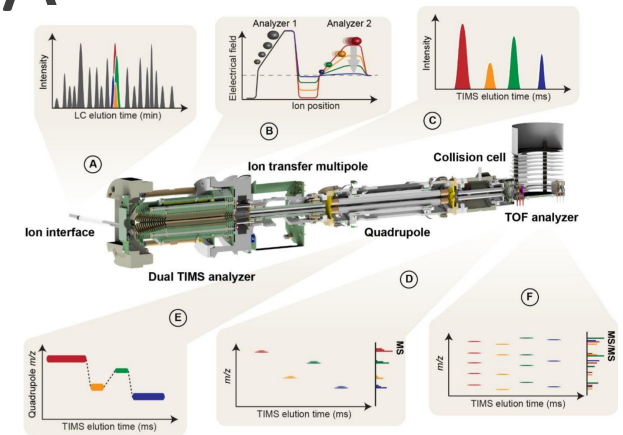
SONAR



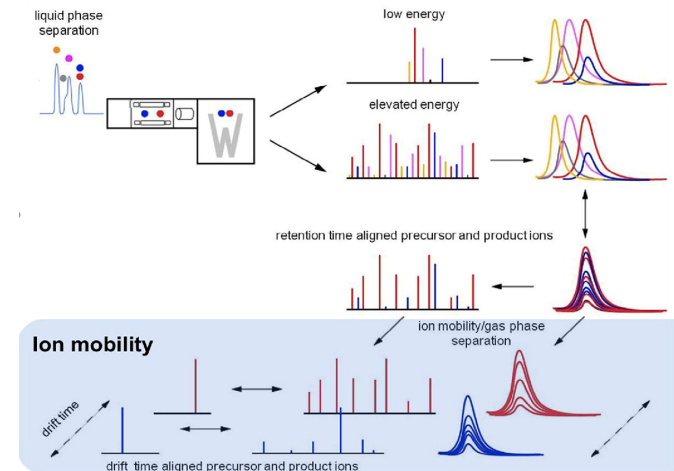
https://sciex.com/community/Asset/00003575/SWATH-Blog-Graphics_Image01.jpg
http://www.waters.com/webassets/cms/category/media/content_blocks/wg_sonar_2.jpg

IMS-eDIA

TIMS



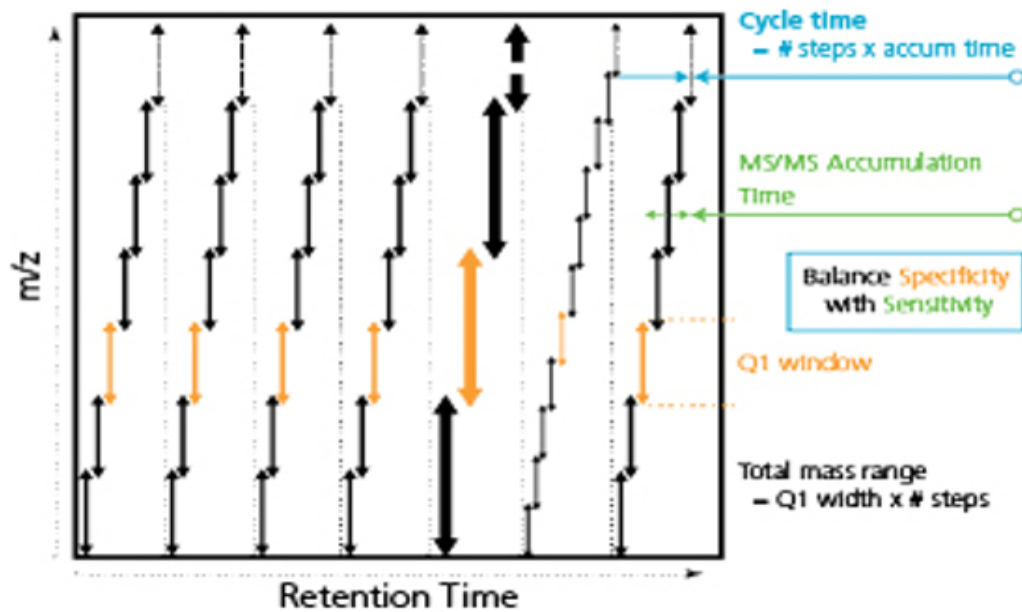
HDMSe



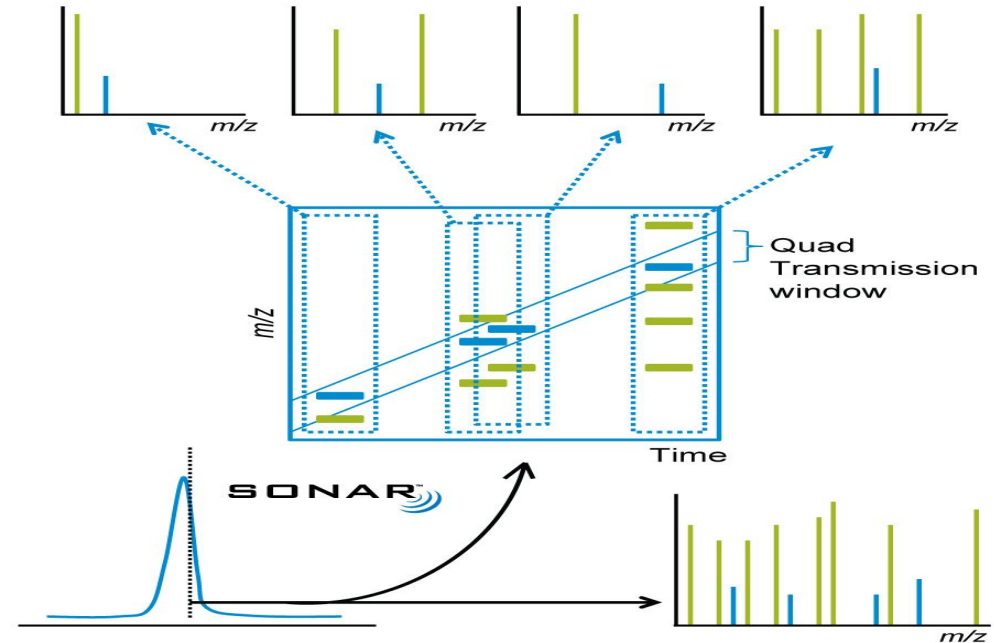
<https://www.biorxiv.org/content/biorxiv/early/2018/06/01/336743.full.pdf>
http://www.waters.com/waters/en_PR/TriWave/nav.htm?locale=en_PR&cid=134663660

Quadrupole-DIA

SWATH



SONAR

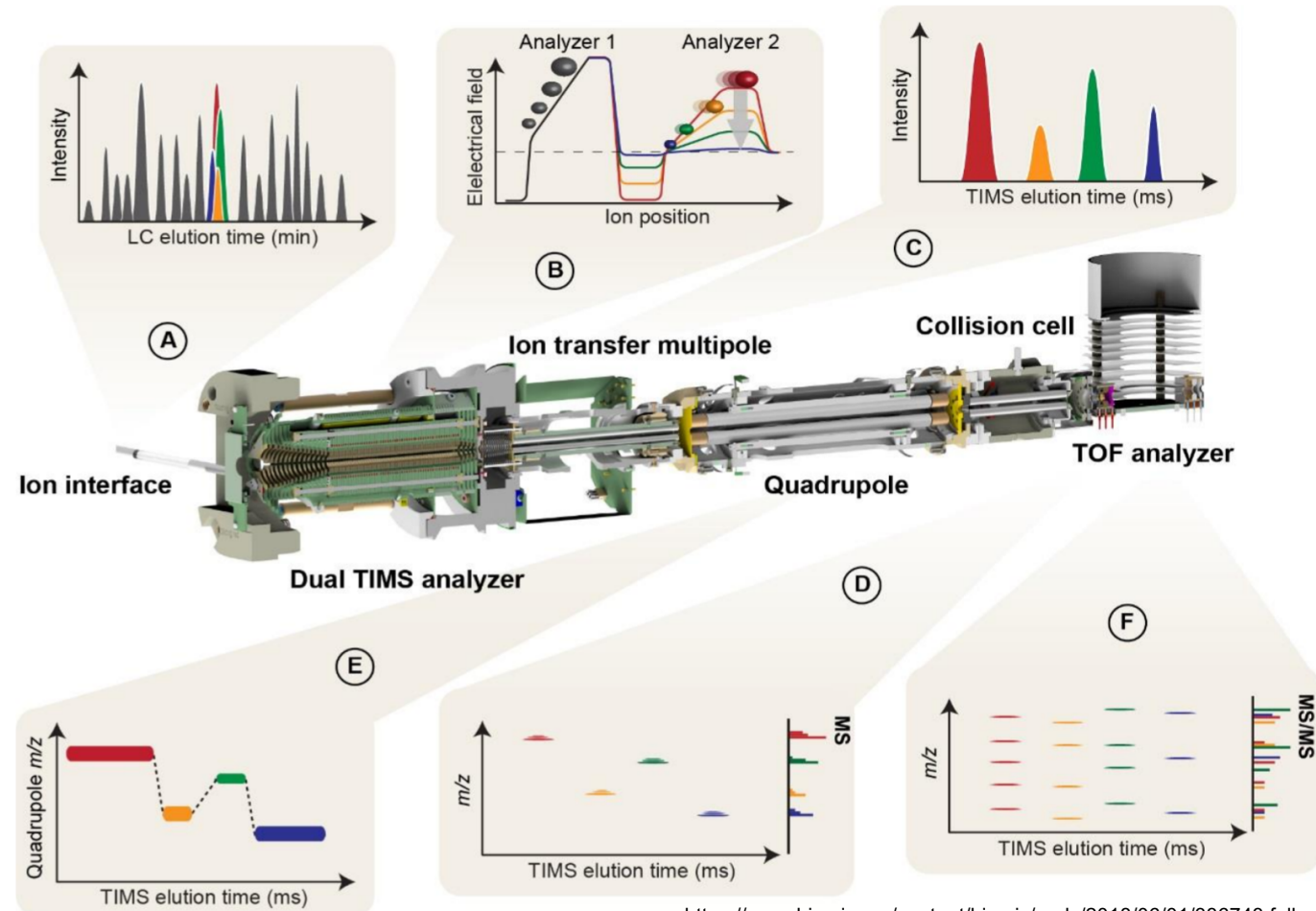


- Active switching/scanning quadrupole used for precursor isolation in a defined m/z range
- Similar to DDA in selectivity
- Unlike DDA, does not lose as much data

TIMS with PACEF

Trapped Ion Mobility Separation with Parallel Accumulation Serial Fragmentation

- Precursor trapping
- Ion mobility separation
- DIA with CE ramp

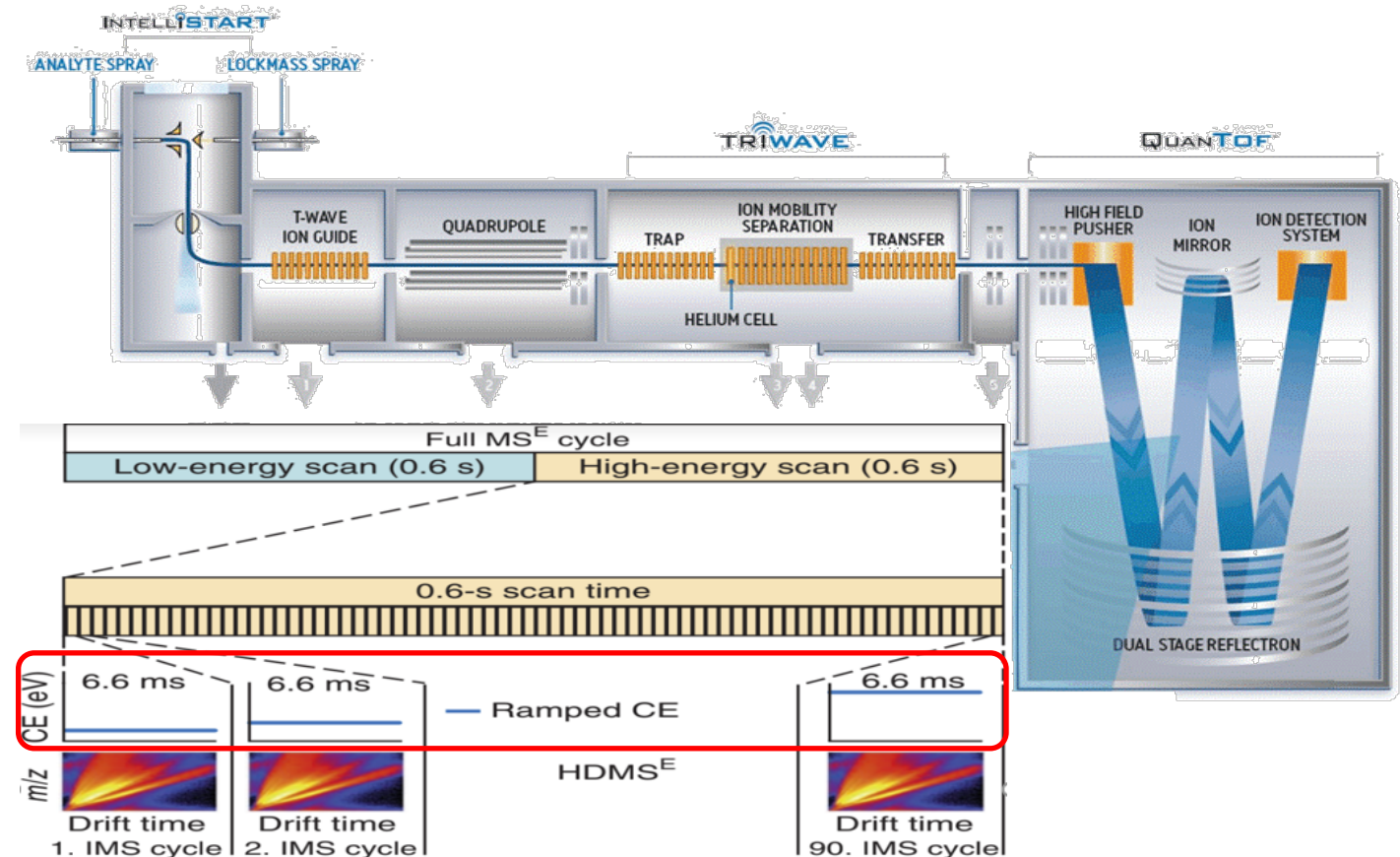


<https://www.biorxiv.org/content/biorxiv/early/2018/06/01/336743.full.pdf>

HDMSe

High Definition MSe

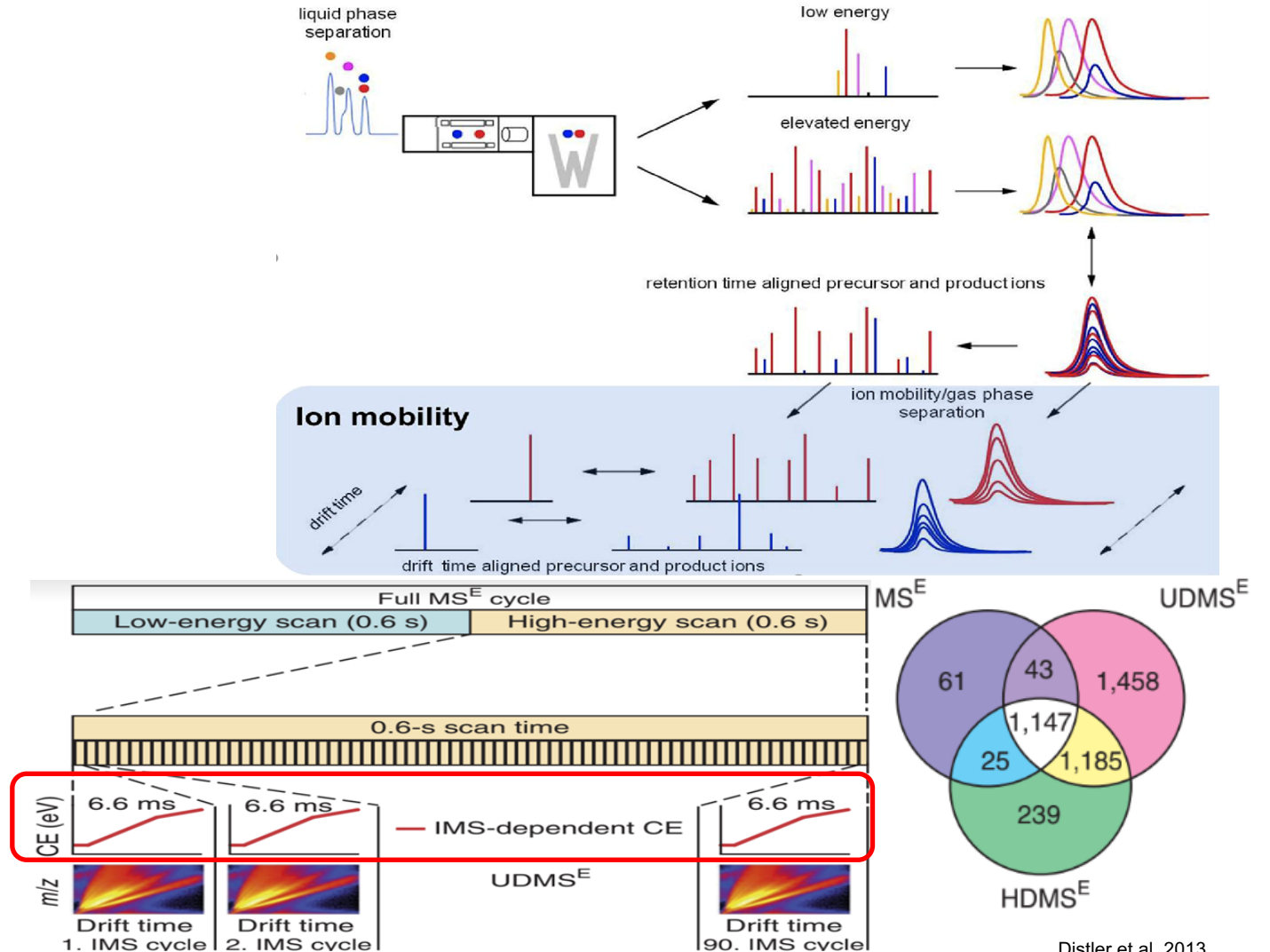
- Precursor trapping
- Ion mobility separation
- CE ramp per MS cycle
- Pre-/Post-IMS fragmentation



UDMS^E

Ultra Definition MS^E

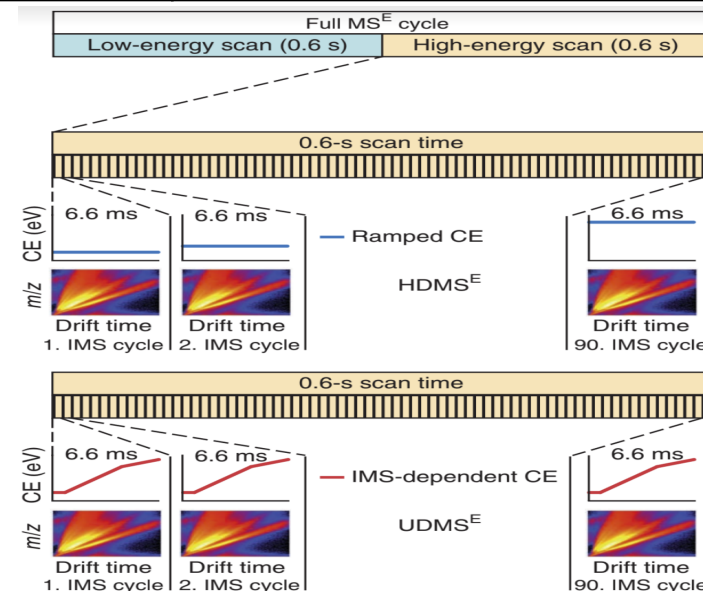
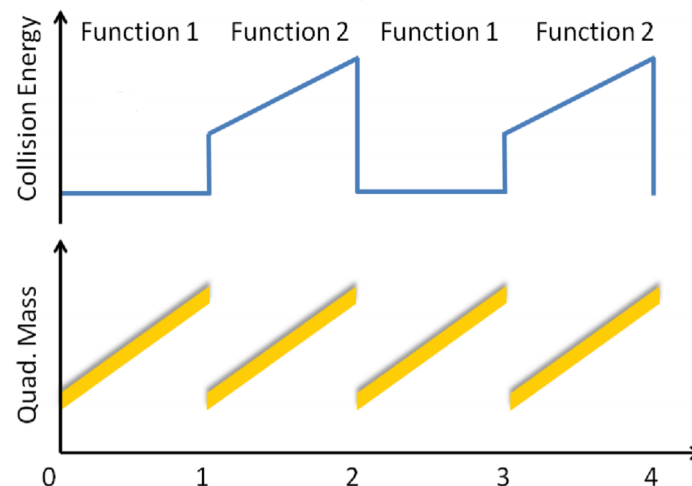
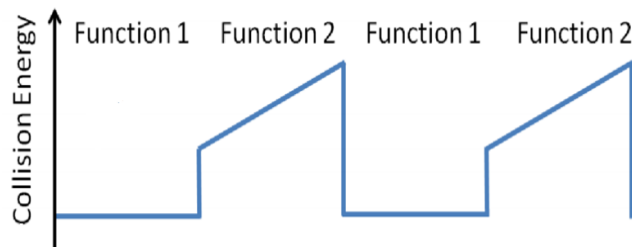
- Precursor trapping
- Ion mobility separation
- CE ramp per IMS cycle
- Pre-/Post-IMS fragmentation



Distler et al, 2013

DIA vs eDIA

	DIA	Quad-eDIA	IMS-eDIA
Sensitivity	High	Low	High
Specificity	Low	High	High



Distler et al, 2013

http://www.waters.com/webassets/cms/library/docs/2016imsc_vissers_system_level_omics.pdf

MS based criteria for ID

1. Mass

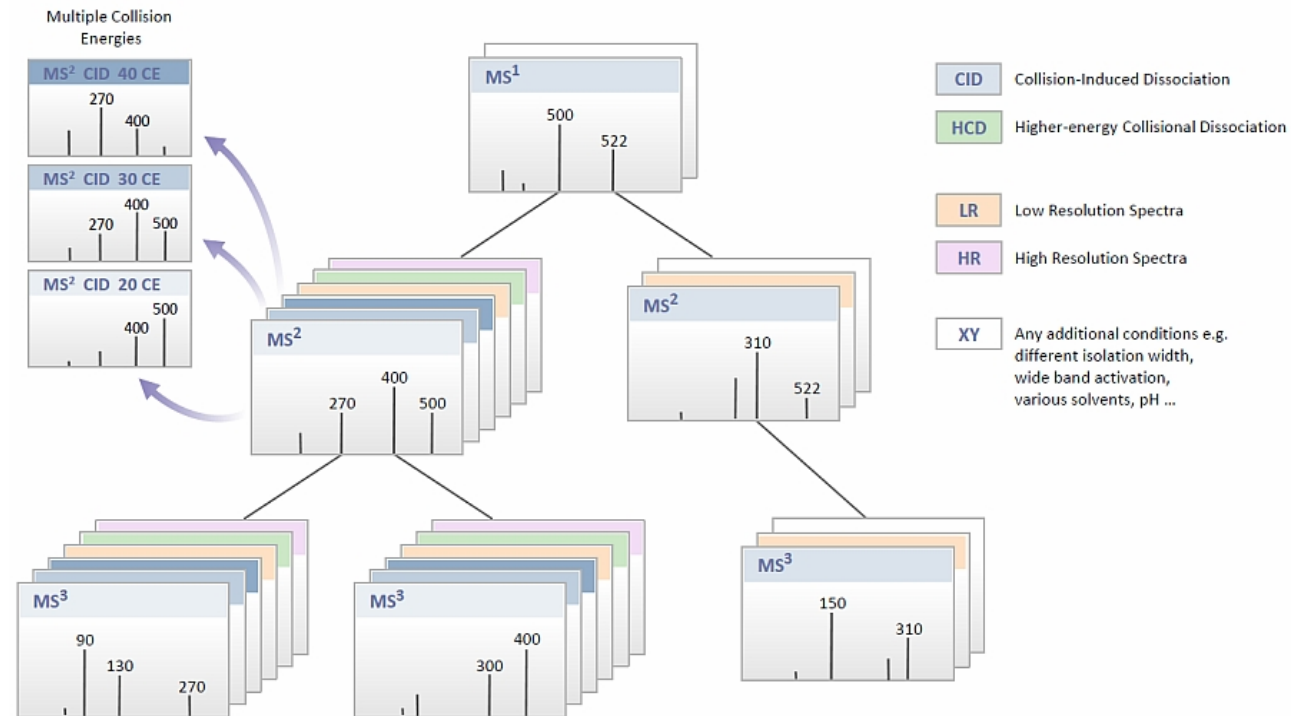
- Accurate
- Resolved
- Peak shape

2. Isotopic distribution

- Isotopes
- Adducts

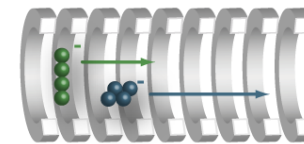
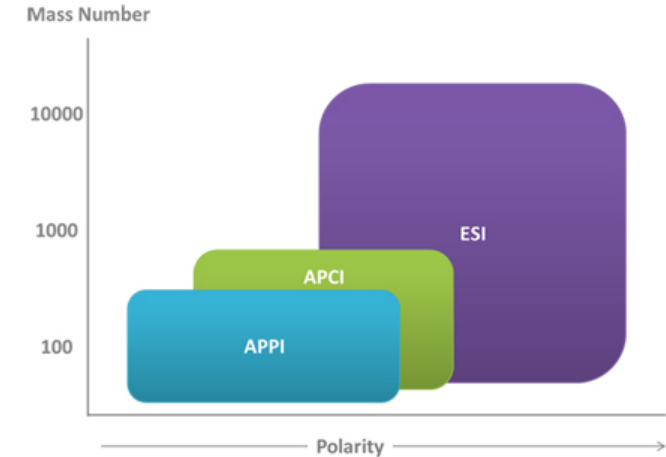
3. Fragmentation spectrum

- Fragmentation mode
- Accurate
- Resolved

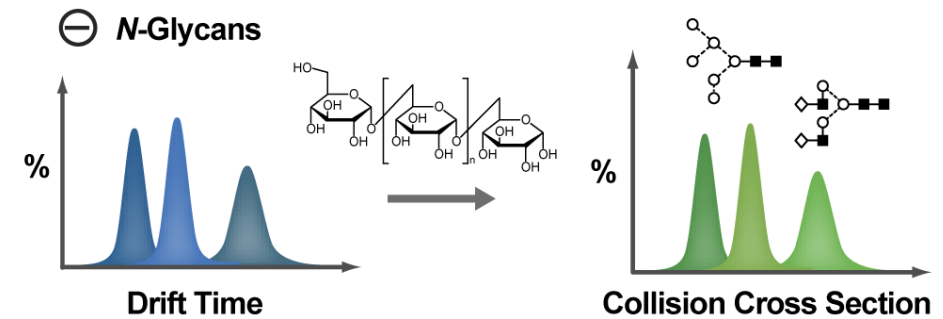


Orthogonal criteria for ID

1. Ionisation compatibility
 - a) Ionisation mode
 - b) Ionisation polarity
2. Ion mobility separation
 - a) Drift time
 - b) Collision Cross Section (CCS)
 - ❖ DMS/FAIMS filter
3. Chromatographic separation
 - a) Retention profile
 - b) Elution profile



TW IM-MS Separation and Dextran Calibration



<https://www.chromacademy.com/images/quick-guide/2016-Oct/LCMS-Ionisation-Modes.jpg>
http://www.fhi-berlin.mpg.de/mp/helden/uploads/Main/neg_CCS_TOC.png

Collision Cross Section (CCS):

- 1.5% difference in CCS is sufficient for separation
- Useful for identification and quantification

	1	2	3	Av CCS	%RSD
Butyric Acid	147.11	147.42	147.42	147.32	0.12
Isobutyric Acid	149.35	149.02	149.11	149.16	0.11
Valeric Acid	160.89	160.95	160.68	160.84	0.09
Isovaleric Acid	160.38	160.30	160.17	160.28	0.07

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