



**UNESCO/IUPAC Postgraduate Course in
Polymer Science**

Lecture:

**Molecular weight and dimensions of
polymers and their assemblies**

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Polymers

M gives independent information

M affects

properties such as density, degree of crystallization, Young modulus, melt viscosity, glass transition temperature etc

Consequently, M affects application use and processing methods

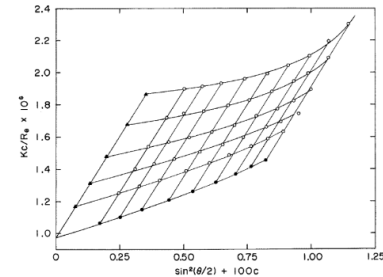
Classical methods for determination of molecular weight of polymers (see Polymer solutions in a nutshell)

Osmotic pressure (absolute, $5 \cdot 10^3$ - 10^6)

$$\Pi_{c \rightarrow 0} = RT \frac{c}{M}$$

Static Light scattering (absolute, 10^4 - 10^7)

$$\left(\frac{Kc}{R_\theta} \right)_{c \rightarrow 0} = \frac{1}{M} \left[1 + \frac{16\pi^2 n^2}{3\lambda} \langle R_g^2 \rangle \sin^2 \left(\frac{\theta}{2} \right) + \dots \right]$$



Zimm plot (2 D plot for 2 independent variables) $\Rightarrow M, A_2, R_g$

Intrinsic viscosity (relative, $>10^3$)

$$[\eta] = KM^a \quad (\text{Mark-Houwink Eq.})$$

And many more - analytical ultracentrifugation, ebullioscopy, end-group analysis, vapor pressure osmometry,

Polymer sample (usually) contains molecules of various polymerization degree

Experimental methods give us only some average of the molecular weight

$$\left(\frac{Y}{c}\right)_{c \rightarrow 0} = KM^a \quad Y = \sum_i Y_i \quad cKM^a = \sum_i c_i KM_i^a \quad \bar{M} = \left(\sum_i w_i M_i^a\right)^{\frac{1}{a}}$$

$$a_{\Pi} = -1 \quad a_{LS} = 1 \quad a_{\eta} = 0.5 - 0.8 \text{ flexible} > 0.8 \text{ rigid}$$

Averages with integer a can be defined as the ratio of moments around the origin

$$M_n = \left(\sum_i w_i M_i^{-1}\right)^{-1} = \frac{\sum_i w_i M_i^0}{\sum_i w_i M_i^{-1}}$$

$$M_w = \sum_i w_i M_i = \frac{\sum_i w_i M_i^1}{\sum_i w_i M_i^0}$$

$$M_z = \frac{\sum_i w_i M_i^2}{\sum_i w_i M_i^1}$$

number-average

weight-average

z-average mol. weight

$$M_n = \left(\sum_i x_i M_i\right)^{-1} = \frac{\sum_i x_i M_i^1}{\sum_i x_i M_i^0}$$

$$M_w = \frac{\sum_i x_i M_i^2}{\sum_i x_i M_i^1}$$

$$M_z = \frac{\sum_i x_i M_i^3}{\sum_i x_i M_i^2}$$

w weight fraction, x molar fraction

Combined averages give only partial information on the sample molecular weight non-uniformity : polydispersity index M_w/M_n

Full information:

relative amount of each polymerization degree – a distribution function

number DF - x_i , weight (mass) DF – w_i

cumulative $\sum_{j=1}^i x_j$ $\sum_{j=1}^i w_j$ discrete vs continuous DF

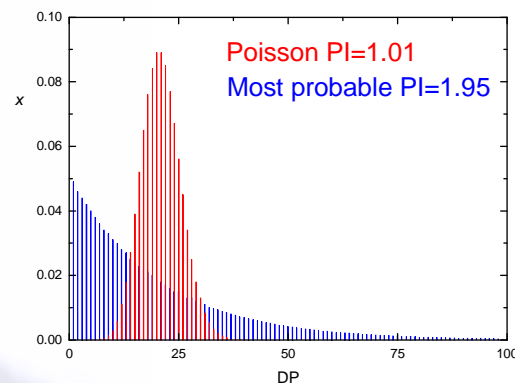
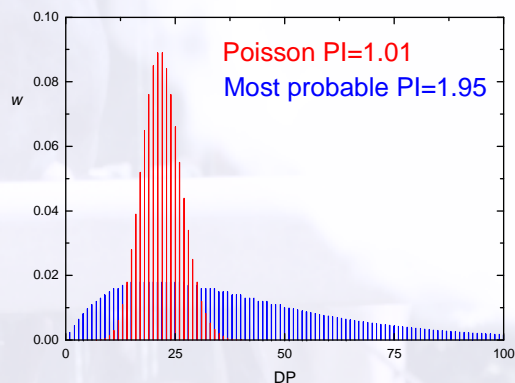
cumulative vs differential DF $\text{difDF} = \frac{dcumDF}{dM}$

Mathematically defined DF

Discrete DF

Poisson $w_P = \frac{P e^{-a} a^{P-1}}{(a+1)(P-1)!}$

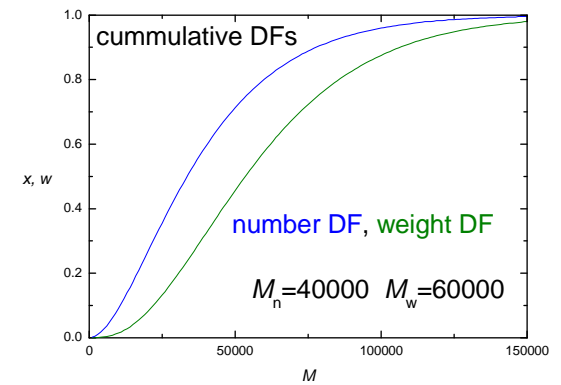
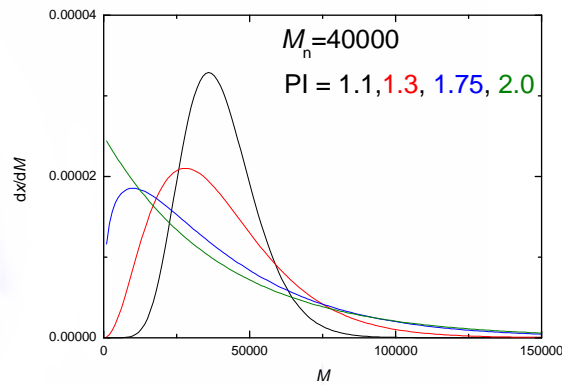
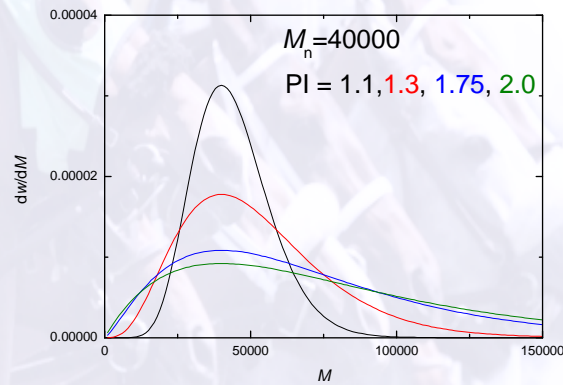
most-probable $w_P = a^2 P(1-a)^{P-1}$



Continuous DF

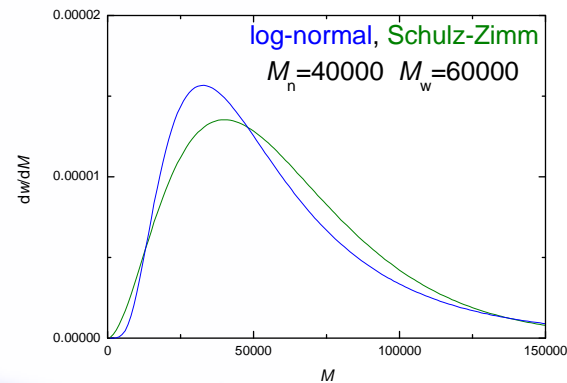
Schulz-Zimm

$$dw = \frac{a^{b+1}}{\Gamma(b+1)} M^b \exp(-aM) dM$$

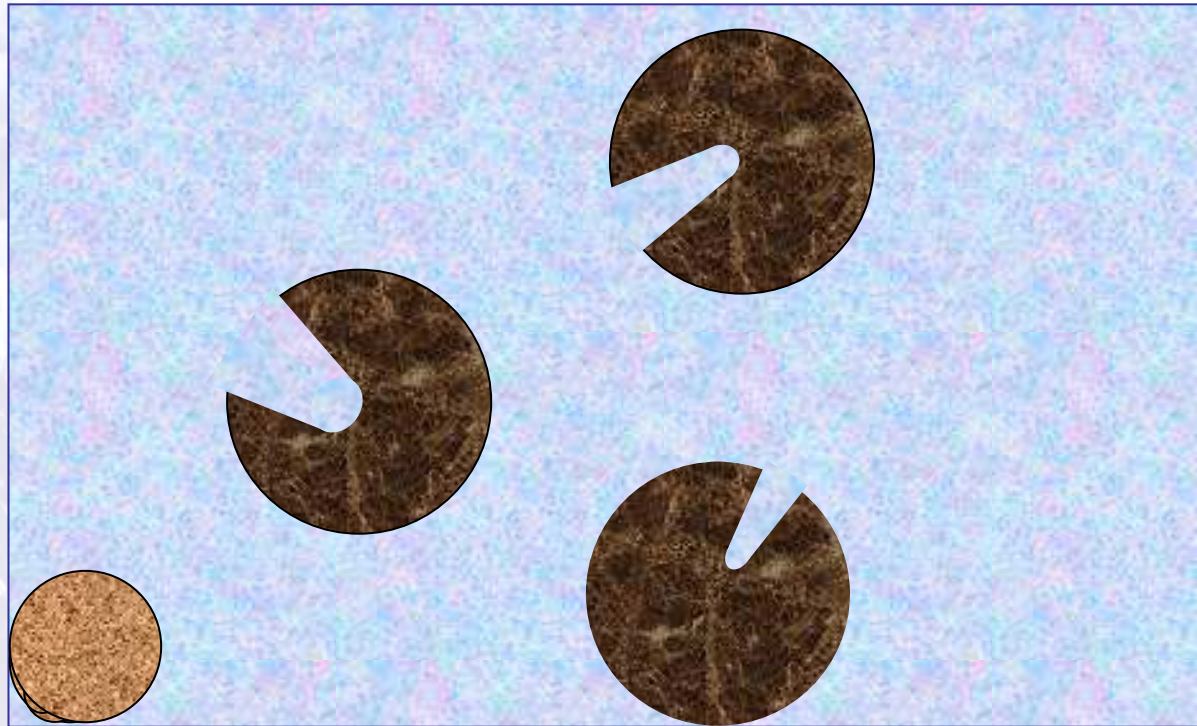


logarithmic normal

$$dw = \frac{1}{a\sqrt{\pi M}} \exp\left(-\frac{1}{a^2} \ln^2 \frac{M}{b}\right) dM$$



Principle of Size Exclusion Chromatography

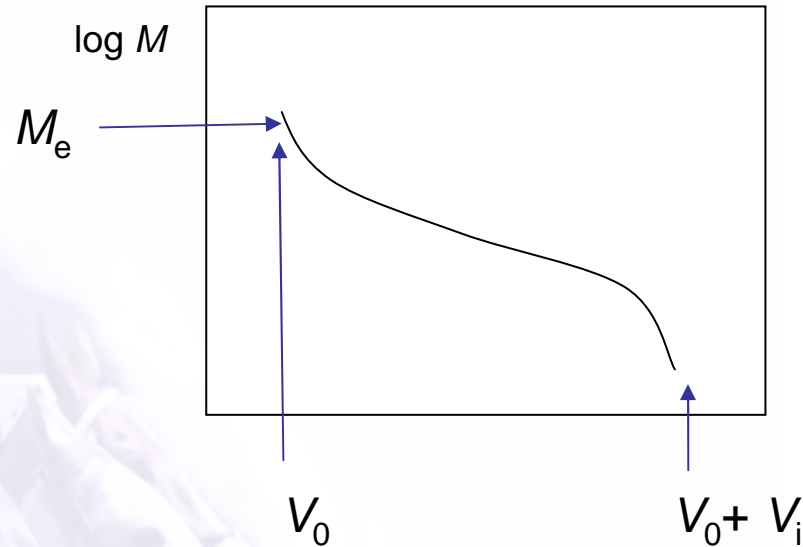


———— solvent flow —————>

Partition between the flowing solvent and the solvent in the pores

Elution time (volume) is a function of the particle (hydrodynamic) size

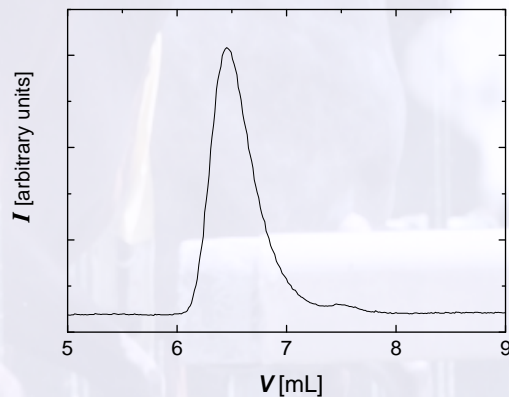
Above certain size all particles are equal, flow only through the interstitial volume



$$\log M = a + b V + \dots$$

- Detectors: (i) mass sensitive (refractometer, evaporative light scattering detection)
 (ii) molecularly sensitive (end group UV absorption)
 (iii) molecular-mass sensitive (light scattering, viscometric)

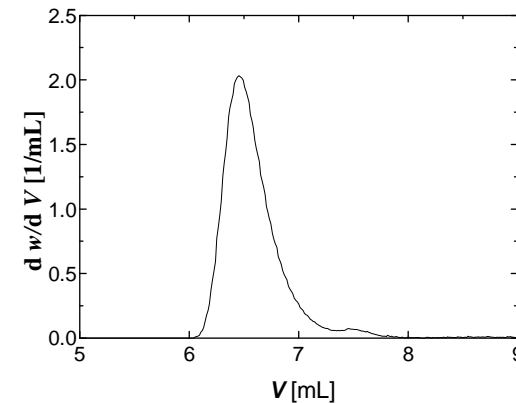
Standard configuration (i); up-to-date = multidetector (i)&(iii)



Baseline subtraction

Normalization

$$w(V) = \frac{I(V)}{\int_{V_L}^{V_R} I(V) dV}$$

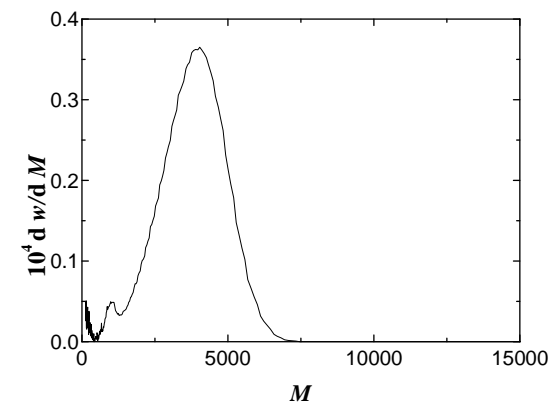
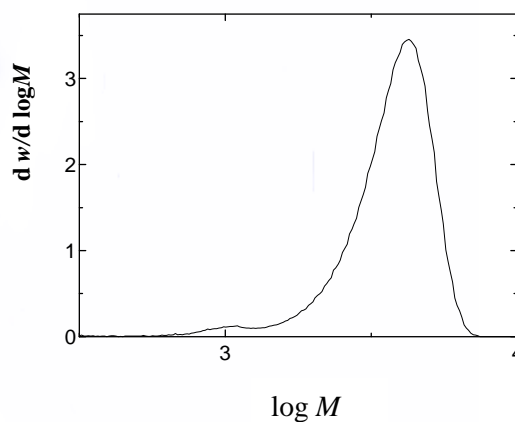
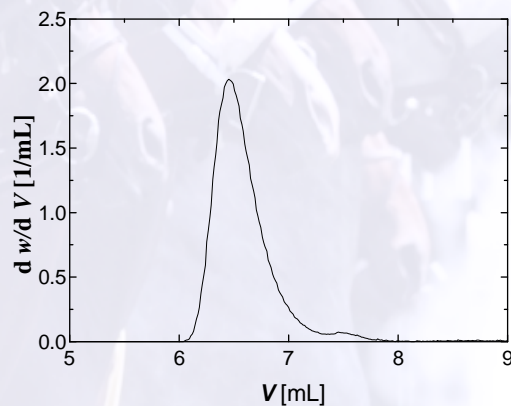


Point to point correspondence of cumulative V and M or $\log M$ distributions

$$\int_{\log M_L}^{\log M} w(\log M) d\log M = \int_V^{V_L} w(V) dV = \int_{\log M_L}^{\log M} w(V) \frac{dV}{d\log M} d\log M$$

$$w(\log M) = \frac{-w(V)}{\frac{d \log M}{dV}}$$

$$w(M) = \frac{w(\log M)}{2.303M}$$



$$\int_0^{\infty} \frac{dw}{d \log M} d\log M = \int_0^{\infty} \frac{dw}{dM} dM = 1$$

$$M_n = 3100$$

$$M_w = 3780$$

$$PI = 1.22$$

$M(V)$ – valid for the column, polymer, solvent etc

SEC with a mass detector only

- calibration by polymer standards
- universal calibration
 - hydrodynamic volume $[\eta]M(V)$ Mark-Houwink Eq. $\log [\eta]M = \log K + (1+a)\log M$
- polystyrene calibration

SEC with mass & molecular-mass detectors

viscosity detector – gives M through the universal calibration without Mark-Houwink parameters

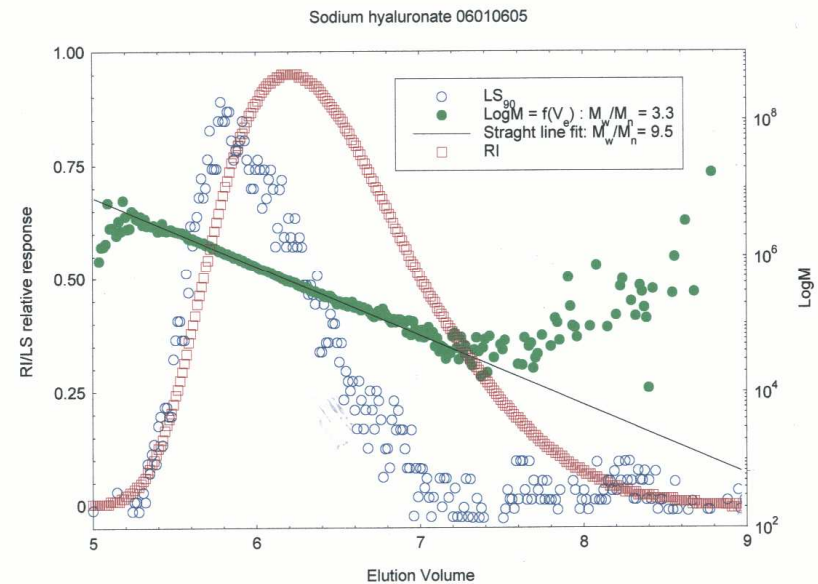
static light-scattering detector

Averages of M :

directly according discrete definitions

Distribution: in two steps

- LS data are used for the calibration equation
- RI data are treated in standard way

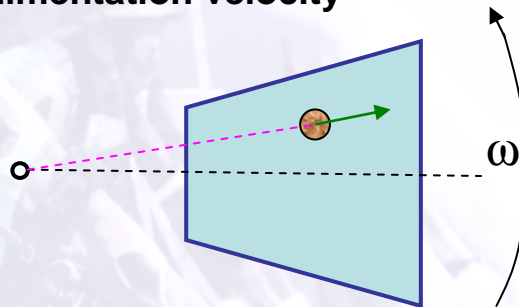


Sedimentation Analysis – Analytical Ultracentrifuge

(macromolecular archeology? – Swedberg 1923, Nobel prize 1926)

Declared clinically dead in 1980's but then resurrected (natural macromolecules)

sedimentation velocity



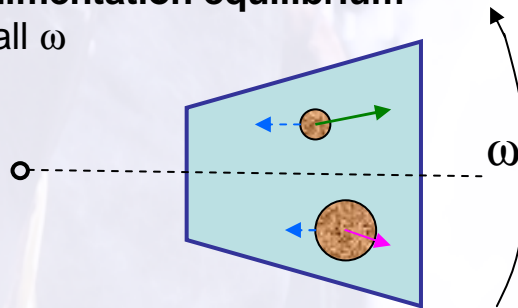
centrifugal force = friction resistance ($f u$) => **sedimentation velocity u**

sedimentation coefficient s

$$s = \frac{u}{\omega^2 r} = \frac{M(1 - \bar{v}\rho)}{N_A f} = \frac{MD(1 - \bar{v}\rho)}{RT}$$

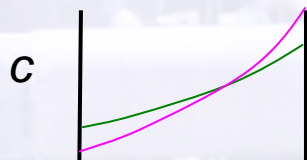
sedimentation equilibrium

small ω

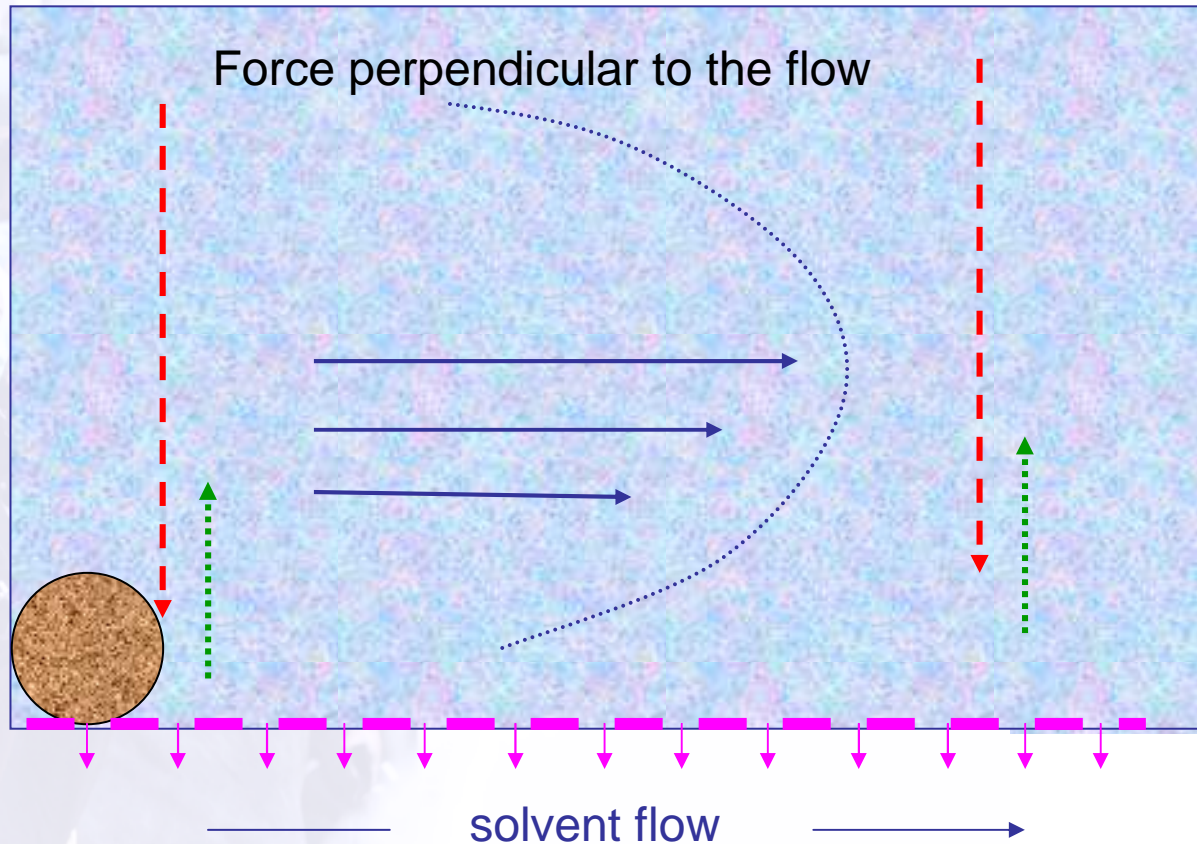


sedimentation creates temporal concentration gradient which is opposed by diffusion, equilibrium gradient is achieved

$$\frac{1}{r} \frac{dc}{dr} \sim M$$



Principle of Field –Flow Fractionation (J. C. Giddings)



field
thermal, electrical..
assymetrical flow



Elution time (volume) is a function of the particle (hydrodynamic) size
bigger particles (up to 0.1 mm vs. SEC <100 nm) smaller adsorption
change of mechanism (bigger particles first), absolute detection LS

Mass Spectrometry

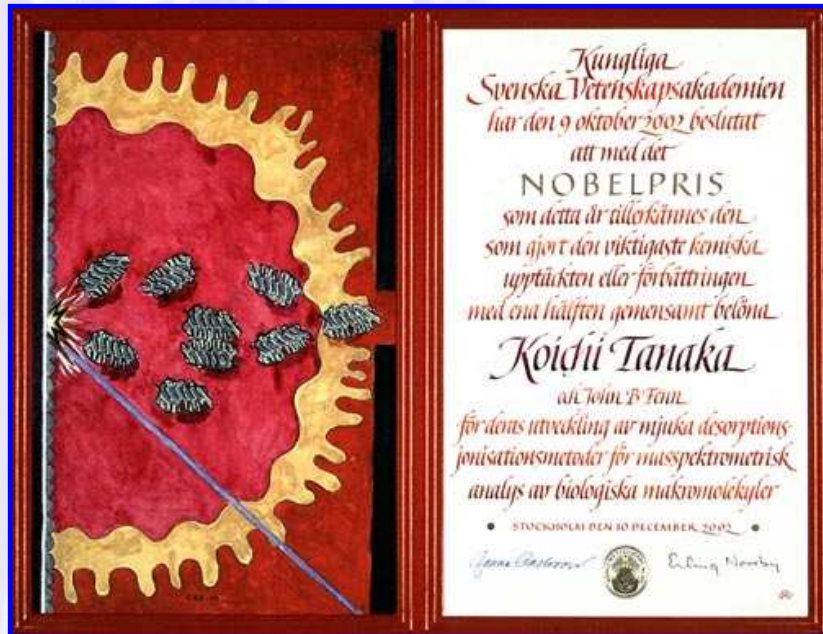
Why MS if we have SEC?

MS: $M/w_{1/2}=10000$

SEC: $N_{tp}=5.54(V/w_{1/2})^2=10000$

$V/w_{1/2}=42$

Resolution



The Nobel Prize in Chemistry 2002

“for the development of soft desorption ionisation methods for mass spectrometric analyses of biological macromolecules”

MALDI-TOF mass spectrometry

Mass spectrometry

Principle:

a charge particle is accelerated in electromagnetic field

In electric field

$$\frac{1}{2}mv^2 = zeU$$

For measurement of molecular weight, M ,

- (i) the sample must be vaporized and charged (ion source)
- (ii) particles must be separated according to M/z (mass analyzer)
- (iii) particles with the same M/z must be counted (detector)

Low-molecular-weight compounds:

M is used for identification

vaporization puts an upper limit on measured M

the most widely used electron impact ionizations fragments the sample molecules

Fragmentation gives information on the structure of the compound

For a long time, polymer researches used MS only for analyzing

polymer additives



pyrolysis products



etc...

At the same time, they were fascinated by the MS precision

M a t r i x
A s s i t e d
L a s e r
D e s o r p t i o n
I o n i z a t i o n

T i m e
O f
F l i g h t

M a s s
S p e c t r o m e t r y

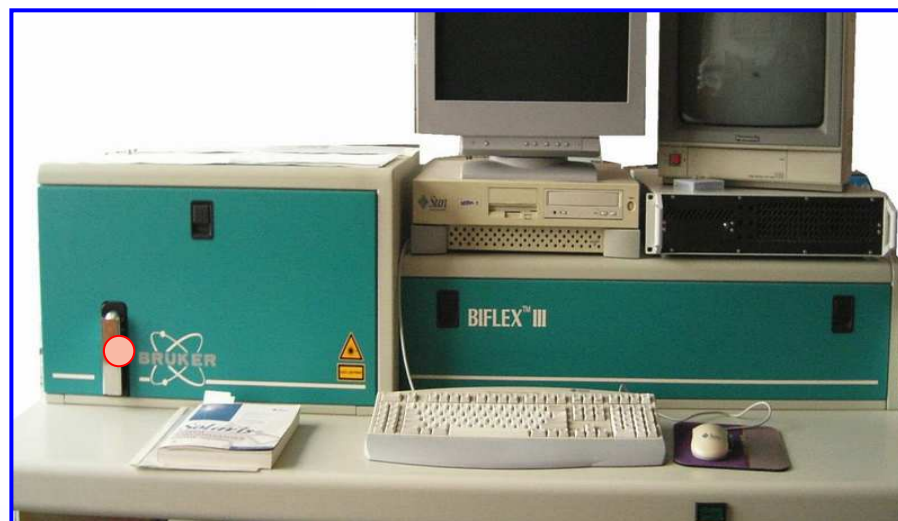
Matrix:

2,5-dihydroxybenzoic acid

1,8,9-trihydroxyanthracene

Laser:

337 nm, pulse <4 ns, 40 kW/4mW



Sample preparation

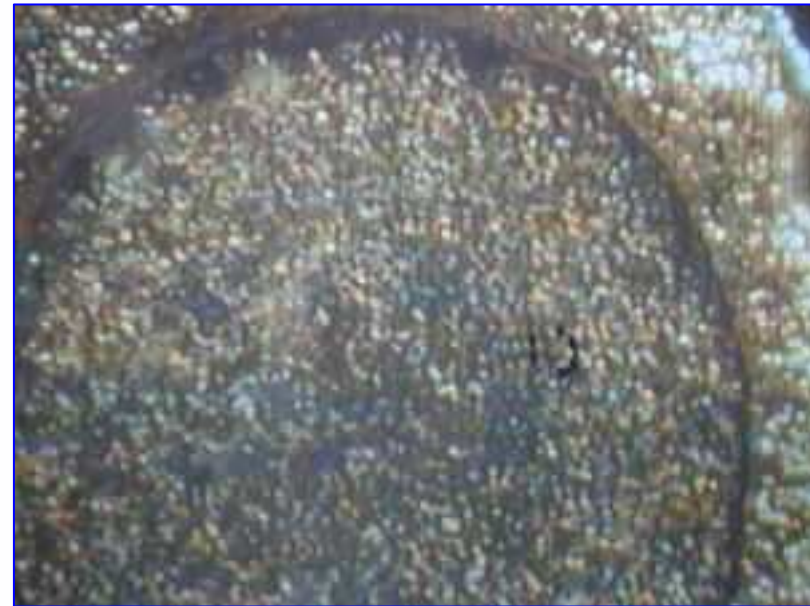


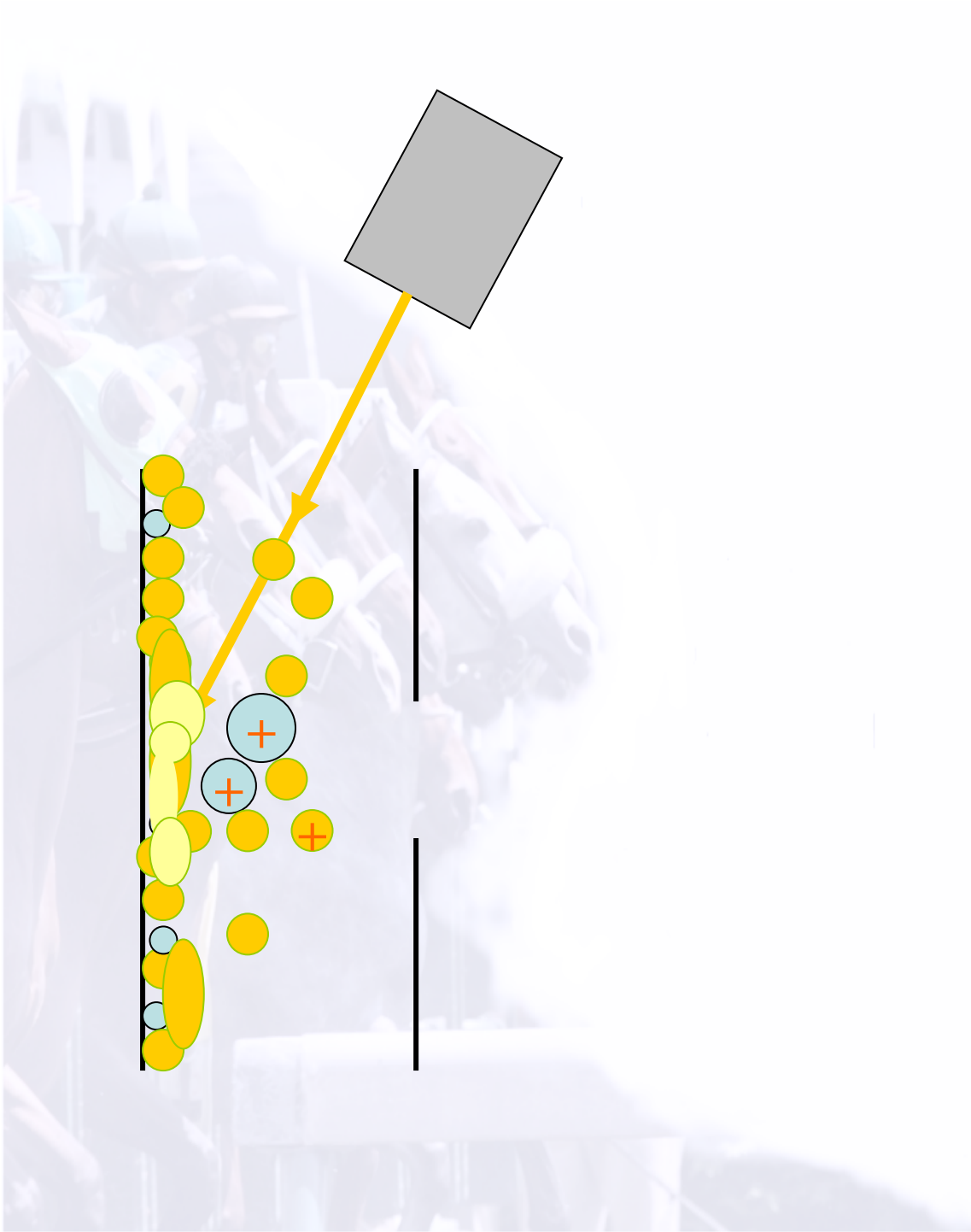
1- 2 μ L per spot (2-10x)

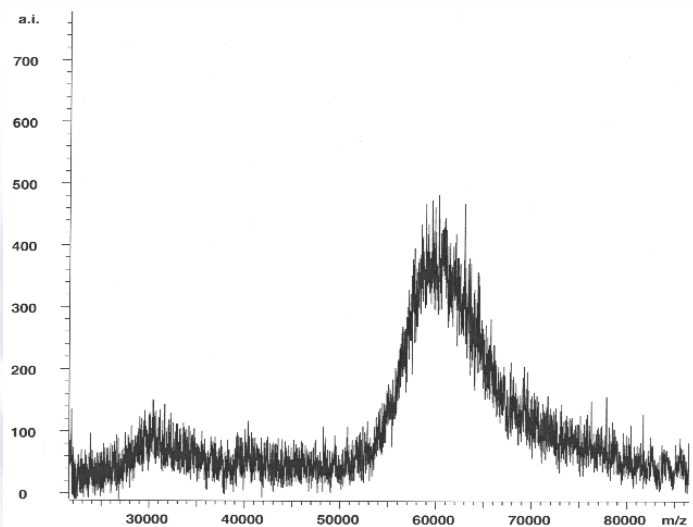
0.2% sample

1-2% matrix

& ionization agent (NaCl, AgTFA)



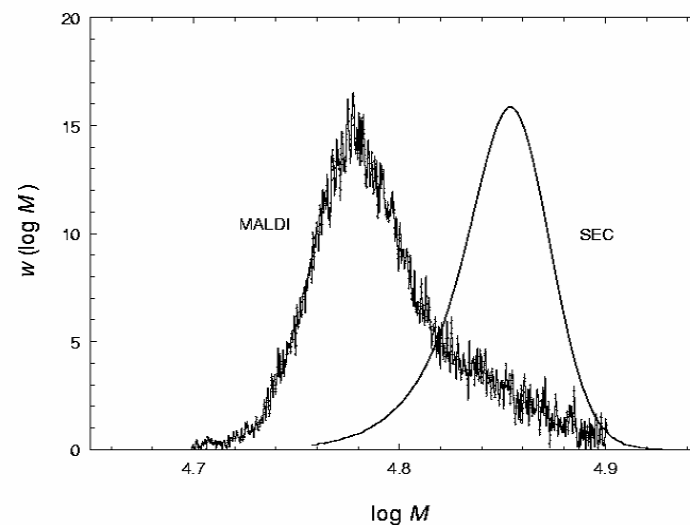




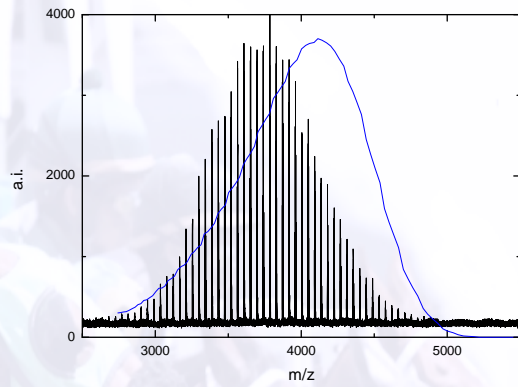
PST M_w/M_n (kDa)

MALDI 62.3/61.9

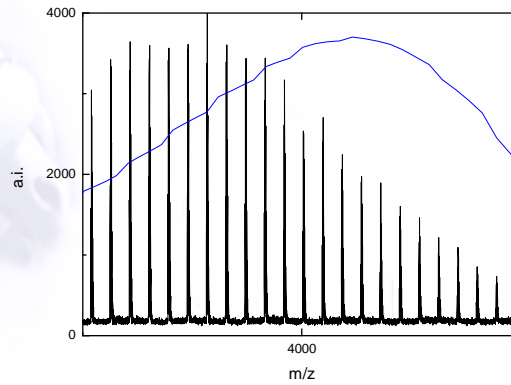
SEC 71.3/71.1



For samples with $M > 20\ 000$ multidetector SEC is the first choice

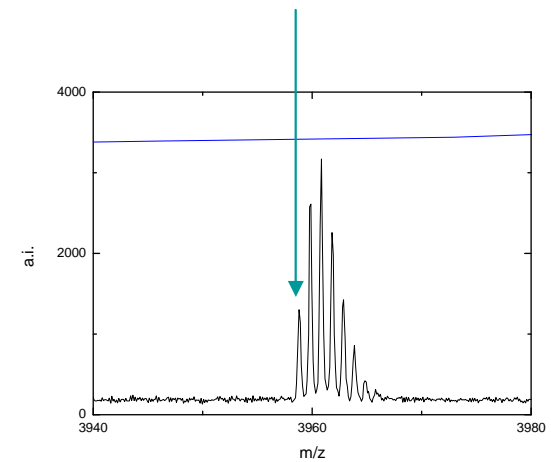


MALDI-TOF MS can distinguish individual oligomers



and even isotopic resolution
(in reflector mode)

Monoisotopic peak
(C^{12} only)

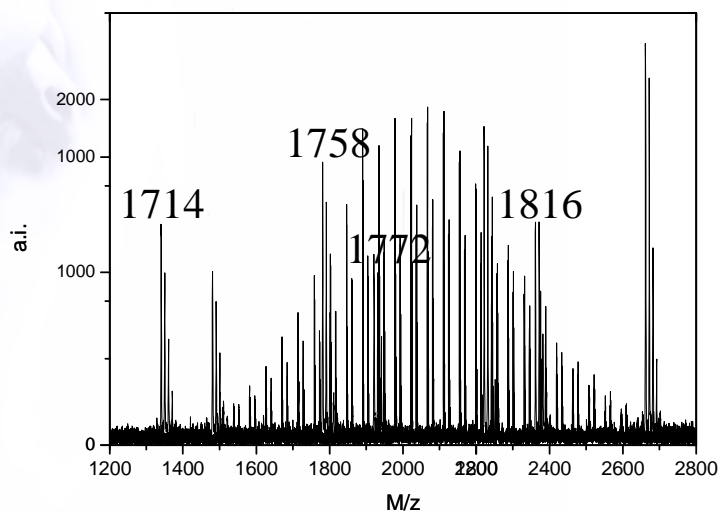


The strength of MALDI-TOF is with samples $M < 20000$
 (For samples with $M > 20\ 000$, the first choice is the multi-detector SEC)

$$M = M_{\text{eg1}} + n M_{\text{m}} + M_{\text{eg2}} + M_{\text{ia}}$$

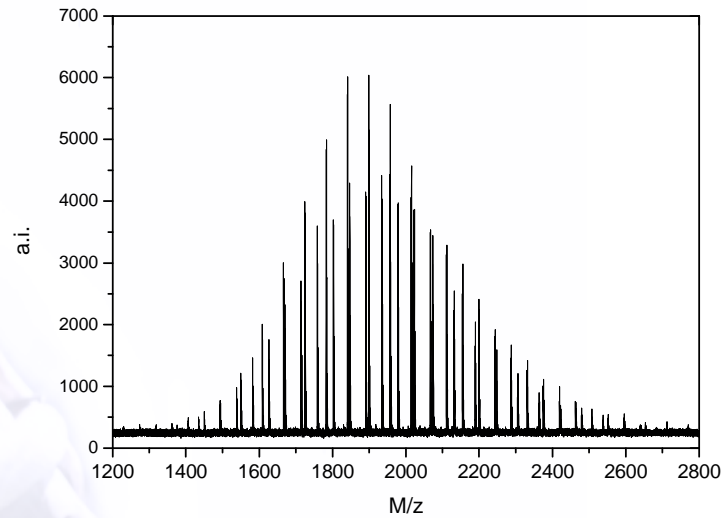


PEG:MPEG
 1 : 1



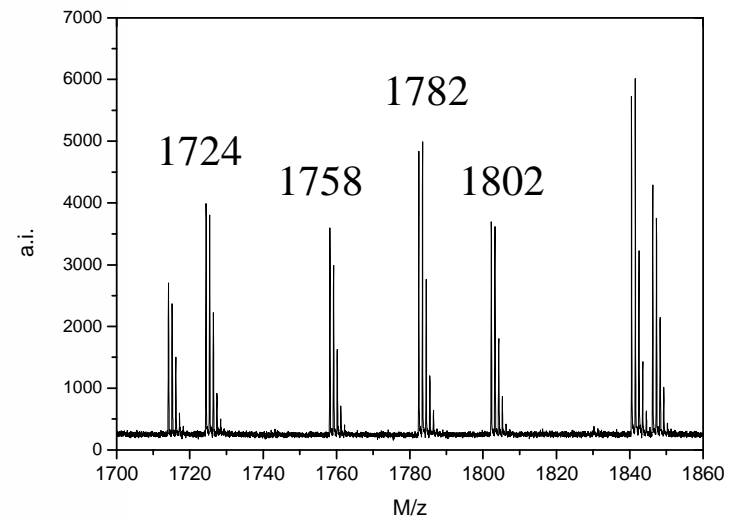
$$17 + 39 * 44 + 1 + 23 = 1758$$

Mixture of two homopolymers

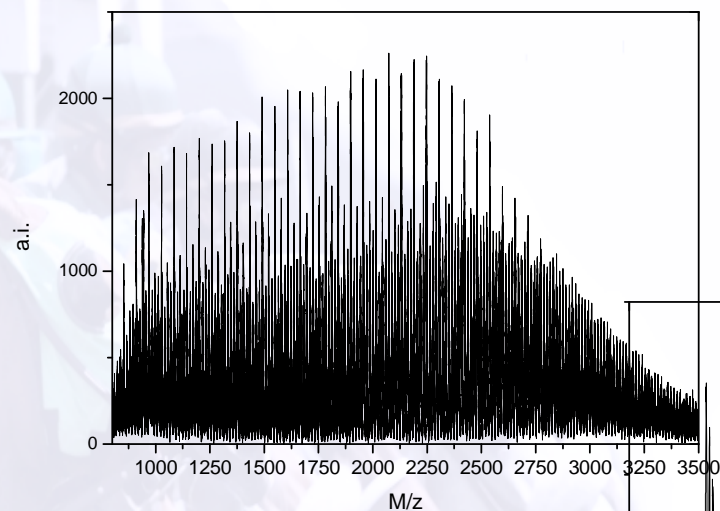


PEG:PPG

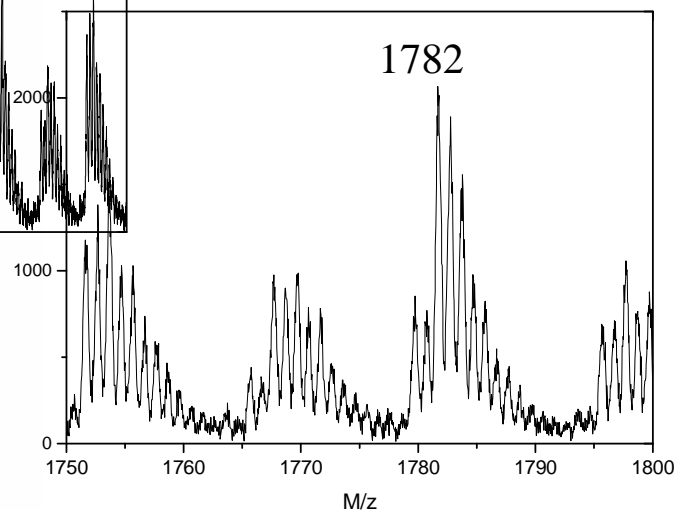
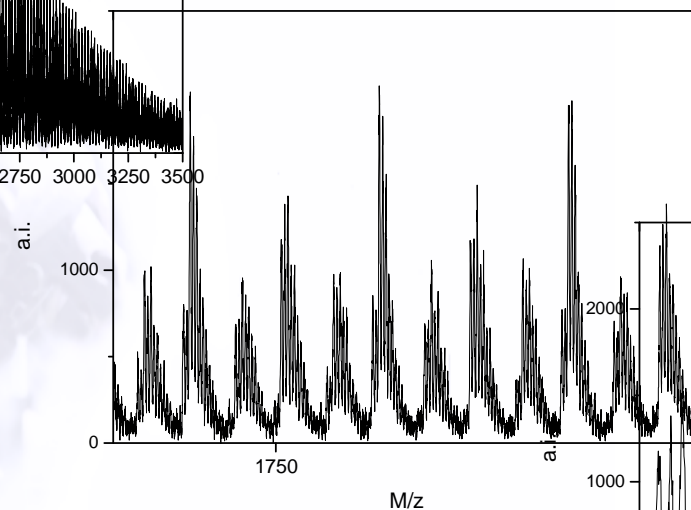
PEG : PPG
2 : 1



Binary copolymers (PEG/PPG -Pluronic)



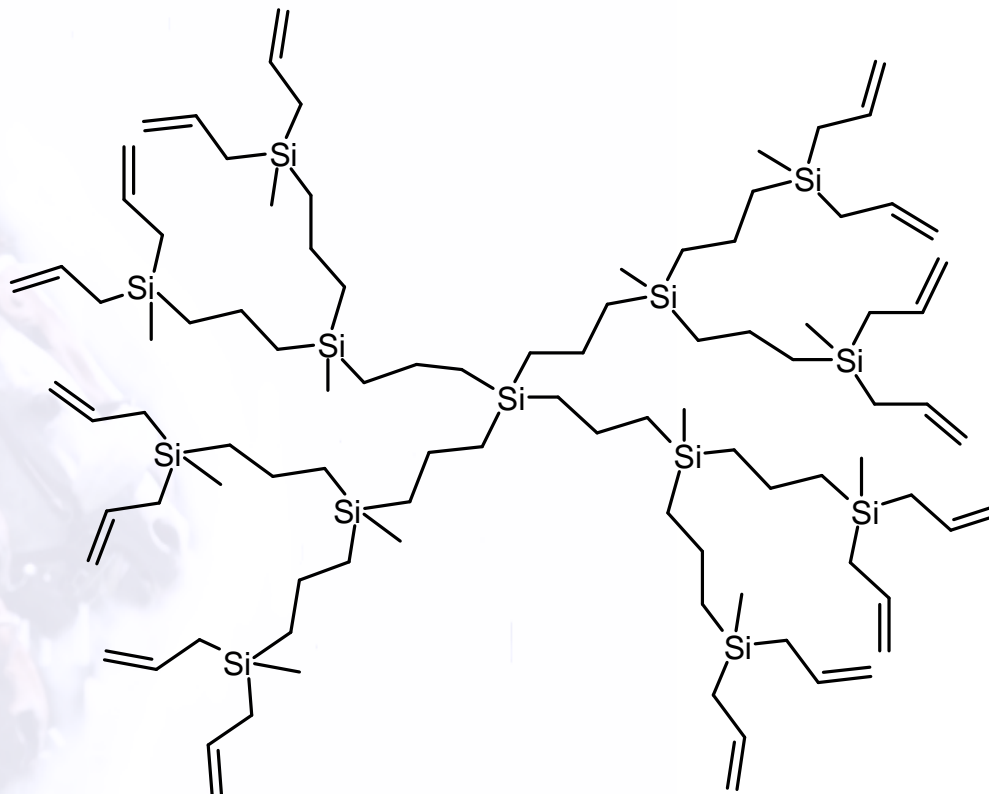
$$M = M_{eg1} + n M_a + m M_b + M_{eg2} + M_{ia}$$



$$1782 = 17 + 30 * 58 + 1 + 23$$

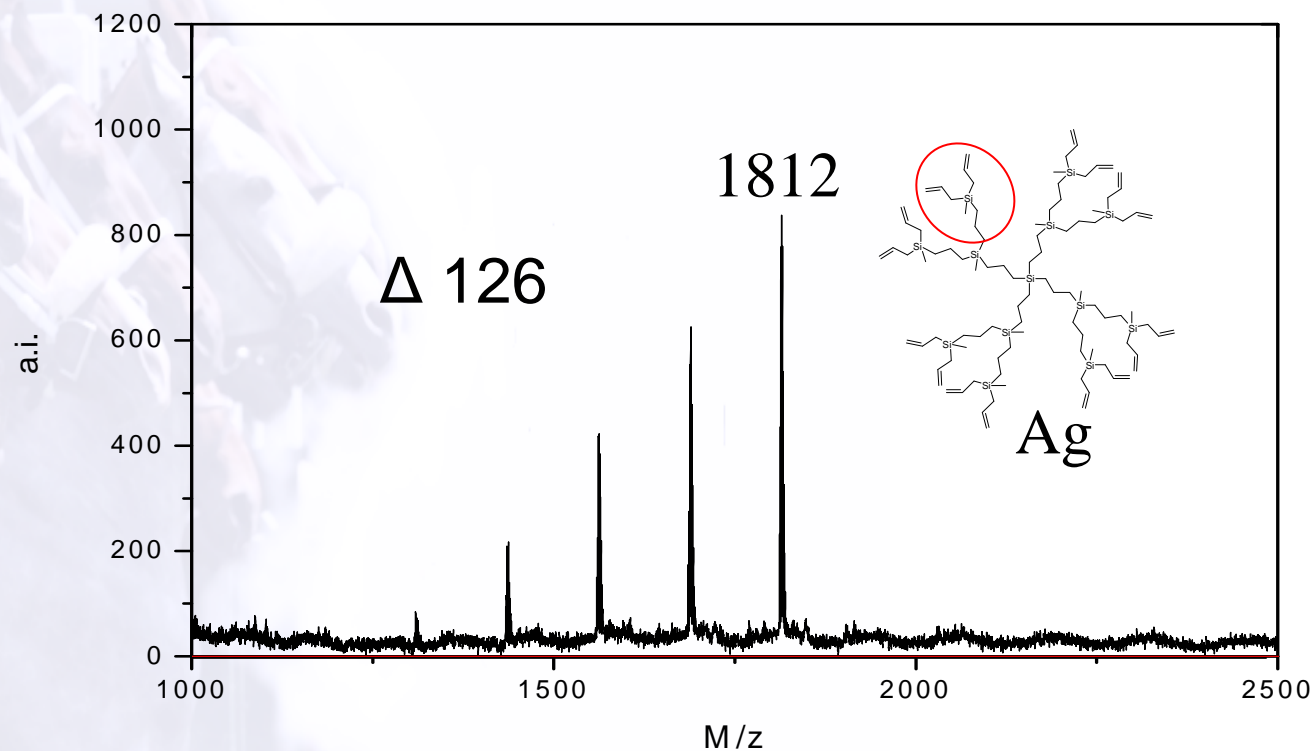
$$1782 = 17 + 29 * 44 + 8 * 58 + 1 + 23$$

$$22 * 58 = 29 * 44$$



d e n d r i m e r

MALDI-TOF mass spektrum of 2nd generation carbosilane dendrimer (defect detection)





Literature:

Montaudo G et al. Prog. Polym. Sci 31, 277-357 (2006)

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Kostanski LK et al. J. Biochem. Biophys. Methods 58, 159–186 (2004)



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