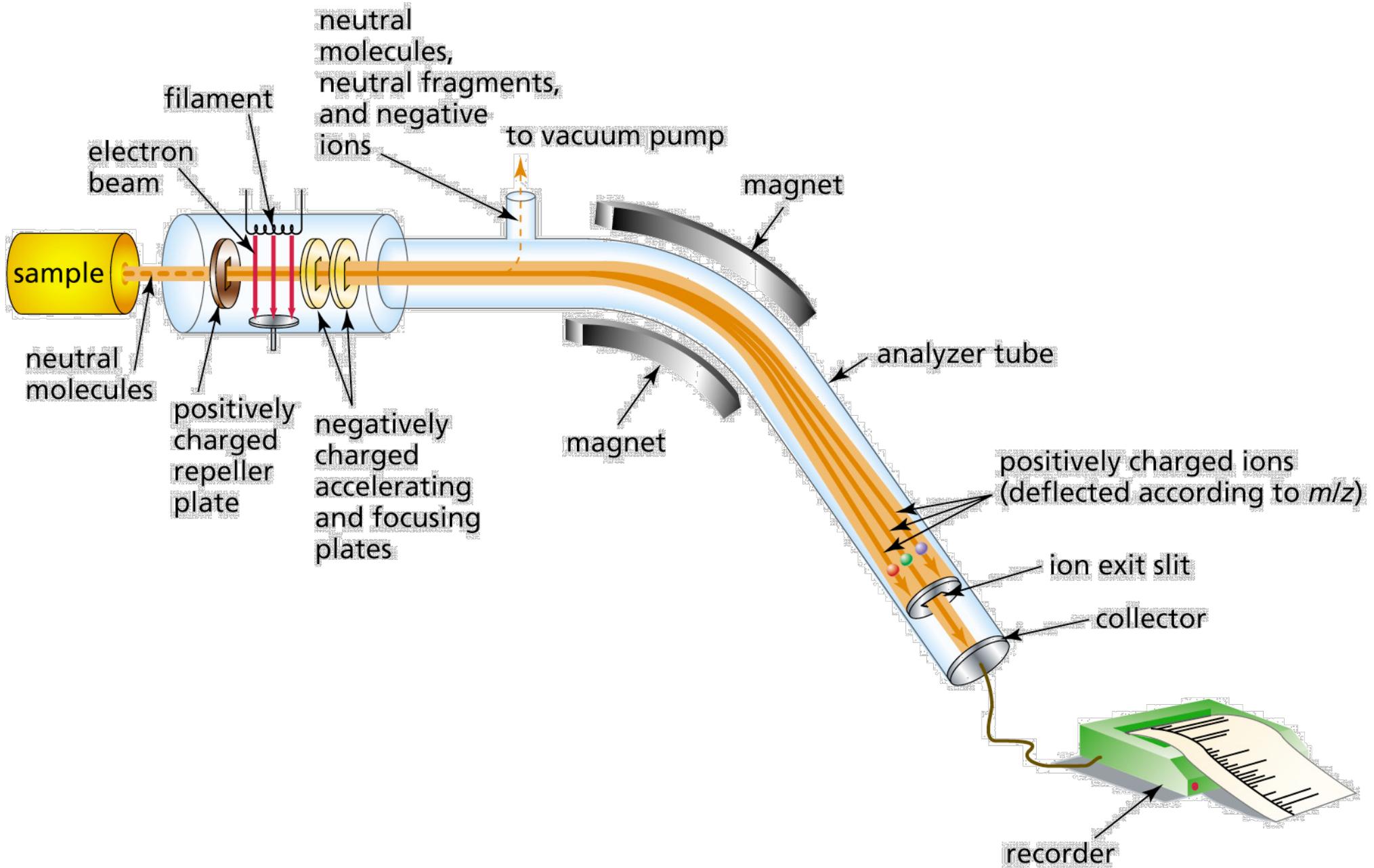


# Making Elephants Fly\*

\*“Well, in homely terms, we learned how to make elephants fly, as it were.”

John B. Fenn during an interview on *News Hour with Jim Lehrer*, October 9, 2002

# Mass Spectrometry



## MS for Small Organic Molecules

Small molecules are easily vaporized

Electron beam ionization (10,000–20,000 V) conveniently ionizes organic molecules

Fragmentation pattern caused by electron beam ionization provides clues about the structure of the molecule

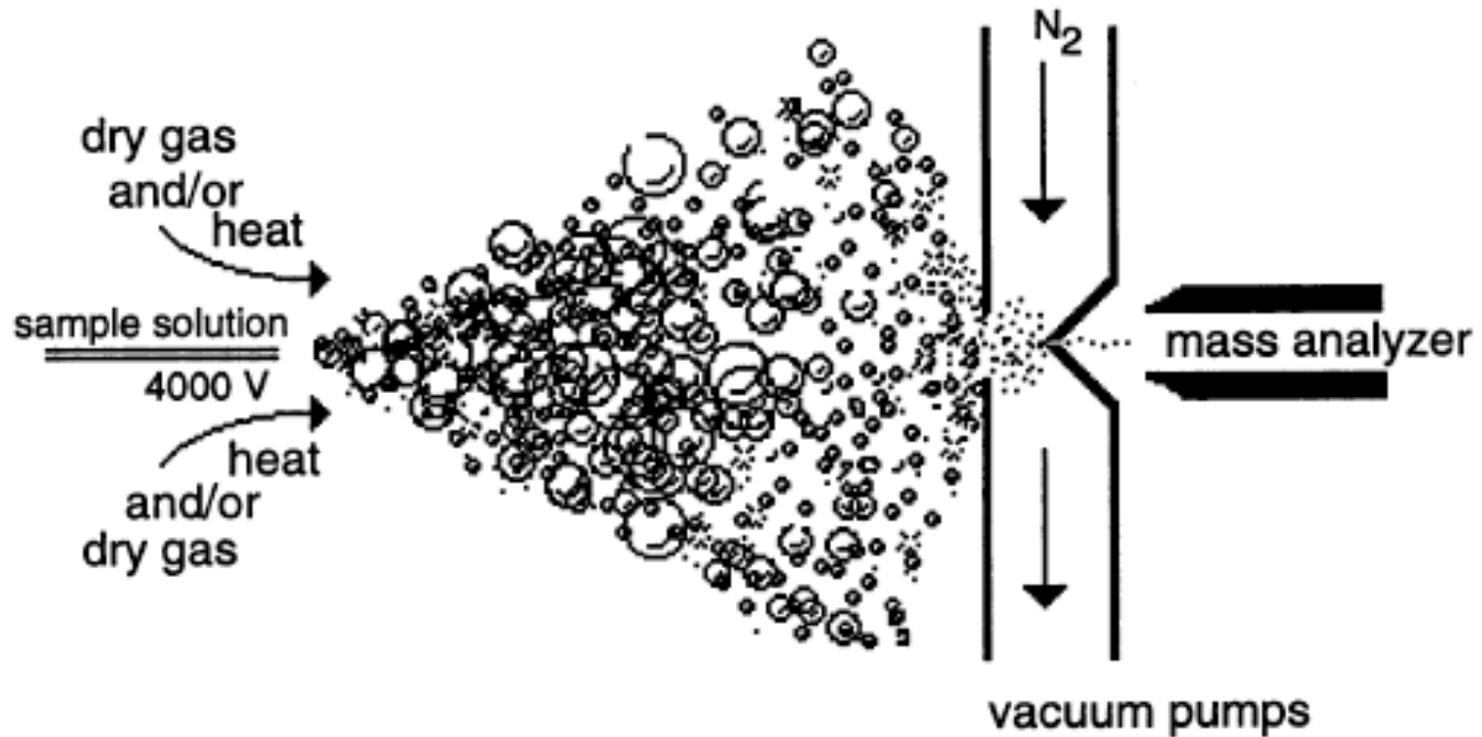
## MS for Proteins

Proteins are not easily vaporized

Electron beam ionization (10,000–20,000 V) easily ionizes (cooks) proteins...

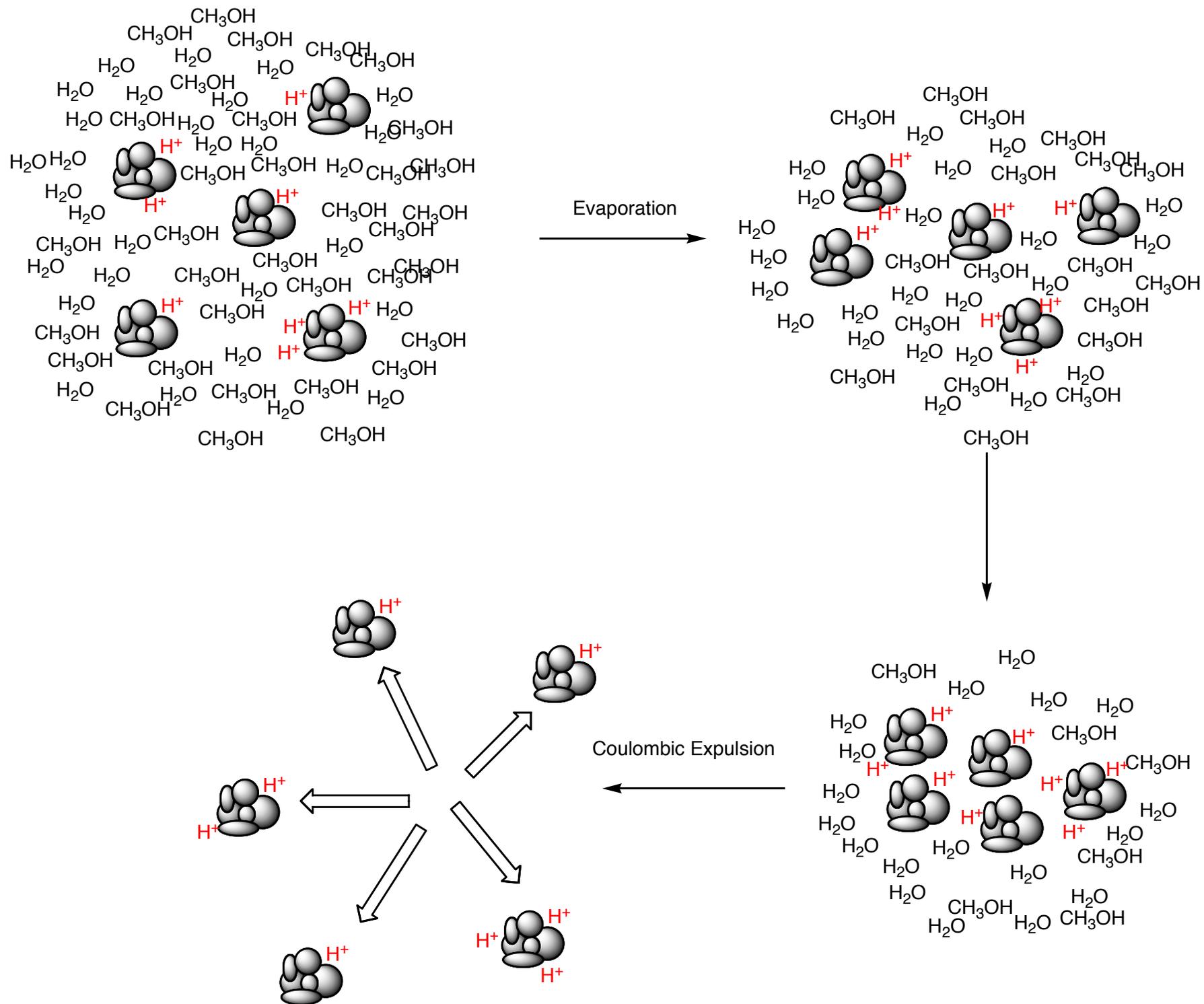
Fragmentation patterns produced by electron beam ionization are too complicated to analyze

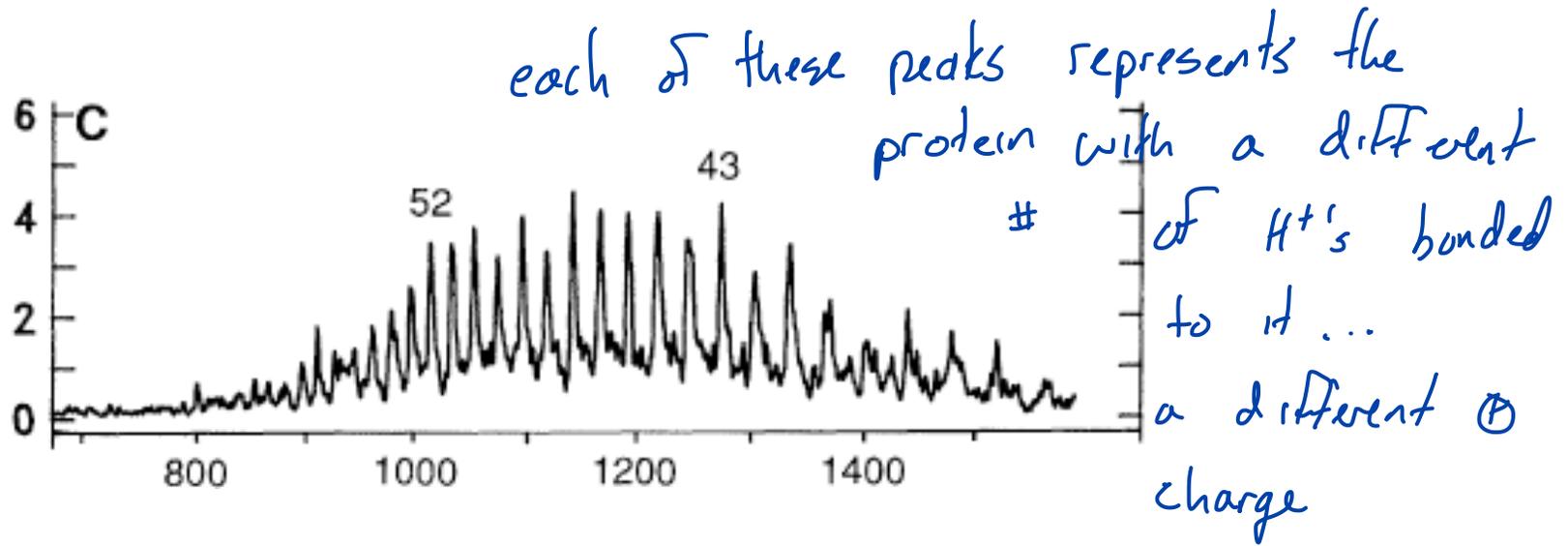
# Electrospray Ionization (ESI)



Gary Siuzdak

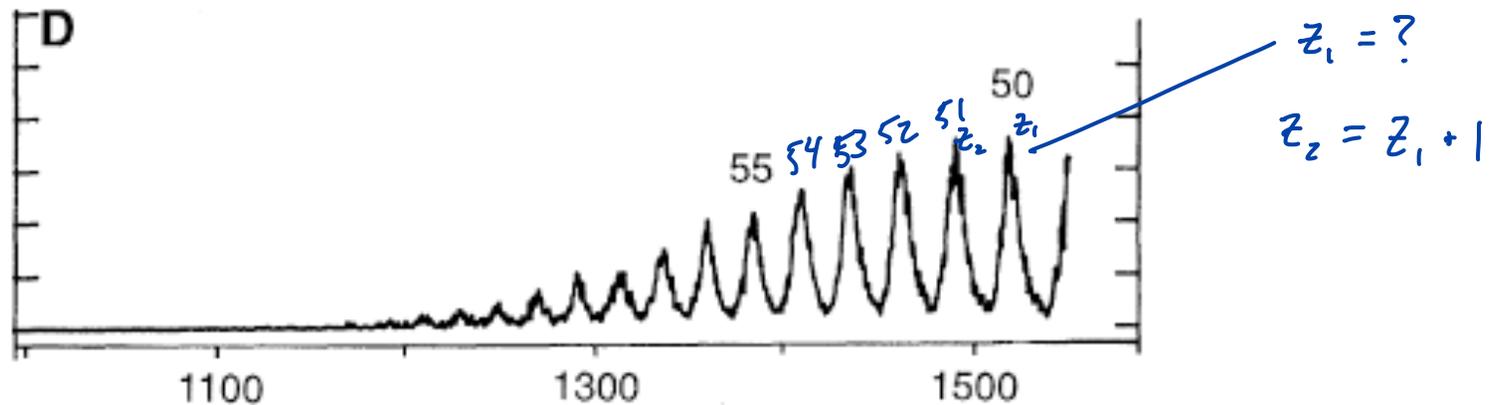
*Proceedings of the National Academy of Sciences of the United States of America*, Vol. 91, No. 24. (Nov. 22, 1994), pp. 11290-11297.





## $\alpha$ -analyse: 54,700 da

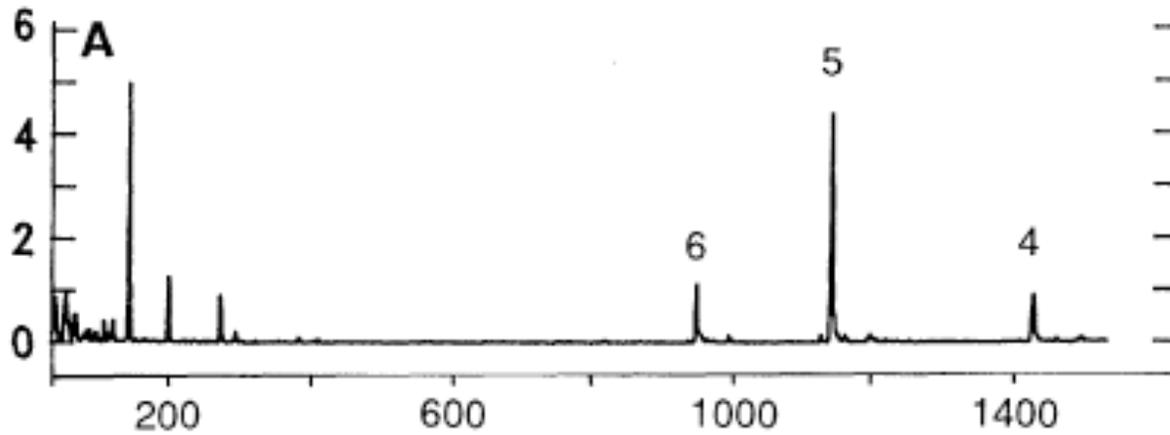
We don't know the charge, but we know that adjacent peaks are separated by a charge of +1



## conalbumin: 76,000 da

John B. Fenn; Matthias Mann; Chin Kai Meng; Shek Fu Wong; Craig M. Whitehouse

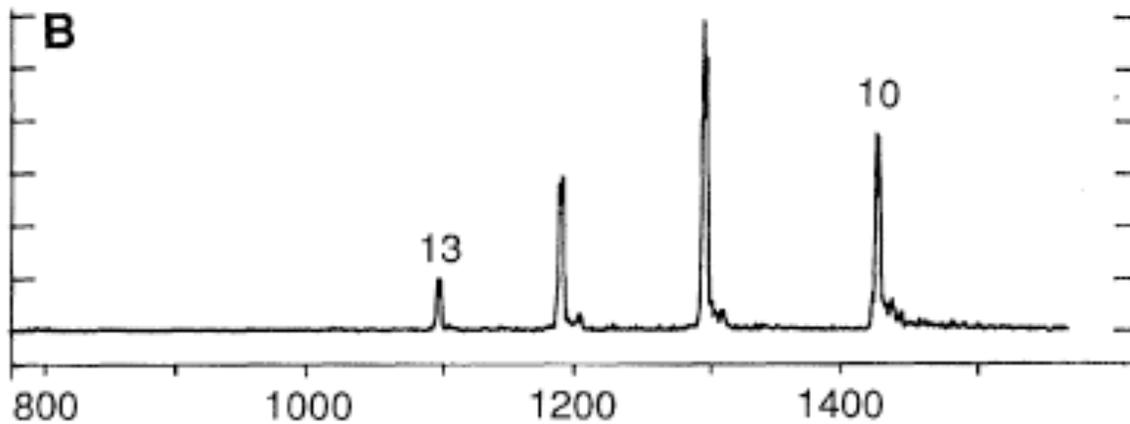
*Science*, New Series, Vol. 246, No. 4926. (Oct. 6, 1989), pp. 64-71.



Insulin: 5730 da

$m/z$	$m/z \times z$
1433	$1433 * 4 = 5732$
1146	$1146 * 5 = 5730$
955	$1433 * 6 = 5730$

↑



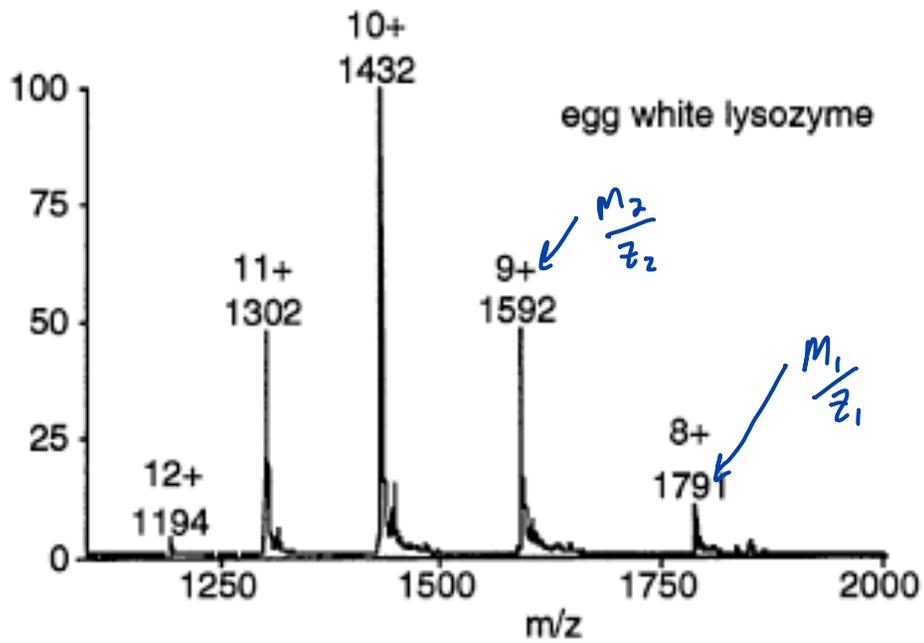
Lysosome: 14300 da

$m/z$	$m/z \times z$
1430	$1430 * 10 = 14,300$
1300	$1300 * 11 = 14,300$
1192	$1192 * 12 = 14,304$
1100	$1100 * 13 = 14,300$

↑

John B. Fenn; Matthias Mann; Chin Kai Meng; Shek Fu Wong; Craig M. Whitehouse

*Science*, New Series, Vol. 246, No. 4926. (Oct. 6, 1989), pp. 64-71.



— mass of the molecule

$$(m/z_1)_1 z_1 = m$$

$$(m/z_2)_2 z_2 = m$$

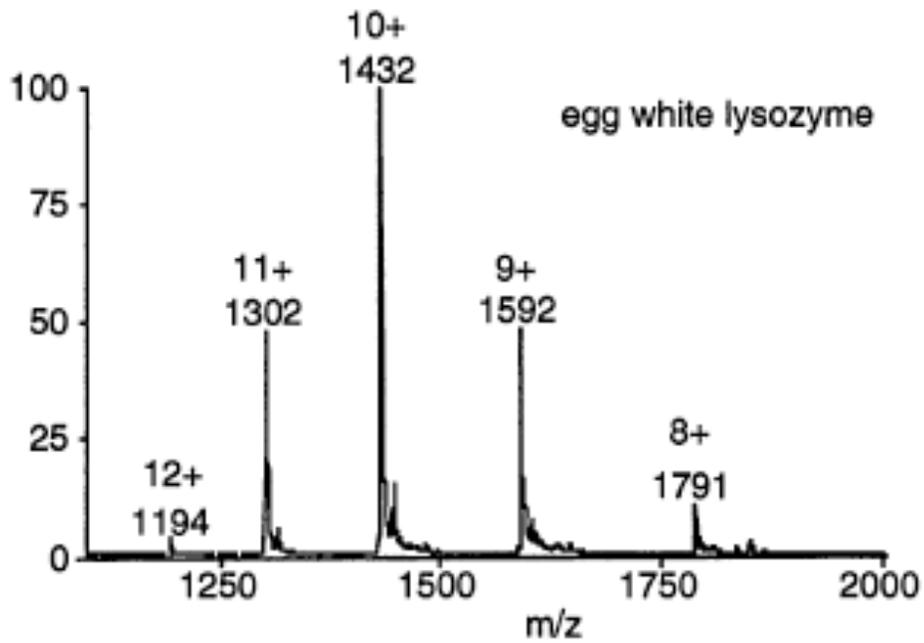
$$1791 z_1 = m$$

$$1592 z_2 = m$$

$$1592 z_2 = 1791 z_1$$

Gary Siuzdak

*Proceedings of the National Academy of Sciences of the United States of America*, Vol. 91, No. 24. (Nov. 22, 1994), pp. 11290-11297.



$$(m/z_1)_{z_1} = m$$

$$(m/z_2)_{z_2} = m$$

$$z_1 + 1 = z_2$$

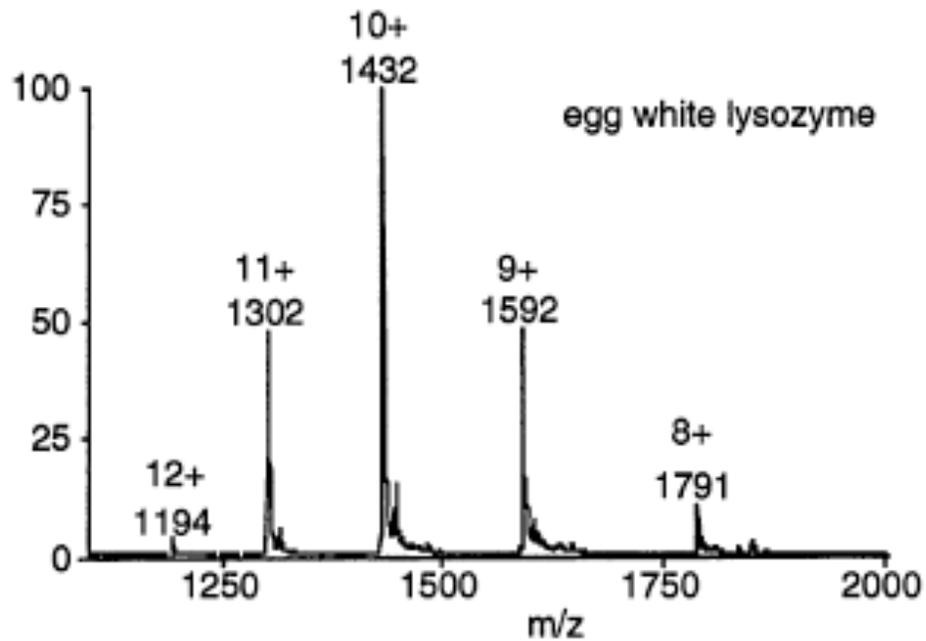
$$1791 \quad z_1 = m$$

$$1592 \quad z_2 = m$$

$$1592 \quad z_2 = 1791 \quad z_1$$

Gary Siuzdak

*Proceedings of the National Academy of Sciences of the United States of America*, Vol. 91, No. 24. (Nov. 22, 1994), pp. 11290-11297.



$$(m/z_1)_1 z_1 = m$$

$$(m/z_2)_2 z_2 = m$$

$$z_1 + 1 = z_2$$

$$1791 z_1 = m$$

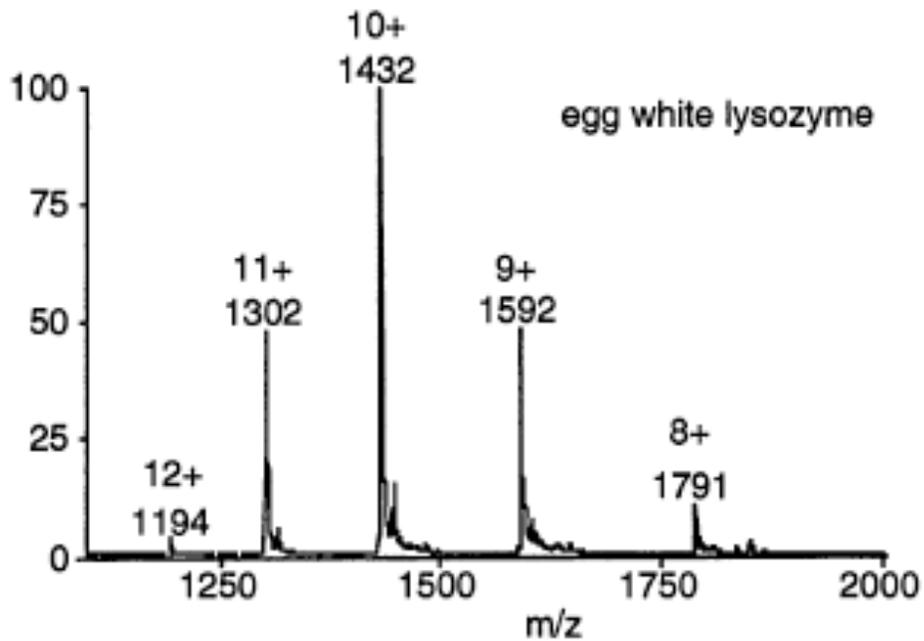
$$1592 z_2 = m$$

$$1592 z_2 = 1791 z_1$$

$$1592 (z_1 + 1) = 1791 z_1$$

Gary Siuzdak

*Proceedings of the National Academy of Sciences of the United States of America*, Vol. 91, No. 24. (Nov. 22, 1994), pp. 11290-11297.



$$(m/z_1)_1 z_1 = m$$

$$(m/z_2)_2 z_2 = m$$

$$z_1 + 1 = z_2$$

$$1791 z_1 = m$$

$$1592 z_2 = m$$

$$1592 z_2 = 1791 z_1$$

$$1592 (z_1 + 1) = 1791 z_1$$

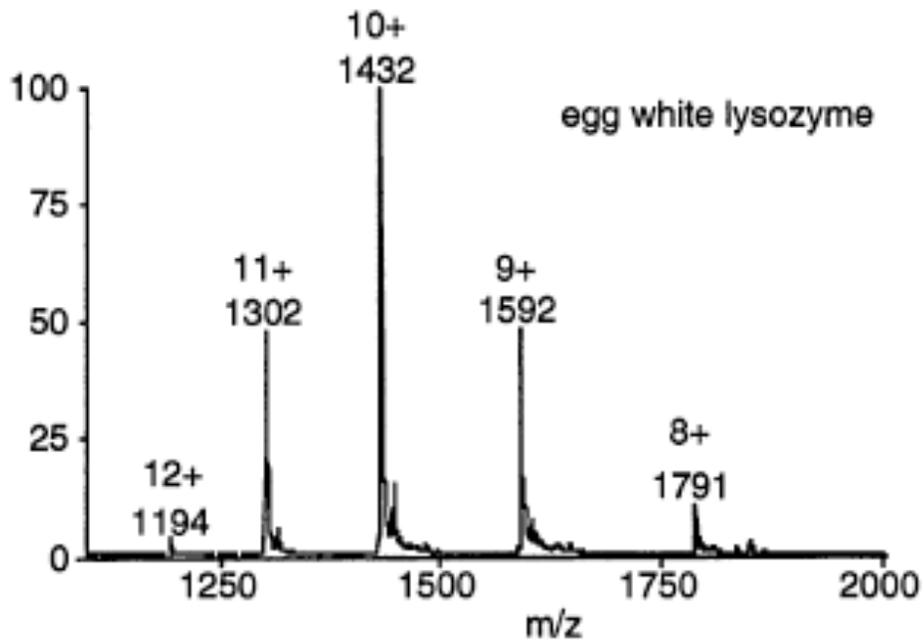
$$- 1592 z_1 + 1592 z_1 + 1592 = 1791 z_1 - 1592 z_1$$

$$1592 = 199 z_1$$

$$8 = z_1$$

Gary Siuzdak

*Proceedings of the National Academy of Sciences of the United States of America*, Vol. 91, No. 24. (Nov. 22, 1994), pp. 11290-11297.



$$(m/z_1)_1 z_1 = m$$

$$(m/z_2)_2 z_2 = m$$

$$z_1 + 1 = z_2$$

$$1791 z_1 = m$$

$$1592 z_2 = m$$

$$1592 z_2 = 1791 z_1$$

$$1791 (8) = m$$

$$1592 (z_1 + 1) = 1791 z_1$$

$$14,328 = m$$

$$1592 z_1 + 1592 = 1791 z_1$$

$$1592 = 199 z_1$$

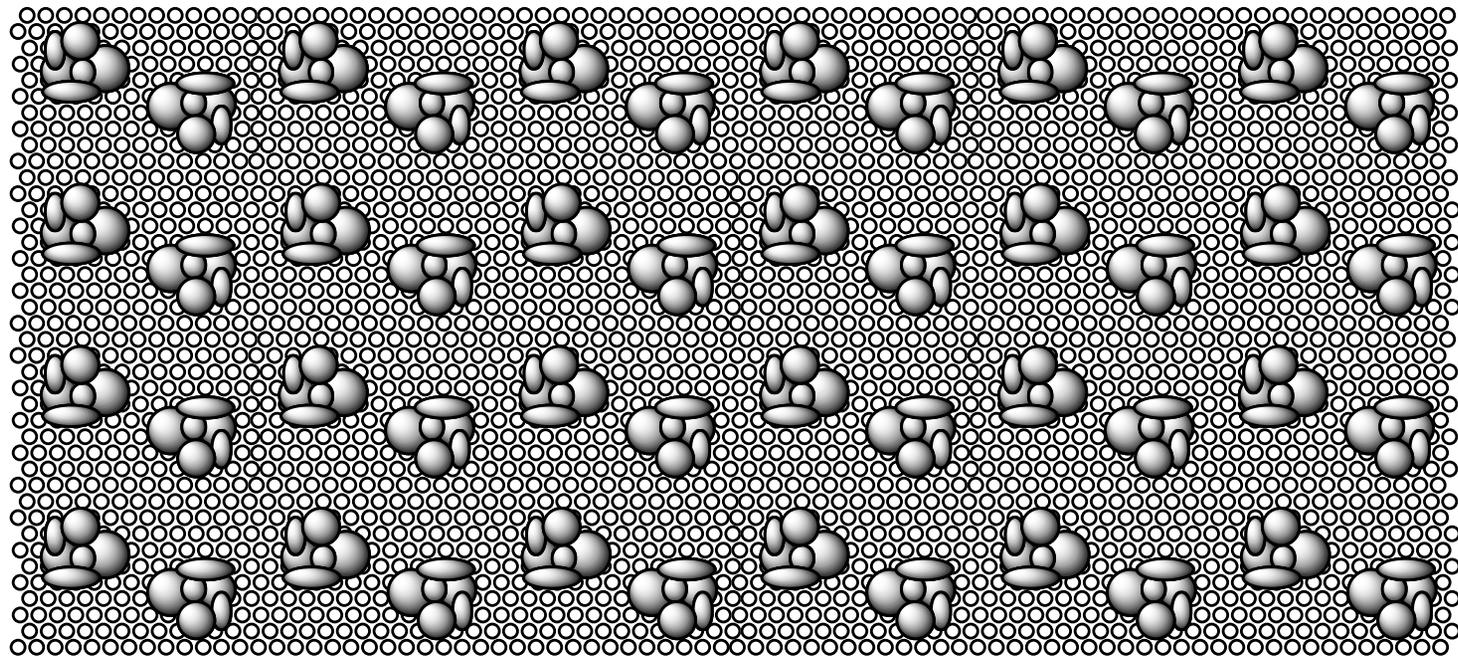
$$8 = z_1$$

Gary Siuzdak

*Proceedings of the National Academy of Sciences of the United States of America*, Vol. 91, No. 24. (Nov. 22, 1994), pp. 11290-11297.

MALDI

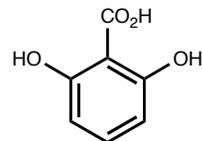
Matrix Assisted Laser Desorption Ionization

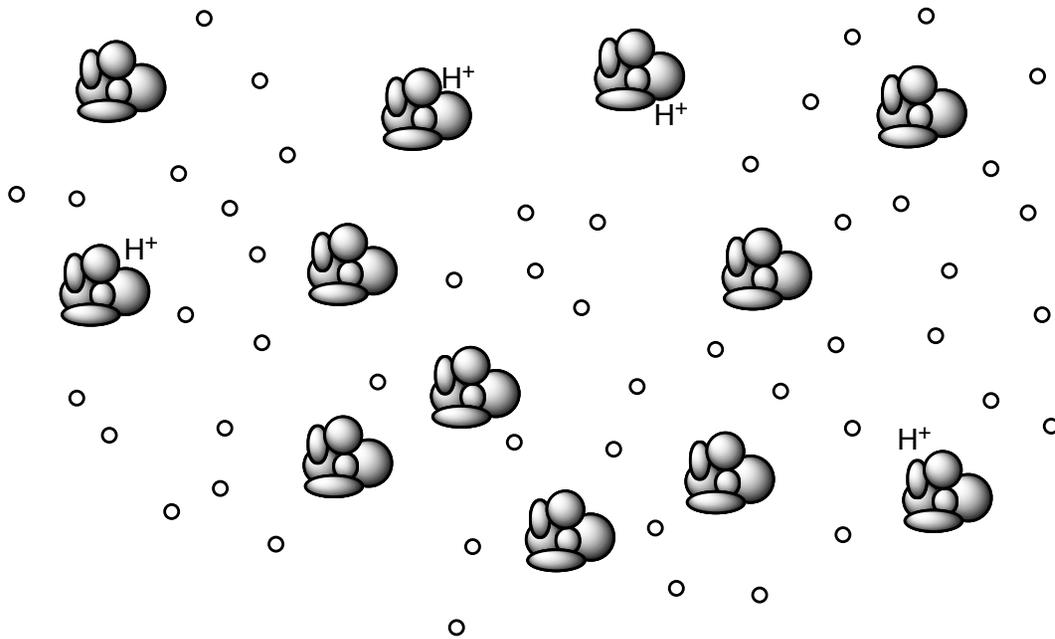


= protein

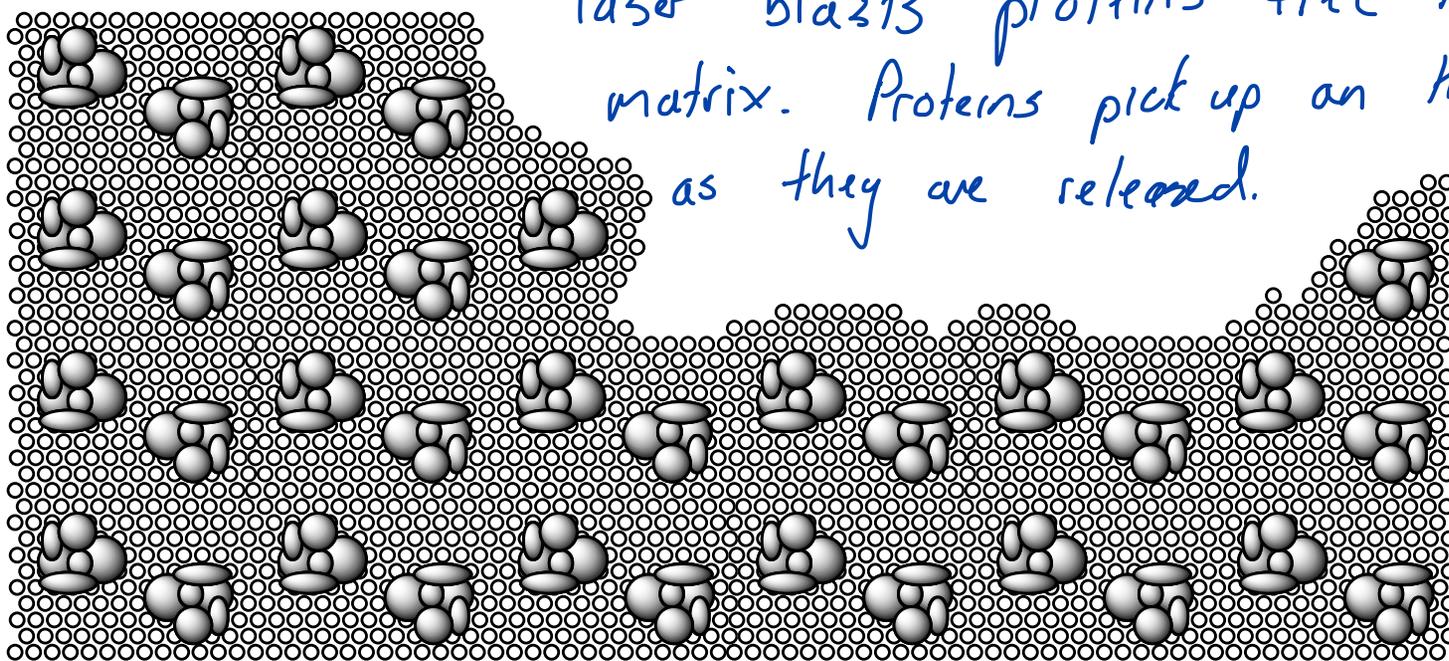


=

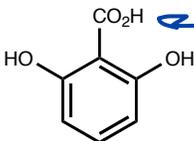




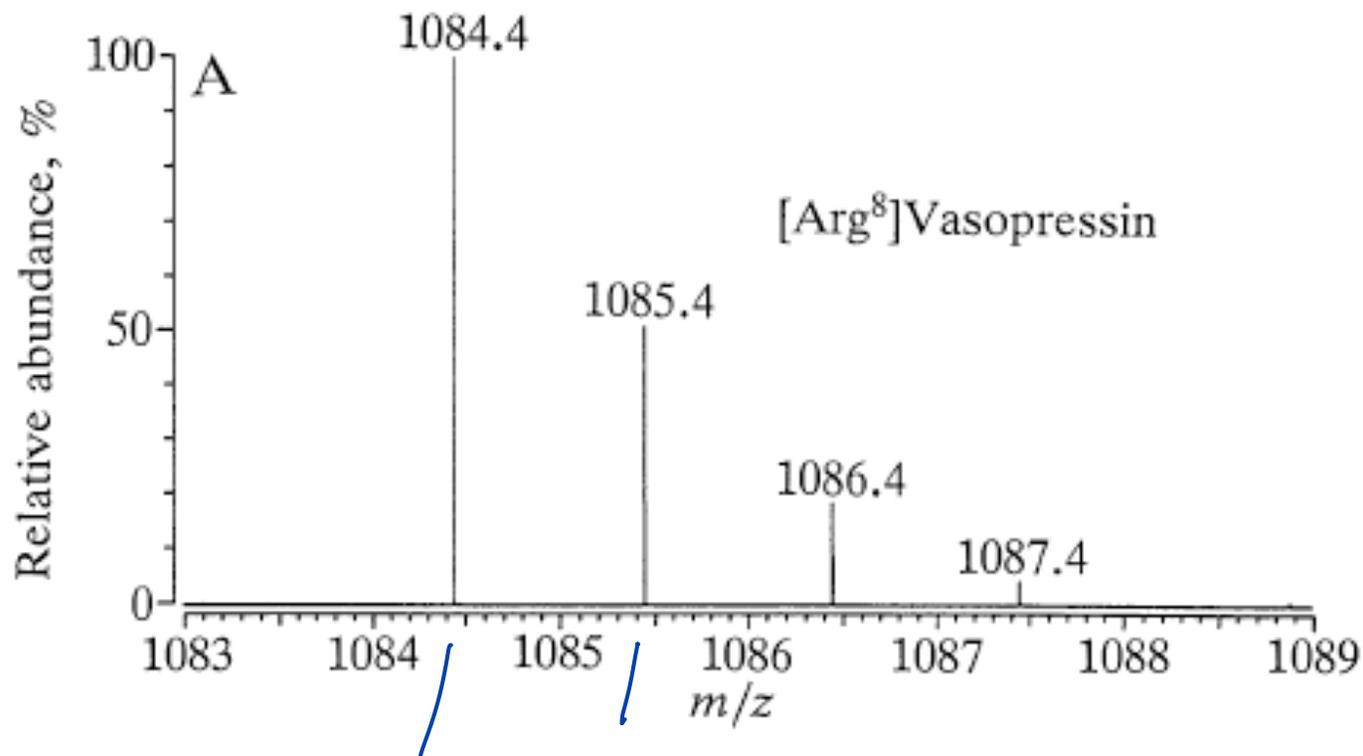
laser "blasts" proteins free from matrix. Proteins pick up an  $H^+$  as they are released.



= protein



← weak acid



all <sup>12</sup>C  
<sup>14</sup>N  
 etc

one <sup>13</sup>C  
 or  
 one <sup>15</sup>N  
 or  
 etc.

<sup>13</sup>C  
 and  
<sup>15</sup>N  
 etc

multiple  
 additional  
 isotopes

Robert T. McIver, Jr.; Yunzhi Li; Richard L. Hunter

*Proceedings of the National Academy of Sciences of the United States of America*, Vol. 91, No. 11. (May 24, 1994), pp. 4801-4805.

# Protein Ladder sequencing

1. 5% phenylisocyanate 95% phenylisothiocyanate
2. Trifluoroacetic acid
3. repeat

[Glu1]fibrinopeptide

PC-Glu-Gly-Val-Asn-Asp-Asn-Glu-Glu-Gly-Phe-Phe-Ser-Ala-Arg

PC-Gly-Val-Asn-Asp-Asn-Glu-Glu-Gly-Phe-Phe-Ser-Ala-Arg

PC-Val-Asn-Asp-Asn-Glu-Glu-Gly-Phe-Phe-Ser-Ala-Arg

PC-Asn-Asp-Asn-Glu-Glu-Gly-Phe-Phe-Ser-Ala-Arg

PC-Asp-Asn-Glu-Glu-Gly-Phe-Phe-Ser-Ala-Arg

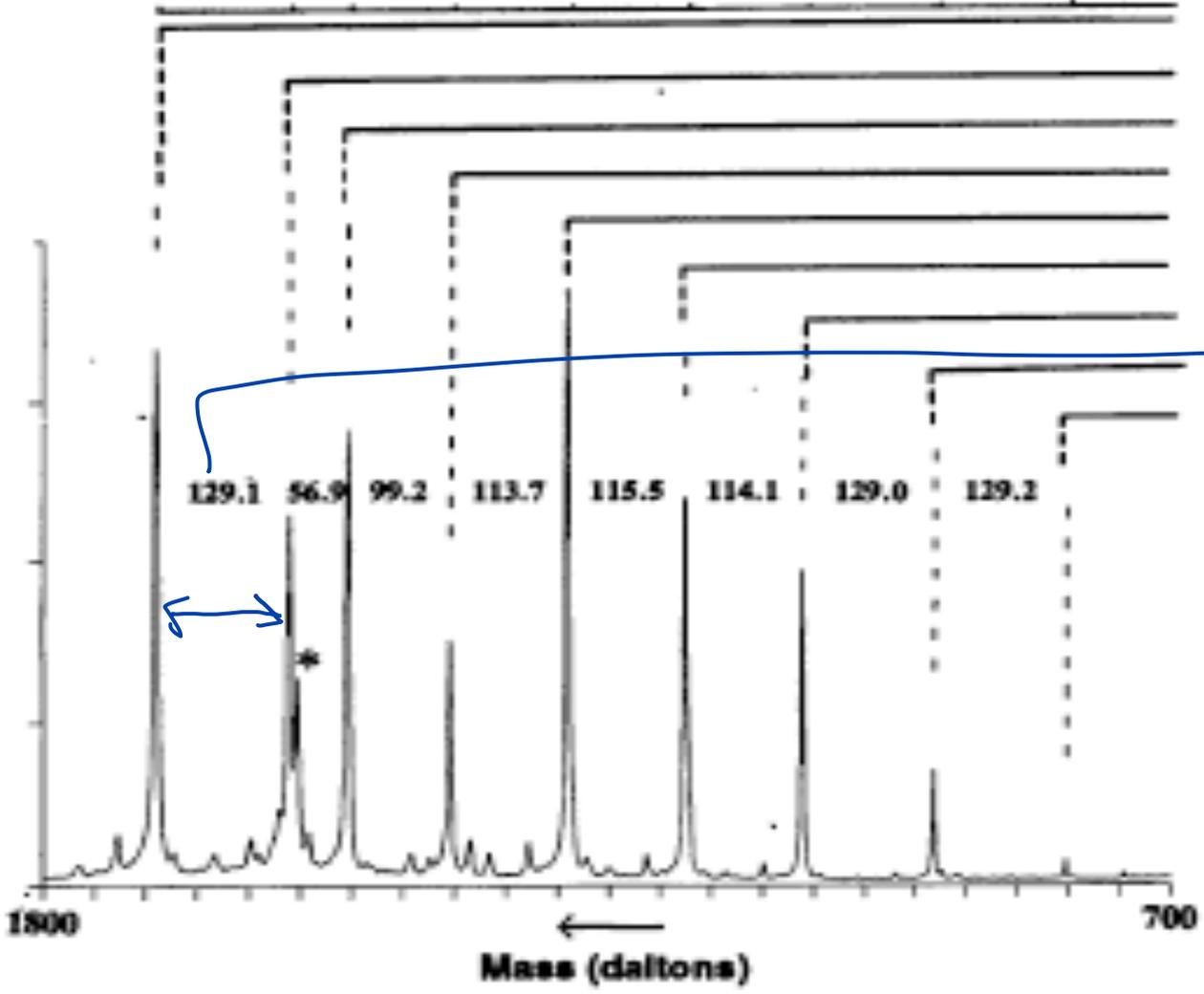
PC-Asn-Glu-Glu-Gly-Phe-Phe-Ser-Ala-Arg

PC = phenylisocyanate

- glu lose mass of 1  
glutamate AA  
- gly  
- val

It's the difference that matters!

glu gly val asn asp asn glu glu arginine  
 E G V N D N E E ..... R



this difference tell us the mass of the amino acid that was lost and we know the masses of the amino acids so we can determine which ones are lost thus the sequence

Brian T. Chait; Rong Wang; Ronald C. Beavis; Stephen B. H. Kent

Science, New Series, Vol. 262, No. 5130, Genome Issue. (Oct. 1, 1993), pp. 89-92.

