

Chimie organique bioorientée

Luc Patiny

<https://biooriented.cheminfo.org>

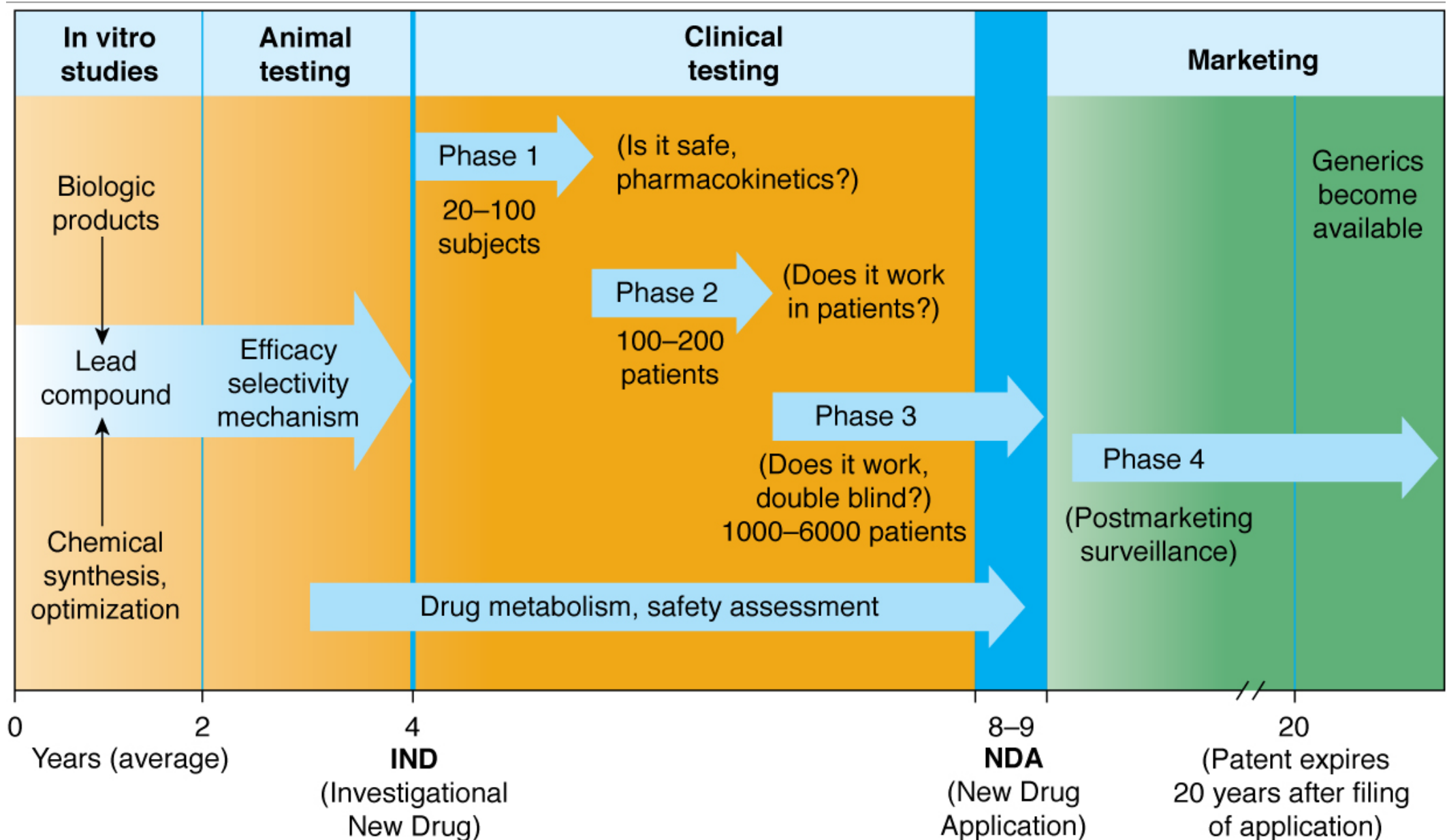
Introduction

En 2020, l'industrie chimique et pharmaceutique a contribué à hauteur de 6,3% au produit intérieur brut. Elle se place ainsi juste derrière l'industrie des machines, mais est en tête pour les exportations. Chaque année des produits chimiques et pharmaceutiques d'une valeur de plus de 116 milliards de francs sont vendus à l'étranger, ce qui représente près de 52% des exportations totales. En 2020, cette industrie employait environ 74'000 personnes en Suisse et plus de 338'000 à l'étranger.

Productivité exceptionnelle en comparaison de branches

Les nouvelles données font encore mieux apparaître l'avance de productivité de l'industrie pharmaceutique. Avec une valeur ajoutée de 332 francs suisses par heure de travail ou 627 000 francs par poste de travail en 2014, la productivité horaire de l'industrie pharmaceutique était environ quatre fois supérieure à celle de l'économie globale et 3,5 fois supérieure à celle de l'ensemble de l'industrie.

Recherche d'un médicament



Plan du cours

- **Introduction**
- **Analyse structurale**
 - Spectrométrie de masse
 - Degré d'insaturation
 - Spectrométrie infrarouge
 - Résonance Magnétique Nucléaire
- **Acides aminés, peptides et protéines**
 - Acides aminés
 - Synthèse peptidique
 - Protéine et JsMol
- **Conclusions**
 - Interaction protéine / inhibiteur
 - Exemple avec la 'peptide deformylase'

Organisation pratique

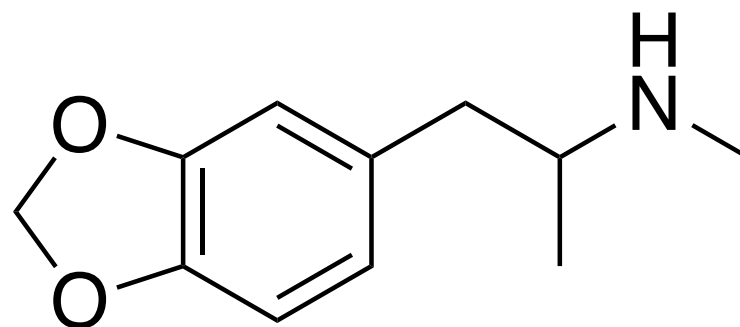
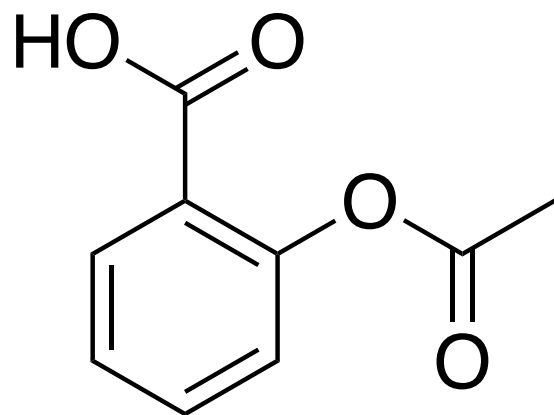
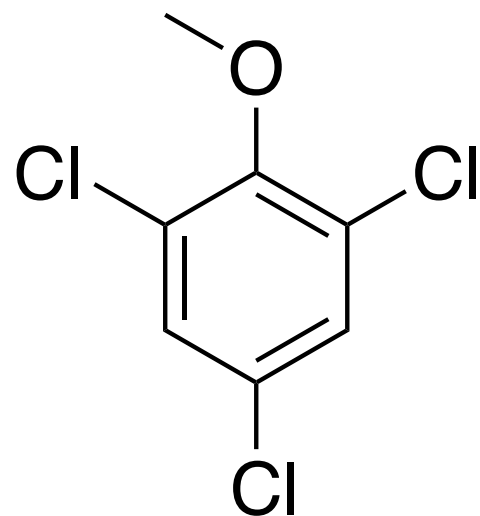
- **Cours théorique** toutes les 2 semaines
- **Exercices pratiques** toutes les semaines
- **Assistant:**
 - Shubhanga Balla - shubhanga.ballal@epfl.ch
- **Contrôle continu:**
 - 2/6: travail JsMol (présentation le 12 ou 19 décembre)
 - 4/6: test écrit (12 décembre)

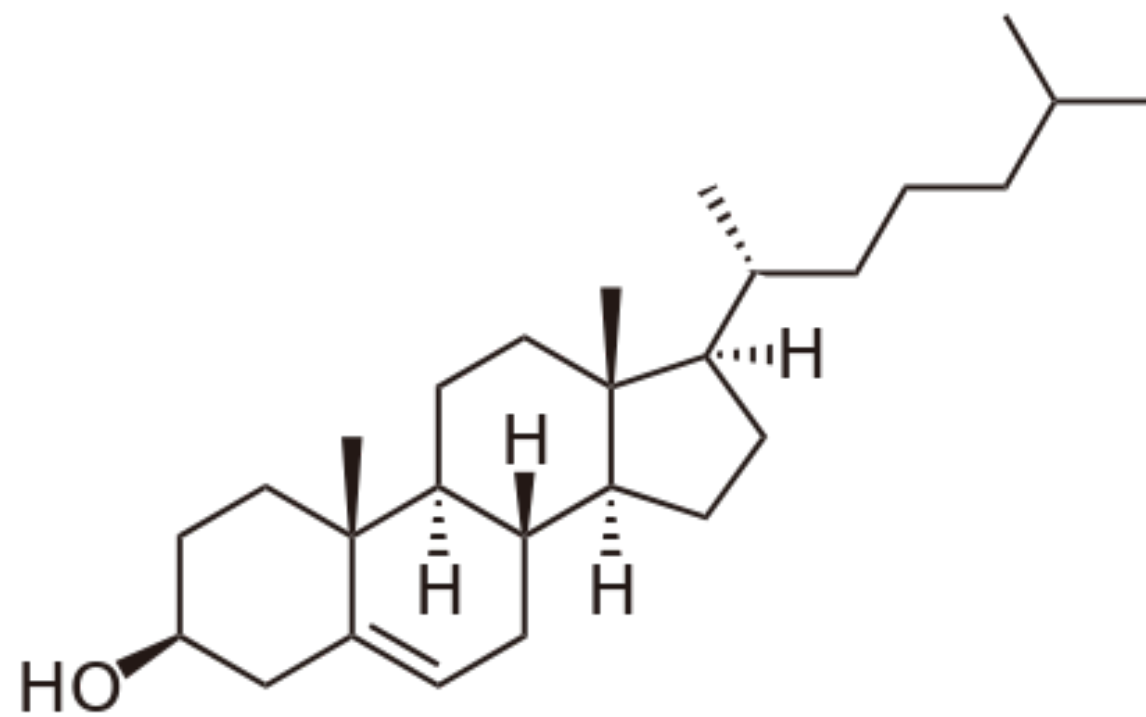
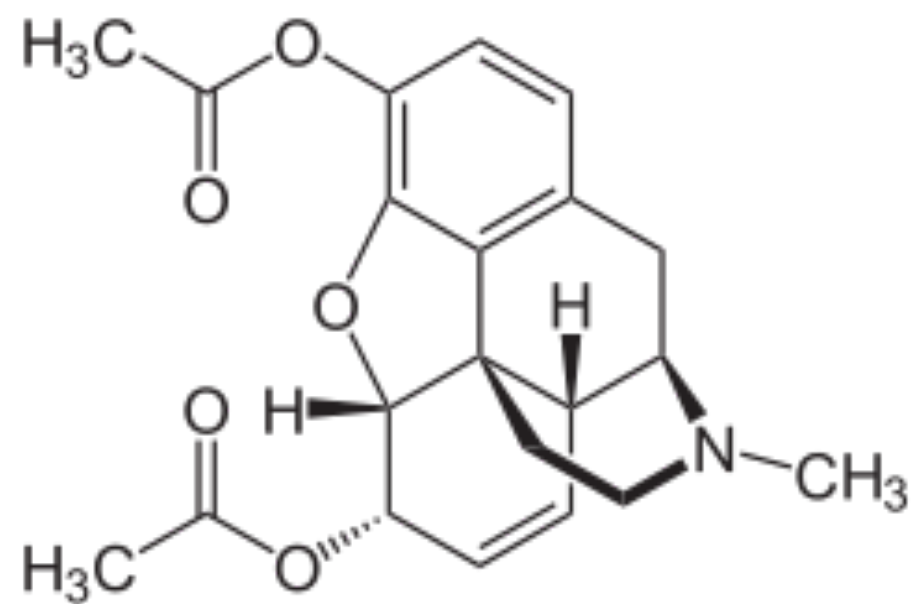
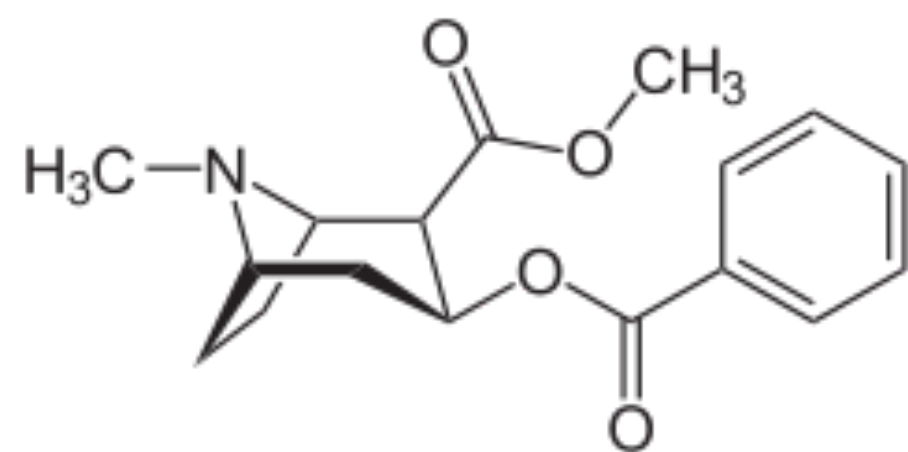
Support

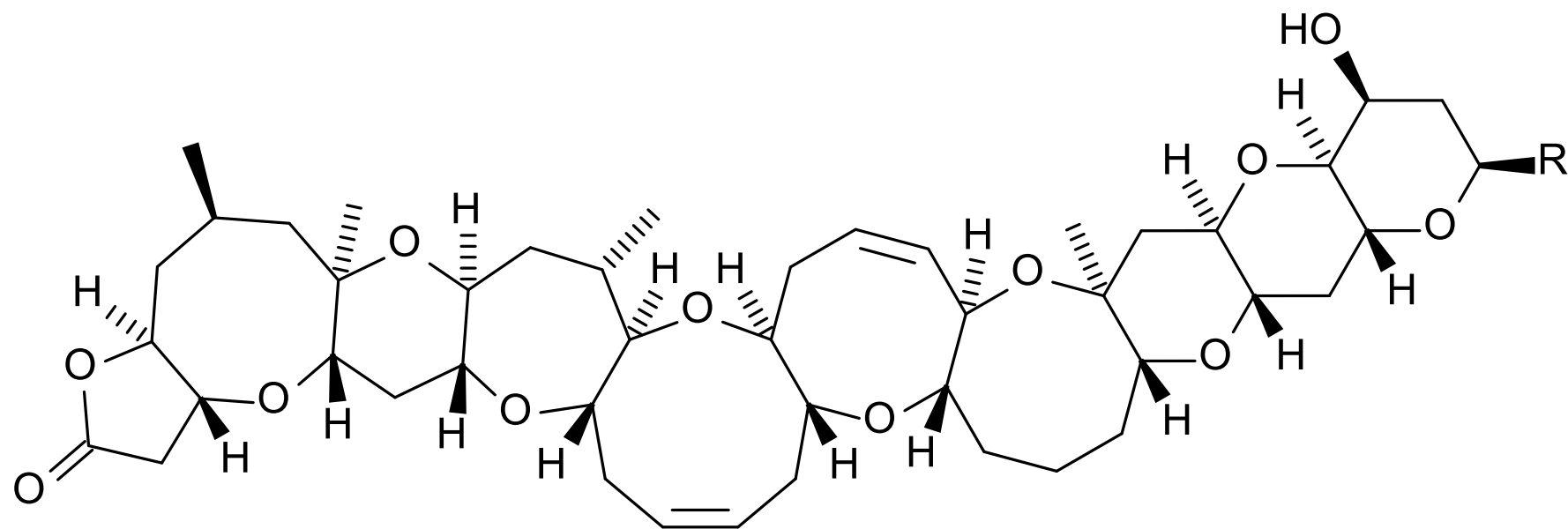
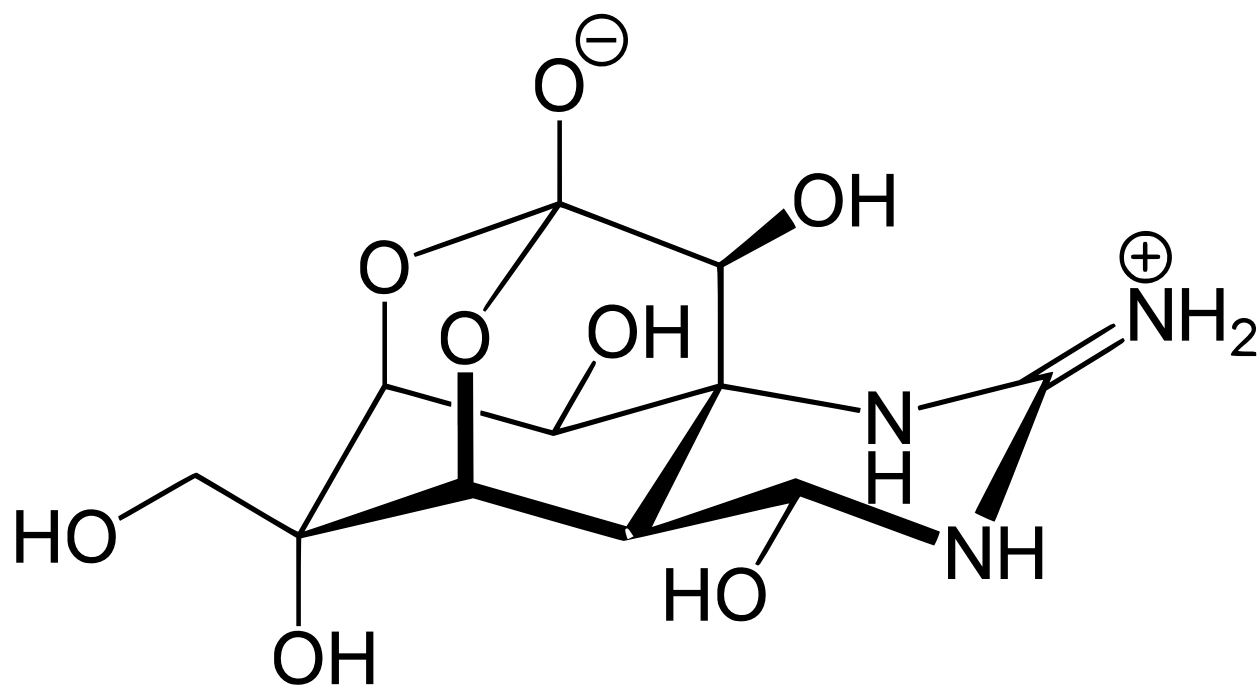
- <https://moodle.epfl.ch/course/view.php?id=16403>
- <https://biooriented.cheminfo.org>

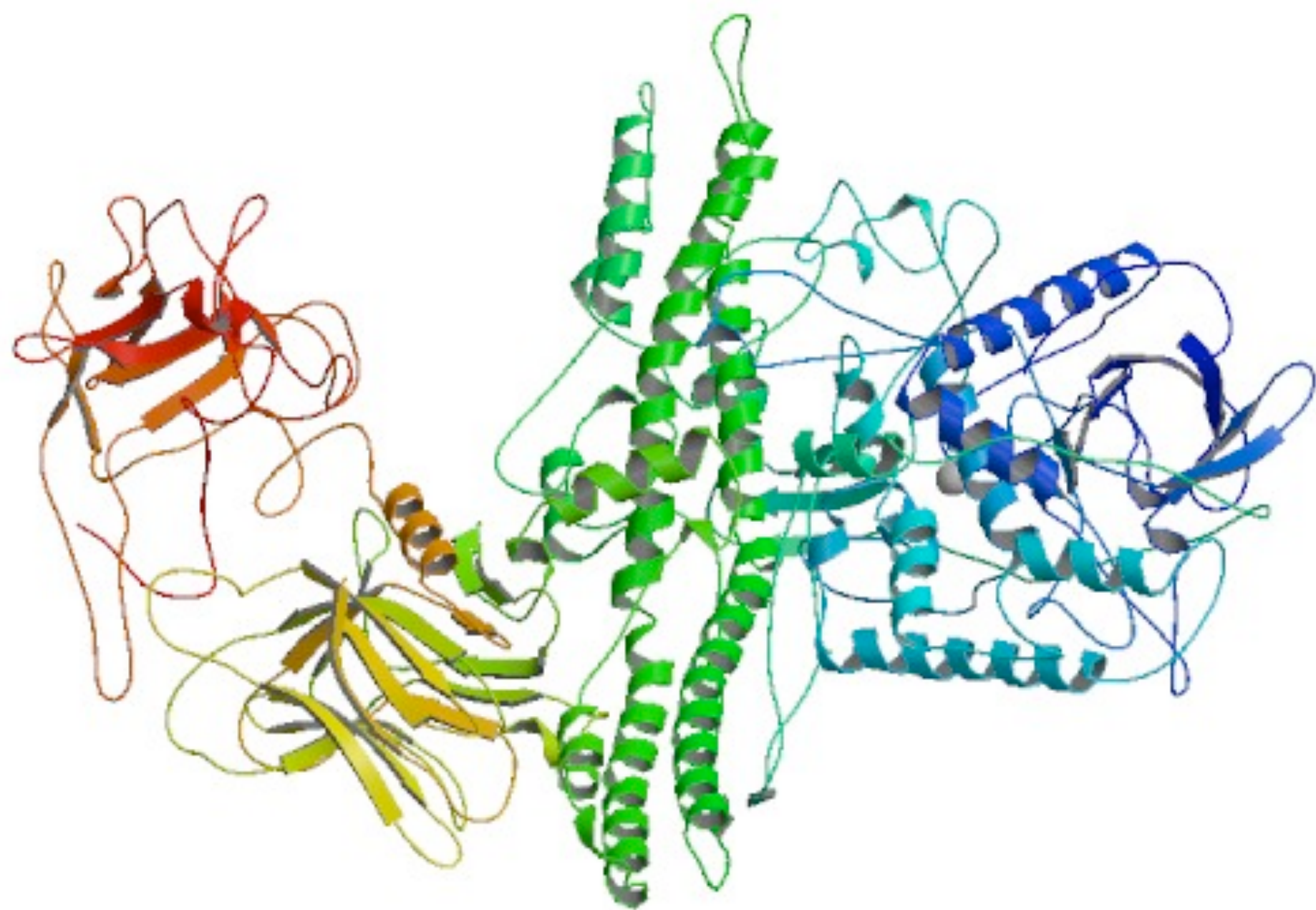
Analyse structurale

Détermination de la structure d'un produit inconnu









DOUZE CAS, UN MORT... CE QUE L'ON SAIT SUR LES CAS DE BOTULISME DÉTECTÉS EN FRANCE

Sophie Cazaux Le 13/09/2023 à 11:47



12 cas de botulisme ont été identifiés en France ces derniers jours, liés à des sardines servies dans un restaurant de Bordeaux. Un décès a été recensé en Île-de-France. En raison du délai d'incubation de la maladie, les autorités s'attendent à détecter des cas jusqu'à ce week-end.

Link

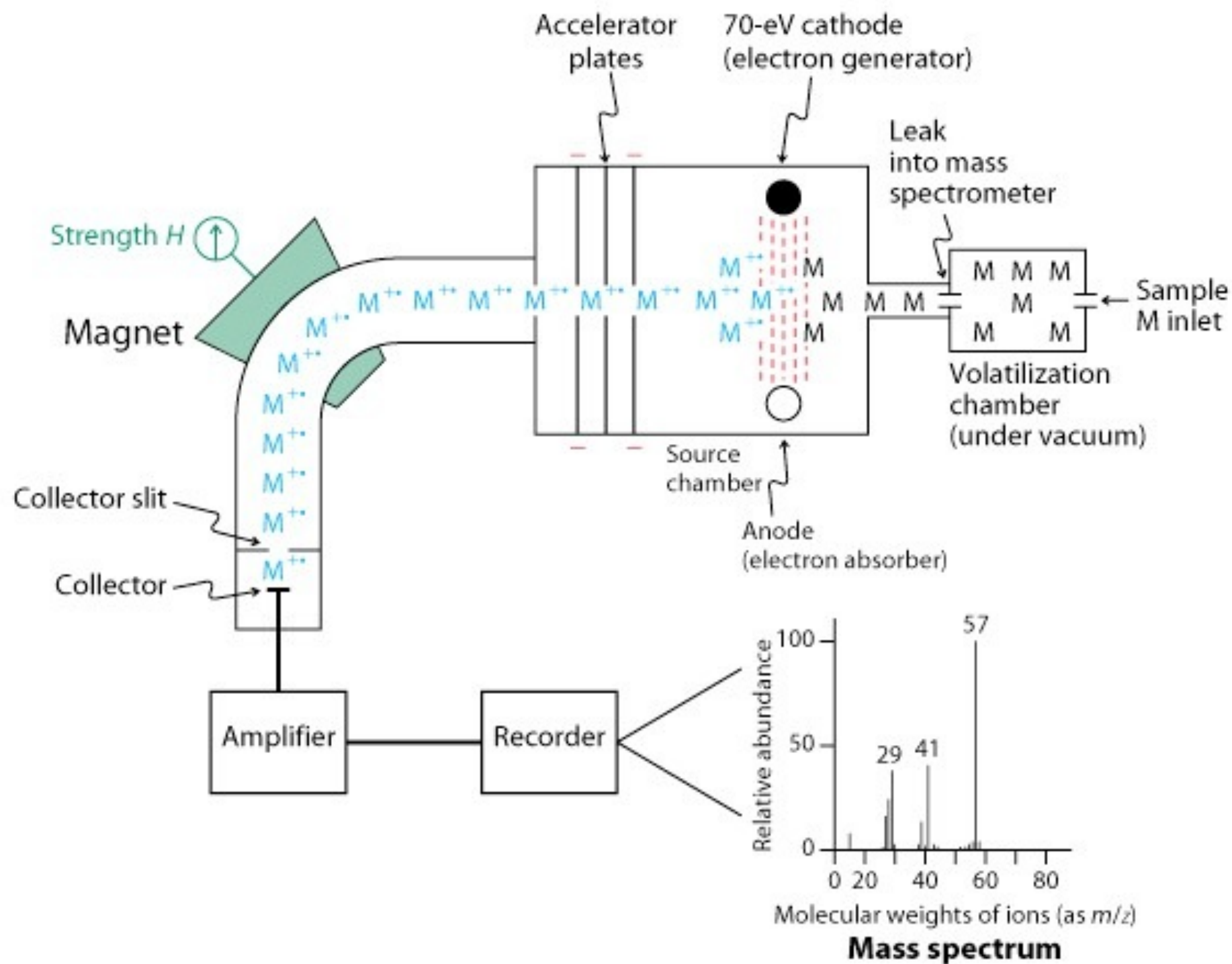
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18			
1	1 H 1.0082		Alkali metals		Lanthanoids	Nonmetals												2 He 4.002...			
2	3 Li 6.942	4 Be 9.012...		Alkaline earth metals				Actinoids	Halogens							5 B 10.812	6 C 12.0112	7 N 14.0072	8 O 15.9992	9 F 18.99...	10 Ne 20.1797
3	11 Na 22.98...	12 Mg 24.3059		Transition metals				Post- transition metals	Noble gases							13 Al 26.98...	14 Si 28.0854	15 P 30.97...	16 S 32.062	17 Cl 35.452	18 Ar 39.948
4	19 K 39.0983	20 Ca 40.078	21 Sc 44.95...	22 Ti 47.867	23 V 50.9415	24 Cr 51.9961	25 Mn 54.93...	26 Fe 55.845	27 Co 58.93...	28 Ni 58.6934	29 Cu 63.546	30 Zn 65.38	31 Ga 69.723	32 Ge 72.63	33 As 74.9216	34 Se 78.96	35 Br 79.9049	36 Kr 83.798			
5	37 Rb 85.4678	38 Sr 87.62	39 Y 88.90...	40 Zr 91.224	41 Nb 92.90...	42 Mo 95.96	43 Tc 98	44 Ru 101.07	45 Rh 102.9...	46 Pd 106.42	47 Ag 107.8...	48 Cd 112.411	49 In 114.818	50 Sn 118.71	51 Sb 121.76	52 Te 127.6	53 I 126.9...	54 Xe 131.293			
6	55 Cs 132.9...	56 Ba 137.327	57-71	72 Hf 178.49	73 Ta 180.9...	74 W 183.84	75 Re 186.207	76 Os 190.23	77 Ir 192.217	78 Pt 195.084	79 Au 196.9...	80 Hg 200.592	81 Tl 204.389	82 Pb 207.2	83 Bi 208.9...	84 Po 209	85 At 210	86 Rn 222			
7	87 Fr 223	88 Ra 226		89-103	104 Rf 267	105 Db 268	106 Sg 269	107 Bh 270	108 Hs 269	109 Mt 278	110 Ds 281	111 Rg 281	112 Cn 285	113 Nh 286	114 Fl 289	115 Mc 289	116 Lv 293	117 Ts 294	118 Og 294		
				57 La 138.9...	58 Ce 140.116	59 Pr 140.9...	60 Nd 144.242	61 Pm 145	62 Sm 150.36	63 Eu 151.964	64 Gd 157.25	65 Tb 158.9...	66 Dy 162.5	67 Ho 164.9...	68 Er 167.259	69 Tm 168.9...	70 Yb 173.054	71 Lu 174.9...			
				89 Ac 227	90 Th 232.0...	91 Pa 231.0...	92 U 238.0...	93 Np 237	94 Pu 244	95 Am 243	96 Cm 247	97 Bk 247	98 Cf 251	99 Es 252	100 Fm 257	101 Md 258	102 No 259	103 Lr 266			

I II III IV V VI VII

1 H 1.0082						
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37 Rb 85.4678	38 Sr 87.62	49 In 114.818	50 Sn 118.71	51 Sb 121.76	52 Te 127.6	53 I 126.9...

Stratégie

Spectrométrie de masse



<https://forms.gle/edM9eWG49uRh59GQ9>

Signal correspondant à un carbone chargé positivement en spectrométrie de masse

1 carbone

- ☐ < 12u
- ☐ = 12u
- ☐ > 12u
- ☐ Impossible d'être certain



Isotope		Abondance (%)	Masse isotopique [u]
H	1	99.99	1.0078
	2	0.01	2.0141
C	12	98.93	12.0000
	13	1.07	13.0033
N	14	99.64	14.0030
	15	0.36	15.0001
O	16	99.76	15.9949
	17	0.04	16.9991
	18	0.20	17.9991
			Electron: 0.0005



Exercice

- Dessiner le spectre de masse théorique de C_2^{++}

Isotope		Abondance (%)	Masse isotopique [u]
H	1	99.99	1.0078
	2	0.01	2.0141
C	12	98.93	12.0000
	13	1.07	13.0033

Electron: 0.0005

<https://www.cheminfo.org/flavor/biooriented>

<https://biooriented.cheminfo.org>

Exercice pour déterminer la charge de la molécule
observée en masse

Isotope		Abondance (%)	Masse isotopique [u]
H	1	99.99	1.0078
	2	0.01	2.0141
C	12	98.93	12.0000
	13	1.07	13.0033
N	14	99.64	14.0030
	15	0.36	15.0001
O	16	99.76	15.9949
	17	0.04	16.9991
	18	0.20	17.9991

Electron: 0.0005

Définitions

Unité de masse atomique unifiée

Unité égale à (quasi *) $1/12$ de la masse d'un isotope 12 du carbone

=

$1.660539 \cdot 10^{-27} \text{ kg}$

Unité: Da (dalton) ou u

* exactement jusqu'au 20 mai 2019

Isotope		Abondance (%)	Masse isotopique [u]
H	1	99.99	1.0078
	2	0.01	2.0141
C	12	98.93	12.0000
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	15	0.36	15.0001
O	16	99.76	15.9949
	17	0.04	16.9991
	18	0.20	17.9991

Electron: 0.0005

Masse atomique

Moyenne pondérée des masses des isotopes naturels stables d'un élément donné

Isotope		Abondance (%)	Masse isotopique [u]
H	1	99.99	1.0078
	2	0.01	2.0141
C	12	98.93	12.0000
	13	1.07	13.0033

Electron: 0.0005

Masse moléculaire

Masse calculée en utilisant la masse atomique de chaque élément.

Masse nominale

Masse calculée en utilisant la masse entière de l'isotope majoritaire de chaque élément.

	Isotope	Abondance (%)	Masse isotopique [u]
H	1	99.99	1.0078
	2	0.01	2.0141
C	12	98.93	12.0000
	13	1.07	13.0033
N	14	99.64	14.0030
	15	0.36	15.0001
O	16	99.76	15.9949
	17	0.04	16.9991
	18	0.20	17.9991

Masse isotopique

Masse calculée en utilisant les masses exactes des isotopes considérés

Masse monoisotopique

Masse calculée en utilisant les masses exactes des isotopes majoritaires de chaque élément

Les chimistes organiciens appellent parfois cela "masse exacte"

	Masse nominale	Abondance relative (%)	Abondance (%)	Masse isotopique [u]	Masse atomique
H	1	100	99.99	1.007825	1.008
	2	0.01	0.01	2.014101	
C	12	100	98.93	12.000000	12.011
	13	1.08	1.07	13.003354	
N	14	100	99.64	14.003074	14.007
	15	0.37	0.36	15.000108	
O	16	100	99.76	15.994914	15.999
	17	0.04	0.04	16.999131	
	18	0.20	0.20	17.999161	
P	31	100	100	30.973761	30.974
S	32	100	94.99	31.972071	32.065
	33	0.79	0.75	32.971458	
	34	4.47	4.25	33.967866	
	36	0.01	0.01	35.967080	
F	19	100	100	18.998403	18.998
Cl	35	100	75.76	34.968852	35.453
	37	32.00	24.24	36.965902	
Br	79	100	50.69	78.918337	79.903
	81	97.28	49.31	80.916290	
I	127	100	100	126.904473	126.904

Electron: 0.00054858

<https://biooriented.cheminfo.org>

Déterminer la masse monoisotopique de la molécule non ionisée

<https://forms.gle/ps6voMgXnJkzmvNT6>

Quelle formule brute correspond le mieux à une molécule mono chargée positivement dont la masse observée est 30.0450

30.0450

☐ CH₂O

☐ C₂H₆

☐ NO



Answer



Type	Abondance (%)	Masse isotopique [u]
C	1	99.99
	2	0.01
	12	98.93
	13	1.07
N	14	99.64
	15	0.36
O	16	99.76
	17	0.04
	18	0.20

Electron: 0.0005

Distribution isotopique

1 seul atome

Exercice

- **Dessinez le spectre de masse de :**
 - C^{+}
 - Cl^{+}
 - Br^{+}
 - S^{+}

C⁺ - Cl⁺ - Br⁺ - S⁺

	Masse nominale	Abondance relative (%)	Abondance (%)	Masse isotopique [u]	Masse atomique
H	1	100	99.99	1.007825	1.008
	2	0.01	0.01	2.014101	
C	12	100	98.93	12.000000	12.011
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P	31	100	100	30.973761	30.974
S	32	100	94.99	31.972071	32.065
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F	19	100	100	18.998403	18.998
Cl	35	100	75.76	34.968852	35.453
	37	32.00	24.24	36.965902	
Br	79	100	50.69	78.918337	79.903
	81	97.28	49.31	80.916290	

Electron: 0.00054858

Element	A (masse)	A (%)	A+1 (masse)	A+1 (%)	A+2 (masse)	A+2 (%)	A+4 (masse)	A+4 (%)
H	1	100	2	0.01				
C	12	100	13	1.08				
N	14	100	15	0.37				
O	16	100	17	0.04	18	0.20		
P	31	100						
S	32	100	33	0.79	34	4.47	36	0.01
F	19	100						
Cl	35	100			37	32.00		
Br	79	100			81	97.28		
I	127	100						

Elem	A	A	A+1	A+1	A+2	A+2	A+4	A+4
H	1	100	2	0.01				
C	12	100	13	1.08				
N	14	100	15	0.37				
O	16	100	17	0.04	18	0.20		
P	31	100						
S	32	100	33	0.79	34	4.47	36	0.01
F	19	100						
Cl	35	100			37	32.00		
Br	79	100			81	97.28		
I	127	100						

Distribution isotopique - plusieurs atomes

Isotopomères

2 molécules ayant le même nombre de chacun des isotopes à des positions différentes.

Isotopologues

2 molécules différents uniquement par leur composition isotopique

Isotopologue majoritaire

Composition isotopique la plus abondante.

Distribution isotopique

Ensemble des isotopologues avec leur masse et intensité relative respective

<https://www.chemcalc.org>

Exercice

- Dessiner la distribution isotopique de:
 - $\text{C}_2^{+\bullet}$
 - $\text{Cl}_2^{+\bullet}$
 - $\text{Br}_2^{+\bullet}$

Elem	A	A	A+1	A+1	A+2	A+2	A+4	A+4
H	1	100	2	0.01				
C	12	100	13	1.08				
N	14	100	15	0.37				
O	16	100	17	0.04	18	0.20		
P	31	100						
S	32	100	33	0.79	34	4.47	36	0.01
F	19	100						
Cl	35	100			37	32.00		
Br	79	100			81	97.28		
I	127	100						

<https://biooriented.cheminfo.org>

Trouver la MF au départ de la distribution isotopique

Autres exercices sur <https://www.chemcalc.org>

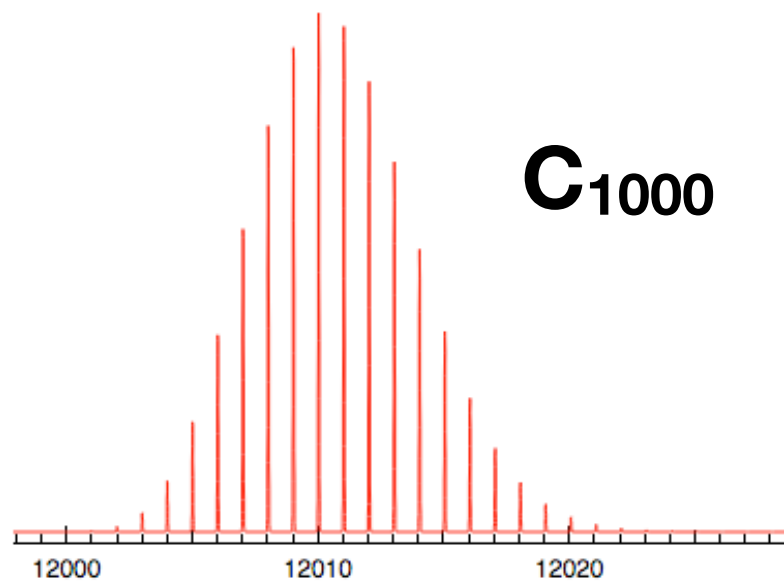
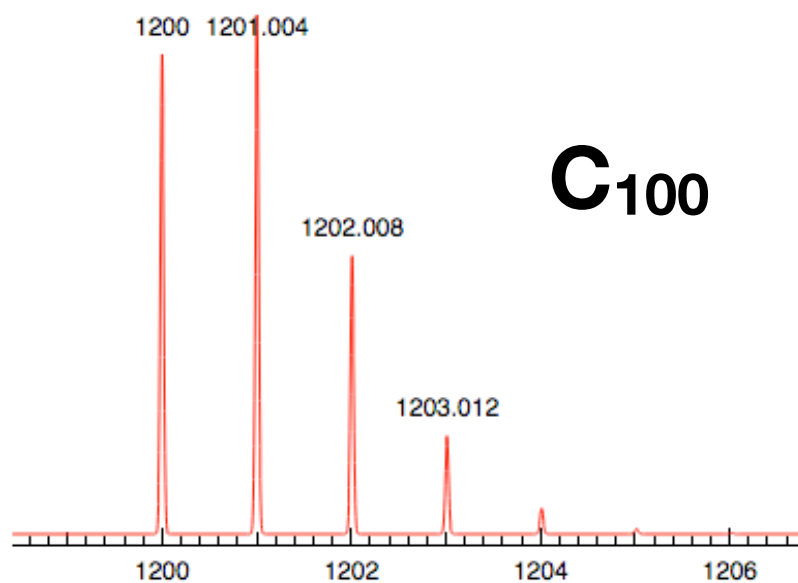
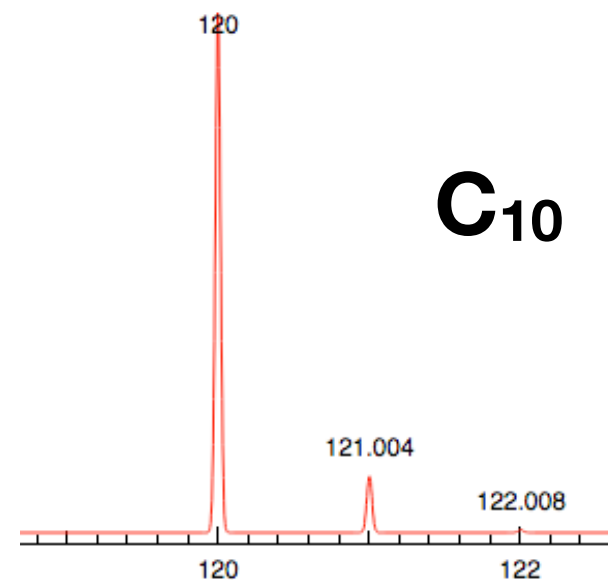
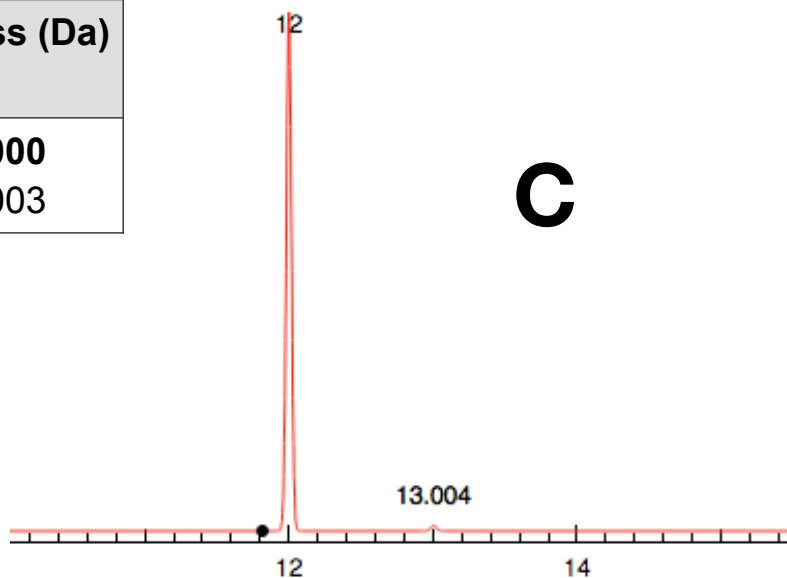
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	2	0.01	0.01	2.014101	
C	12	100	98.93	12.000000	12.011
	13	1.08	1.07	13.003354	
N	14	100	99.64	14.003074	14.007
	15	0.37	0.36	15.000108	
O	16	100	99.76	15.994914	15.999
	17	0.04	0.04	16.999131	
	18	0.20	0.20	17.999161	
P	31	100	100	30.973761	30.974
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	33	0.79	0.75	32.971458	
	34	4.47	4.25	33.967866	
	36	0.01	0.01	35.967080	
F	19	100	100	18.998403	18.998
Cl	35	100	75.76	34.968852	35.453
	37	32.00	24.24	36.965902	
Br	79	100	50.69	78.918337	79.903
	81	97.28	49.31	80.916290	
I	127	100	100	126.904473	126.904



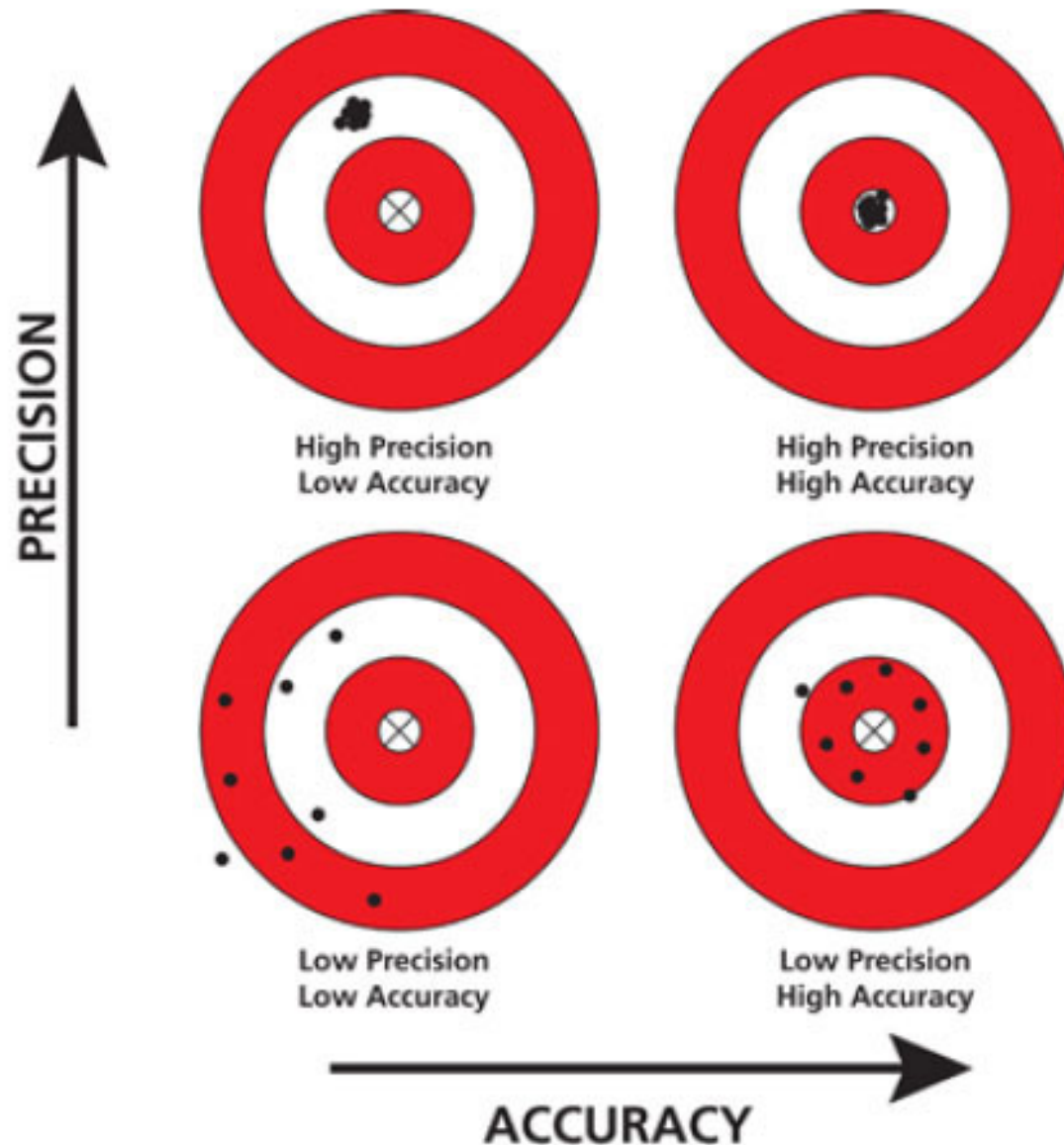
Electron: 0.00054858

Plusieurs carbones

	Nominal mass	Abundance (%)	Mass (Da)
C	12	98.93	12.000
	13	1.07	13.003



Répétabilité / Exactitude



■ ■ Répétabilité

=

🇬🇧 precision

■ ■ Exactitude

=

🇬🇧 accuracy

Exactitude (accuracy)

$$\textit{Exactitude} = \textit{Mass accuracy} = \frac{m_{\textit{experimental}} - m_{\textit{theory}}}{m_{\textit{theory}}} * 10^6 \textit{ppm}$$

Mass defect

	Isotope	Abondance (%)	Masse isotopique [u]
H	1	99.99	1.008
	2	0.01	2.014
C	12	98.93	12.000
	13	1.07	13.003
N	14	99.64	14.003
	15	0.36	15.000
O	16	99.76	15.995
	17	0.04	16.999
	18	0.20	17.999
S	32	94.99	31.972
	33	0.75	32.971
	34	4.25	33.968
	36	0.01	35.967

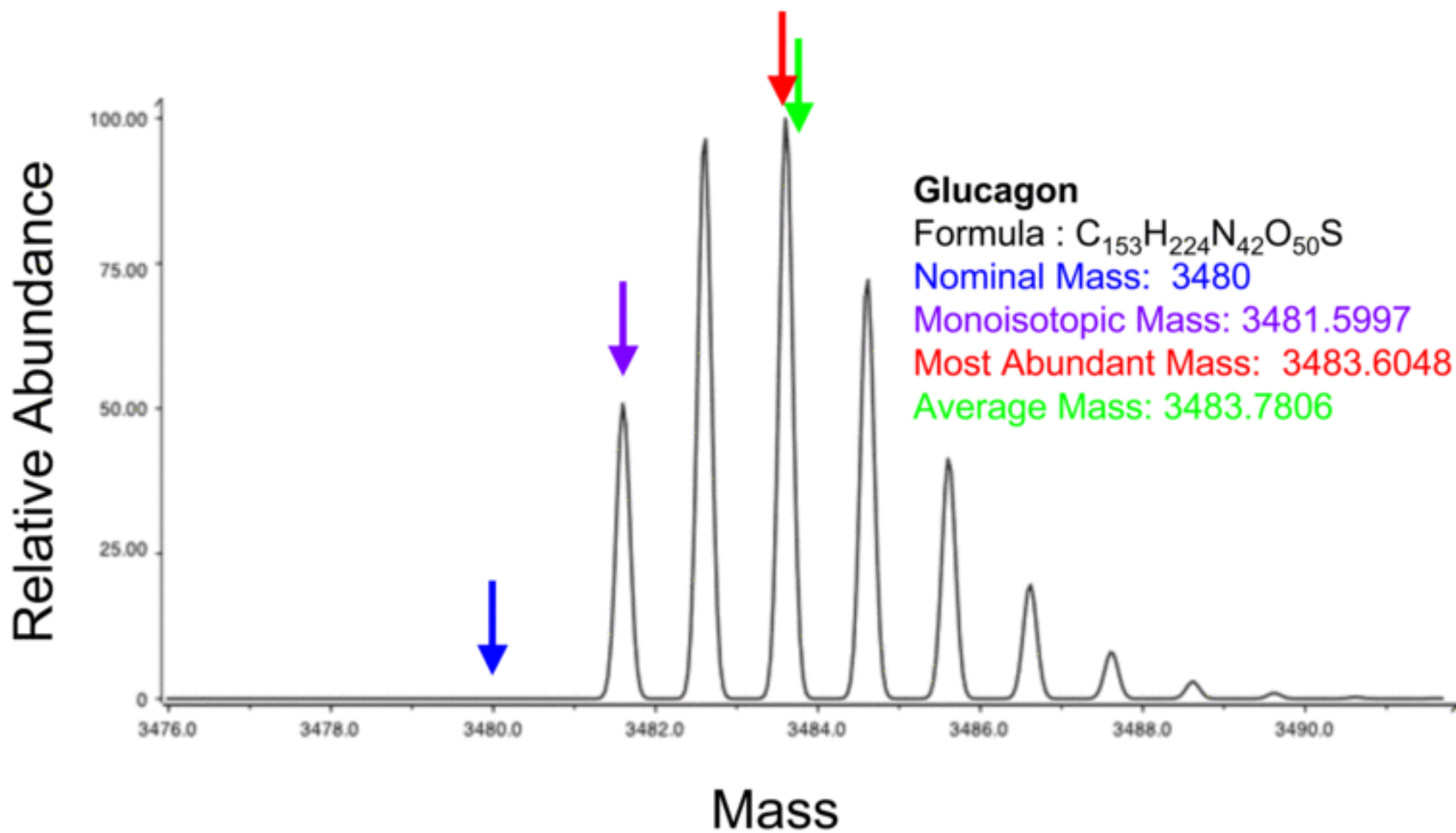
SCN⁻



Masse majoritaire

Masse correspondante au pic majoritaire observé dans le spectre de masse

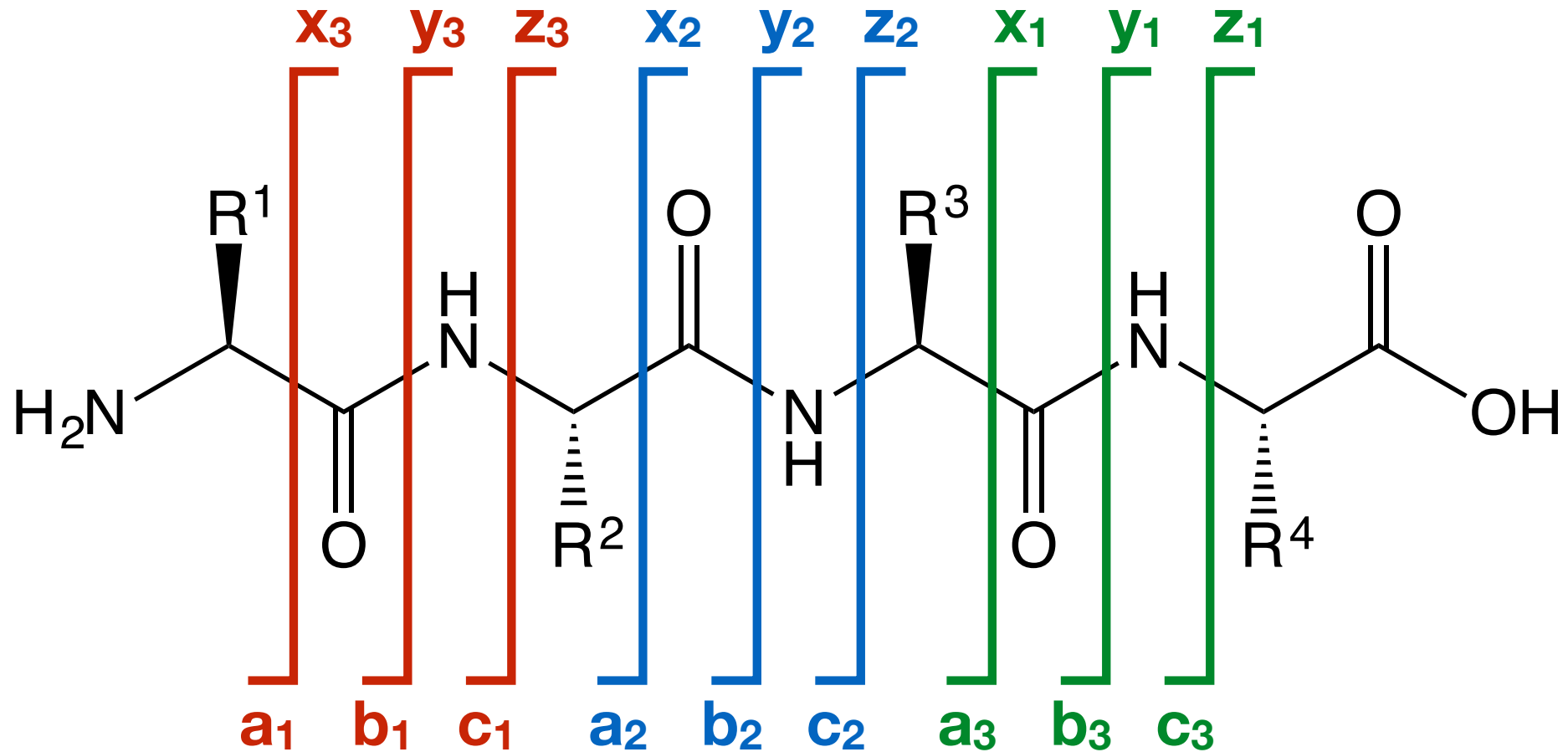
Dépend de la largeur des pics (résolution)



Cys100

Exercices intégrés

Peptide fragmentation



Proteomics

Protein digestion

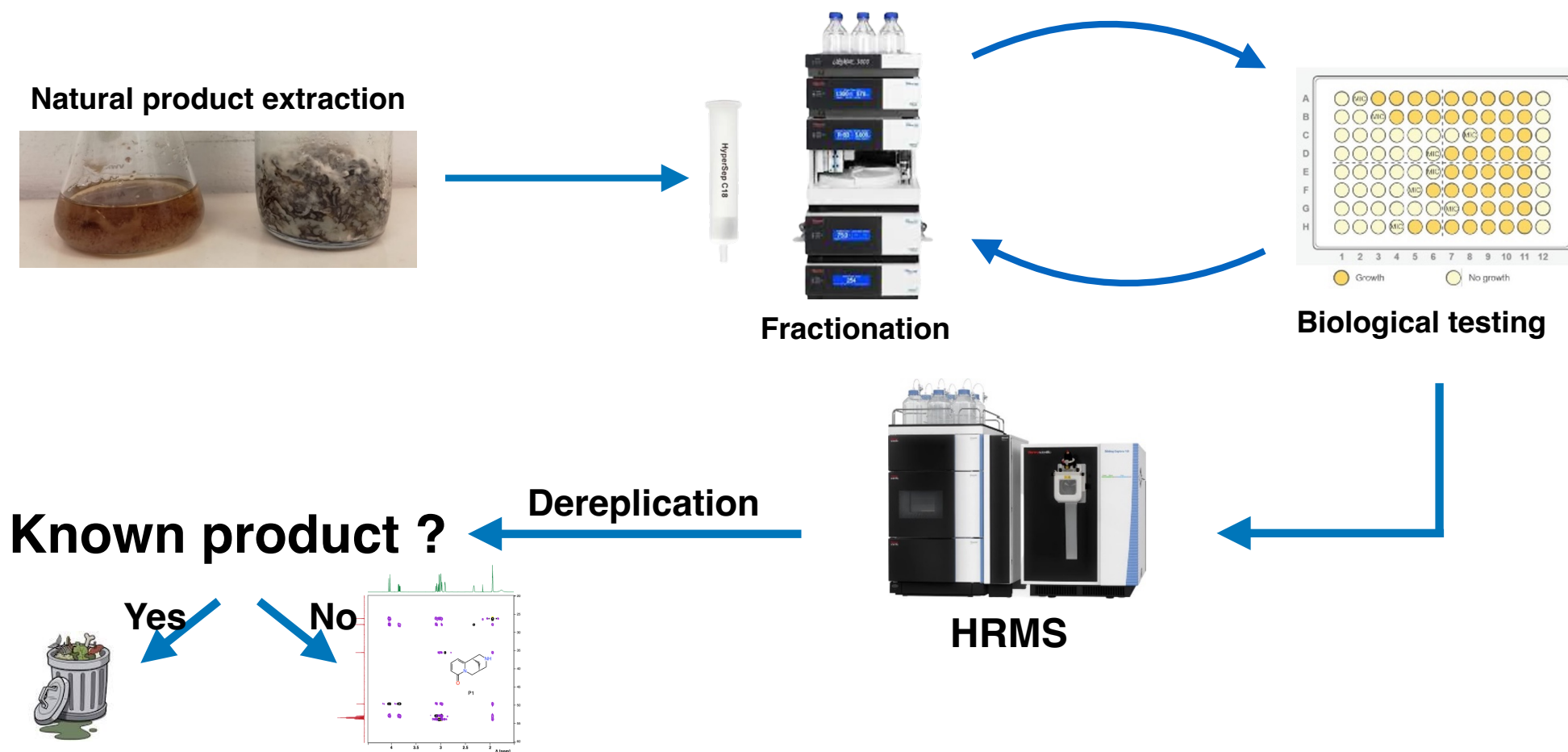
ASP	GLU	ILE	LYS	ILE	VAL	LYS	TYR	PRO	ASP	PRO	ILE	LEU
ARG	ARG	ARG	SER	GLU	VAL	THR	ASN	PHE	ASP	ASP	ASN	LEU
LYS	ARG	VAL	VAL	ARG	LYS	MSE	PHE	ASP	ILE	MSE	TYR	GLU
SER	LYS	GLY	ILE	GLY	LEU	SER	ALA	PRO	GLN	VAL	ASN	ILE
SER	LYS	ARG	ILE	ILE	VAL	TRP	ASN	ALA	LEU	TYR	GLU	LYS
ARG	LYS	GLU	GLU	ASN	GLU	ARG	ILE	PHE	ILE	ASN	PRO	SER
ILE	VAL	GLU	GLN	SER	LEU	VAL	LYS	LEU	LYS	LEU	ILE	GLU
GLY	CYS	LEU	SER	PHE	GLY	ILE	GLU	GLY	LYS	VAL	GLU	ARG
PRO	SER	ILE	VAL	SER	ILE	SER	TYR	TYR	ASP	ILE	ASN	GLY
TYR	LYS	HIS	LEU	LYS	ILE	LEU	LYS	GLY	ILE	HIS	SER	ARG
ILE	PHE	GLN	HIS	GLU	PHE	ASP	HIS	LEU	ASN	GLY	THR	LEU
PHE	ILE	ASP	LYS	MSE	THR	GLN	VAL	ASP	LYS	LYS	LYS	VAL
ARG	PRO	LYS	LEU	ASN	GLU	LEU	ILE	ARG	ASP	TYR	LYS	ALA
THR	HIS	SER	GLU	GLU	PRO	LEU	GLU	HIS	HIS	HIS	HIS	HIS
HIS												

Example: digestion of peptide deformylase by chymotrypsin

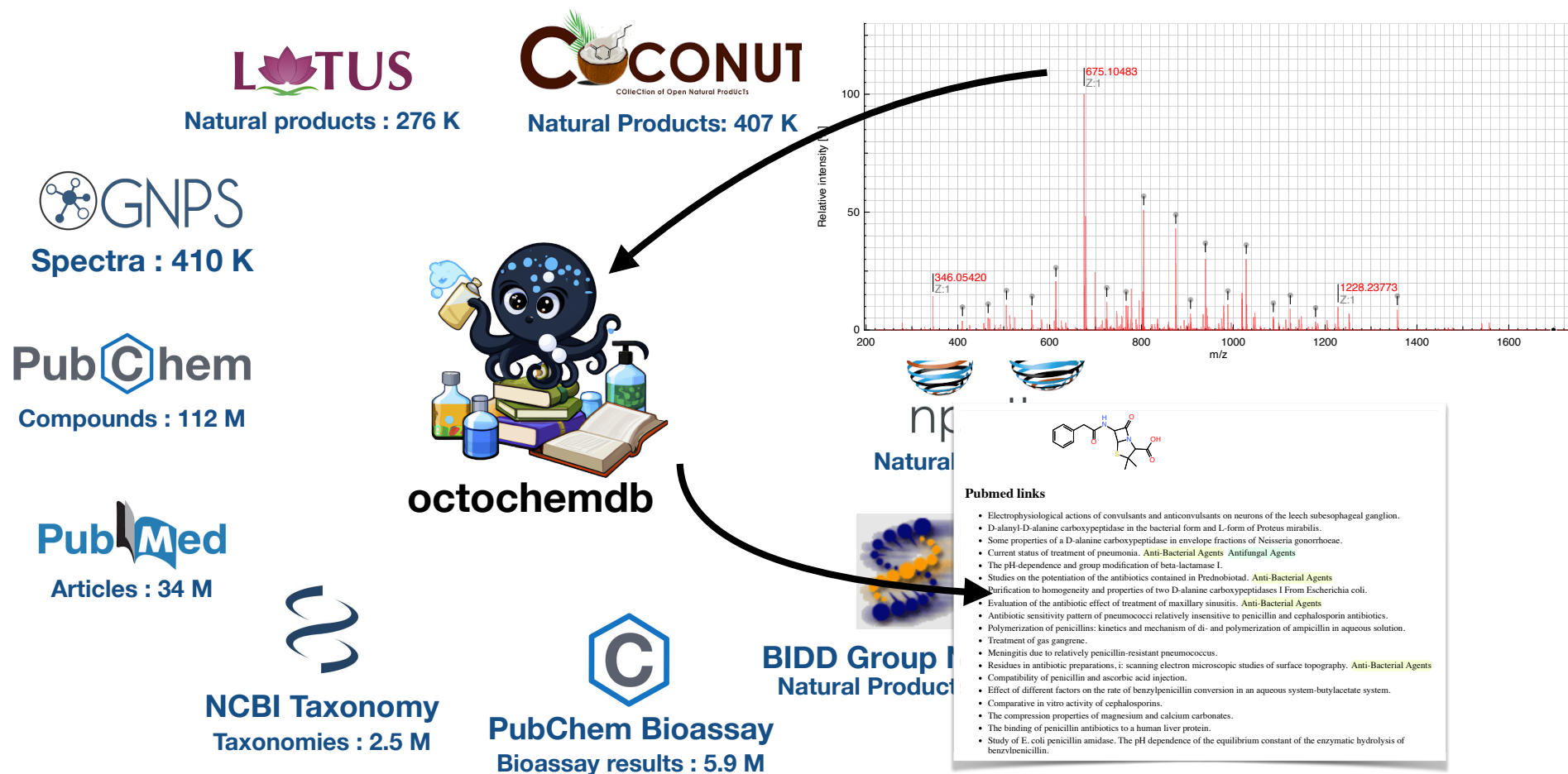
Déréplication

<https://octochemdb.cheminfo.org>

Natural product: dereplication

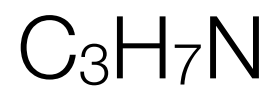


Searching for existing information



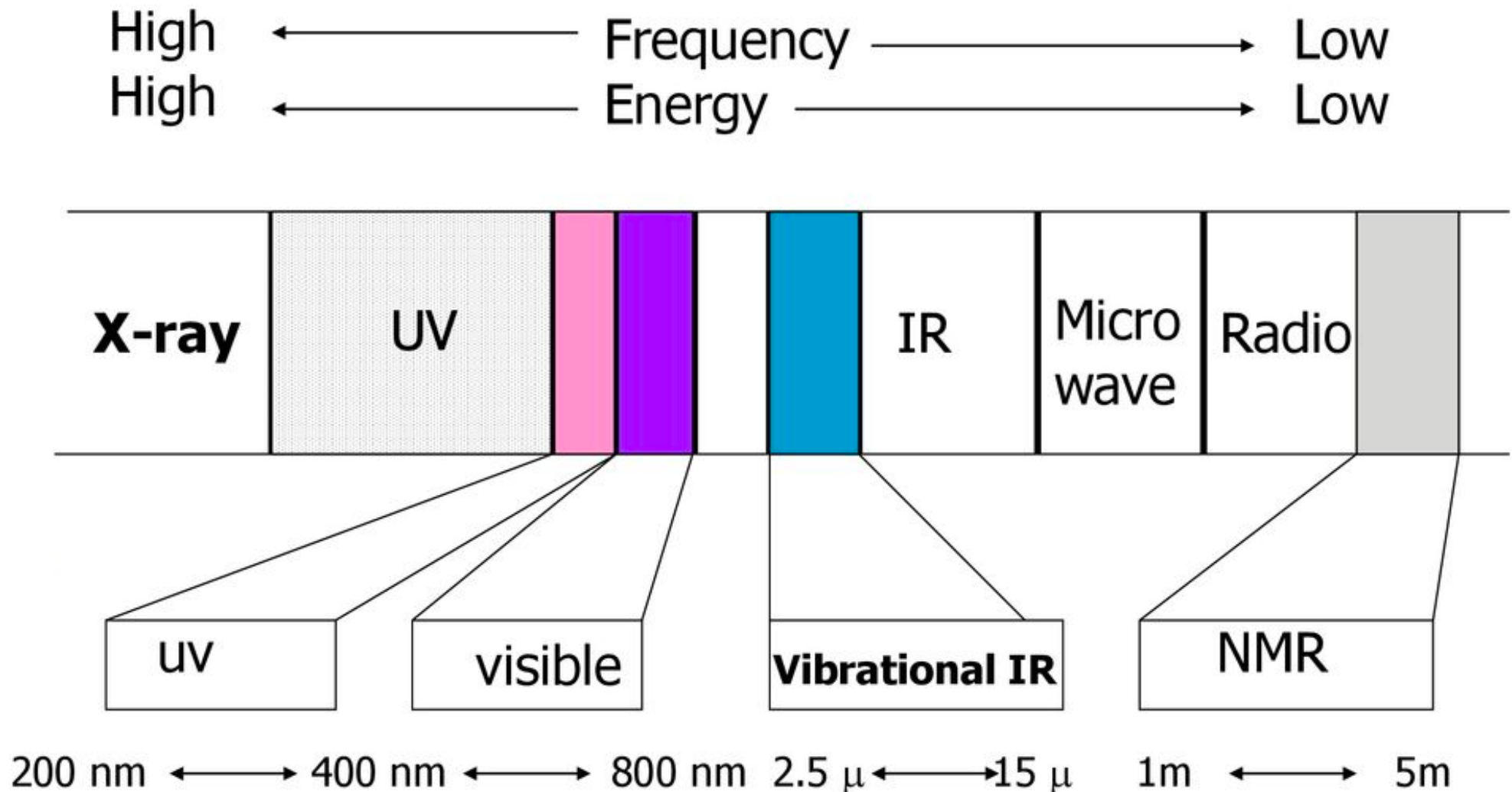
Degré d'insaturation

Isomères de structure

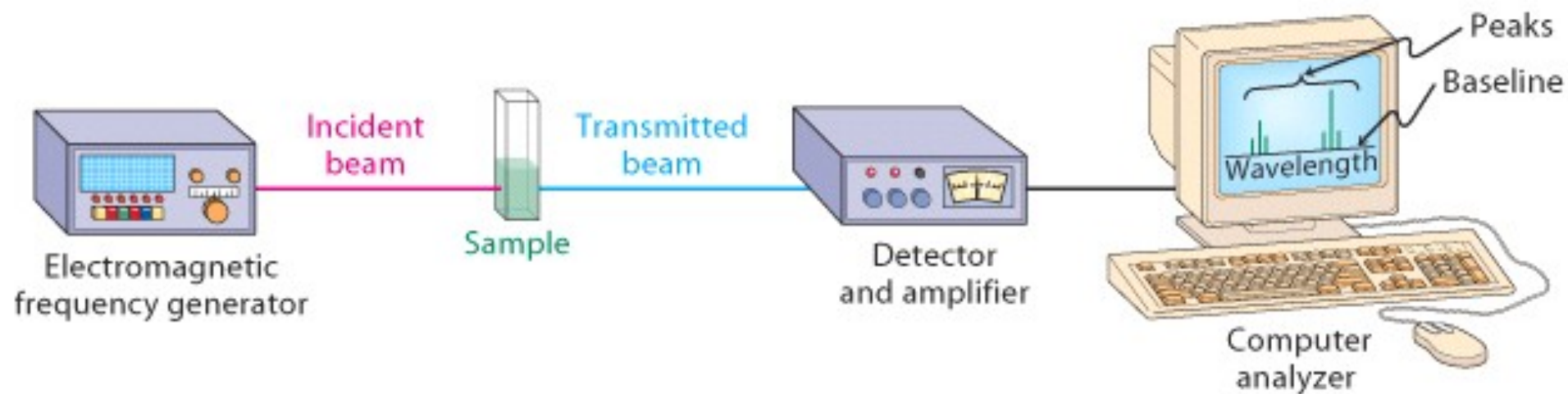


Spectroscopie infrarouge

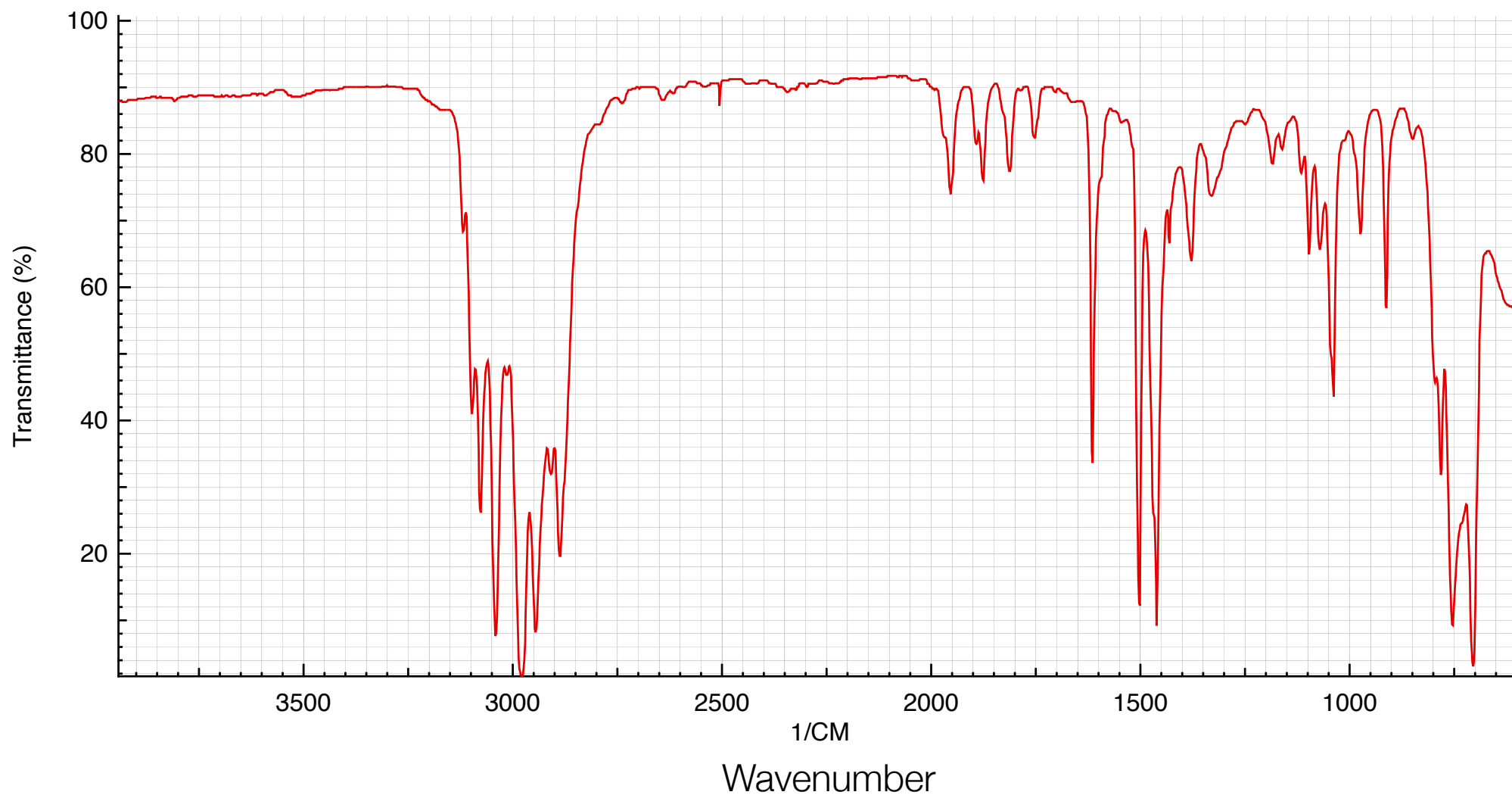
Electromagnetic spectrum



IR spectrophotometer



IR of ethylbenzene



Loi de Hooke



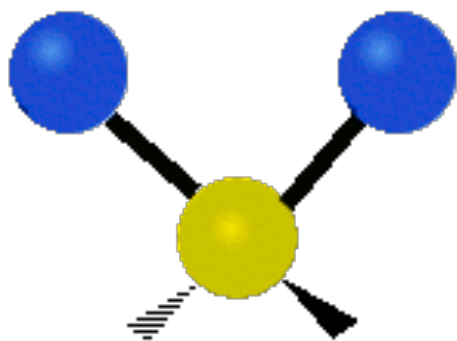
A $\longleftrightarrow$ B

Frequency (ν)

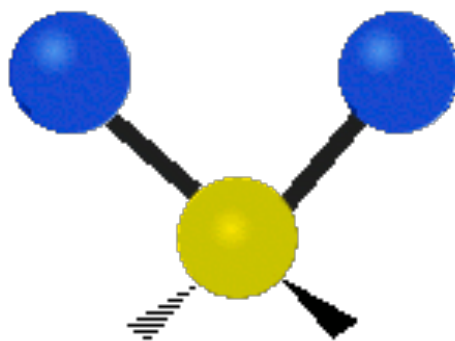
$$\bar{\nu} = k \sqrt{f \frac{m_1 + m_2}{m_1 m_2}}$$

$$\bar{v} = k \sqrt{f \frac{m_1 + m_2}{m_1 m_2}}$$

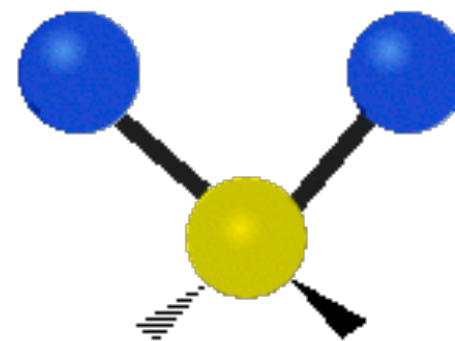
Vibrations moléculaires



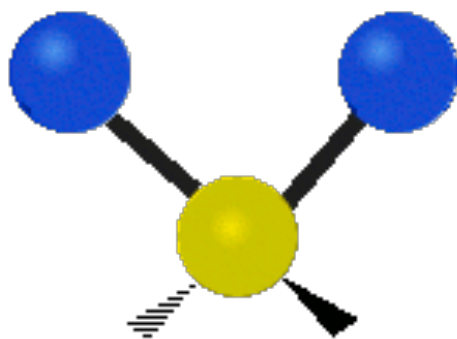
Symmetrical stretching



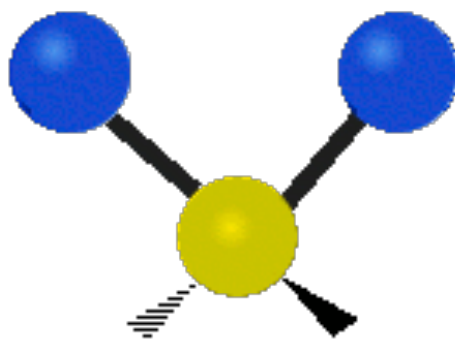
Scissoring



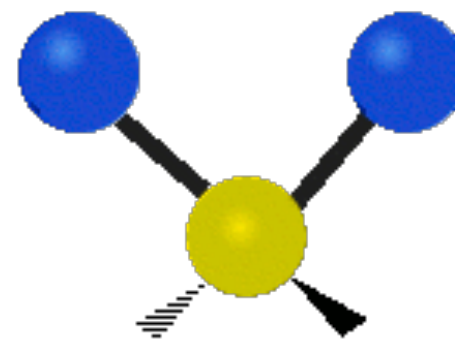
Wagging



Asymmetrical stretching

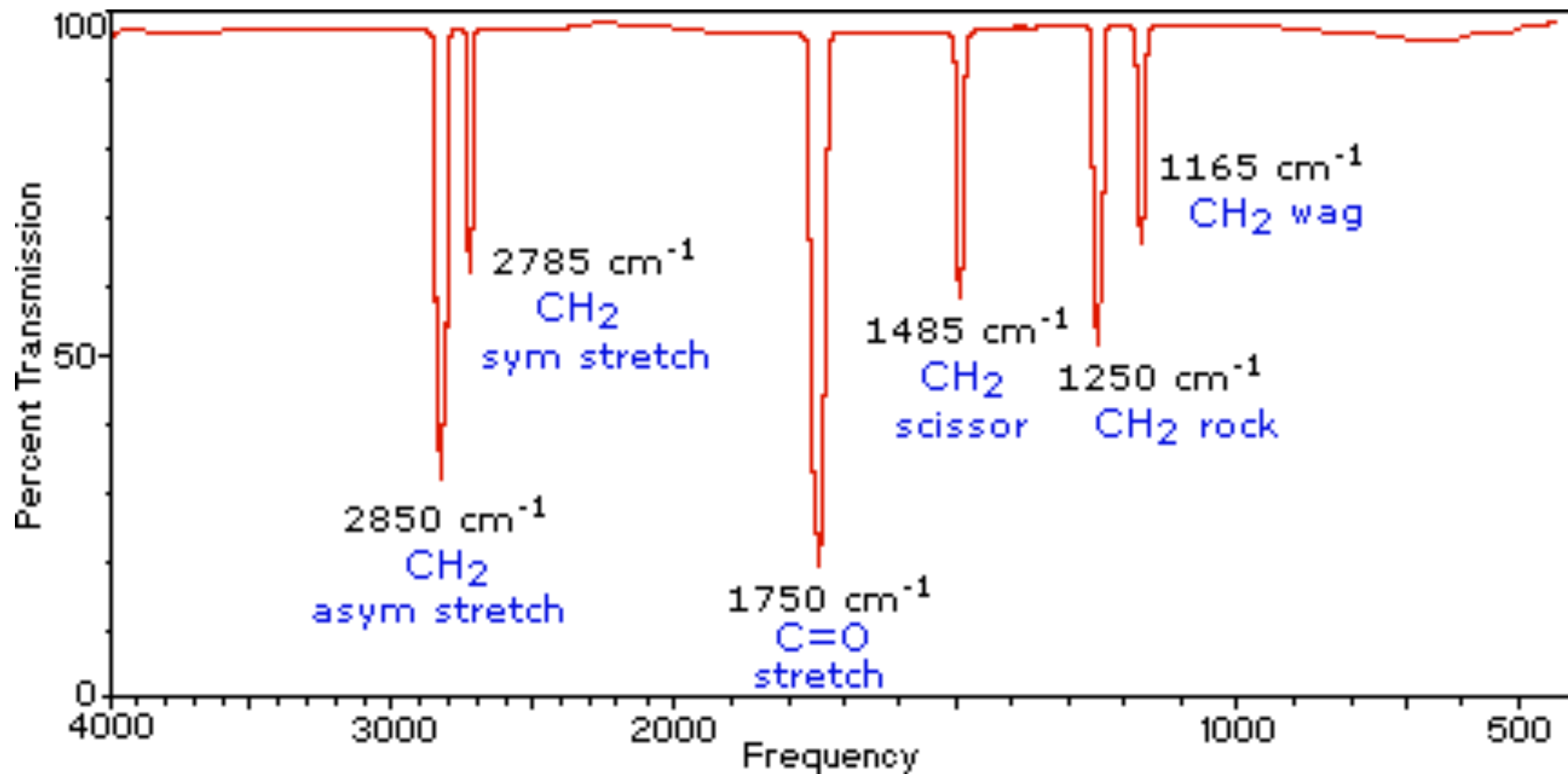


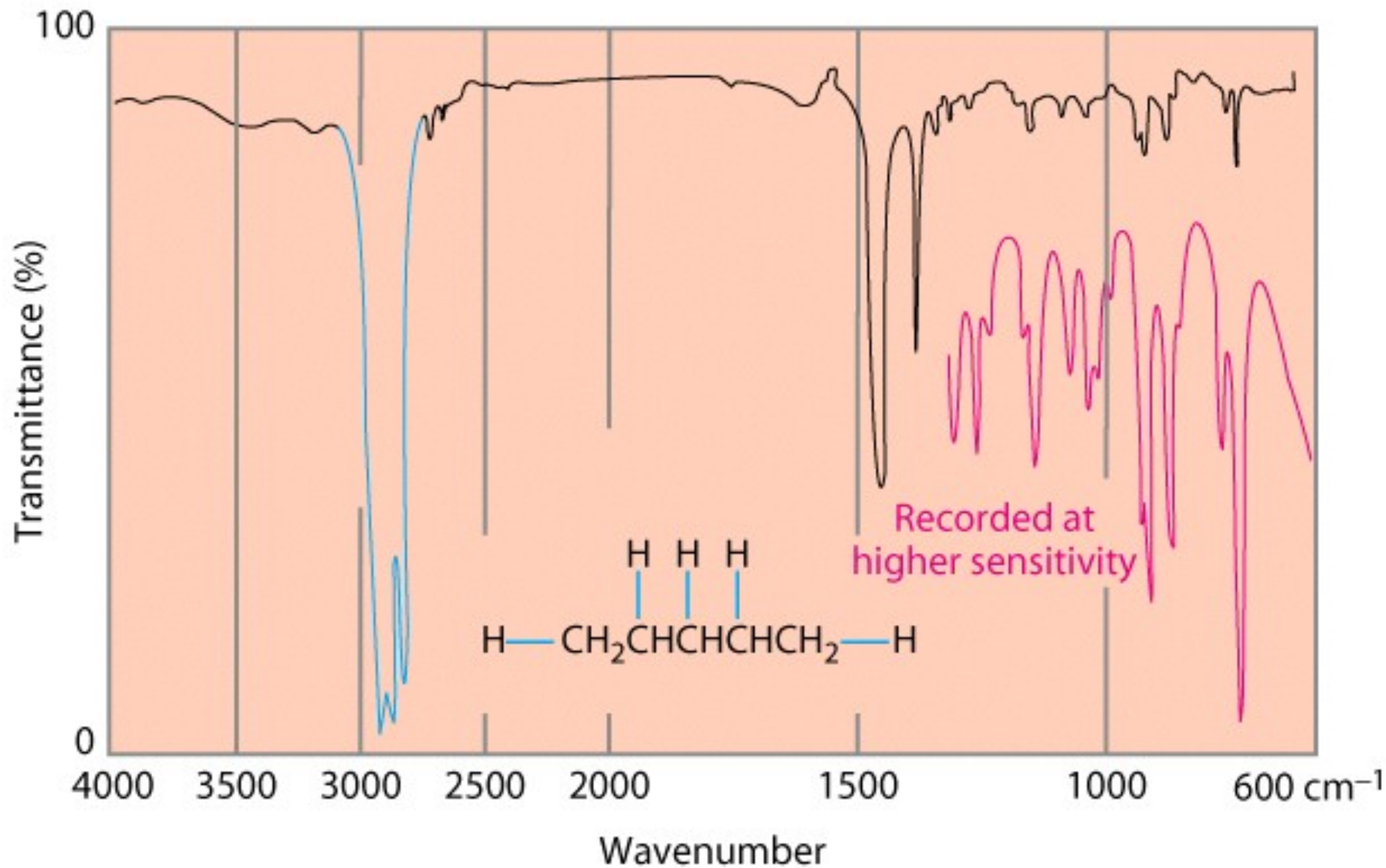
Rocking

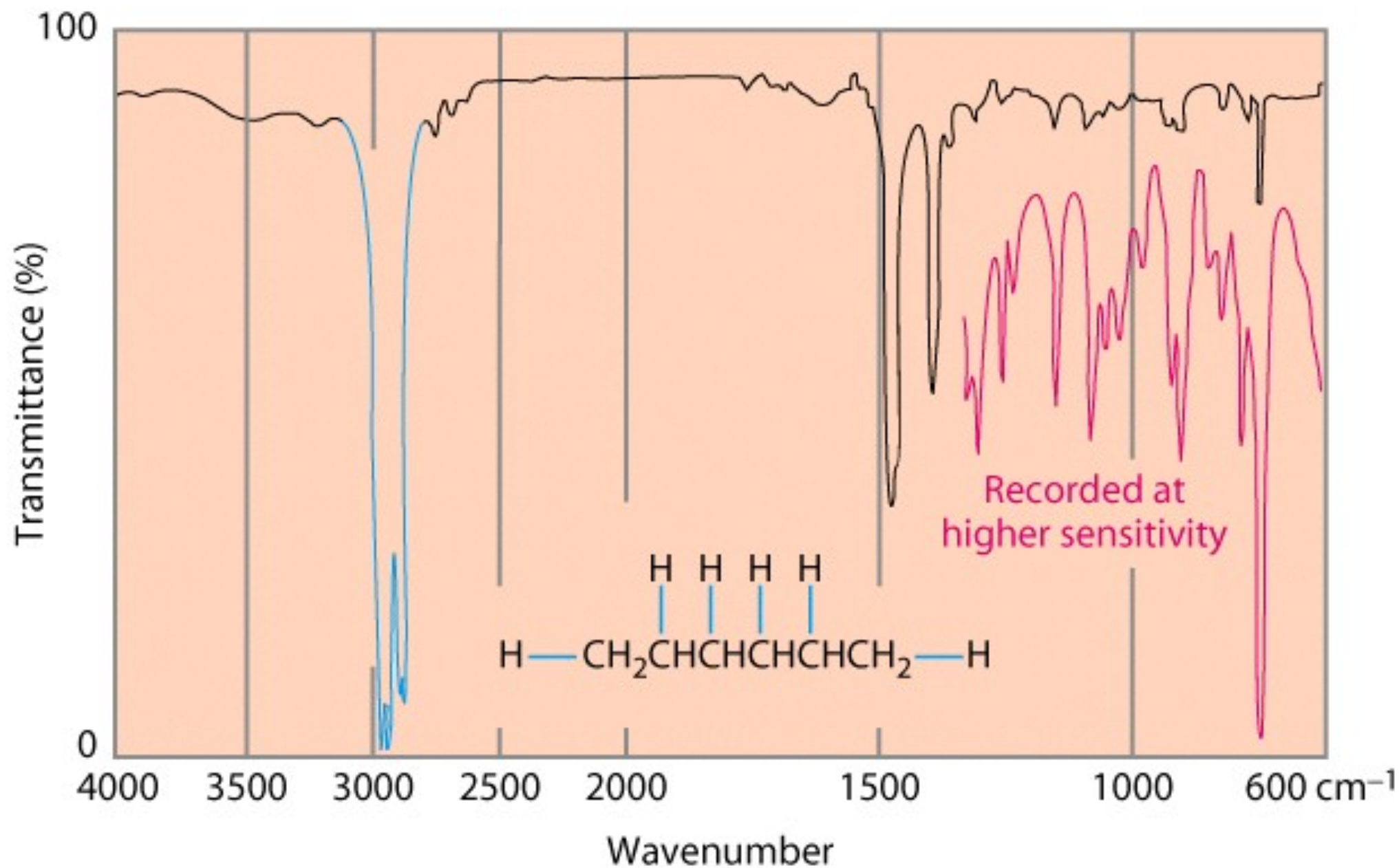


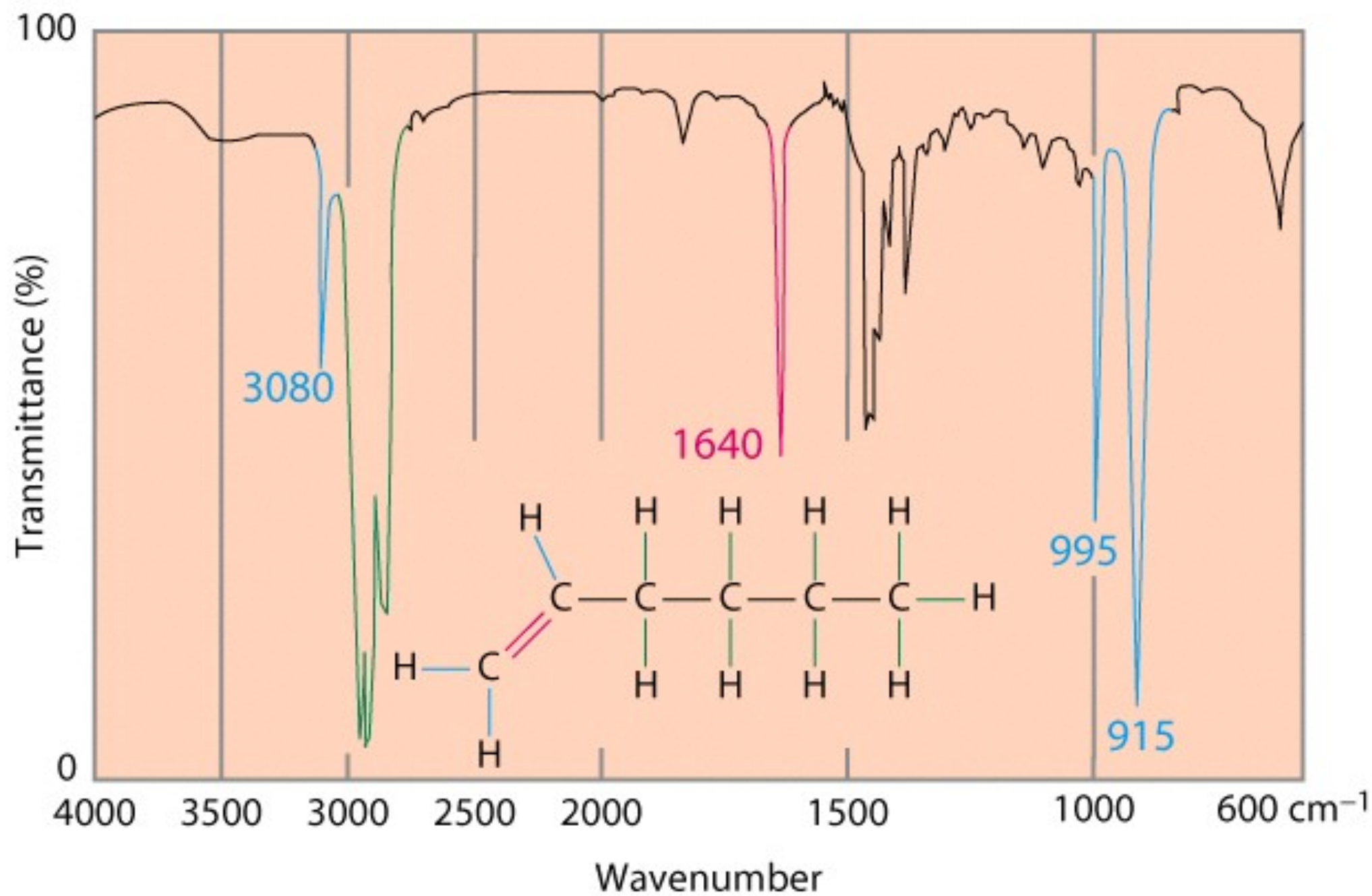
Twisting

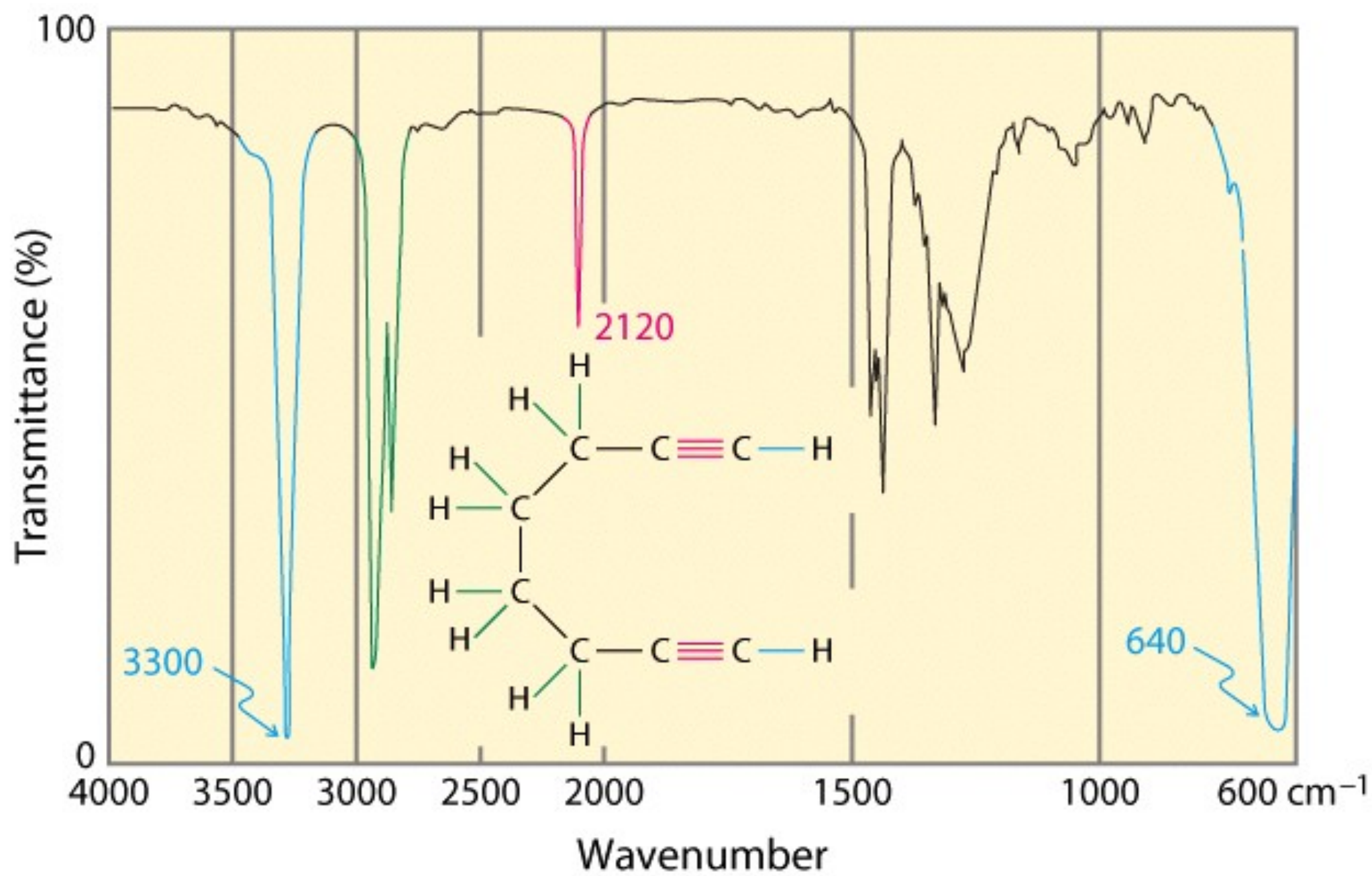
Formaldehyde

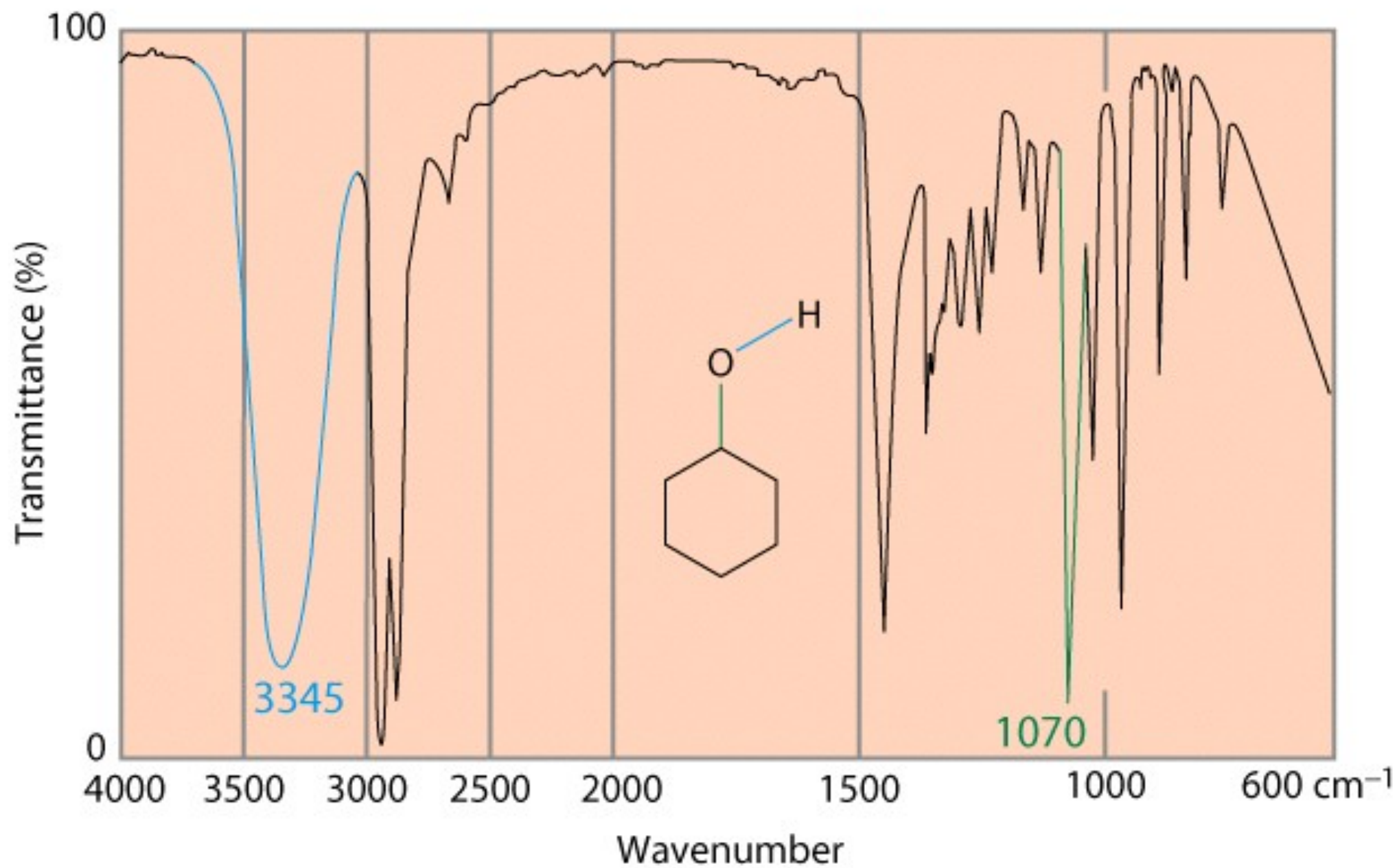


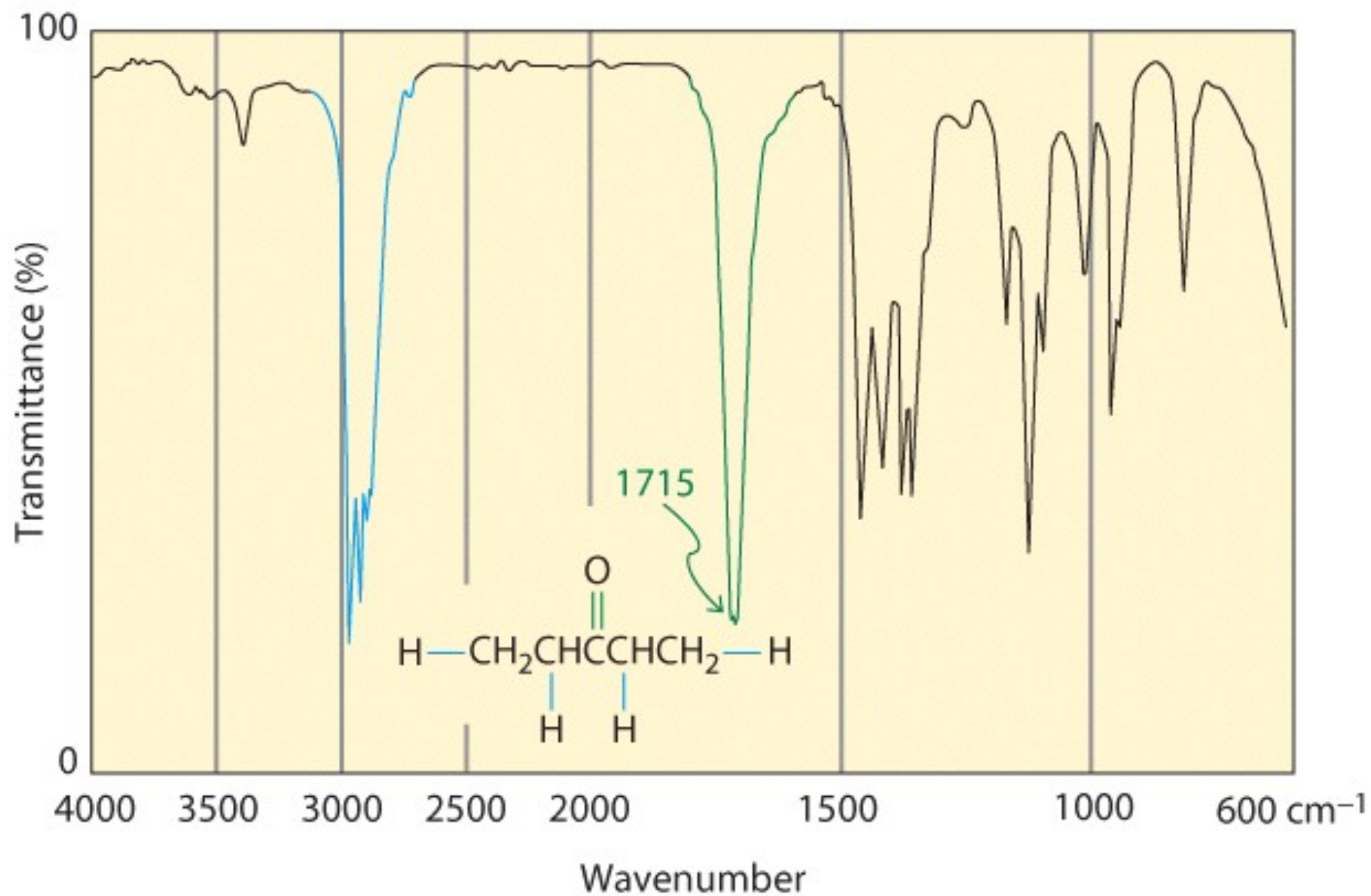


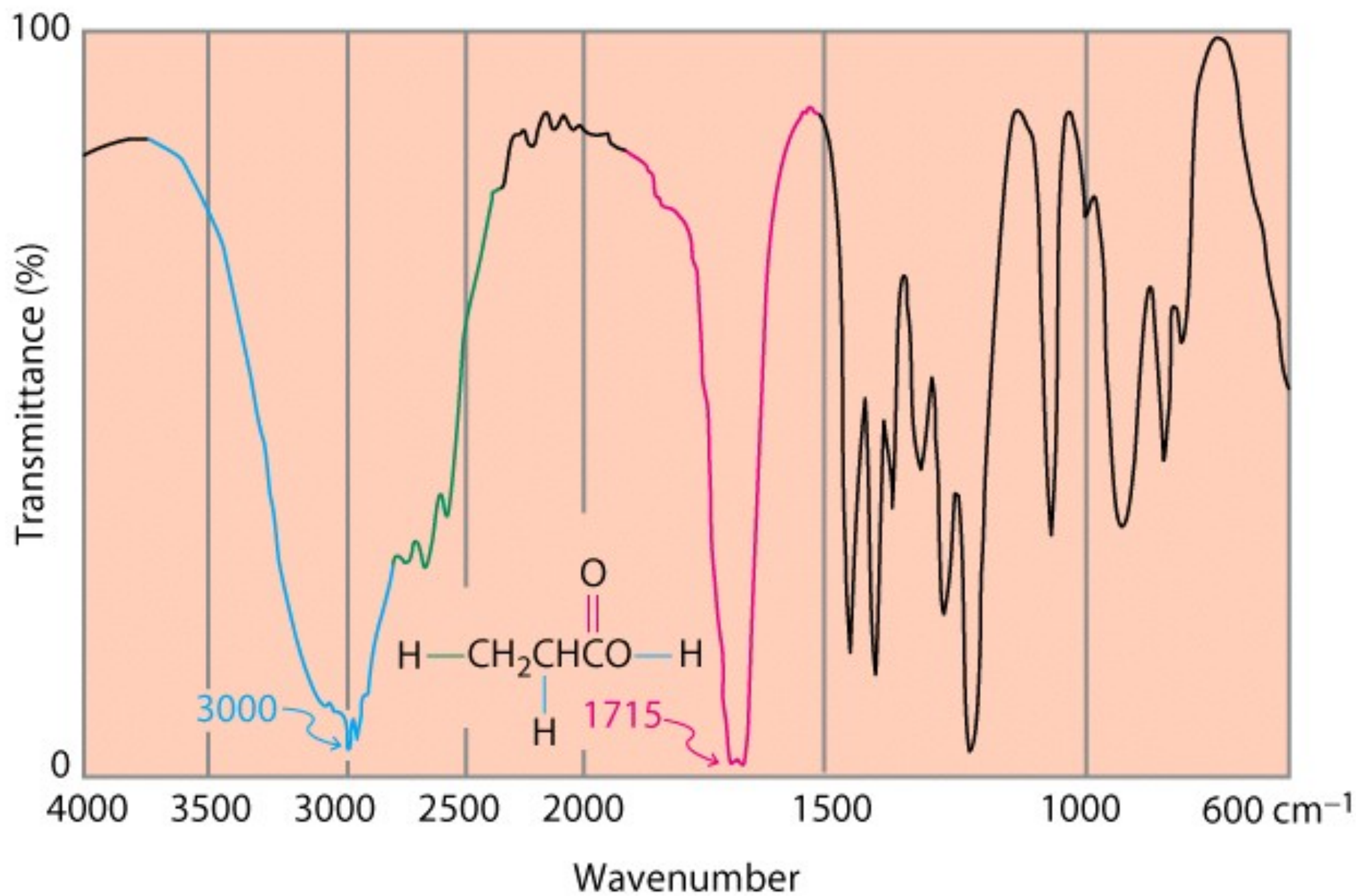


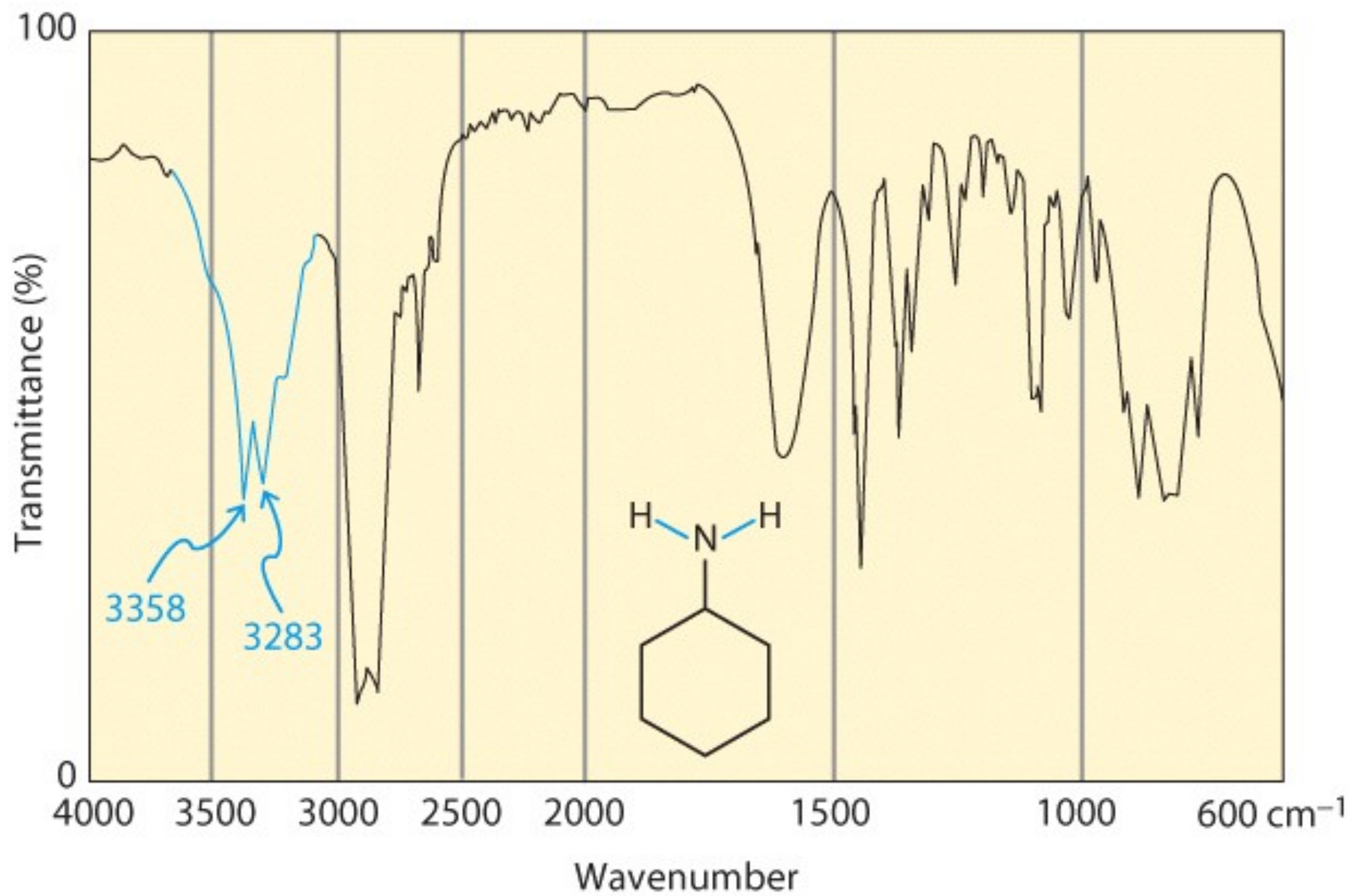












<https://biooriented.cheminfo.org>

Structure du produit inconnu au départ du spectre IR

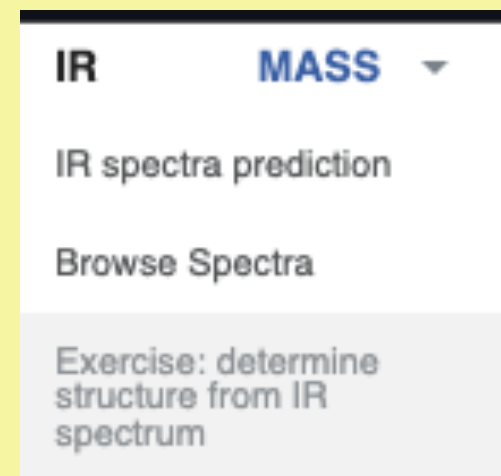


TABLE 11-4

Characteristic Infrared Stretching Wavenumber Ranges of Organic Molecules

Bond or functional group	$\tilde{\nu}$ (cm ⁻¹)	Bond or functional group	$\tilde{\nu}$ (cm ⁻¹)
RO—H (alcohols)	3200–3650	RC≡N (nitriles)	2220–2260
$\begin{array}{c} \text{O} \\ \parallel \\ \text{RCO—H} \end{array}$ (carboxylic acids)	2500–3300	$\begin{array}{c} \text{O} \quad \text{O} \\ \parallel \quad \parallel \\ \text{RCH, RCR}' \end{array}$ (aldehydes, ketones)	1690–1750
R ₂ N—H (amines)	3250–3500	$\begin{array}{c} \text{O} \\ \parallel \\ \text{RCOR}' \end{array}$ (esters)	1735–1750
RC≡C—H (alkynes)	3260–3330	$\begin{array}{c} \text{O} \\ \parallel \\ \text{RCOH} \end{array}$ (carboxylic acids)	1710–1760
$\begin{array}{c} \diagup \quad \diagdown \\ \text{C}=\text{C} \\ \diagdown \quad \diagup \\ \text{H} \end{array}$ (alkenes)	3050–3150	$\begin{array}{c} \diagup \quad \diagdown \\ \text{C}=\text{C} \\ \diagdown \quad \diagup \end{array}$ (alkenes)	1620–1680
$\begin{array}{c} \\ \text{—C—H} \\ \end{array}$ (alkanes)	2840–3000	$\begin{array}{c} \\ \text{RC—OR}' \\ \end{array}$ (alcohols, ethers)	1000–1260
RC≡CH (alkynes)	2100–2260		

ALDEHYDES

DIALKYL

AROMATIC

CARBOXYLIC ACIDS

DIMER

CARBOXYATE ION

ESTERS

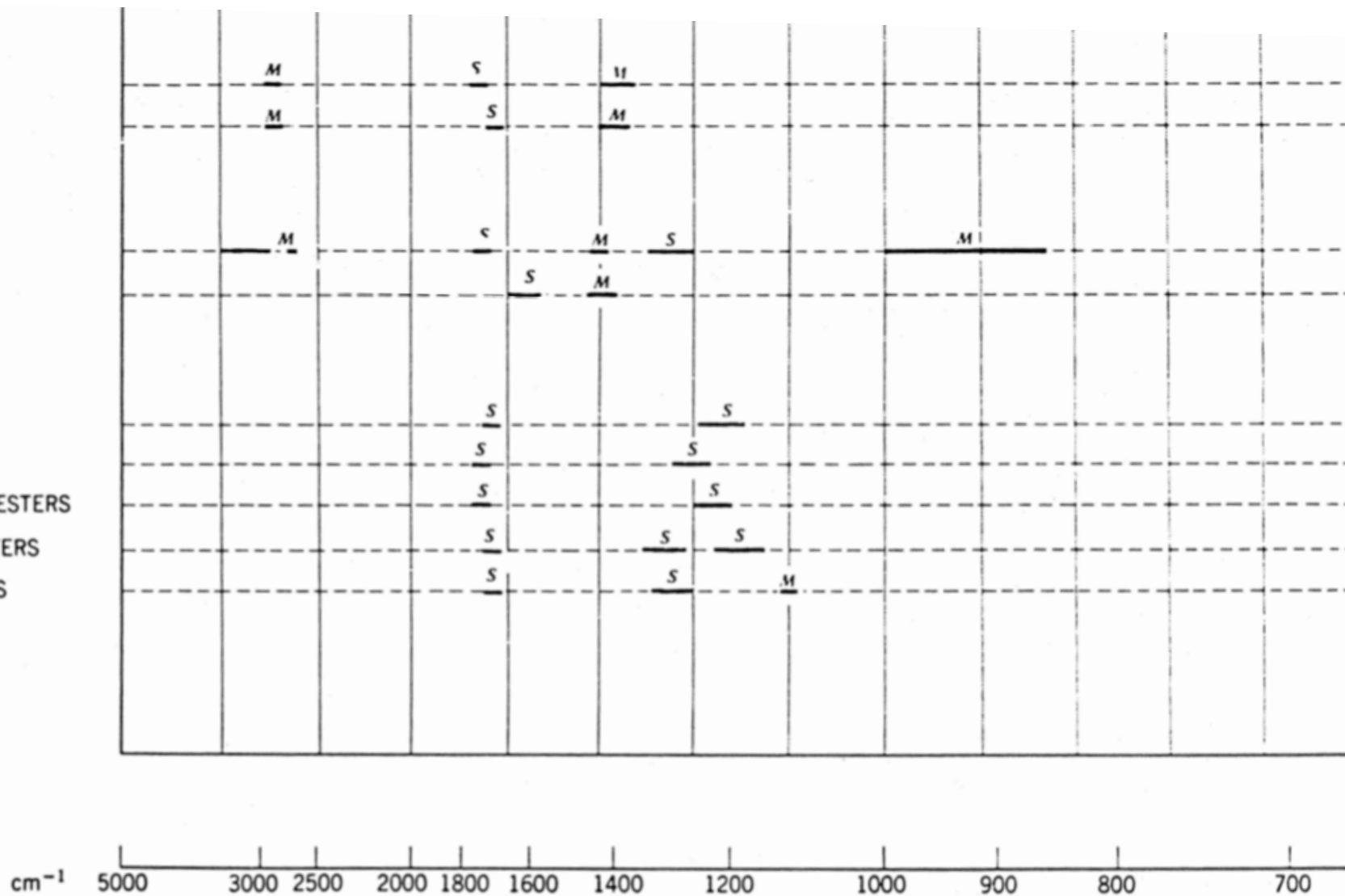
FORMATES

ACETATES

OTHER UNCONJ. ESTERS

CONJUGATED ESTERS

AROMATIC ESTERS



*Three bands, sometimes a fourth band for ketals and a fifth band for acetals.

Atomes “équivalents”

diethyl ether



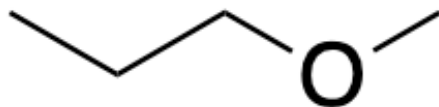
Combien d'hydrogènes différents ?

- ☐ 1
- ☐ 2
- ☐ 3
- ☐ 4
- ☐ 5
- ☐ 10



Answer

methyl propyl ether



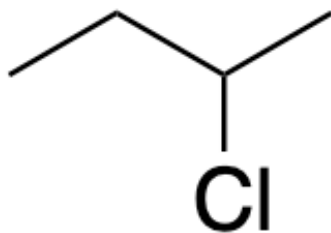
Combien d'hydrogènes différents ?

- ☐ 1
- ☐ 2
- ☐ 3
- ☐ 4
- ☐ 5
- ☐ 10



Answer

2-chlorobutane



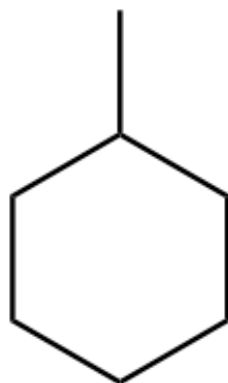
Combien d'hydrogènes différents ?

- ☐ 1
- ☐ 2
- ☐ 3
- ☐ 4
- ☐ 5
- ☐ 9



Answer

methylcyclohexane



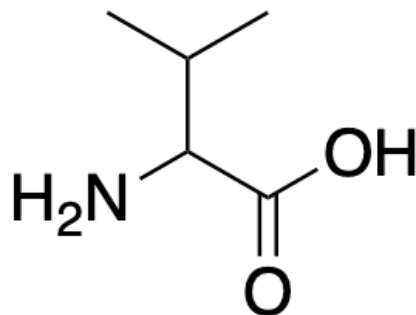
How many kind of protons

- ☐ 5
- ☐ 6
- ☐ 7
- ☐ 8
- ☐ 9
- ☐ 10



Answer

valine



Combien d'hydrogènes différents ?

- ☐ 1
- ☐ 2
- ☐ 3
- ☐ 4
- ☐ 5
- ☐ 6
- ☐ 7



Answer

<https://biooriented.cheminfo.org>

Nombre d'hydrogènes différents

NMR	IR	MASS	PDB	UI
Exercises		3. Find the structure from predicted 1H NMR		
Tools		2.5 Assign 1H NMR spectra to molecule		
has been designed as a co		4. Find the structure of experimental 1H NMR		cl
ral Analysis		6. 1H NMR spectra of Boc amino acids		is
Mass spectrometry: monois		1. Number of different Hs		
Infrared dspectroscopy		2 1H number of signals		
Degree of unsaturation		5. 1H NMR integrate and find the structure		
Diastereotopic protons		7. Integrated: EM, IR and NMR 1H		
Nuclear magnetic resonance				
synthesis				
protected amino acids				
Protein database and a wor				

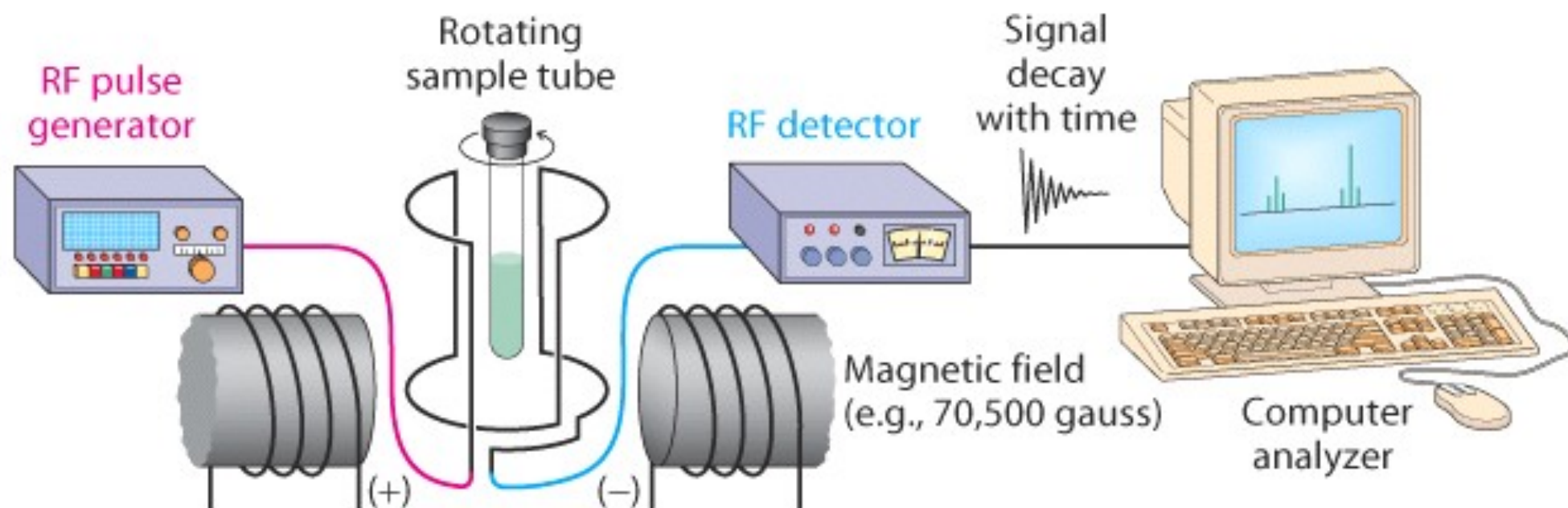
RMN

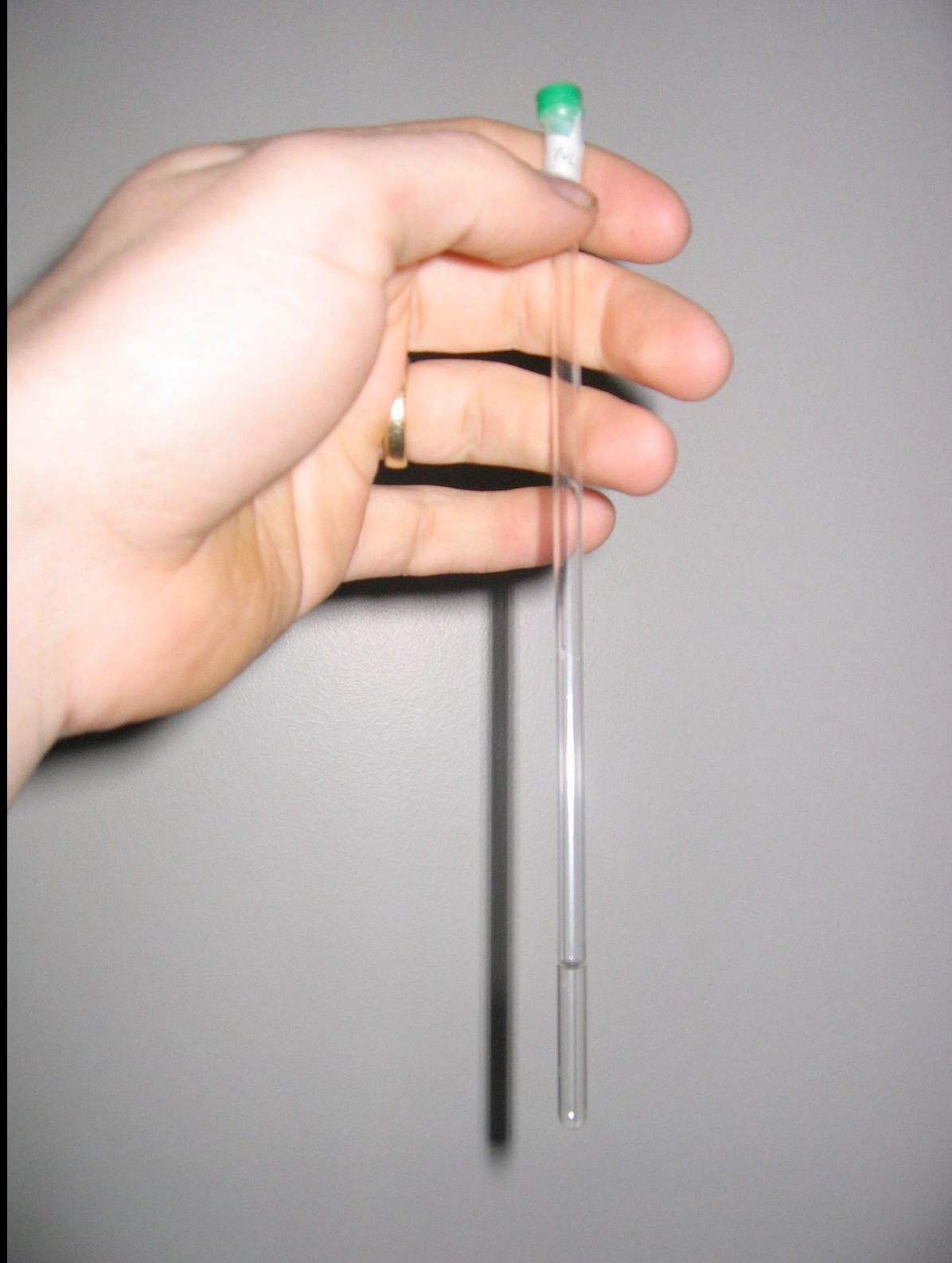
Résonance Magnétique Nucléaire

Prix Nobel:

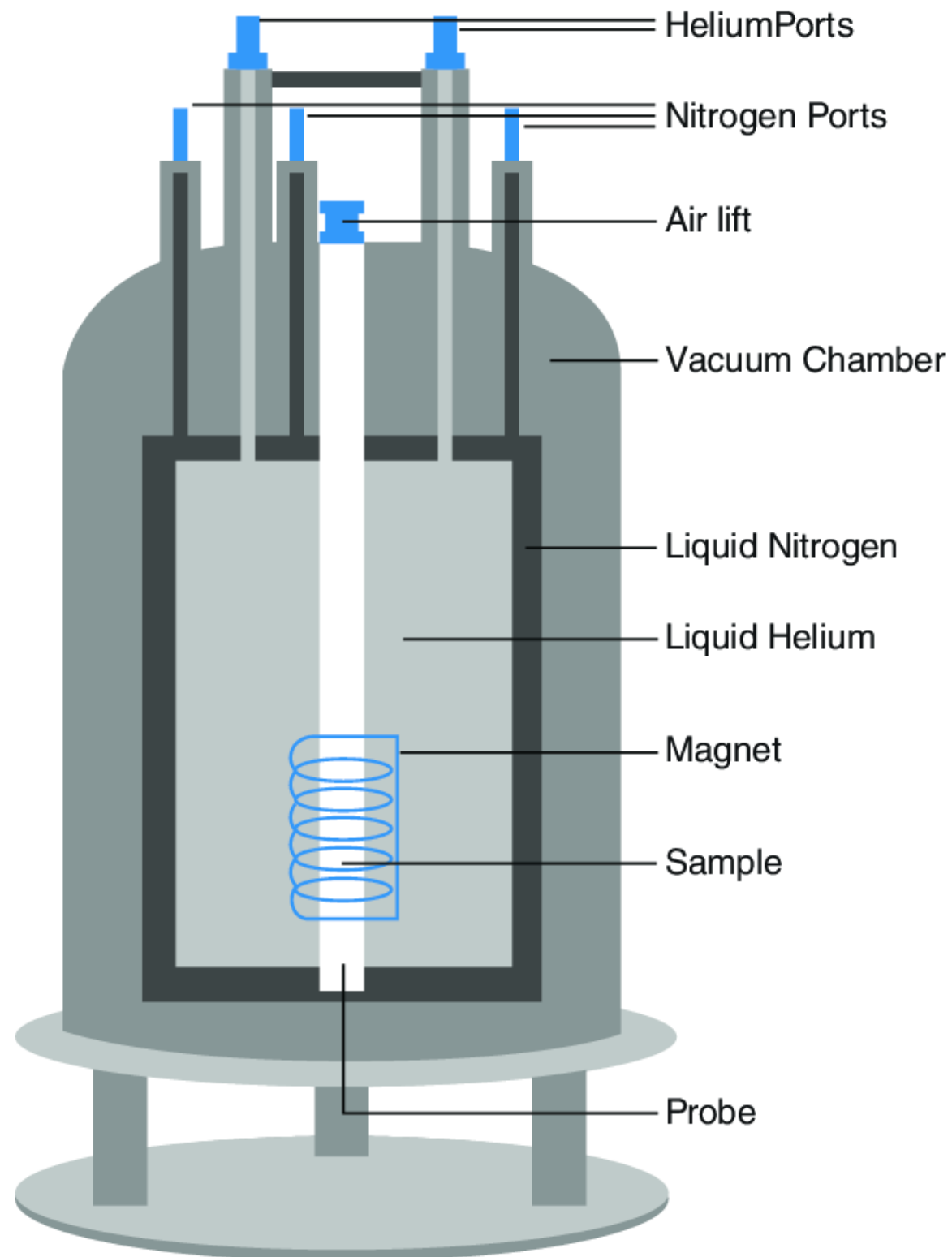
- 1991 Richard Ernst
- 2002 Kurt Wüthrich

NMR spectroscopy



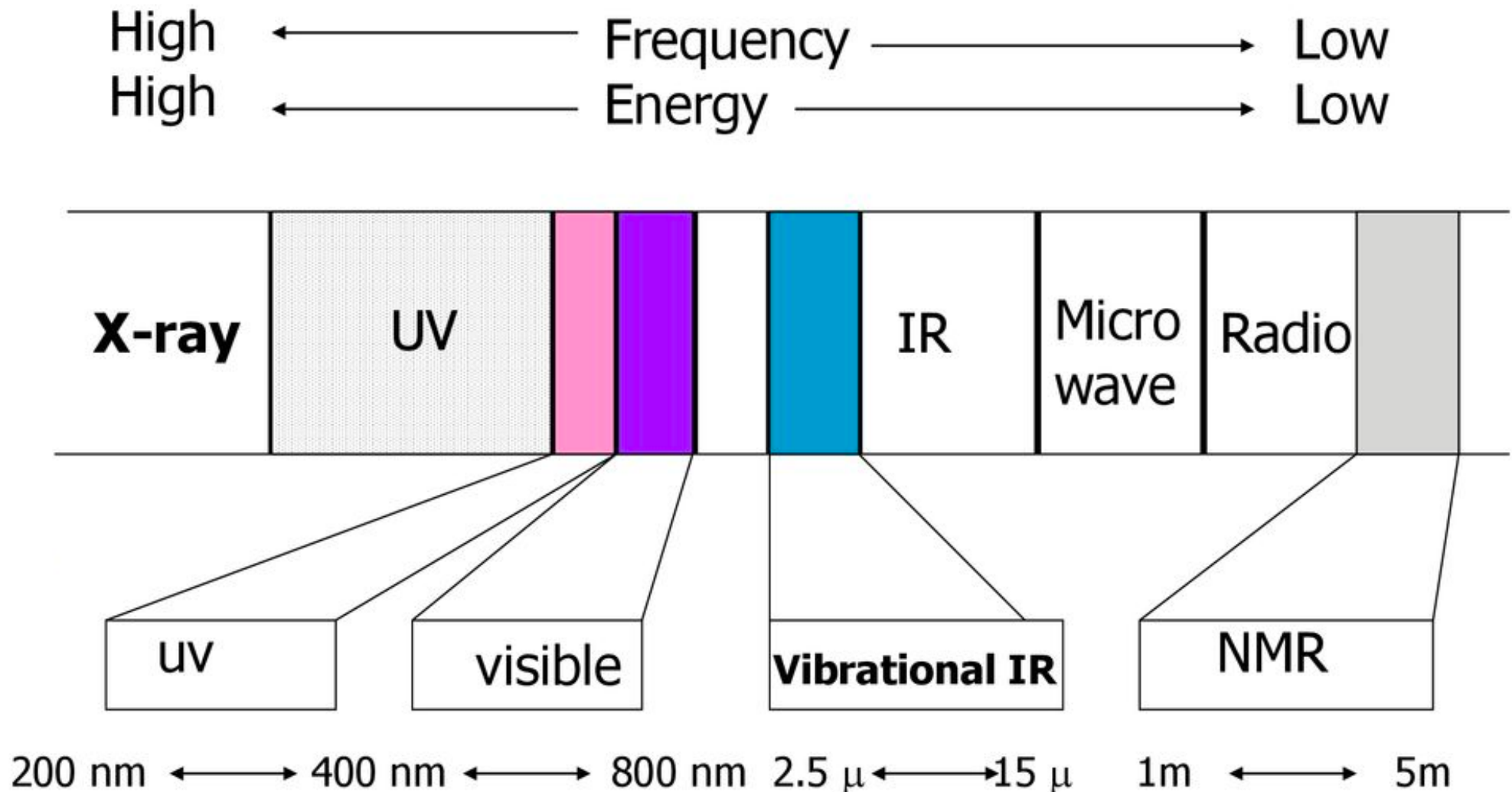








Electromagnetic spectrum



United Kingdom

- 380–399.9 MHz: [Terrestrial Trunked Radio](#) (TETRA) service for emergency use
- 430–440 MHz: Amateur radio ([70 cm band](#))
- 446.0–446.2 MHz : European unlicensed PMR service => [PMR446](#)
- 457–464 MHz: Scanning telemetry and telecontrol, assigned mostly to the water, gas, and electricity industries
- 606–614 MHz: Radio microphones and radio-astronomy
- 470–862 MHz: Previously used for [analogue TV channels 21–69](#) (until 2012).
 - Currently channels 21–37 and 39–48 are used for [Freeview](#) digital TV.^[6] Channels 55-56 were previously used by temporary muxes COM7 and COM8, channel 38 was used for radio astronomy but has been cleared to allow [PMSE](#) users access on a licensed, shared basis.
 - 694-790 MHz:^[7] i.e. Channels 49-60 have been cleared, to allow these channels to be allocated for 5G cellular communication.
 - 791–862 MHz,^[8] i.e. channels 61–69 inclusive were previously used for licensed and shared wireless microphones (channel 69 only), has since been allocated to 4G cellular communications.
- 863–865 MHz: Used for licence-exempt wireless systems.
- 863–870 MHz: [Short range devices](#), [LPWAN IoT](#) devices such as [NarrowBand-IoT](#).
- 870–960 MHz: Cellular communications (GSM900 - Vodafone and O2 only) including GSM-R and future TETRA
- 1240–1325 MHz: Amateur radio ([23 cm band](#))

Caractéristiques des principaux noyaux

Noyau	Spin I	Abondance naturelle (%)	ν obs. (MHz) ($B_0=2.3488$ T)	Rapport gyromagnétique γ [10^7 rad T ⁻¹ s ⁻¹]	Relative sensibility
¹ H	1/2	99.98	100	26.7519	100
² H	1	0.016	15.3	4.1066	0.96
¹⁰ B	3	19.58	10.7	2.8746	1.99
¹¹ B	3/2	80.42	32.0	8.5843	16.5
¹² C	0	98.9	—	—	—
¹³ C	1/2	1.108	25.1	6.7283	1.59
¹⁴ N	1	99.63	7.2	1.9338	0.10
¹⁵ N	1/2	0.37	10.1	−2.712	0.10
¹⁶ O	0	99.96	—	—	—
¹⁷ O	5/2	0.037	13.6	−3.6279	2.91
¹⁹ F	1/2	100	97.1	25.181	83.3
²⁹ Si	1/2	4.70	19.9	−5.3188	0.78
³¹ P	1/2	100	40.4	10.841	6.63

ethyl acetate

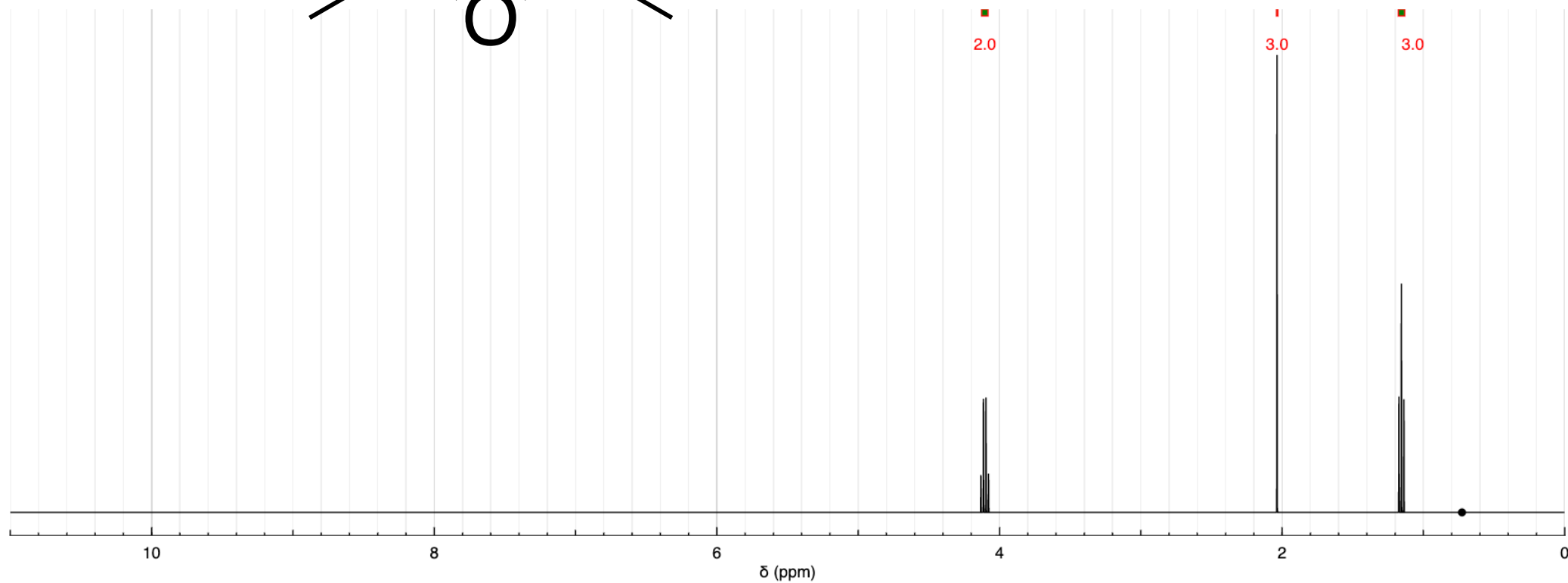
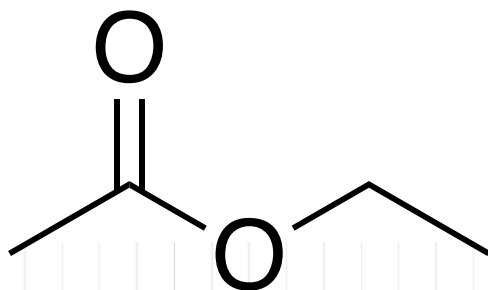
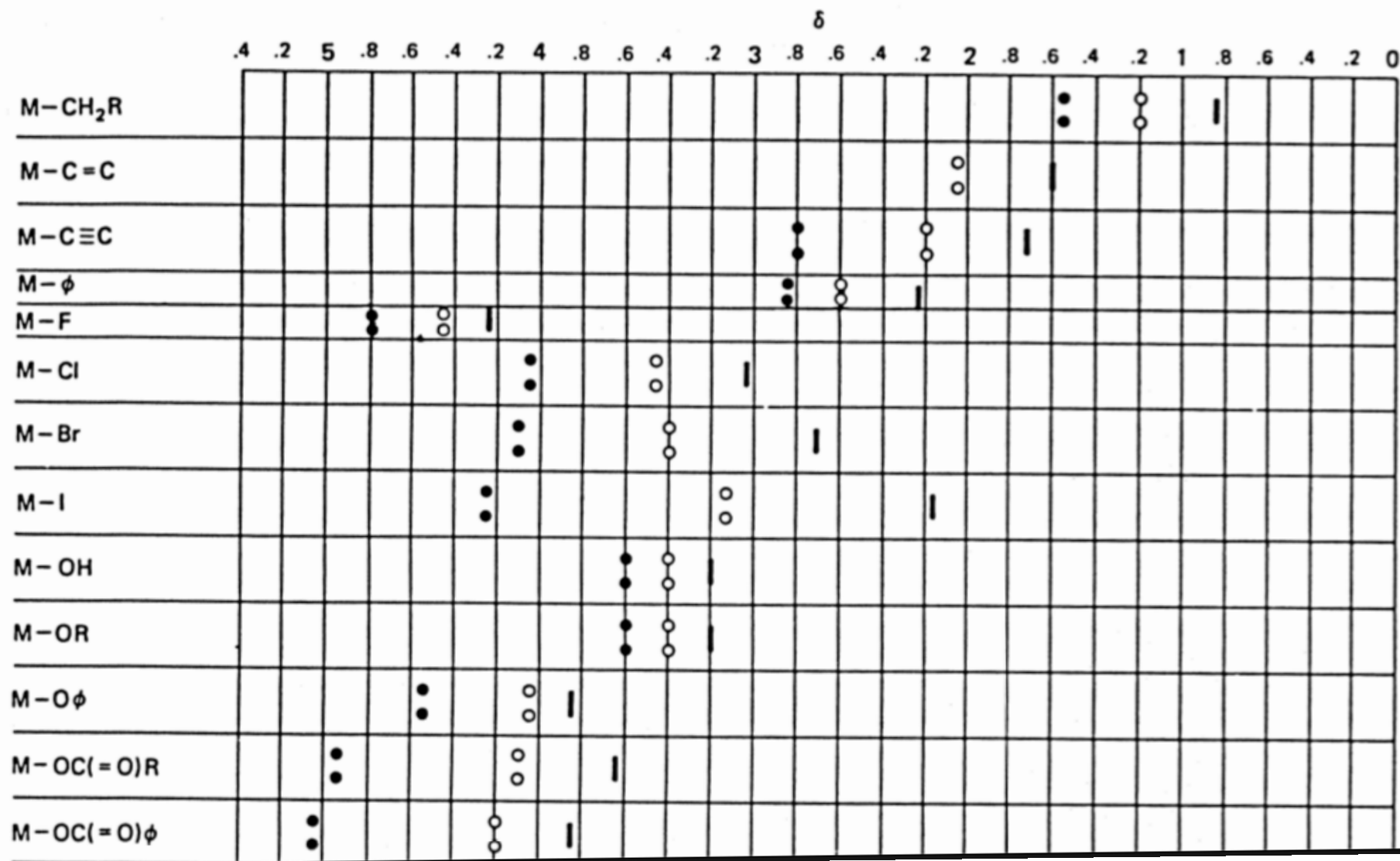


CHART 1. CHEMICAL SHIFTS OF PROTONS ON A CARBON ATOM ADJACENT (α - POSITION) TO A FUNCTIONAL GROUP IN ALIPHATIC COMPOUNDS (M—Y).

- | M = methyl
 ∅ M = methylene
 • M = methine



$$\delta_{\text{CH}_2\text{R}_1\text{R}_2} = 1.25 + \sum_1^2 z_i \quad \delta_{\text{CHR}_1\text{R}_2\text{R}_3} = 1.50 + \sum_1^3 z_i$$

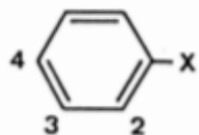
Substituent	z_i
-alkyl	0.0
C -C=C-	0.8
-C≡C-	0.9
-phenyl	1.3
H -Cl	2.0
A -Br	1.9
L -I	1.4
-OH	1.7
-O-alkyl	1.5
O -O-phenyl	2.3
-OCO-alkyl	2.7
-OCO-phenyl	2.9
-NH ₂	1.0
N -N-alkyl ₂	1.0
-NO ₂	3.0
S -S-alkyl	1.0
-CHO	1.2
O -CO-alkyl	1.2
 -COOH	0.8
C -COO-alkyl	0.7
/ \ -CN	1.2

$$\delta_{\text{CH}_2\text{R}_1\text{R}_2} = 0.23 + Z_{\text{R}_1} + Z_{\text{R}_2}$$

Substituent R	Z_{R}
-alkyl	see p. H17
-C=C-	1.33
-C $\equiv$ CH	1.52
C -C $\equiv$ Calkyl	1.52
-C $\equiv$ Cphenyl	1.77
-phenyl	1.85
H -F	3.15
A -Cl	2.48
L -Br	2.29
-OH	2.46
-Oalkyl	2.27
O -Ophenyl	2.89
-OCOalkyl	2.98
-OCOPhenyl	3.23
-NH ₂	1.69
-NHalkyl	1.60
-N(alkyl) ₂	1.41
-NHphenyl	2.15
N -N(alkyl)phenyl	2.39
-NH ₃ ⁺	2.31
-NH ₂ ⁺ alkyl	2.31
-NH ⁺ (alkyl) ₂	2.46
-N ⁺ (alkyl) ₃	2.56
-NHCOalkyl	2.23
-N(alkyl)COalkyl	2.23
-NHCOphenyl	2.33
-SH	1.63
S -Salkyl	1.63
-Sphenyl	1.92
-COalkyl	1.58
-COPhenyl	2.08
O -COOH	1.49
-COOalkyl	1.49
C -COOPhenyl	1.74
// -CONH ₂	1.39
-CON(alkyl) ₂	1.39
-CONHphenyl	1.59
-C $\equiv$ N	1.73

for D₂O a)

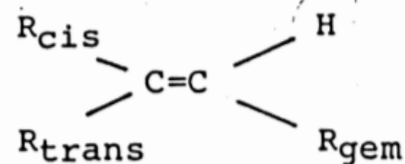
for D₂O b)



$$\delta_{H_i} = 7.26 + z_i$$

Substituent X		z_2	z_3	z_4
C	-H	0	0	0
	-CH ₃	-0.20	-0.12	-0.22
	-CH ₂ CH ₃	-0.14	-0.06	-0.17
	-CH(CH ₃) ₂	-0.13	-0.08	-0.18
	-C(CH ₃) ₃	0.02	-0.08	-0.21
	-CH ₂ Cl	0.00	0.00	0.00
	-CF ₃	0.32	0.14	0.20
	-CCl ₃	0.64	0.13	0.10
	-CH ₂ OH	-0.07	-0.07	-0.07
	-CH=CH ₂	0.06	-0.03	-0.10
	-CH=CH-phenyl	0.15	-0.01	-0.16
	-C≡CH	0.15	-0.02	-0.01
	-C≡C-phenyl	0.19	0.02	0.00
	-phenyl	0.37	0.20	0.10
H A L	-F	-0.26	0.00	-0.20
	-Cl	0.03	-0.02	-0.09
	-Br	0.18	-0.08	-0.04
	-I	0.39	-0.21	0.00
O	-OH	-0.56	-0.12	-0.45
	-OCH ₃	-0.48	-0.09	-0.44
	-OCH ₂ CH ₃	-0.46	-0.10	-0.43
	-O-phenyl	-0.29	-0.05	-0.23
	-OCOCH ₃	-0.25	0.03	-0.13
	-OCO-phenyl	-0.09	0.09	-0.08
	-OSO ₂ CH ₃	-0.05	0.07	-0.01

$$\delta_{C=CH} = 5.25 + z_{gem} + z_{cis} + z_{trans}$$



Substituent R		z_{gem}	z_{cis}	z_{trans}
C	-H	0	0	0
	-alkyl	0.45	-0.22	-0.28
	-alkyl ring ¹⁾	0.69	-0.25	-0.28
	-CH ₂ -aromatic	1.05	-0.29	-0.32
	-CH ₂ X, X: F, Cl, Br	0.70	0.11	-0.04
	-CHF ₂	0.66	0.32	0.21
	-CF ₃	0.66	0.61	0.32
	-CH ₂ O	0.64	-0.01	-0.02
	-CH ₂ N	0.58	-0.10	-0.08
	-CH ₂ S	0.71	-0.13	-0.22
	-CH ₂ CO, CH ₂ CN	0.69	-0.08	-0.06
	-C=C isolated	1.00	-0.09	-0.23
	-C=C conjugated ²⁾	1.24	0.02	-0.05
	-C≡C	0.47	0.38	0.12
	-aromatic free rotation	1.38	0.36	-0.07
	-aromatic fixed ³⁾	1.60	-	-0.05
H A L	-aromatic o-substituted	1.65	0.19	0.09
	-F	1.54	-0.40	-1.02
	-Cl	1.08	0.18	0.13
	-Br	1.07	0.45	0.55
	-I	1.14	0.81	0.88

<https://moodle.epfl.ch/course/view.php?id=16403>

Exemple avec les solvants

Couplage spin-spin

<https://www.cheminfo.org/flavor/biooriented>

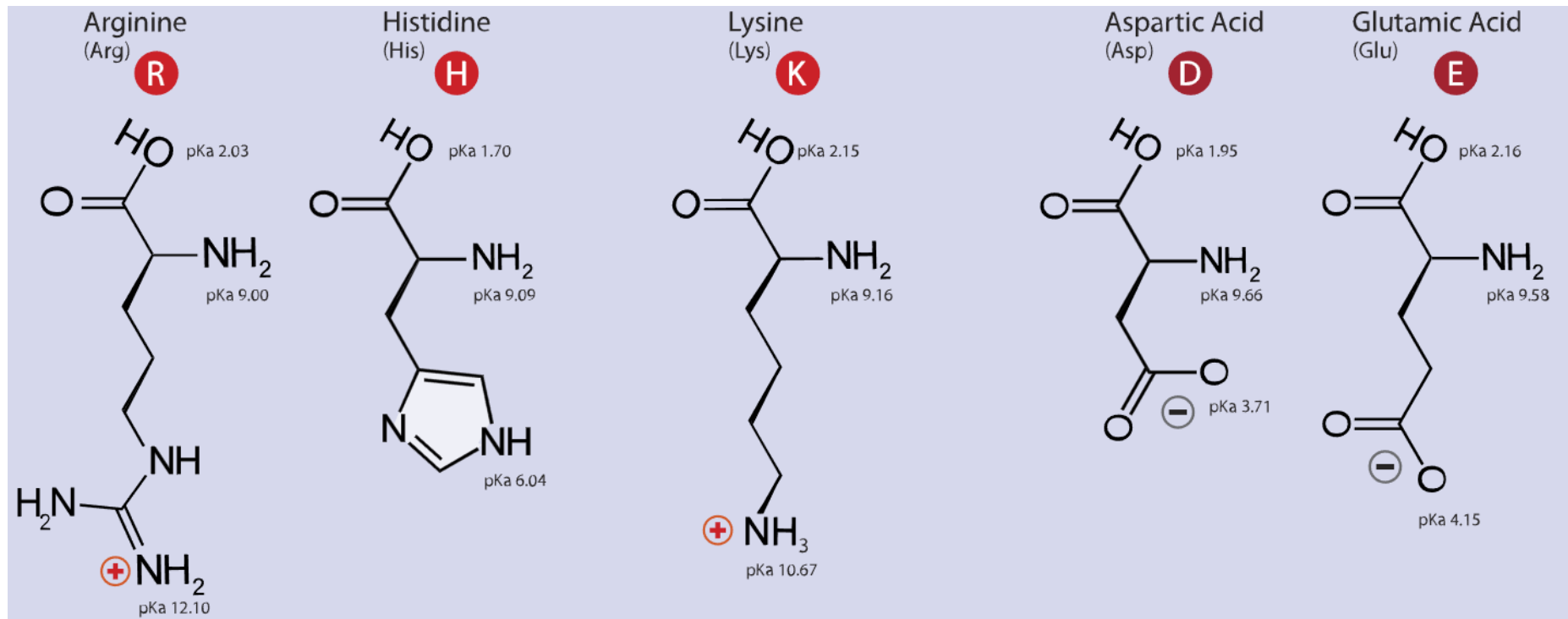
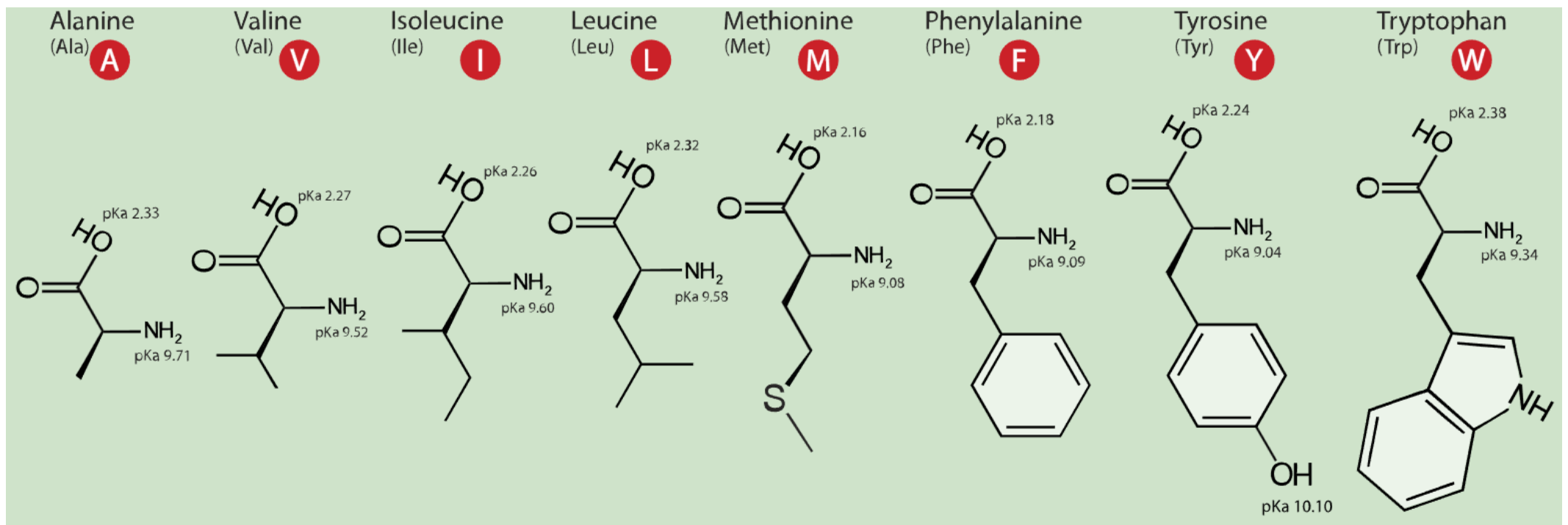
Second order effect

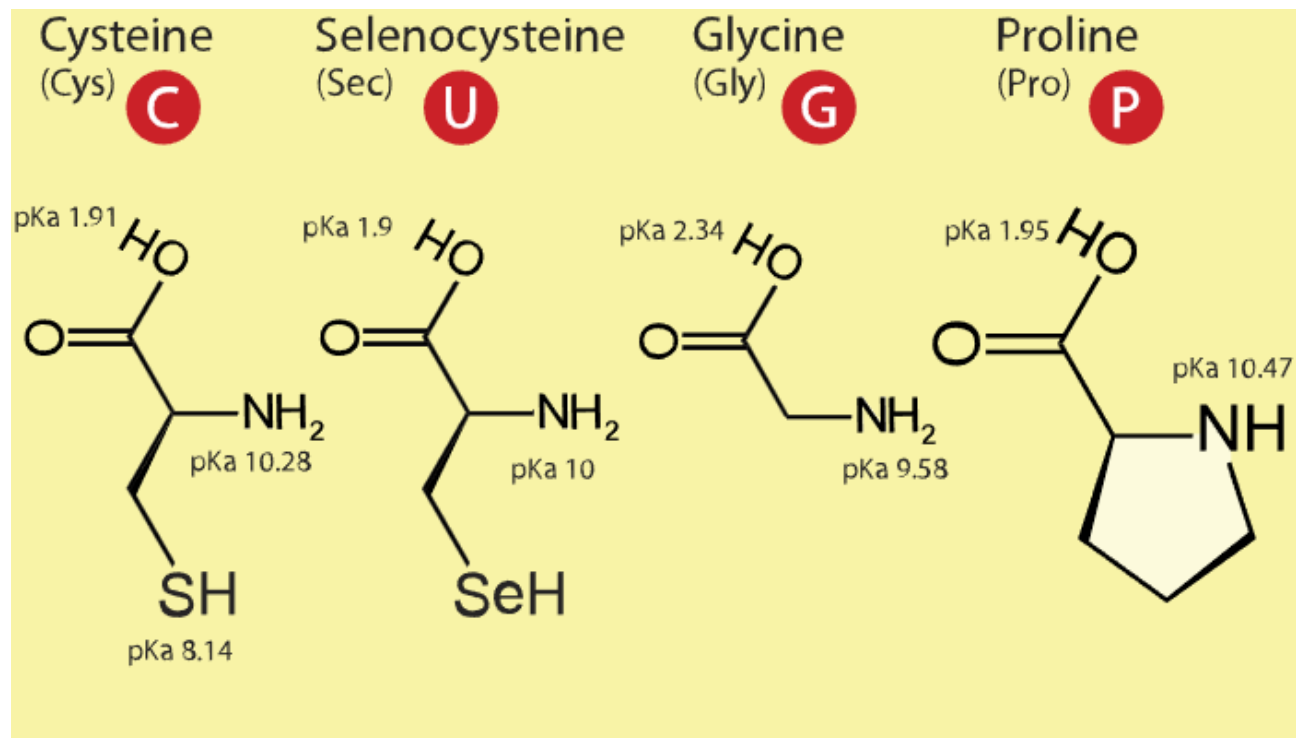
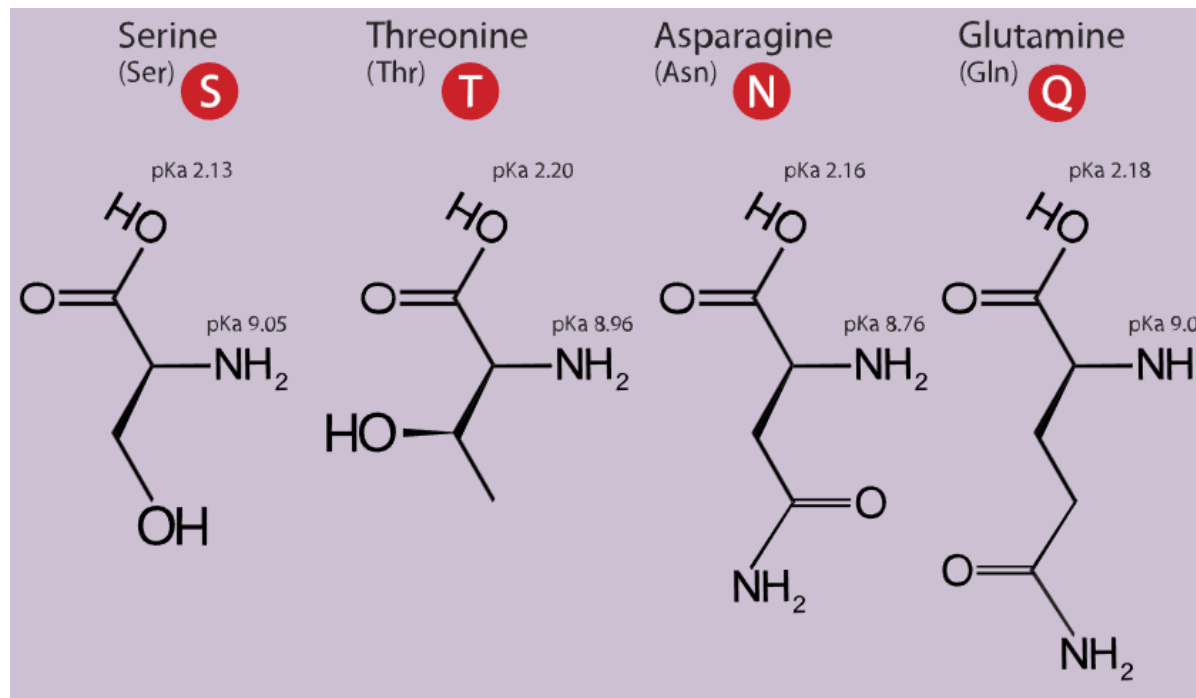
<https://www.cheminfo.org/flavor/biooriented>

NMR

Boc protected amino-acids

Exercices Boc





Exercices intégrés

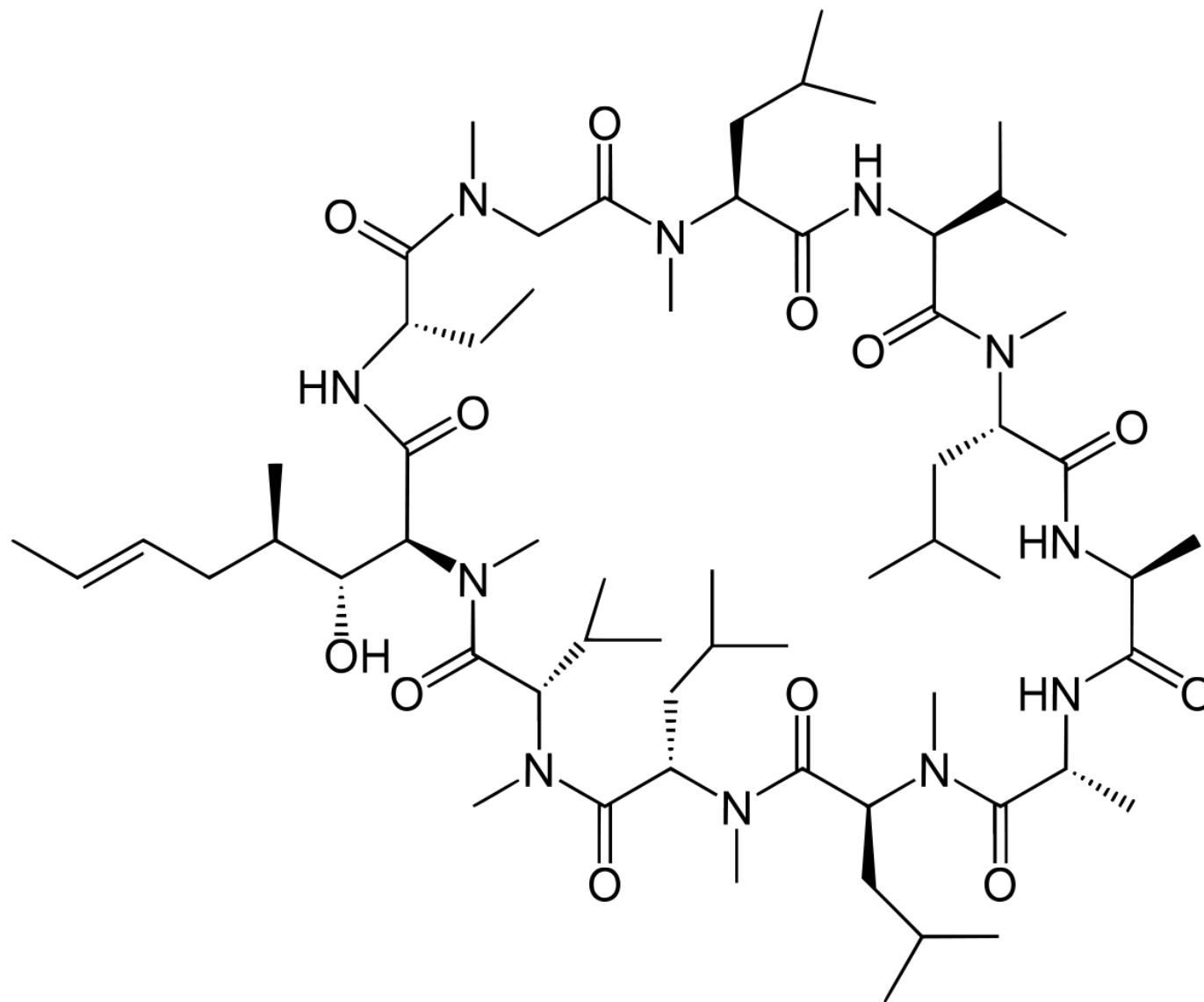
Acides aminés, peptides, protéines

Acides aminés

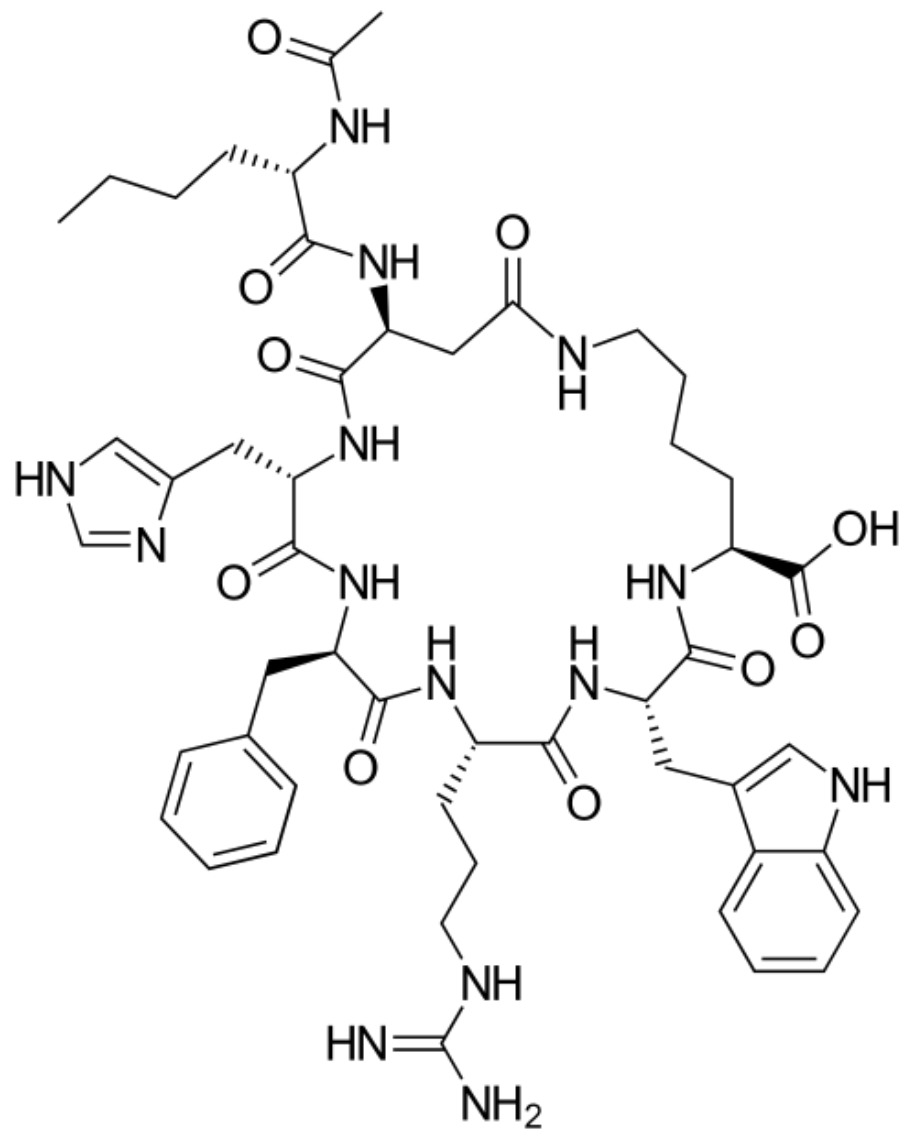
Codification IUPAC des atomes

Synthèse peptique

Cyclosporine



Bremelanotide



[illegible]

[illegible]

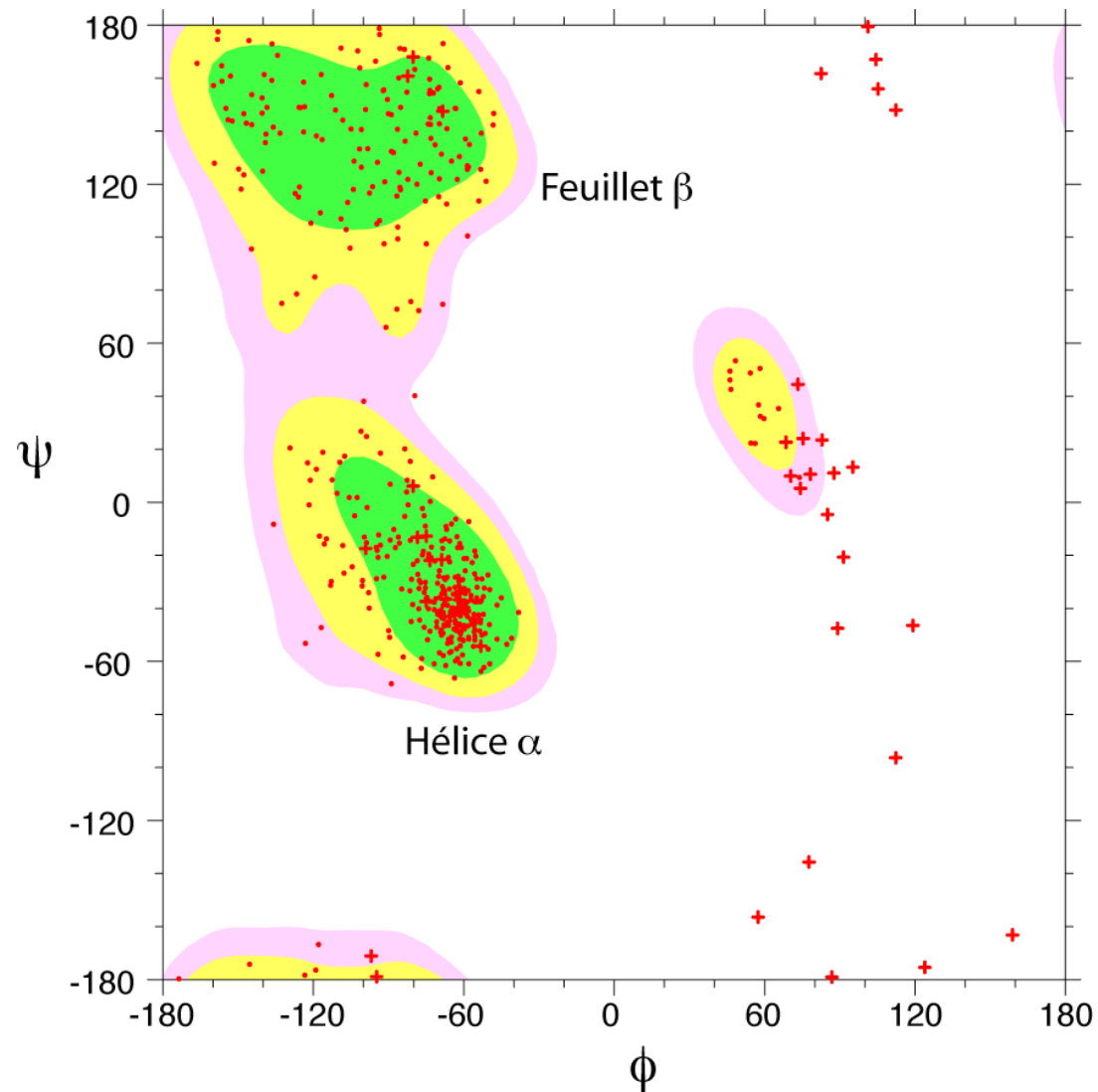
	acide	base conjuguée		pKa
acide très fort	HI	I ⁻	base très faible	-5.2
	HBr	Br ⁻		-4.7
	HCl	Cl ⁻		-2.2
acide le + fort dans l'eau	H ₃ O ⁺	H ₂ O		-1.7
	CF ₃ COOH	CF ₃ COO ⁻		0.2
	HF	F ⁻		3.2
	CH ₃ COOH	CH ₃ COO ⁻		4.7
	H ₂ S	HS ⁻		7.0
	HCN	CN ⁻		9.2
	Me ₃ N ⁺ H	Me ₃ N		9.8
	C ₆ H ₅ OH	C ₆ H ₅ O ⁻		10.0
	EtSH	EtS ⁻		10.6
	H ₂ O	HO ⁻	base la plus + dans l'eau	15.7
	EtOH	EtO ⁻		15.9
	CH ₃ COOEt	⁻ CH ₂ COOEt		24.5
	HCCH	HCC ⁻		25
acide très faible	C ₂ H ₅ NH ₂	C ₂ H ₅ NH ⁻	base très forte	35

Protéine

Feuillet Beta

Diagramme de Ramachandran

Diagramme de Ramachandran



PDB format

- <https://www.rcsb.org/>



Protein Data Bank Contents Guide:
Atomic Coordinate Entry Format Description
Version 2.3, July 9, 1998

<https://www.rcsb.org/structure/1CWA>

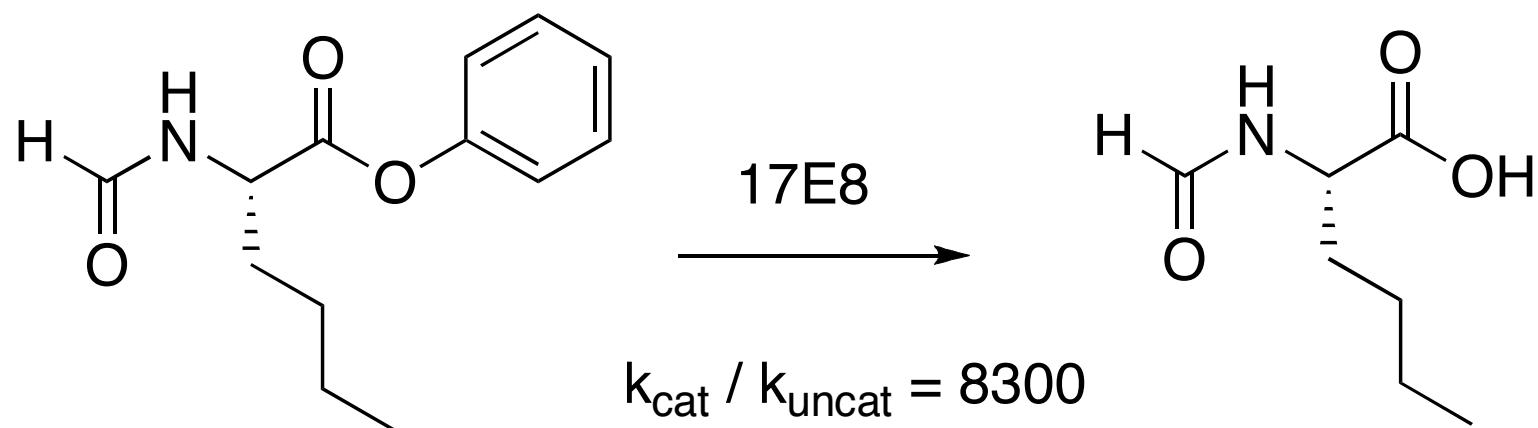
Protéine et travail JSMol

Travail JSMol

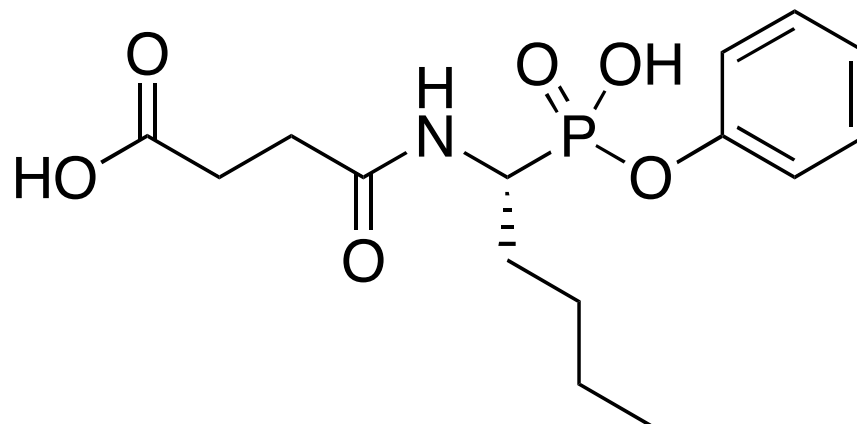
- **Choisir une protéine**
- **Effectuer le travail JSMol**

Réactions bio compatibles

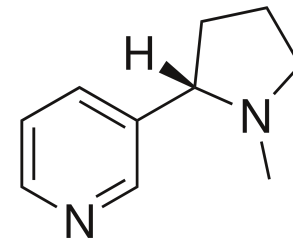
Catalyseur



Hapten:



Vaccin antinicotine



Preclinical Development of a Vaccine ‘Against Smoking’

E. H. Cerny^a R. Lévy^a J. Mauel^b M. Mpandi^c M. Mutter^d C. Henzelin-Nkubana^d L. Patiny^d
G. Tuchscherer^d T. Cerny^e

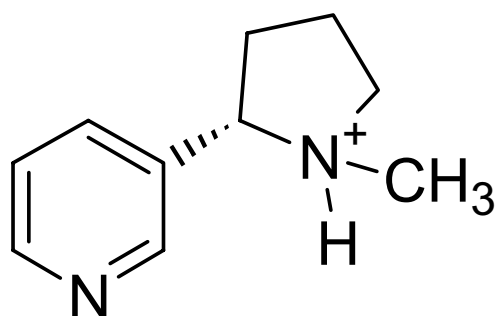
^aChilka Ltd., Lausanne

^bInstitut de Biochimie, ISREC, Epalinges

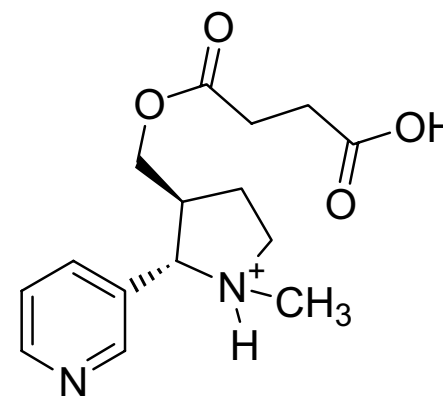
^cSerolab SA, Remaufens

^dInstitut of Molecular and Biological Chemistry, Swiss Federal Institute of Technology, Lausanne

^eDepartment of Oncology/Haematology, Cantonal Hospital St. Gall



nicotine



hapten

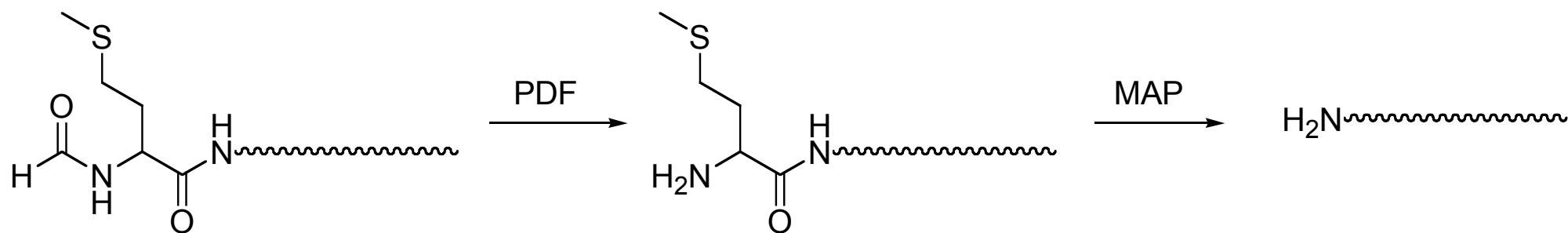
Réactions sur NH₂

Réactions sur SH

Bioconjugaison

Peptide deformylase

PDF and MAP

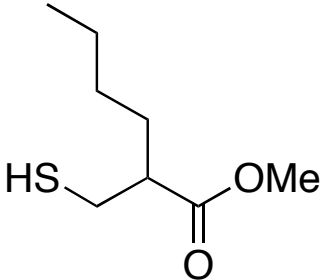
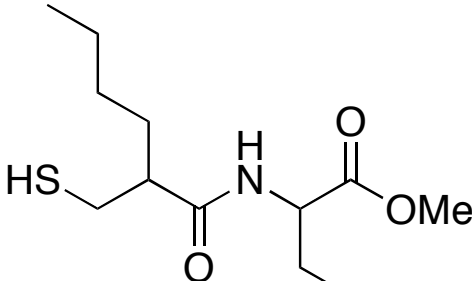
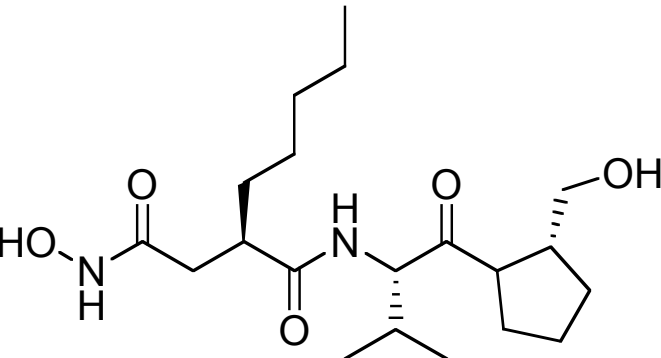


Recherche d'un inhibiteur

But: Structure 3D protéine / inhibiteur

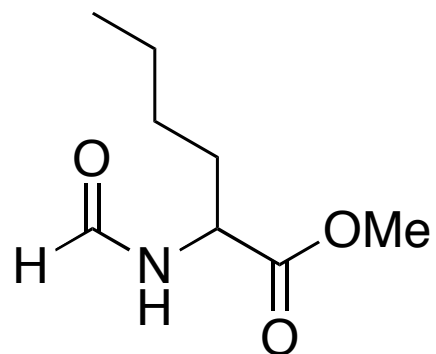
Substrat minimal

Peptide	vitesse relative
Fo-Ala-Ala-Ala-OH	0.20
Fo-Met-Ala-Ser-OH	100
Fo-Nle-Ala-Ser-OH	115
Fo-Leu-Ala-Ser-OH	11
Fo-Met-OMe	27
Fo-Nle-OMe	59
Fo-Met-OH	0.16
Fo-Leu-Ala-OMe	267
Fo-Nle-Arg-NH ₂	839

Peptide	K _i (μM)
H-Met-Ala-Ser-OH	53000
H-Met-Arg.OH	3800
HS-CH ₂ -CH ₂ -OH	10000
	52
	2.5
	64
	actinonine*

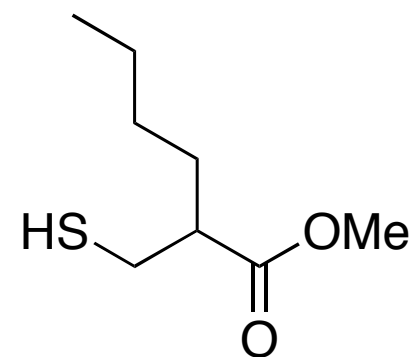
* Antimicrobial Agents and Chemotherapy 2001, 563-570.

substrats

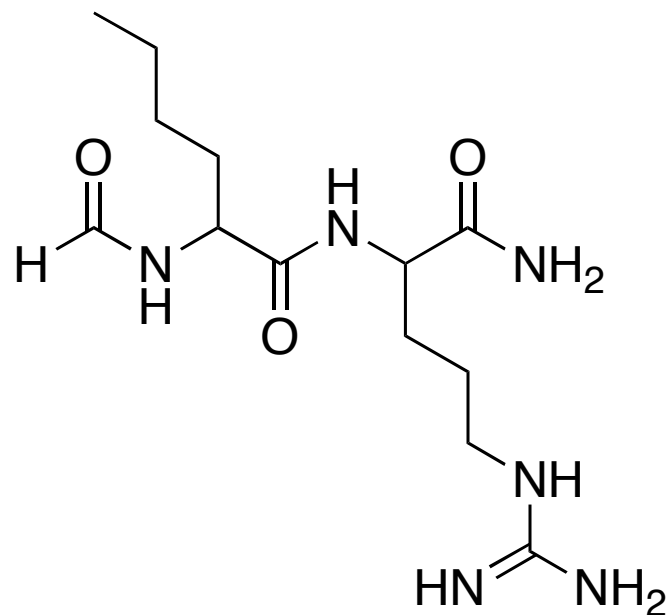


$k_{\text{rel}}=59$

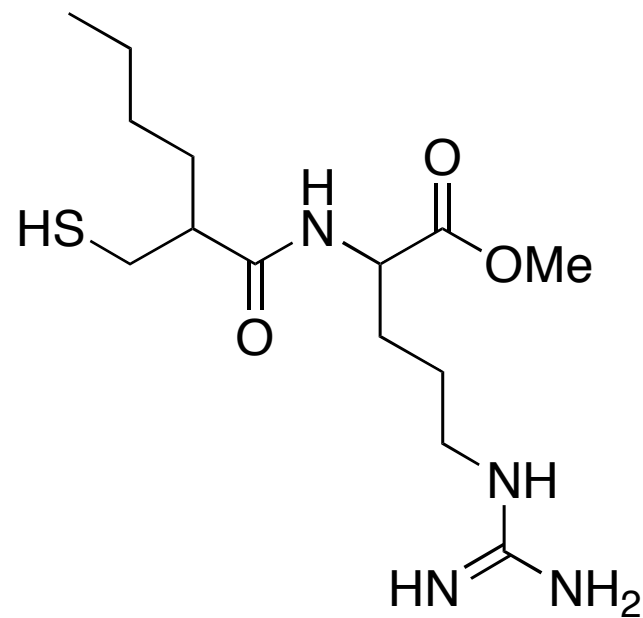
inhibiteurs



$K_i (\mu\text{M})=52$



$k_{\text{rel}}=839$



$K_i (\mu\text{M})=2.5$

Design and Synthesis of Substrate Analogue Inhibitors of Peptide Deformylase[†]

Thierry Meinnel,^{*,‡} Luc Patiny,[§] Stéphane Ragusa,[‡] and Sylvain Blanquet[‡]

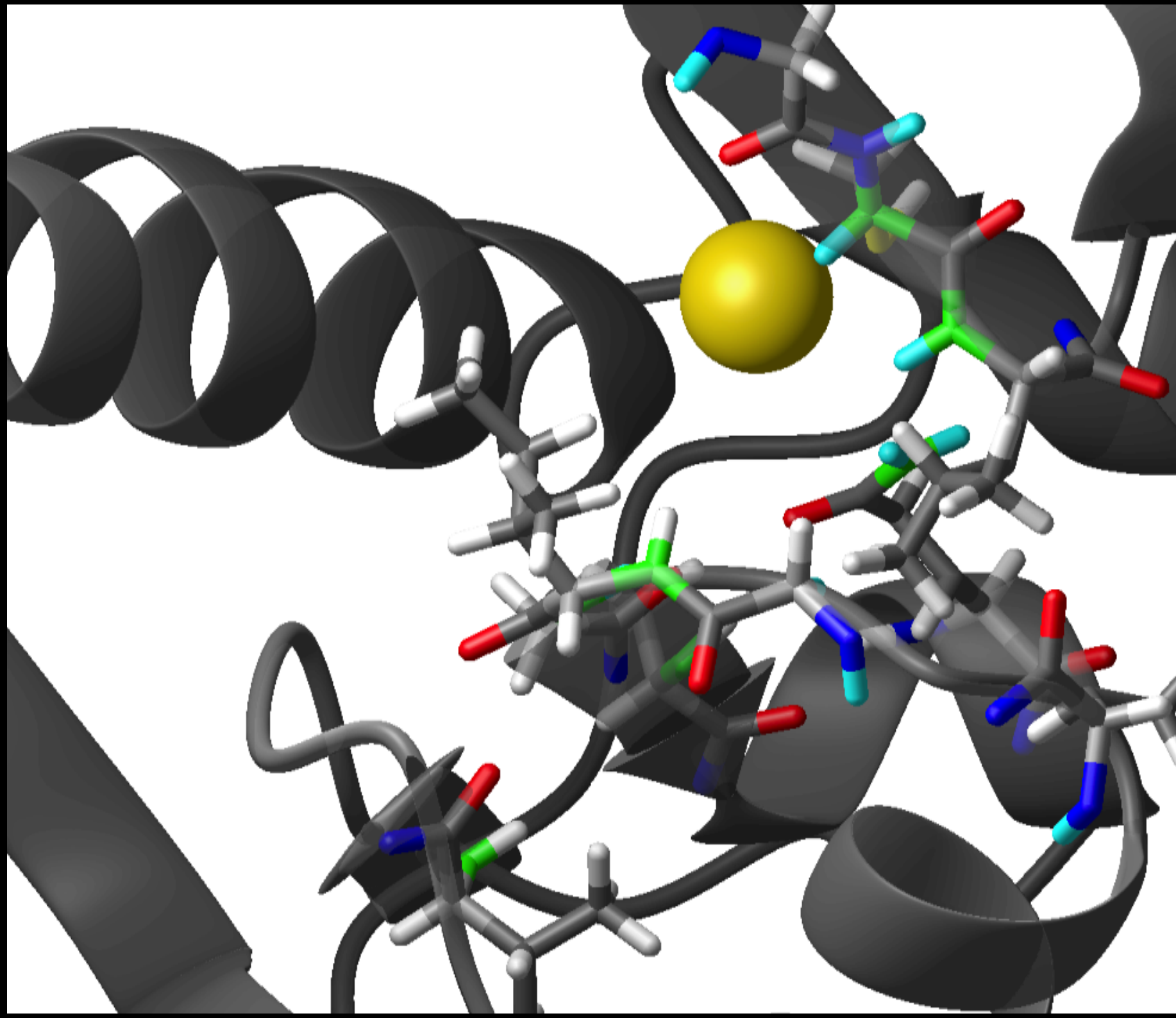
Laboratoire de Biochimie and Département de Chimie et Synthèse Organique, UMR 7654 and 7652 Ecole Polytechnique, Centre National de la Recherche Scientifique, Ecole Polytechnique, F-91128 Palaiseau Cedex, France

Received November 4, 1998; Revised Manuscript Received January 8, 1999

ABSTRACT: Series of substrates derivatives of peptide deformylase were systematically synthesized and studied for their capacities to undergo hydrolysis. Data analysis indicated the requirement for a hydrophobic first side chain and for at least two main chain carbonyl groups in the substrate. For instance, Fo-Met-OCH₃ and Fo-Nle-OCH₃ were the minimal substrates of peptide deformylase obtained in this study, while positively charged Fo-Nle-ArgNH₂ was the most efficient substrate ($k_{\text{cat}}/K_{\text{m}} = 4.5 \times 10^5 \text{ M}^{-1} \cdot \text{s}^{-1}$). On the basis of this knowledge, 3-mercapto-2-benzylpropanoylglycine (thiorphan), a known inhibitor of thermolysin, could be predicted and further shown to inhibit the deformylation reaction. The inhibition by this compound was competitive and proved to depend on the hydrophobicity at the P₁' position. Spectroscopic evidence that the sulfur group of thiorphan binds next to the active site metal ion on the enzyme could be obtained. Consequently, a small thiopseudopeptide derived from Fo-Nle-OCH₃ was designed and synthesized. This compound behaved as a competitive inhibitor of peptide deformylase with $K_{\text{i}} = 52 \pm 5 \mu\text{M}$. Introduction of a positive charge to this thiopeptide via addition of an arginine at P₂' improved the inhibition constant up to $2.5 \pm 0.5 \mu\text{M}$, a value 4 orders of magnitude smaller than that of the starting inhibitors. Evidence that this inhibitor, imino[(5-methoxy-5-oxo-4-[[2-(sulfanylmethyl)-hexanoyl]amino]pentyl)amino]methanamine, binds inside the active site cavity of peptide deformylase, while keeping intact the 3D fold of the protein, was provided by NMR. A fingerprint of the interaction of the inhibitor with the residues of the enzyme was obtained.

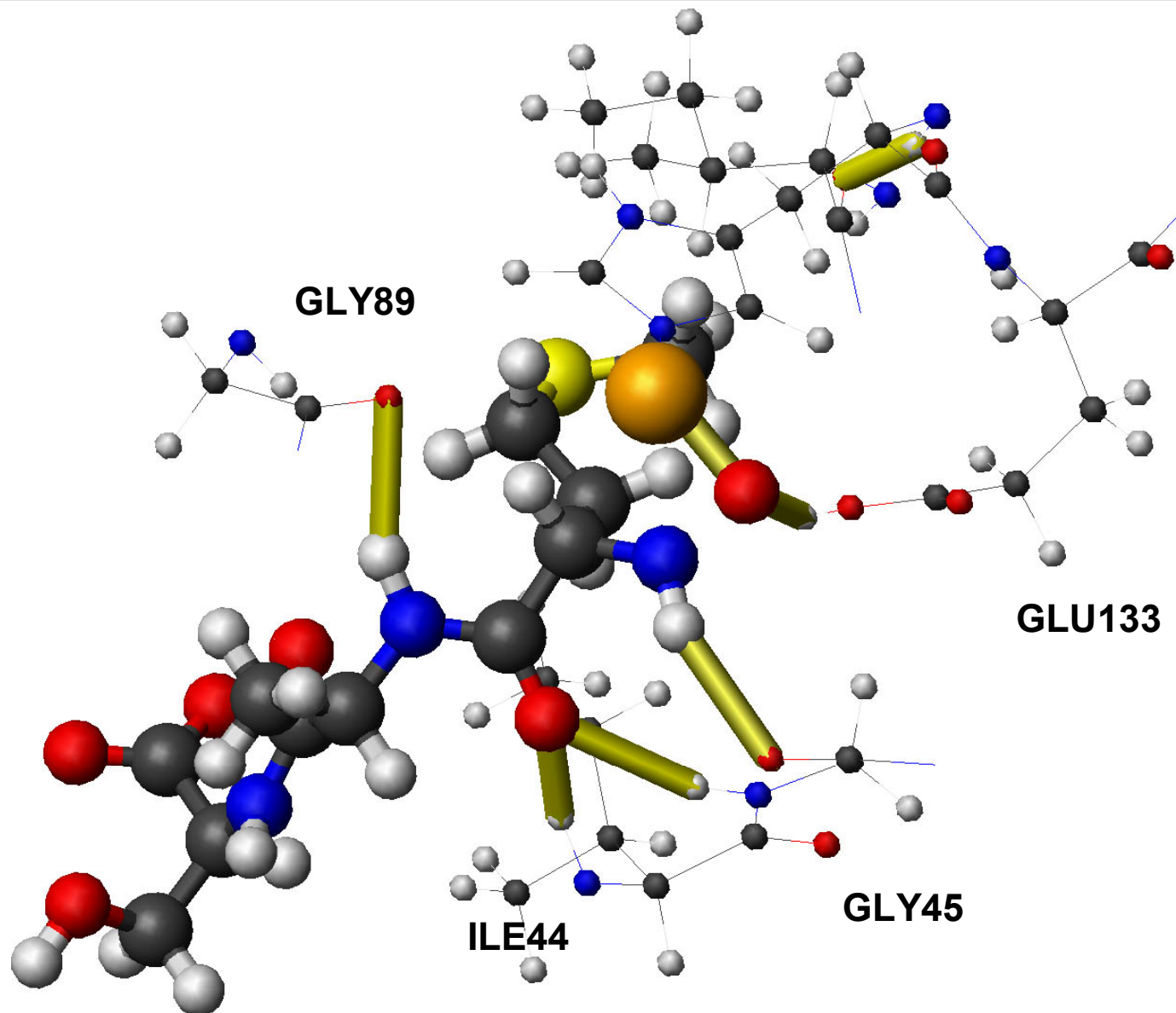
RMN PDF et PDF / inhibiteur

Atom	$\Delta\delta$ ^{15}N or ^{13}C (ppm)	Atom	$\Delta\delta$ ^1H (ppm)
C90 CA	7.2	C90 HA	1.32
Q50 NE2	5.5	Q50 HE21	0.92
L91 N	4.5	L91 HN	0.83
V59 N	3.0	H7 HN	0.57
I86 N	2.0	G89 HN	0.53
I44 N	1.5	Q50 HNE2	0.51
G45 N	1.5	G43 HA1	0.45
A47 N	1.5	E41 HN	0.40
		G45 HN	0.35
		C90 HN	0.34
		G43 HN	0.31

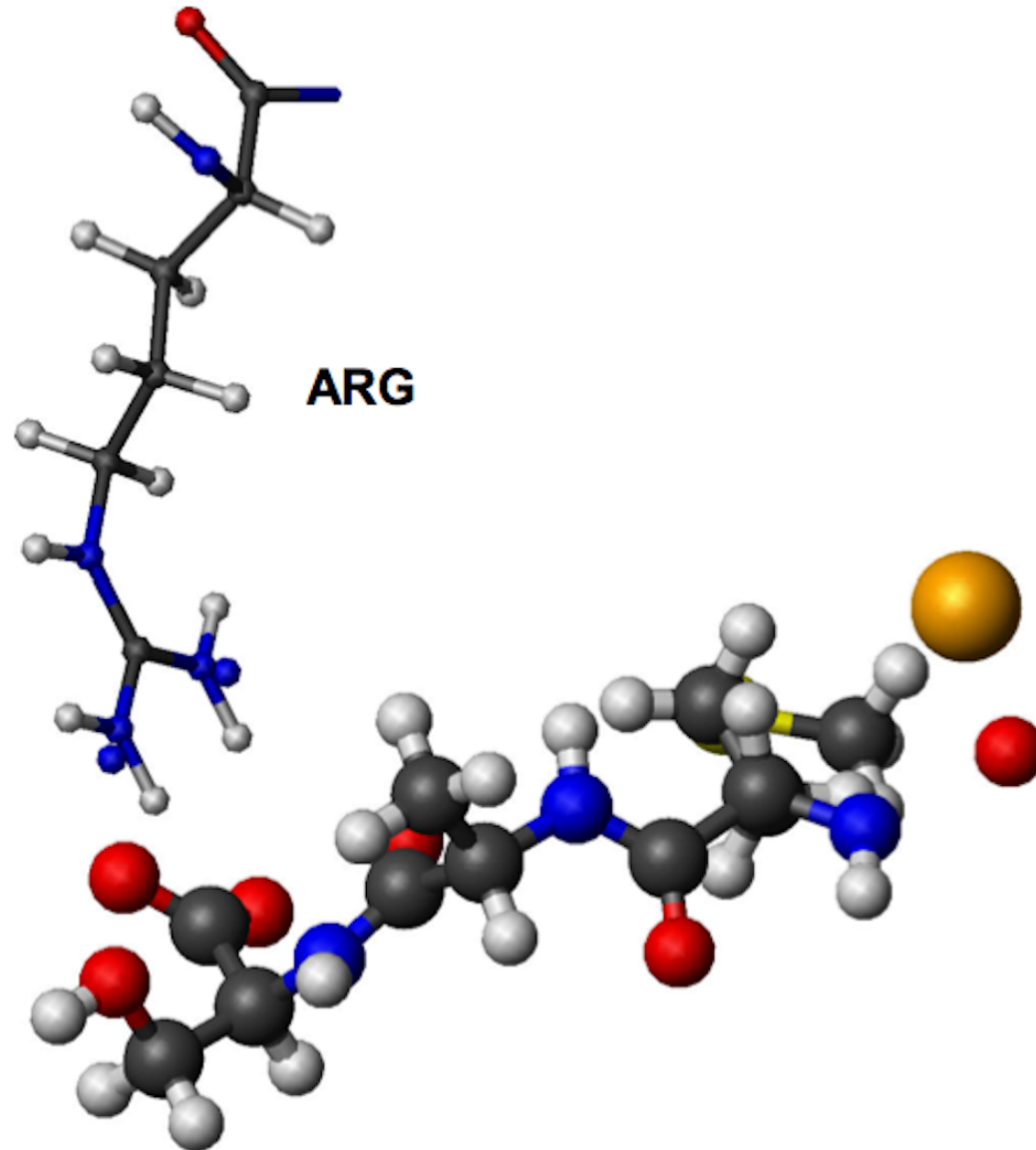


Stabilisation inhibiteur

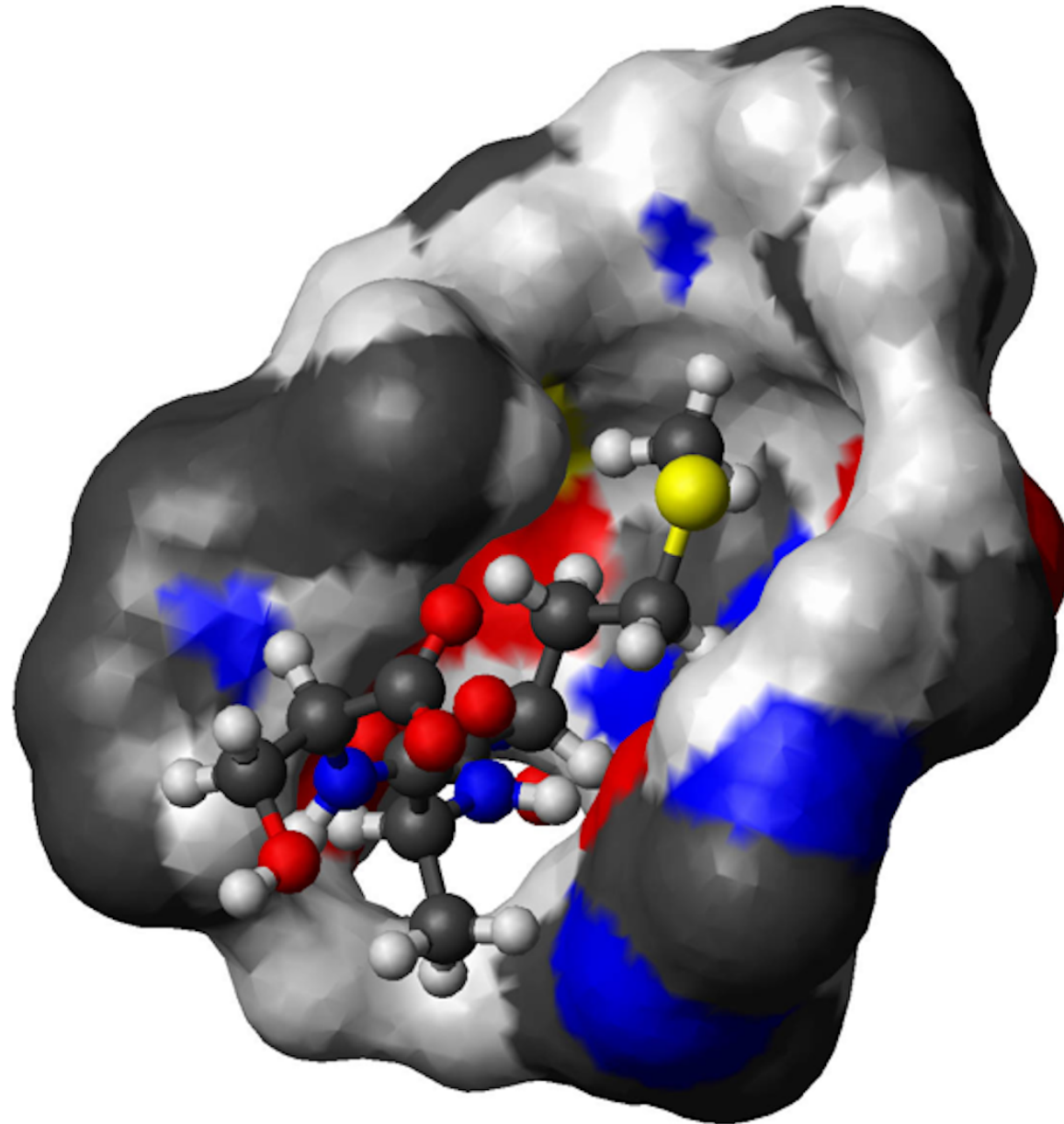
Ponts hydrogènes



Effets électrostatiques



Effets hydrophobes



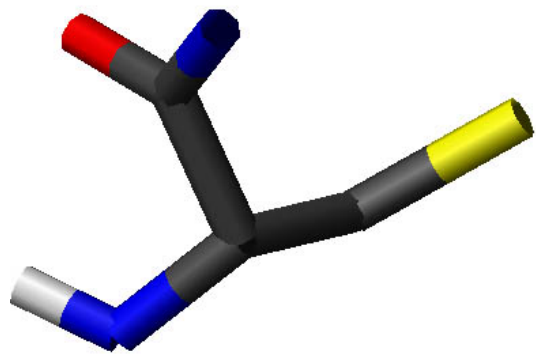
3D structure



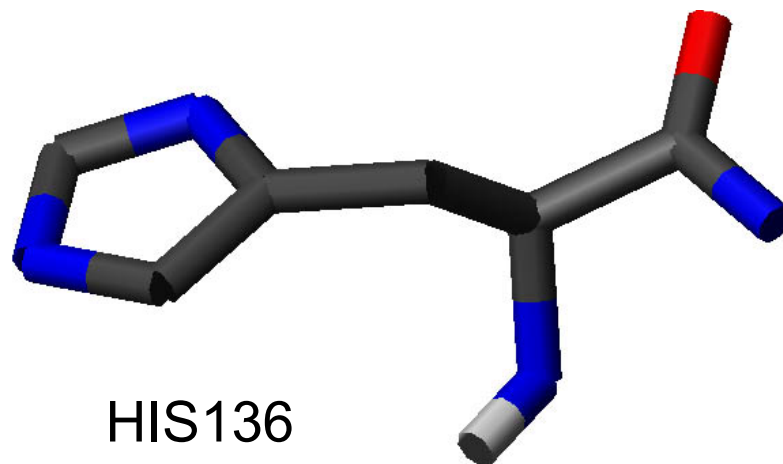
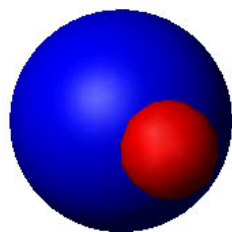
1DEF



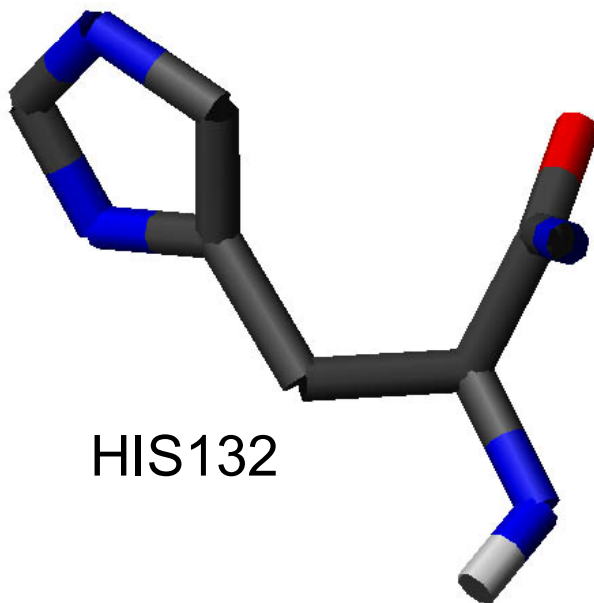
1DFF



CYS90



HIS136



HIS132

Conclusions

Conclusions

- **RMN / Mass / IR:**
 - Déterminer la structure de petites molécules
 - Déterminer la structure de protéines ou l'interaction en inhibiteur et protéine
- **Importance de la structure de la protéine:**
 - Déterminer le site catalytique
 - Comprendre le mécanisme de la réaction (par exemple hydrolase)
 - Améliorer un inhibiteur (charge, poche hydrophobe, ...)
- **Réactions chimiques:**
 - Problème des groupes protecteurs
 - Possibilité de faire des réactions chimiosélective / biocompatible

