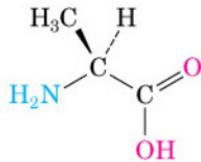


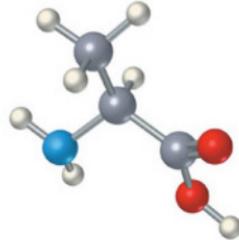
Il codice genetico

	T	C	A	G	
T	TTT <i>Phe (F)</i> TTC " TTA <i>Leu (L)</i> TTG "	TCT <i>Ser (S)</i> TCC " TCA " TCG "	TAT <i>Tyr (Y)</i> TAC " TAA stop TAG stop	TGT <i>Cys (C)</i> TGC " TGA stop TGG <i>Trp (W)</i>	T C A G
C	CTT <i>Leu (L)</i> CTC " CTA " CTG "	CCT <i>Pro (P)</i> CCC " CCA " CCG "	CAT <i>His (H)</i> CAC " CAA <i>Gln (Q)</i> CAG "	CGT <i>Arg (R)</i> CGC " CGA " CGG "	T C A G
A	ATT <i>Ile (I)</i> ATC " ATA " ATG <i>Met (M)</i>	ACT <i>Thr (T)</i> ACC " ACA " ACG "	AAT <i>Asn (N)</i> AAC " AAA <i>Lys (K)</i> AAG "	AGT <i>Ser (S)</i> AGC " AGA <i>Arg (R)</i> AGG "	T C A G
G	GTT <i>Val (V)</i> GTC " GTA " GTG "	GTC <i>Ala (A)</i> GCC " GCA " GCG "	GAT <i>Asp (D)</i> GAC " GAA <i>Glu (E)</i> GAG "	GGT <i>Gly (G)</i> GGC " GGA " GGG "	T C A G

Amminoacidi: composti bifunzionali

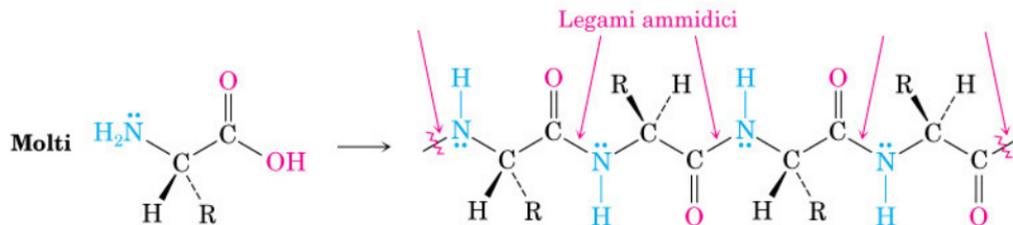


Alanina (un amminoacido)



Contengono un gruppo acido ed uno basico

Amminoacidi: peptidi

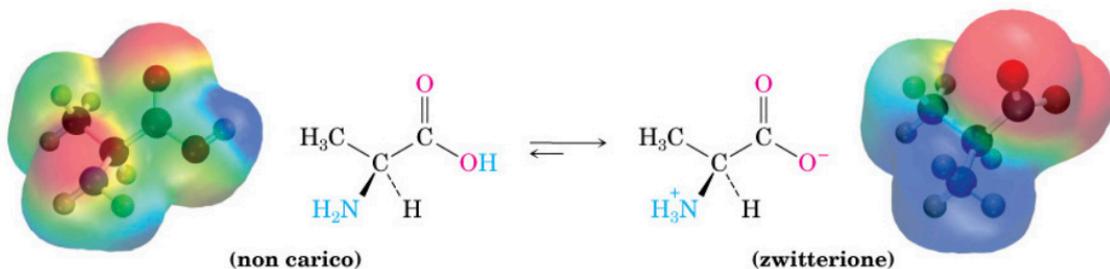


Unità strutturali delle proteine (o peptidi se <50 a.a.)

Amminoacidi: zwitterioni

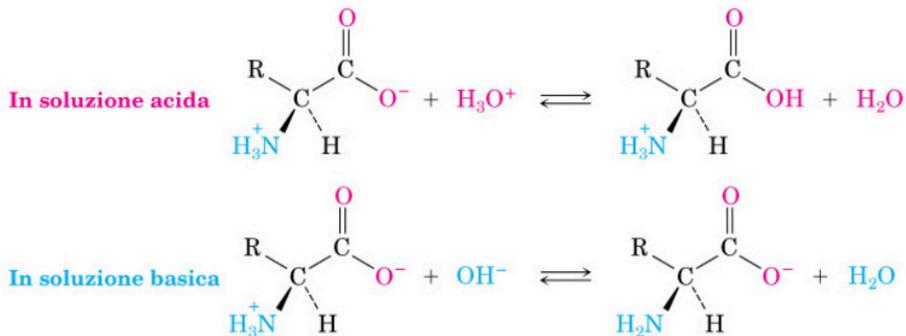
Sono soggetti a reazione acido-base intramolecolare

esistono principalmente in forma di ione dipolare o zwitterione



Alanina

Sono anfoteri (possono reagire sia come basi che come acidi)

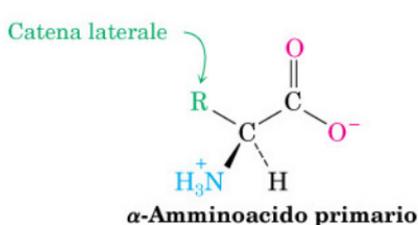


Amminoacidi: alpha-amminoacidi

Gli a.a. comuni presenti nelle proteine sono 20

si tratta di **α-amminoacidi**

19 di 20 sono ammine primarie e differiscono solo per la natura del sostituente in α: la catena laterale
la prolina è secondaria (anello pirrolidinico)

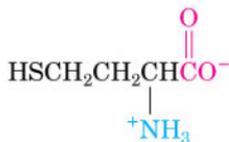


Altri amminoacidi non proteici importanti:



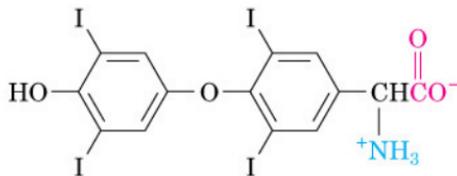
**Acido γ -ammino-
butirrico**

Neurotrasmettitore nel cervello



Omocisteina

Presente nel sangue,
legata a disturbi delle coronarie

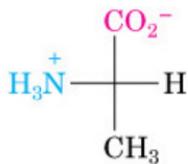


Tiroxina

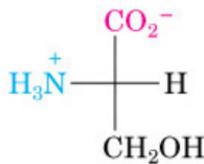
Ormone tiroideo

degli amminoacidi proteici solo la glicina non è chirale

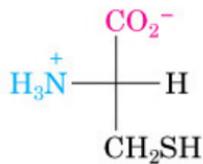
Proiezioni di Fischer



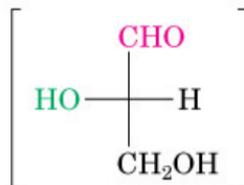
L-Alanina
(S)-Alanina



L-Serina
(S)-Serina



L-Cisteina
(R)-Cisteina



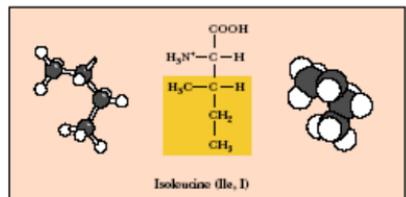
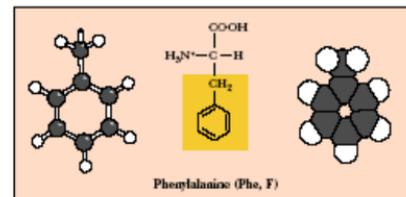
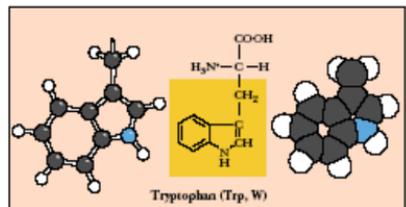
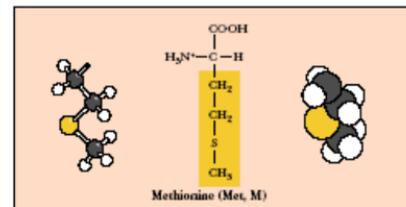
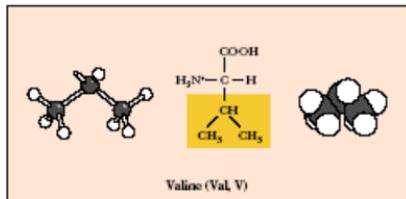
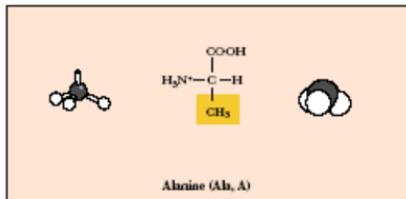
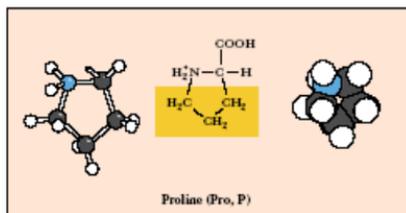
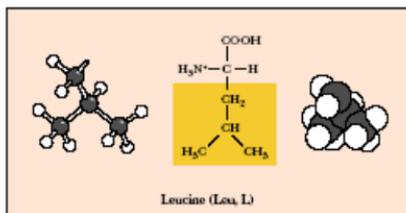
L-Gliceraldeide

L-amminoacidi

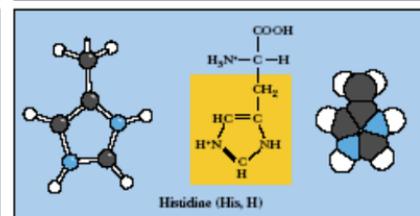
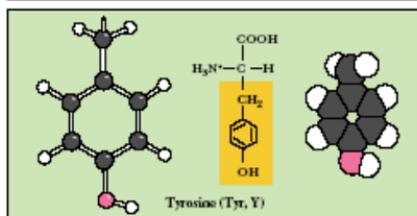
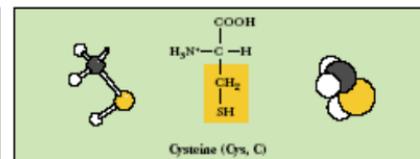
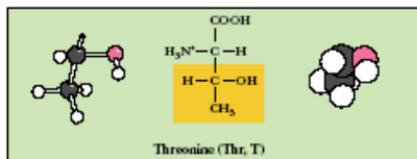
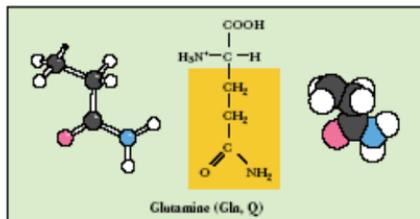
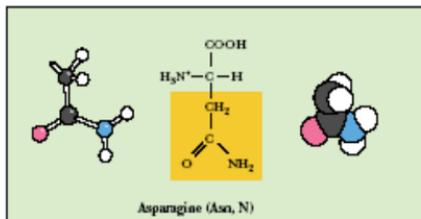
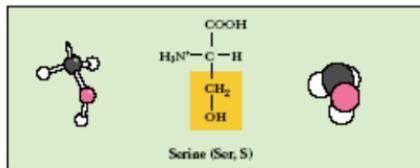
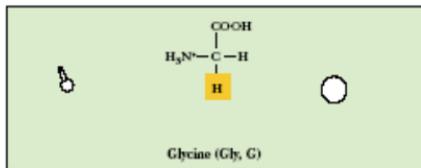
L-carboidrati

Amminoacidi: proprietà

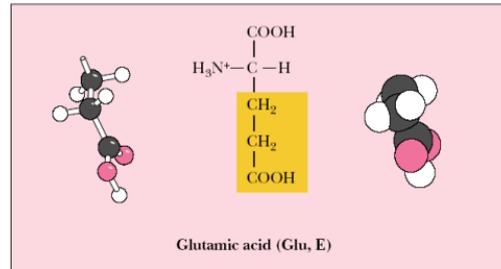
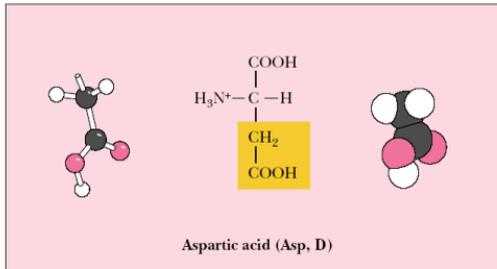
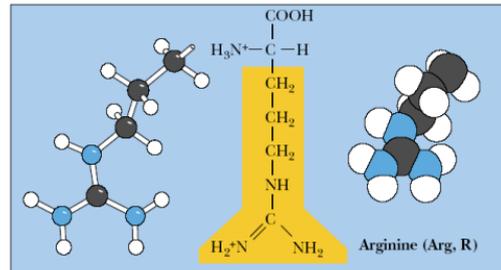
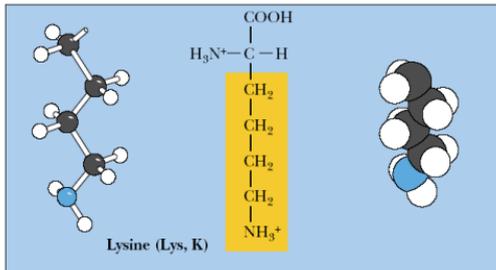
I 20 a.a. comuni sono distinti in neutri, acidi e basici in base alla natura della catena laterale

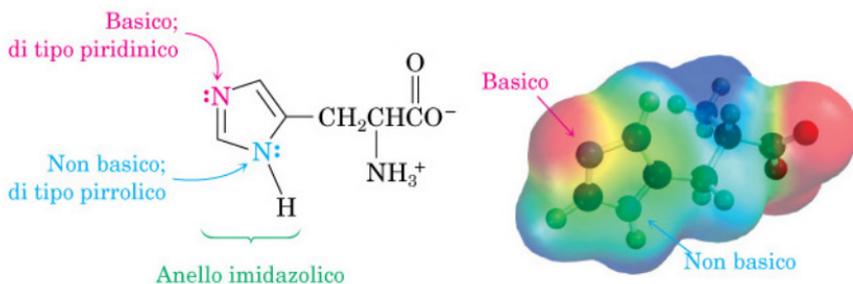


Amminoacidi: proprietà



Amminoacidi: proprietà

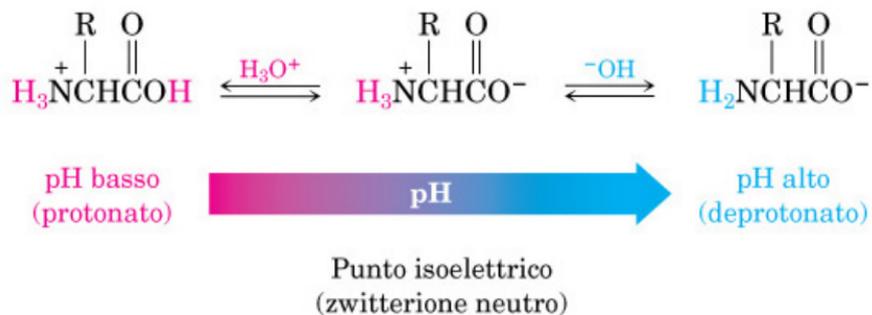




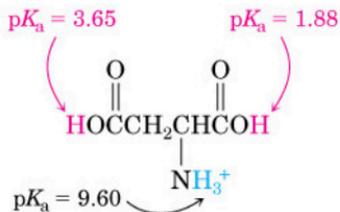
Istidina

La protonazione è influenzata dal pH – quello fisiologico è circa 7.3

Gli esseri umani sono in grado di sintetizzare solo 10 dei 20 a.a. proteici, gli altri (detti a.a. essenziali) devono essere assunti con l'alimentazione



E' il valore di pH in cui l' a.a. è globalmente neutro



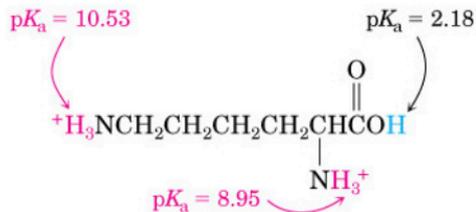
$$pI = \frac{1.88 + 3.65}{2} = 2.77$$

Aminoacido acido
Acido aspartico



$$pI = \frac{2.34 + 9.69}{2} = 6.01$$

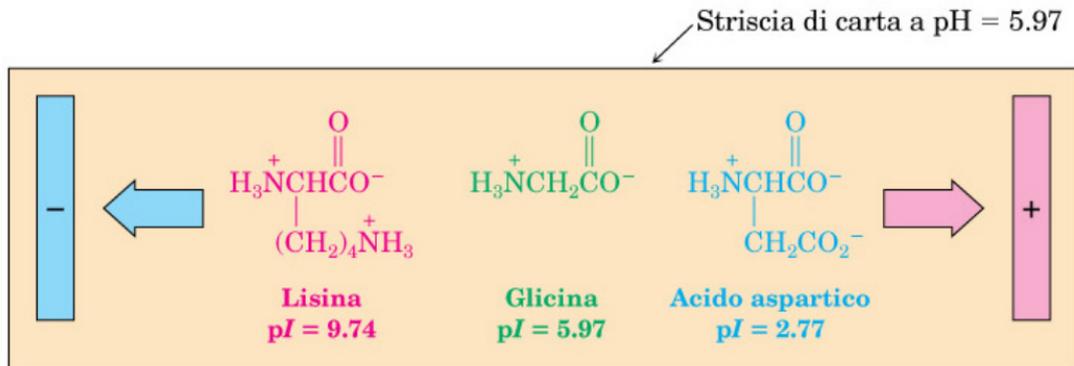
Aminoacido neutro
Alanina



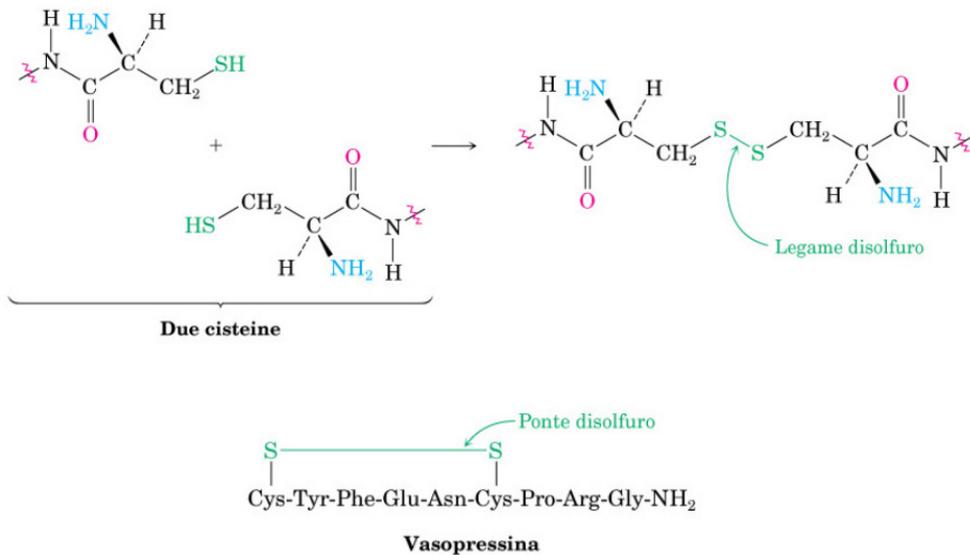
$$pI = \frac{8.95 + 10.53}{2} = 9.74$$

Aminoacido basico
Lisina

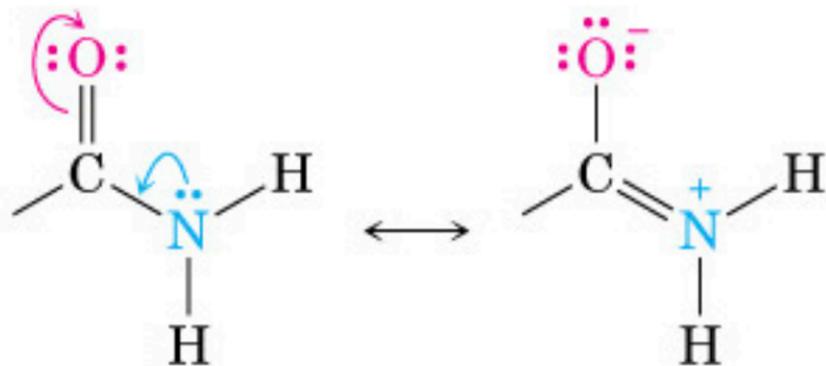
Separazione di una miscela di amminoacidi mediante elettroforesi. A pH = 5.97 le molecole di glicina sono per lo più neutre e non migrano, le molecole di lisina sono protonate e migrano verso l'elettrodo negativo e le molecole di acido aspartico sono deprotonate e migrano verso l'elettrodo positivo.

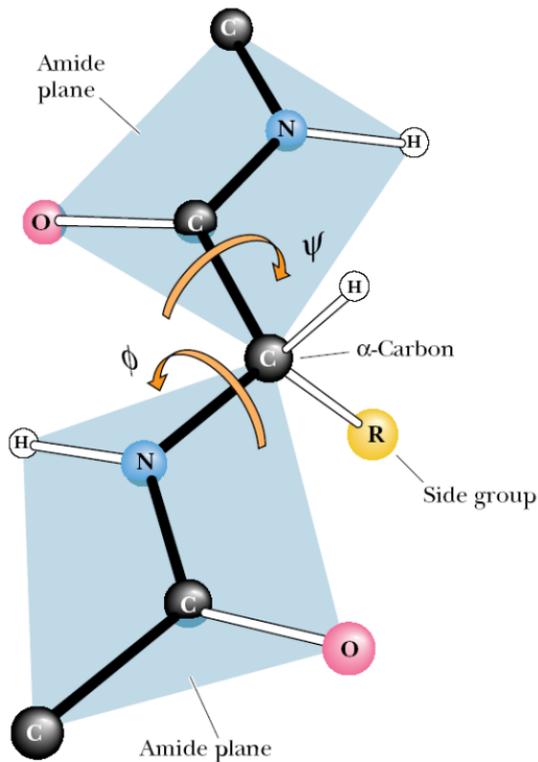


Il legame disolfuro



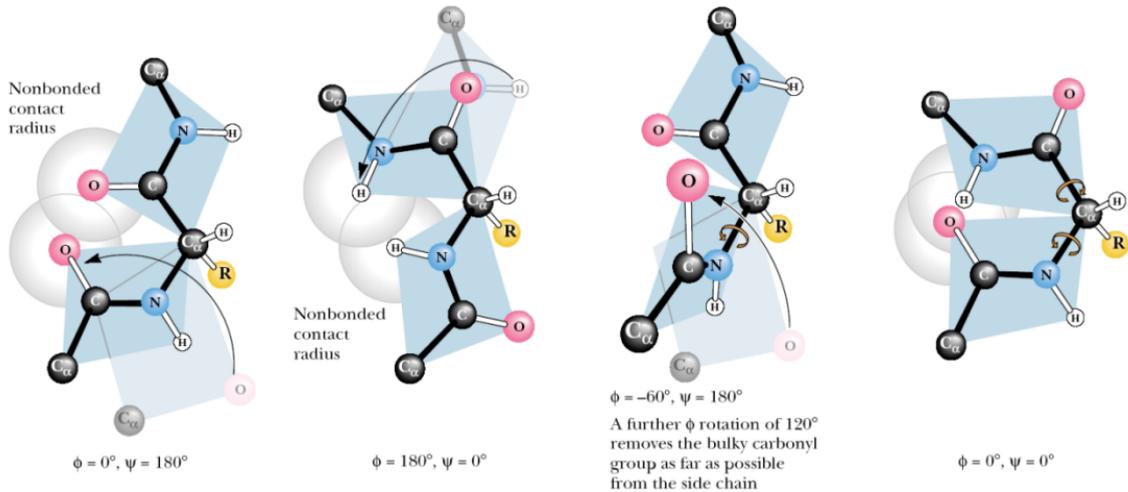
Può unire a.a. della stessa catena o di catene diverse



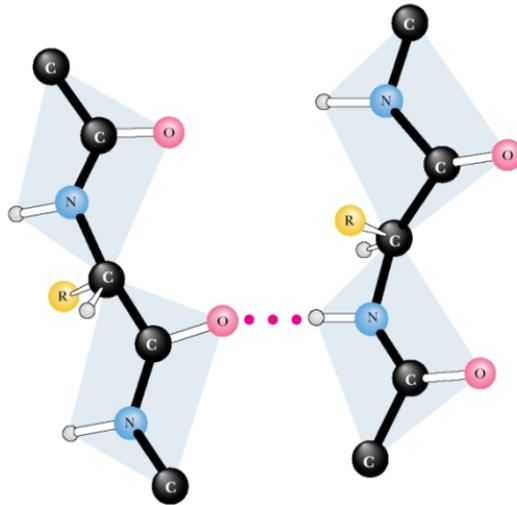


Sul legame ammidico c' è una barriera rotazionale di $88 \sin^2\theta \text{ kJmol}^{-1}$ a causa del parziale carattere di doppio legame

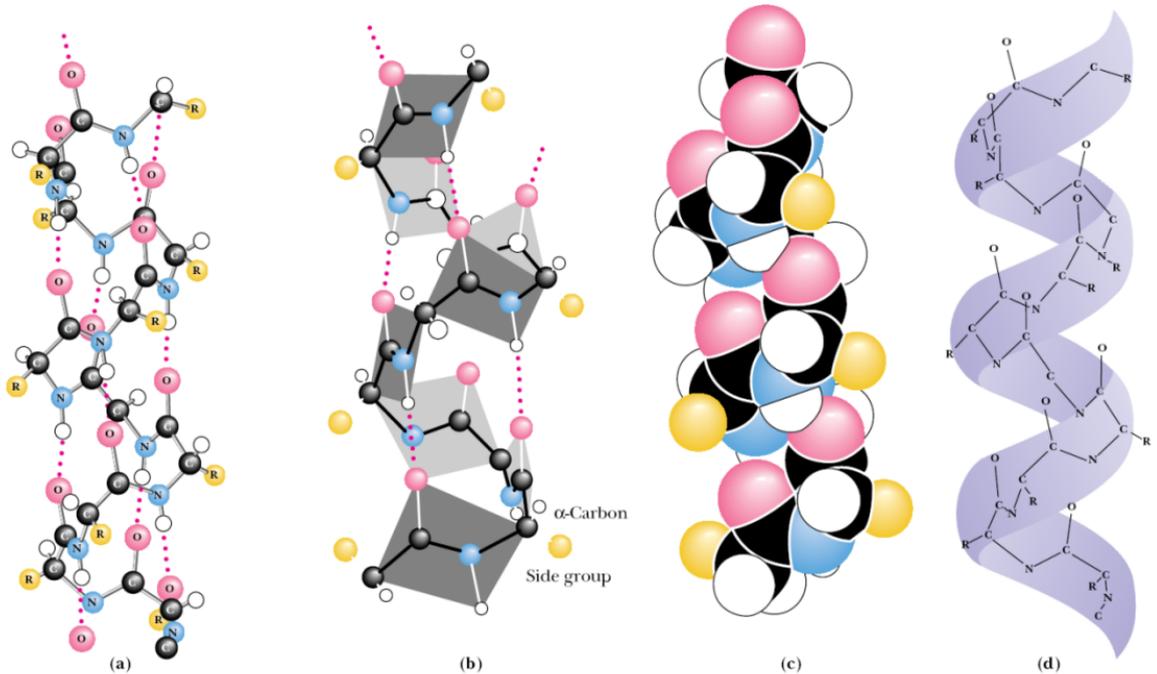
Per ogni amminoacido esistono due gradi di libertà rotazionali



In realtà non tutti gli angoli sono ugualmente possibili ed alcune conformazioni sono più probabili

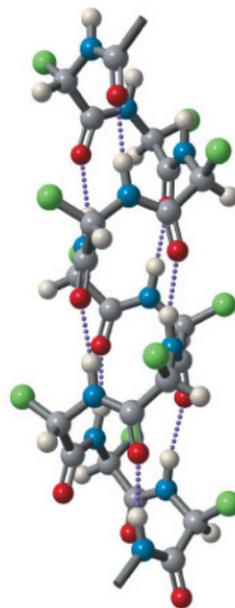
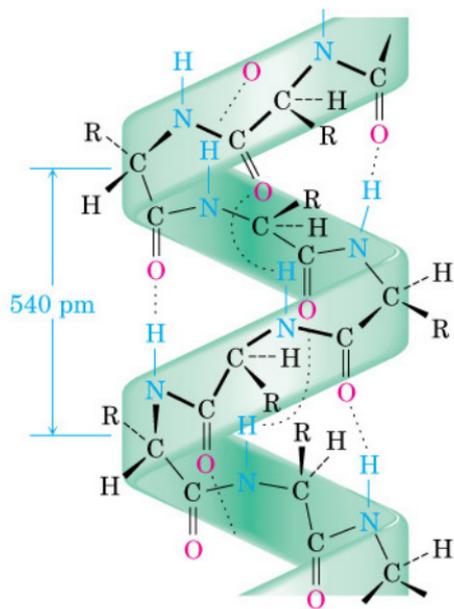


Ulteriori interazioni determinano le conformazioni delle proteine: legami a H

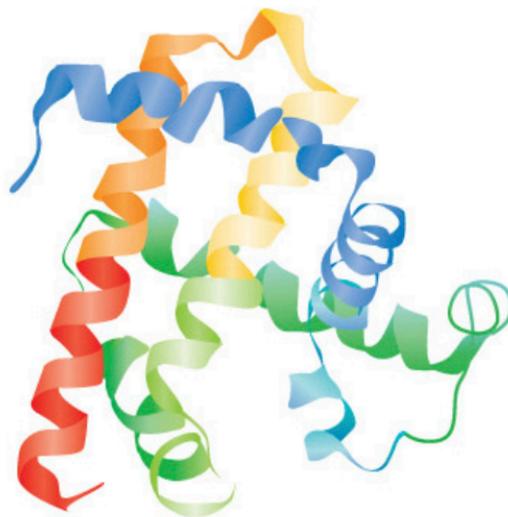


Struttura a elica

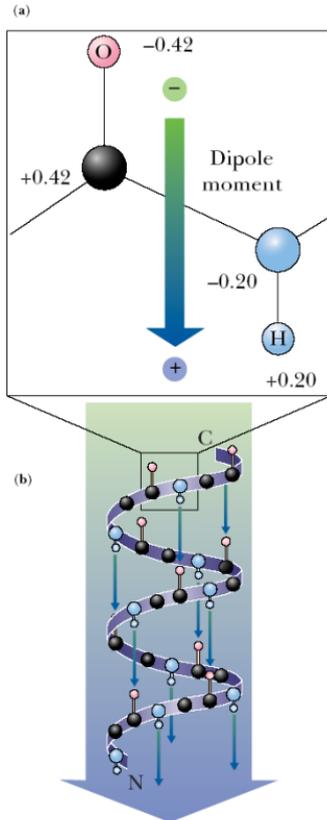
La struttura secondaria ad elica presente nell' α -cheratina.



Struttura secondaria e terziaria della mioglobina, una proteina globulare con estese sezioni ad elica, qui mostrate come nastri.

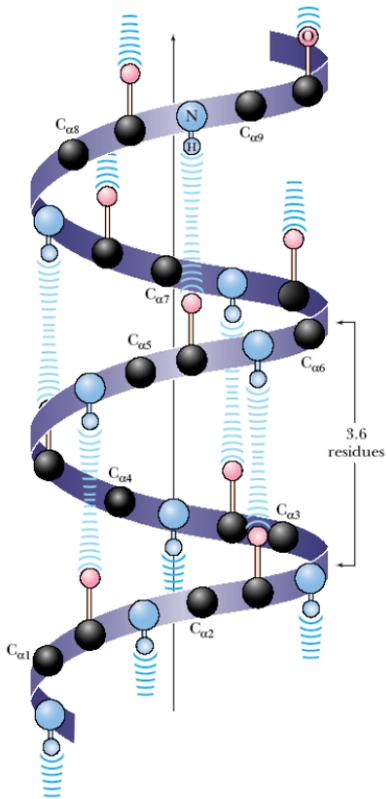


Proteine



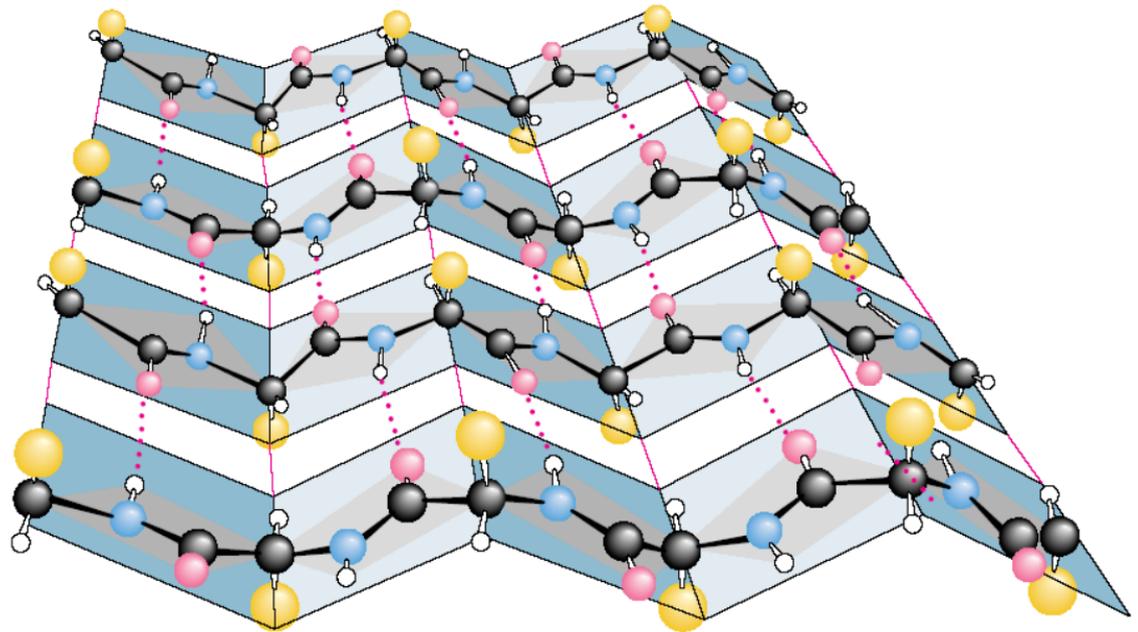
Momenti dipolari dei singoli legami peptidici si sommano in una struttura a elica

Leganti positivi tendono a legarsi in prossimità del C-terminale, negativi dell' N-terminale

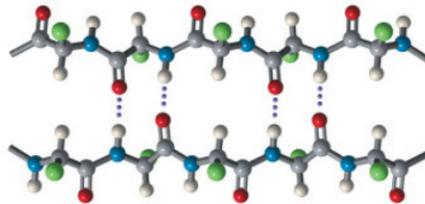
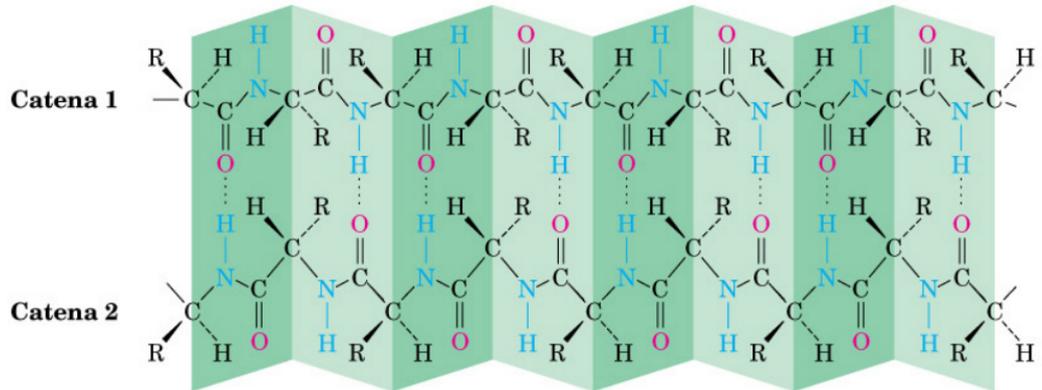


Agli estremi dell' elica vi sono accettori e donatori di legami a H liberi

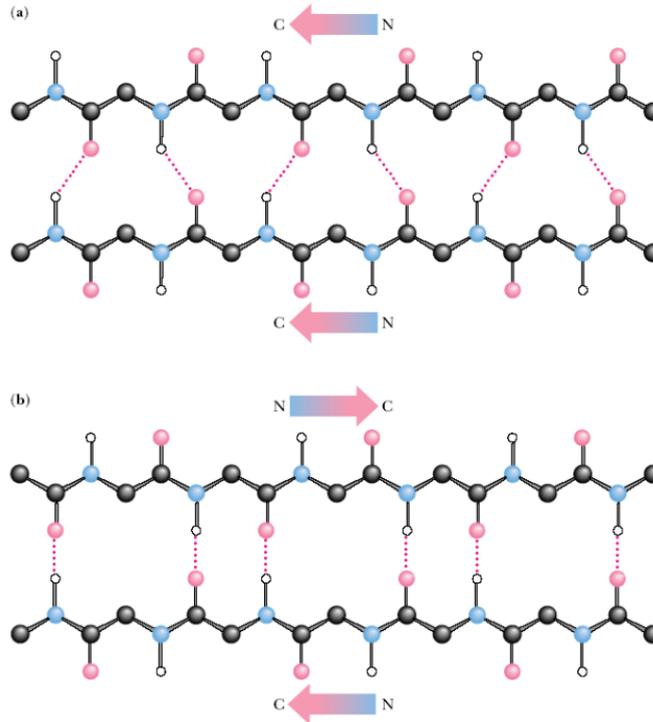
Un altro motivo di struttura secondaria: il β -foglietto



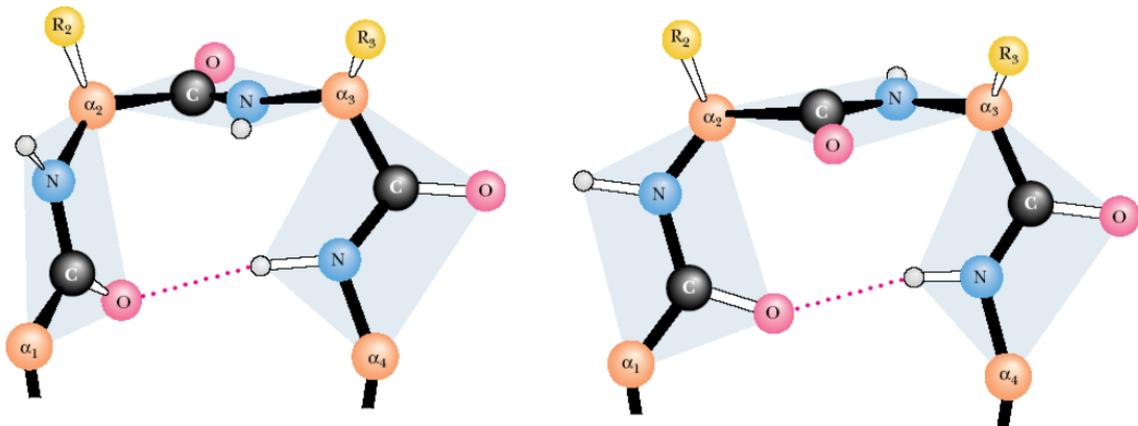
La struttura a foglietto β pieghettato nella fibroina della seta.



foglietto β parallelo e anti-parallelo

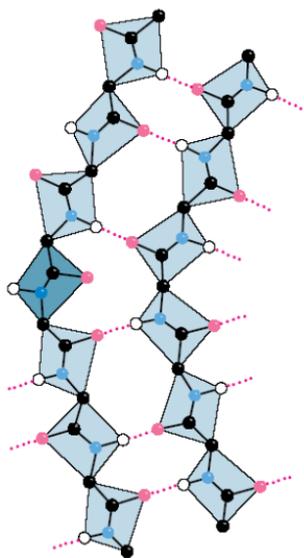


β turn

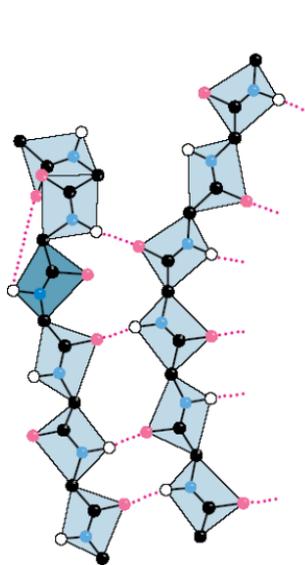


Sono presenti spesso glicine e proline

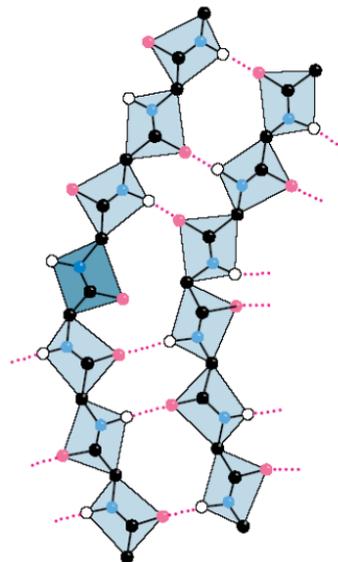
β buldge



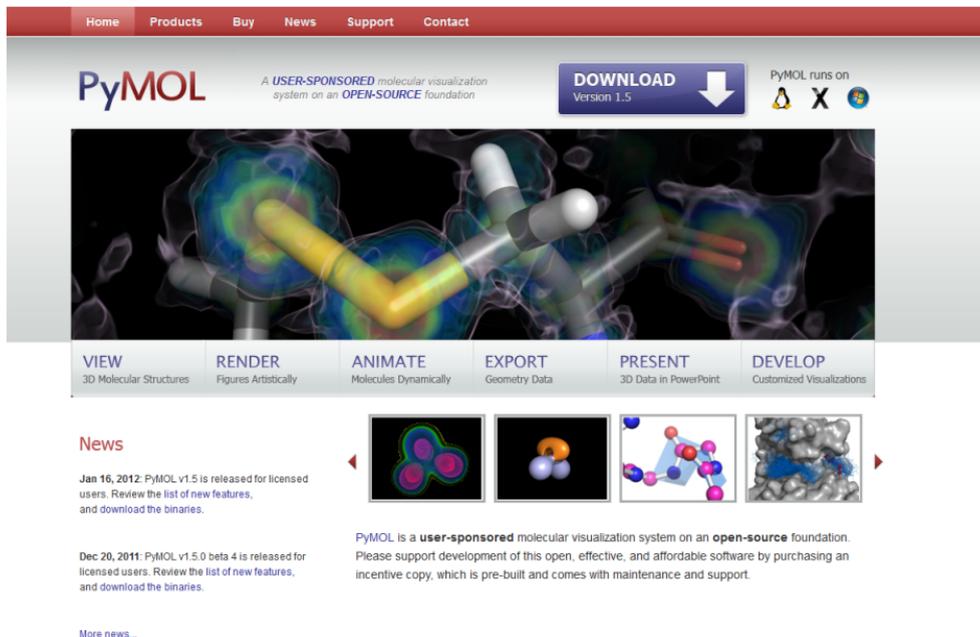
Classic buldge



G-I buldge



Wide buldge



The screenshot shows the PyMOL website homepage. At the top is a red navigation bar with links for Home, Products, Buy, News, Support, and Contact. Below this is a white banner area. On the left, the PyMOL logo is displayed. In the center, a tagline reads: "A USER-SPONSORED molecular visualization system on an OPEN-SOURCE foundation". To the right of the tagline is a blue "DOWNLOAD" button with a white arrow pointing down and the text "Version 1.5". Further right, it says "PyMOL runs on" followed by logos for Linux, X11, and Windows. Below the banner is a large image showing a protein structure with a yellow stick model and a blue electron density map. Underneath this image is a row of six tabs: VIEW (3D Molecular Structures), RENDER (Figures Artistically), ANIMATE (Molecules Dynamically), EXPORT (Geometry Data), PRESENT (3D Data in PowerPoint), and DEVELOP (Customized Visualizations). Below the tabs is a "News" section with a red heading. It contains two news items: "Jan 16, 2012: PyMOL v1.5 is released for licensed users. Review the list of new features, and download the binaries." and "Dec 20, 2011: PyMOL v1.5.0 beta 4 is released for licensed users. Review the list of new features, and download the binaries." To the right of the news items are four small thumbnail images showing different molecular visualization styles: a protein with electron density, a ball-and-stick model, a space-filling model, and a surface representation. Below the news items is a paragraph stating: "PyMOL is a **user-sponsored** molecular visualization system on an **open-source** foundation. Please support development of this open, effective, and affordable software by purchasing an incentive copy, which is pre-built and comes with maintenance and support." At the bottom left of the news section is a link "More news...".

<http://www.pymol.org/>