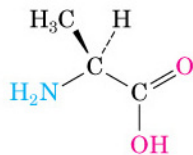


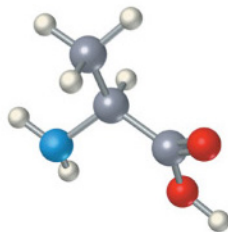
Il codice genetico

	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

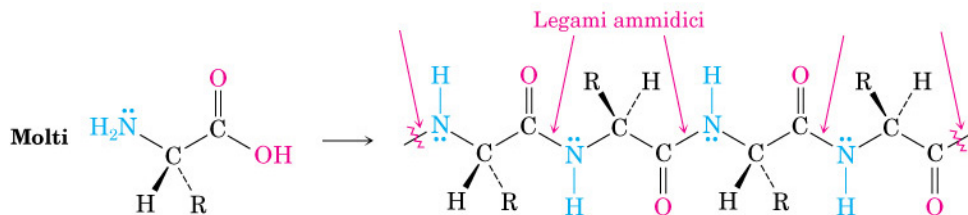
Amminoacidi: composti bifunzionali



Alanina (un amminoacido)



Contengono un gruppo acido ed uno basico

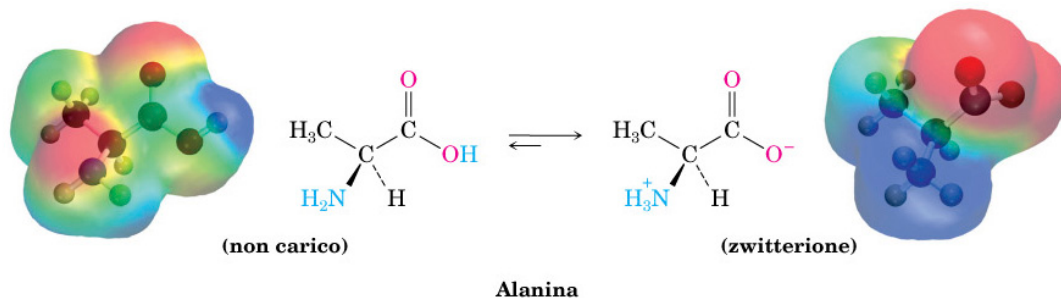


Unità strutturali delle proteine (o peptidi se <50 a.a.)

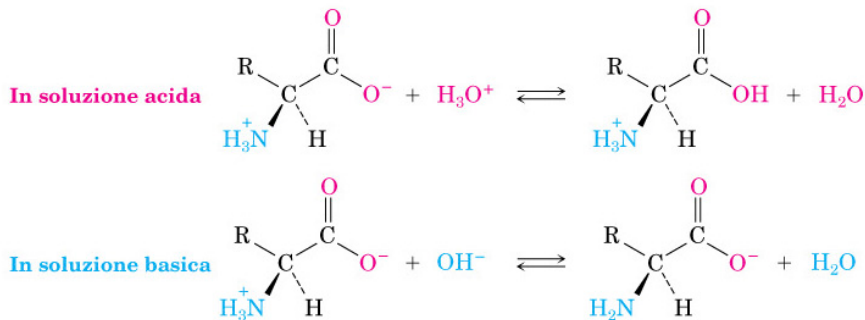
Amminoacidi: zwitterioni

Sono soggetti a reazione acido-base intramolecolare

esistono principalmente in forma di ione dipolare o zwitterione



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

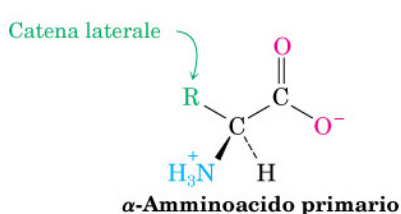


Amminoacidi: alpha-amminoacidi

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 sostituito in α: la catena laterale
la prolina è secondaria (anello pirrolidinico)

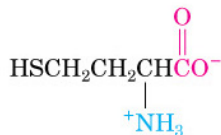


Altri amminoacidi non proteici importanti:



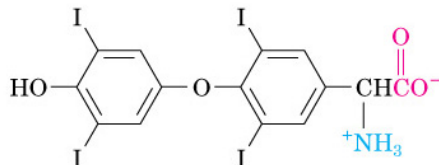
**Acido γ -ammino-
butirrico**

Neurotrasmettitore nel cervello



Omocisteina

Presente nel sangue,
legata a disturbi delle coronarie

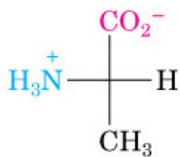


Tiroxina

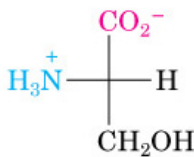
Ormone tiroideo

degli amminoacidi proteici solo la glicina non è chirale

Proiezioni di Fischer



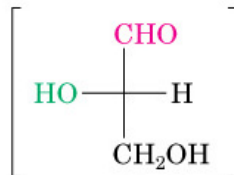
L-Alanina
(S)-Alanina



L-Serina
(S)-Serina



L-Cisteina
(R)-Cisteina



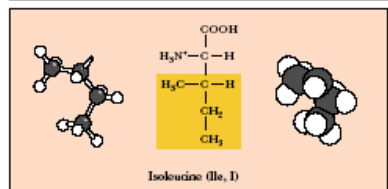
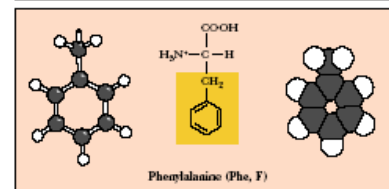
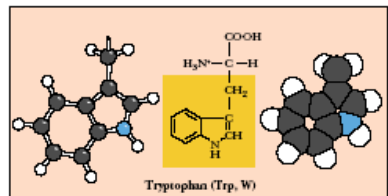
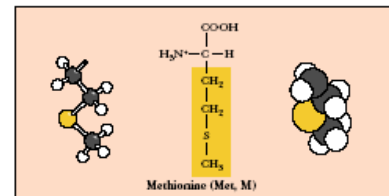
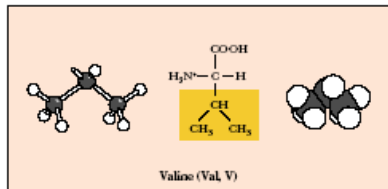
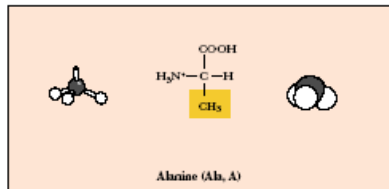
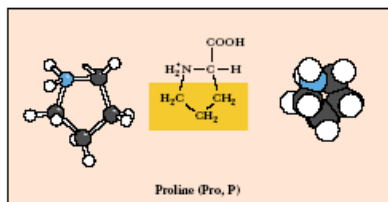
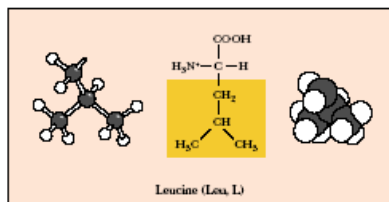
L-Gliceraldeide

L-amminoacidi

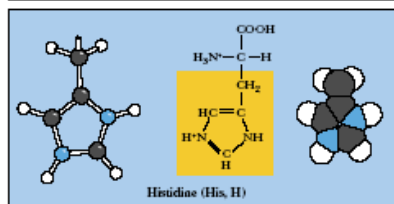
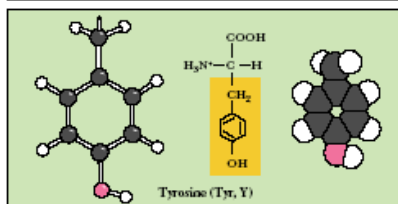
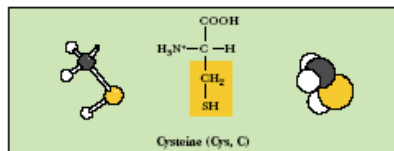
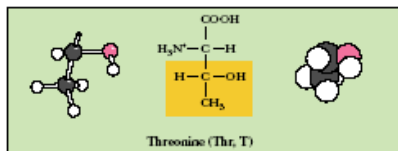
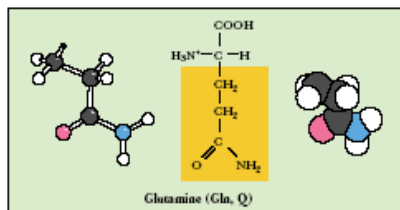
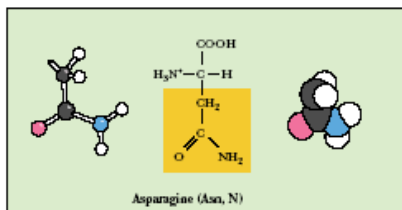
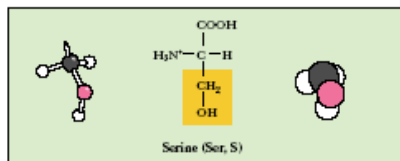
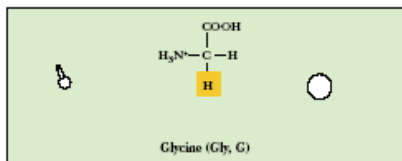
L-carboidrati

Amminoacidi: proprietà

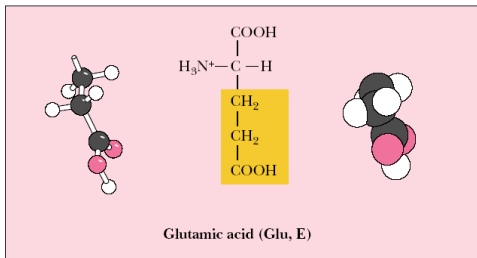
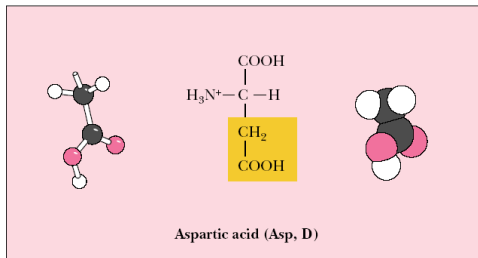
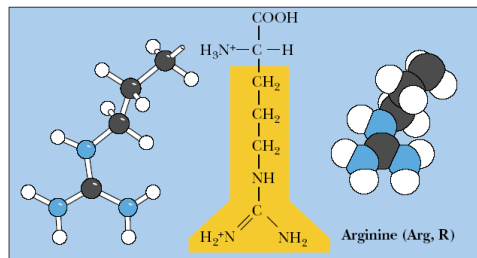
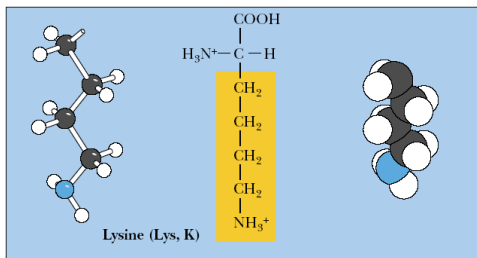
I 20 a.a. comuni sono distinti in neutri, acidi e basici in base alla natura della catena laterale

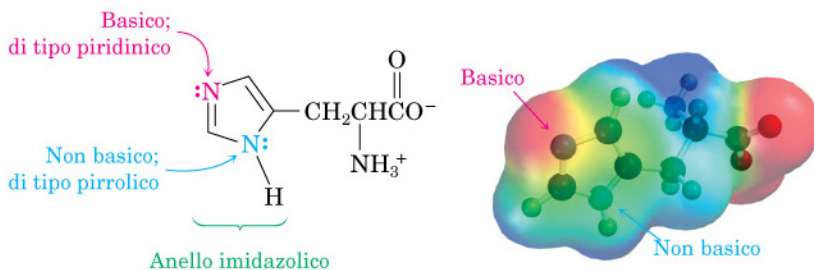


Amminoacidi: proprietà



Amminoacidi: proprietà

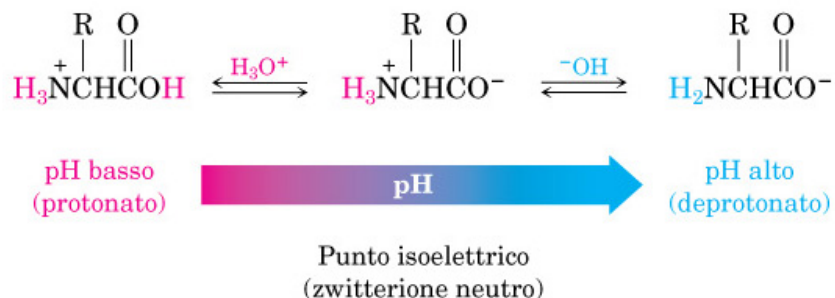




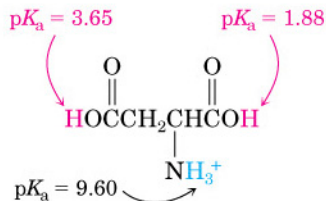
Istidina

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

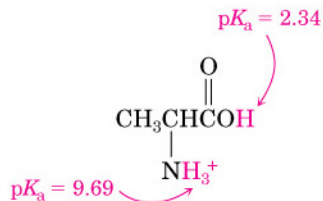


E' il valore di pH in cui l' a.a. è globalmente neutro



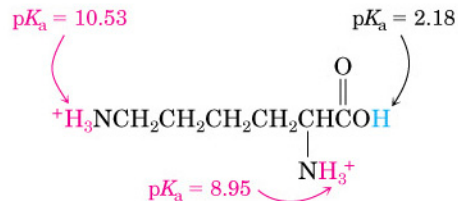
$$pI = \frac{1.88 + 3.65}{2} = 2.77$$

Amminoacido acido
Acido aspartico



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

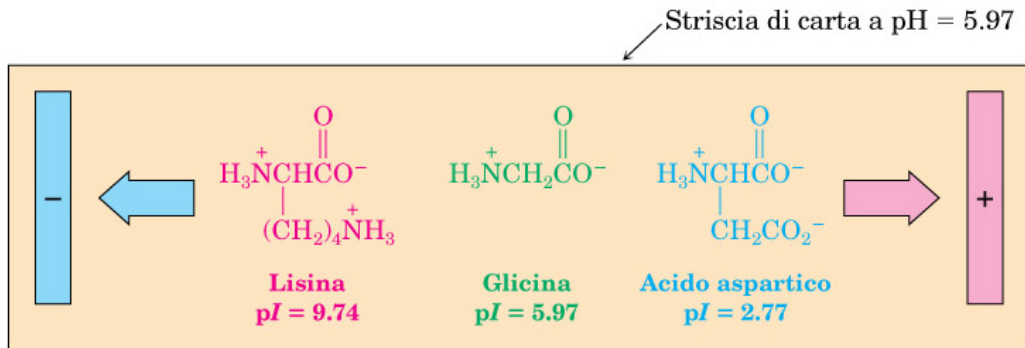
Amminoacido neutro
Alanina



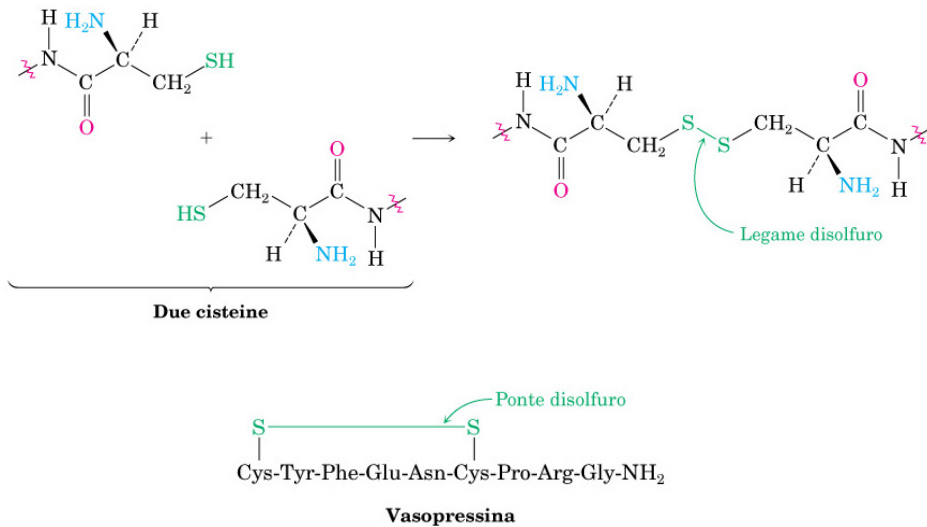
$$pI = \frac{8.95 + 10.53}{2} = 9.74$$

Amminoacido basico
Lisina

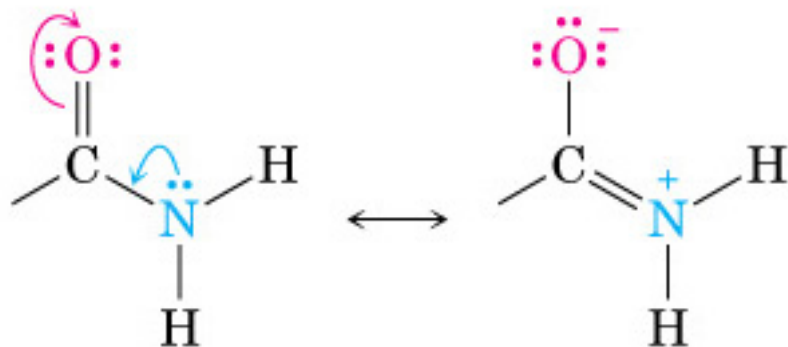
Separazione di una miscela di amminoacidi mediante elettroforesi. A pH = 5.97 le molecole di glicina sono per lo più neutre e non migrano, le molecole di lisina sono protonate e migrano verso l'elettrodo negativo e le molecole di acido aspartico sono deprotonate e migrano verso l'elettrodo positivo.

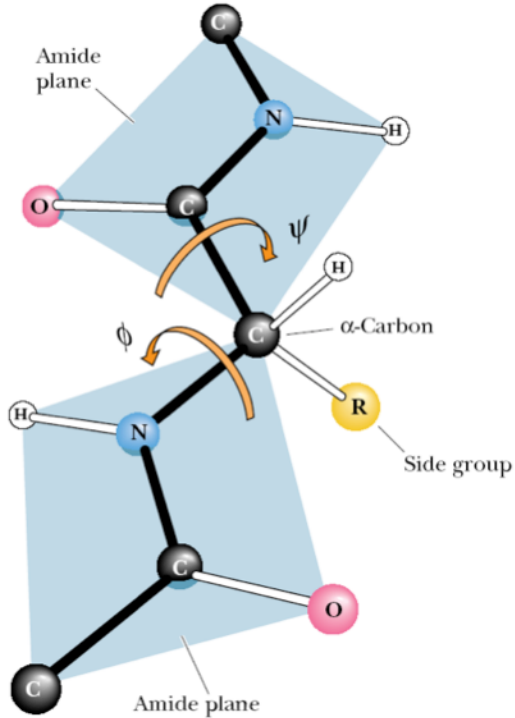


Il legame disolfuro



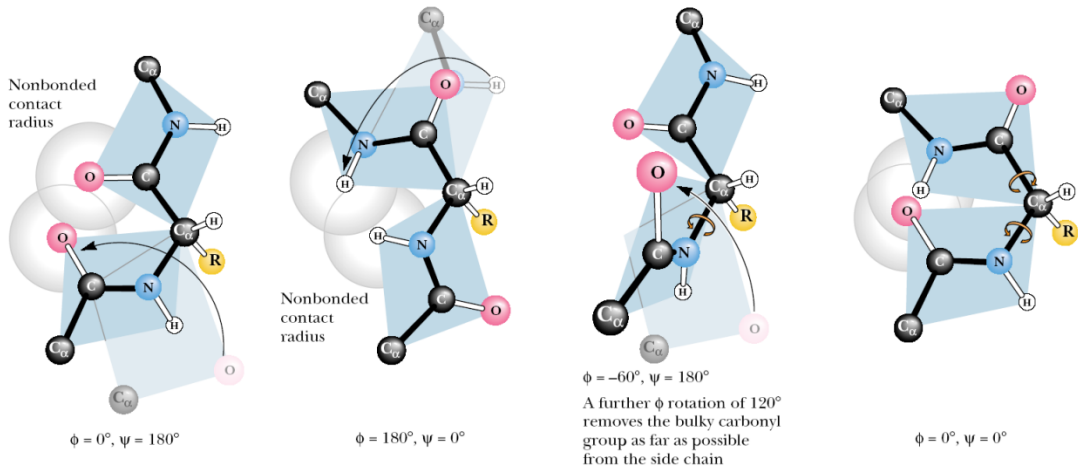
Può unire a.a. della stessa catena o di catene diverse



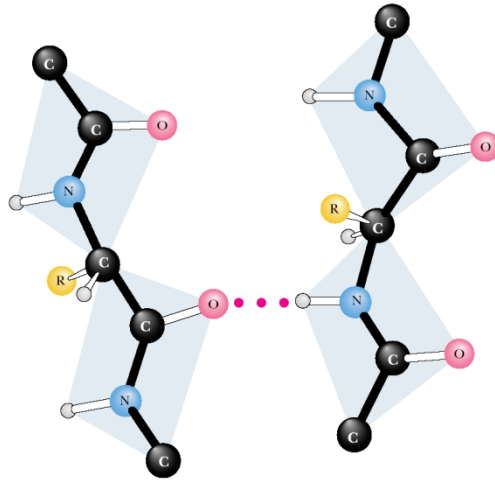


Sul legame ammidico c'è una barriera rotazionale di $88 \sin^2\theta \text{ kJmol}^{-1}$ a causa del parziale carattere di doppio legame

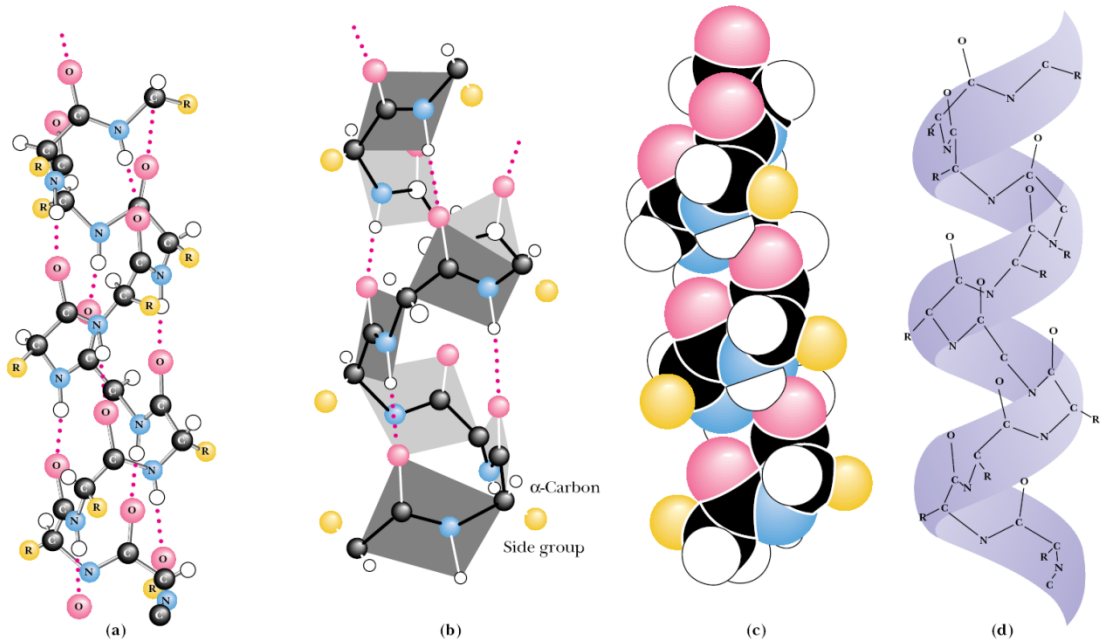
Per ogni amminoacido esistono due gradi di libertà rotazionali



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

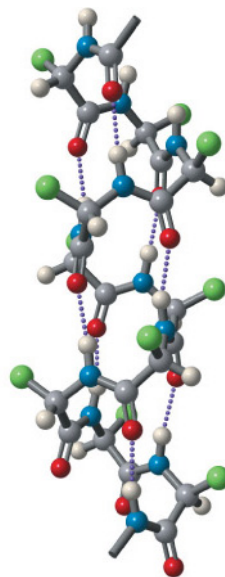
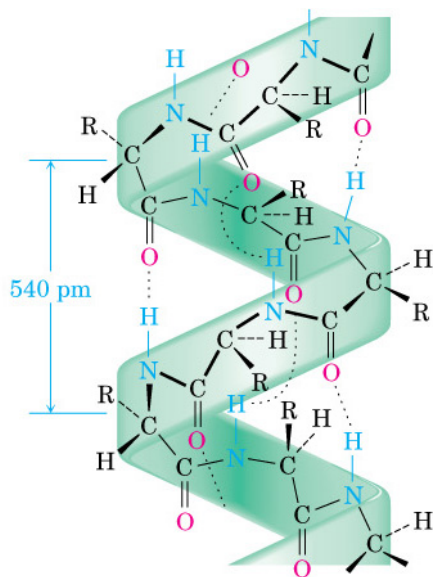


Ulteriori interazioni determinano le conformazioni delle proteine: legami a H

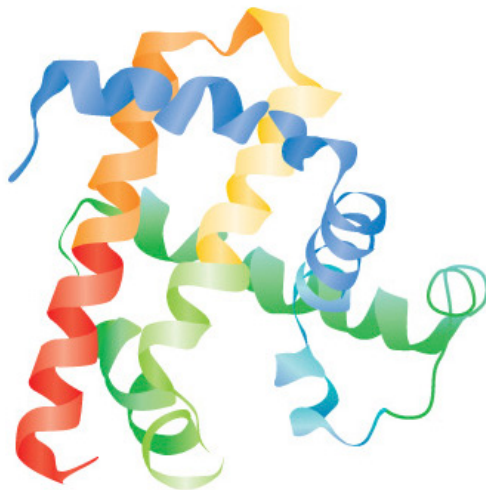


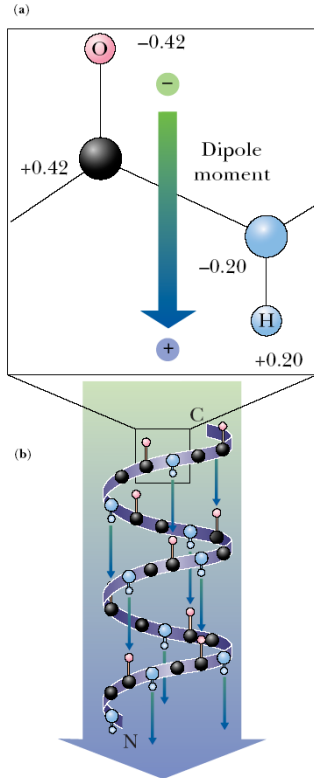
Strutture a elica

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



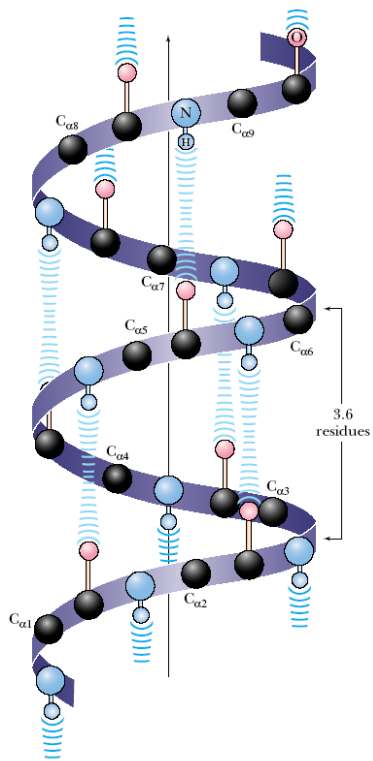
Struttura secondaria e terziaria della mioglobina, una proteina globulare con estese sezioni ad elica, qui mostrate come nastri.





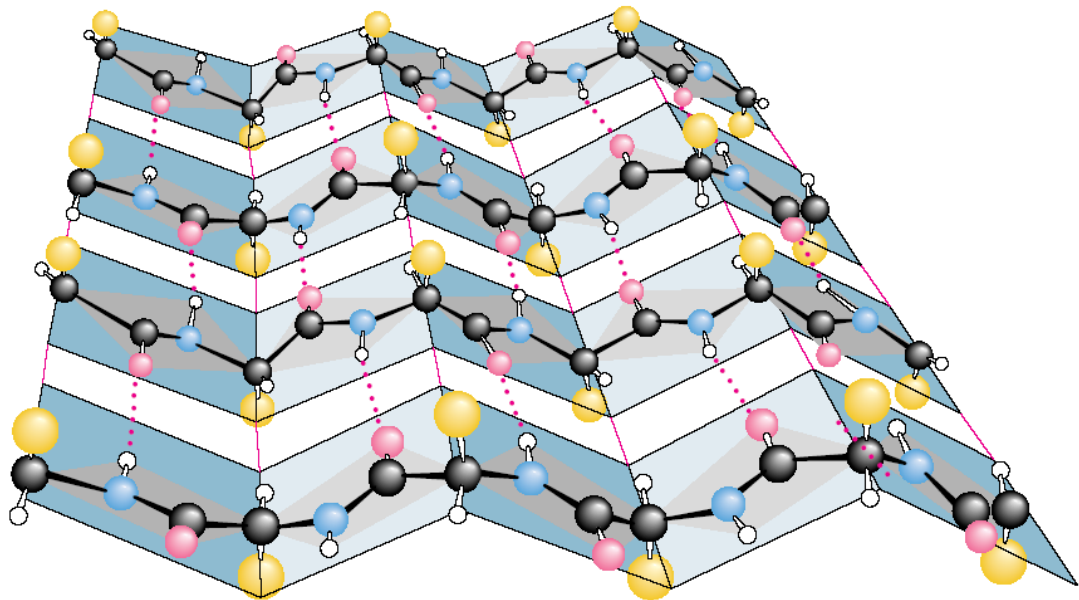
Momenti dipolari dei singoli legami peptidici si sommano in una struttura a elica

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

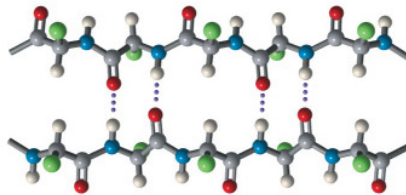
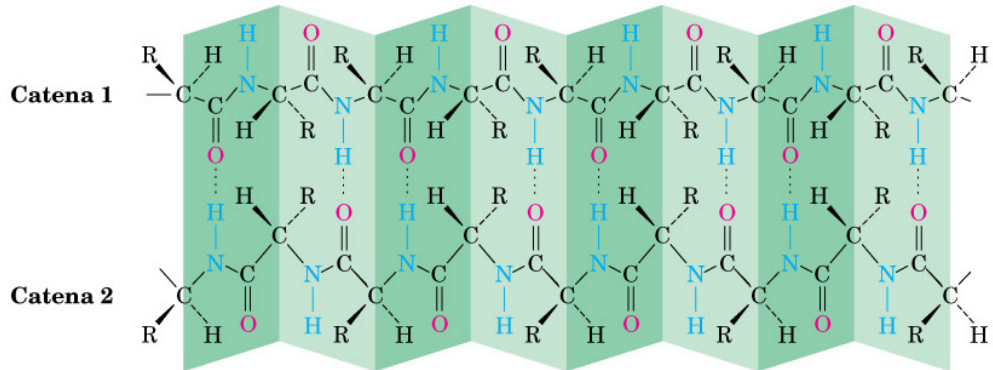


Agli estremi dell' elica vi sono accettori e donatori di legami a H liberi

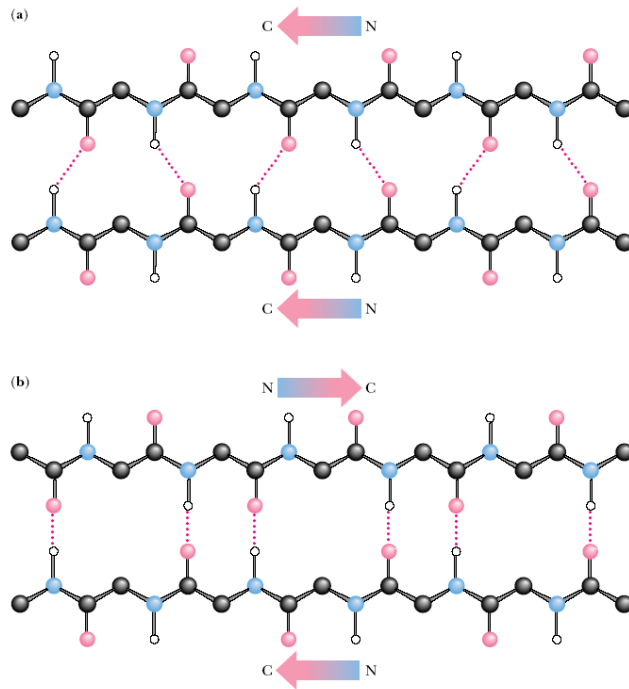
Un altro motivo di struttura secondaria: il β -foglietto



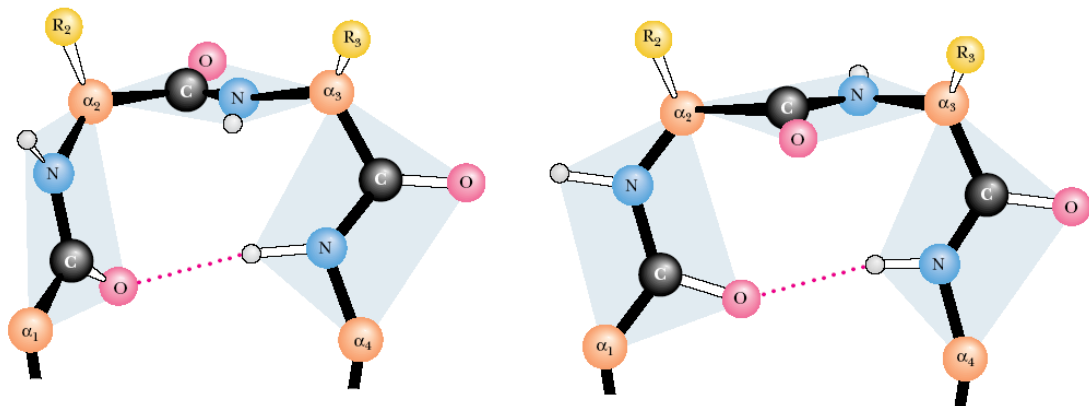
La struttura a foglietto β pieghettato nella fibroina della seta.



foglietto β parallelo e anti-parallelo

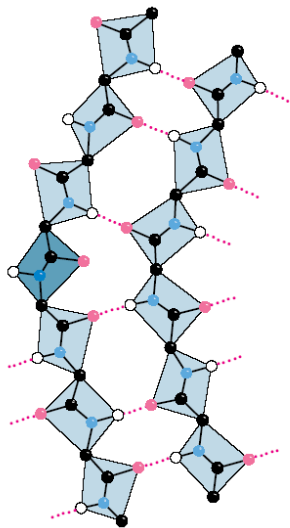


β turn

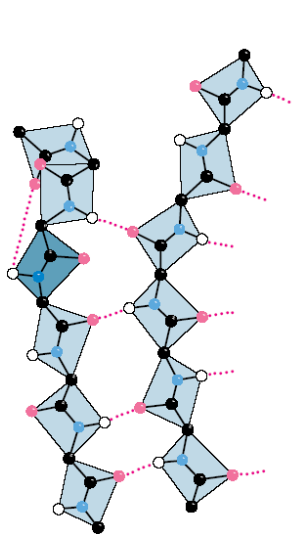


Sono presenti spesso glicine e proline

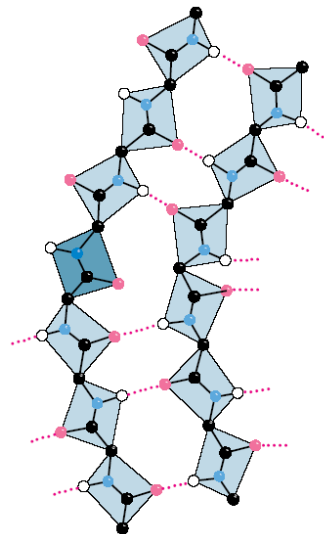
β buldge



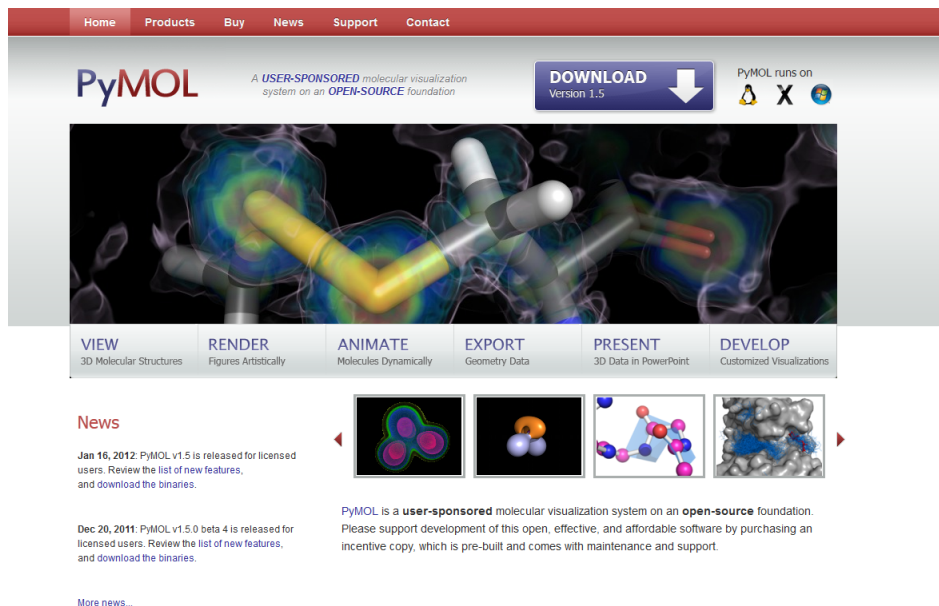
Classic bulge



G-I bulge



Wide bulge



The screenshot shows the PyMOL website homepage. At the top is a red navigation bar with links: Home, Products, Buy, News, Support, and Contact. Below this is a header section with the PyMOL logo, a tagline "A USER-SPONSORED molecular visualization system on an OPEN-SOURCE foundation", a "DOWNLOAD Version 1.5" button with a download icon, and a note "PyMOL runs on" with logos for Linux, Mac OS X, and Windows. The main visual is a large 3D molecular model of a protein-ligand complex with a yellow stick model and a blue electron density map. Below this is a row of six buttons: VIEW (3D Molecular Structures), RENDER (Figures Artistically), ANIMATE (Molecules Dynamically), EXPORT (Geometry Data), PRESENT (3D Data in PowerPoint), and DEVELOP (Customized Visualizations). A "News" section follows, featuring a carousel of four molecular visualization images. The first news item, dated Jan 16, 2012, announces the release of PyMOL v1.5 for licensed users. The second, dated Dec 20, 2011, announces the release of PyMOL v1.5.0 beta 4. A "More news..." link is at the bottom of the news section. A paragraph on the right states that PyMOL is a user-sponsored molecular visualization system on an open-source foundation, encouraging support through purchasing an incentive copy.

Home Products Buy News Support Contact

PyMOL A **USER-SPONSORED** molecular visualization system on an **OPEN-SOURCE** foundation

DOWNLOAD Version 1.5

PyMOL runs on   

VIEW
3D Molecular Structures

RENDER
Figures Artistically

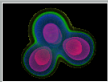
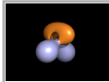
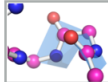
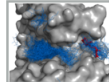
ANIMATE
Molecules Dynamically

EXPORT
Geometry Data

PRESENT
3D Data in PowerPoint

DEVELOP
Customized Visualizations

News

◀     ▶

Jan 16, 2012: PyMOL v1.5 is released for licensed users. Review the [list of new features](#), and download the binaries.

Dec 20, 2011: PyMOL v1.5.0 beta 4 is released for licensed users. Review the [list of new features](#), and download the binaries.

[More news...](#)

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.

www.pymol.org

Database di coordinate di strutture di proteine: www.rcsb.org