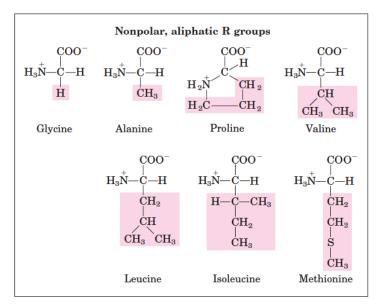
# From amino acids to proteins

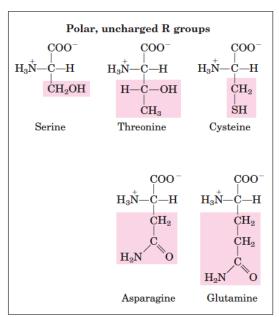
# 王春光

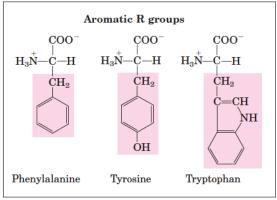
chunguangwang@tongji.edu.cn

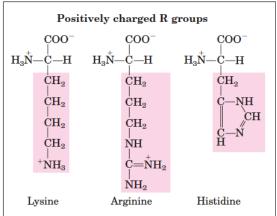
2020-09-18

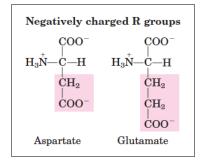
#### 20 common amino acids







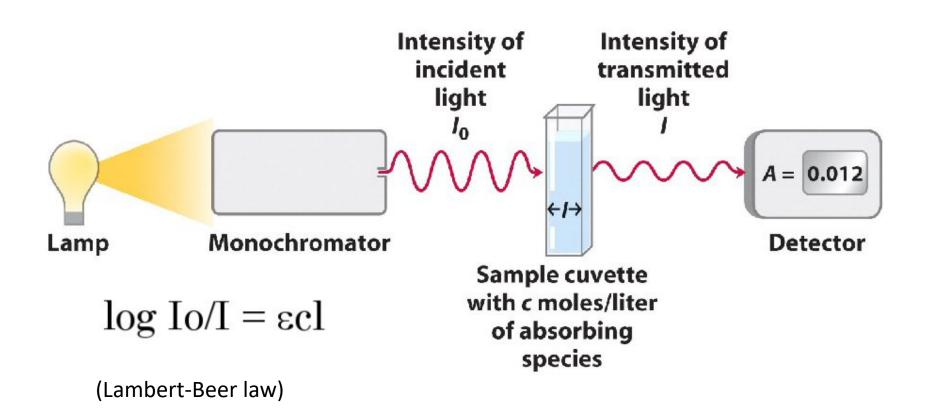




#### From amino acids to proteins

- ➤ Explain the optical absorbance (光吸收);
- Describe the properties of peptide bond (肽键);
- ➤ Interpret the disulfide bond(二硫键);
- ➤ Define the hydrogen bond (氢键);
- $\triangleright$  Illustrate the structural basis of  $\alpha$  helix.

# Optical absorbance(光吸收) Optical density (OD)(光密度)



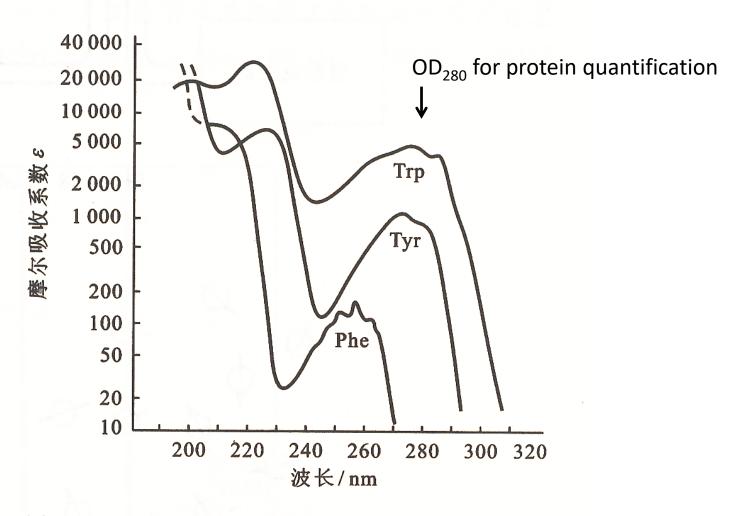


图 3-17 芳香族氨基酸在 pH6 时的紫外吸收光谱

#### 等电点 pl(isoelectric point)

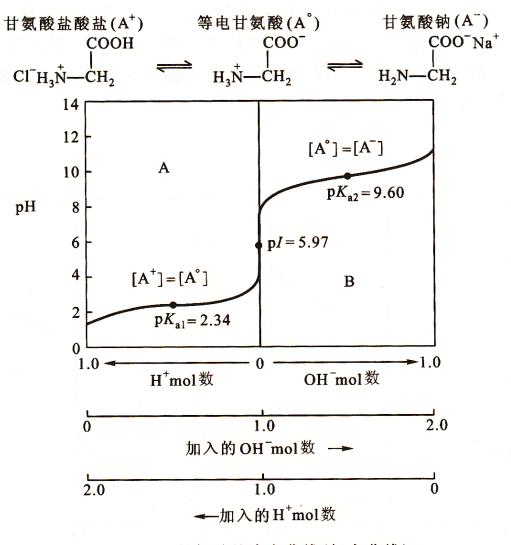


图 3-9 甘氨酸的滴定曲线(解离曲线)

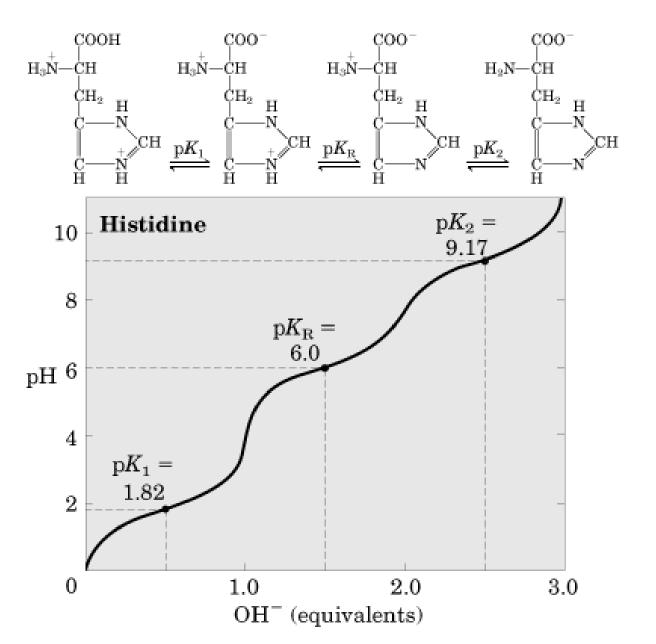


TABLE 3-1 Properties and Conventions Associated with the Common Amino Acids Found in Proteins

			pK <sub>a</sub> values					
Amino acid	Abbreviation/ symbol	$M_r$	рК <sub>1</sub> (—СООН)	рК <sub>2</sub> (—NН <sub>3</sub> +)	pK <sub>R</sub> (R group)	pl	Hydropathy index*	Occurrence in proteins (%) <sup>†</sup>
Nonpolar, aliphatic								
R groups								
Glycine	Gly G	75	2.34	9.60		5.97	-0.4	7.2
Alanine	Ala A	89	2.34	9.69		6.01	1.8	7.8
Proline	Pro P	115	1.99	10.96		6.48	1.6	5.2
Valine	Val V	117	2.32	9.62		5.97	4.2	6.6
Leucine	Leu L	131	2.36	9.60		5.98	3.8	9.1
Isoleucine	lle I	131	2.36	9.68		6.02	4.5	5.3
Methionine	Met M	149	2.28	9.21		5.74	1.9	2.3
Aromatic R groups								
Phenylalanine	Phe F	165	1.83	9.13		5.48	2.8	3.9
Tyrosine	Tyr Y	181	2.20	9.11	10.07	5.66	-1.3	3.2
Tryptophan	Trp W	204	2.38	9.39		5.89	-0.9	1.4
Polar, uncharged								
R groups								
Serine	Ser S	105	2.21	9.15		5.68	-0.8	6.8
Threonine	Thr T	119	2.11	9.62		5.87	-0.7	5.9
Cysteine	Cys C	121	1.96	10.28	8.18	5.07	2.5	1.9
Asparagine	Asn N	132	2.02	8.80		5.41	-3.5	4.3
Glutamine	Gln Q	146	2.17	9.13		5.65	-3.5	4.2
Positively charged								
R groups								
Lysine	Lys K	146	2.18	8.95	10.53	9.74	-3.9	5.9
Histidine	His H	155	1.82	9.17	6.00	7.59	-3.2	2.3
Arginine	Arg R	174	2.17	9.04	12.48	10.76	-4.5	5.1
Negatively charged R groups								
Aspartate	Asp D	133	1.88	9.60	3.65	2.77	-3.5	5.3
Glutamate	Glu E	147	2.19	9.67	4.25	3.22	-3.5	6.3

#### A few examples of other amino acids

$$H$$
 $HO-C$ 
 $CH_2$ 
 $H_2C$ 
 $CH-COO^ H$ 
 $H$ 
 $H$ 
 $H$ 

$$^{\text{COO}^-}$$
 $^{\text{OOC}}$ 
 $^{\text{COO}^-}$ 
 $^{\text{OOC}}$ 
 $^{\text{CH}}$ 
 $^{\text{CH}}$ 
 $^{\text{CH}}$ 
 $^{\text{CH}}$ 
 $^{\text{COO}^-}$ 
 $^{\text{NH}_3}$ 
 $^{\text{Carboxyglutamate}}$ 

$$\begin{array}{c} {\rm H_3 \mathring{N}-CH_2-CH-CH_2-CH_2-CH-COO^-} \\ {\rm OH} & {}^{+}{\rm NH_3} \\ \\ {\rm 5-Hydroxylysine} \end{array}$$

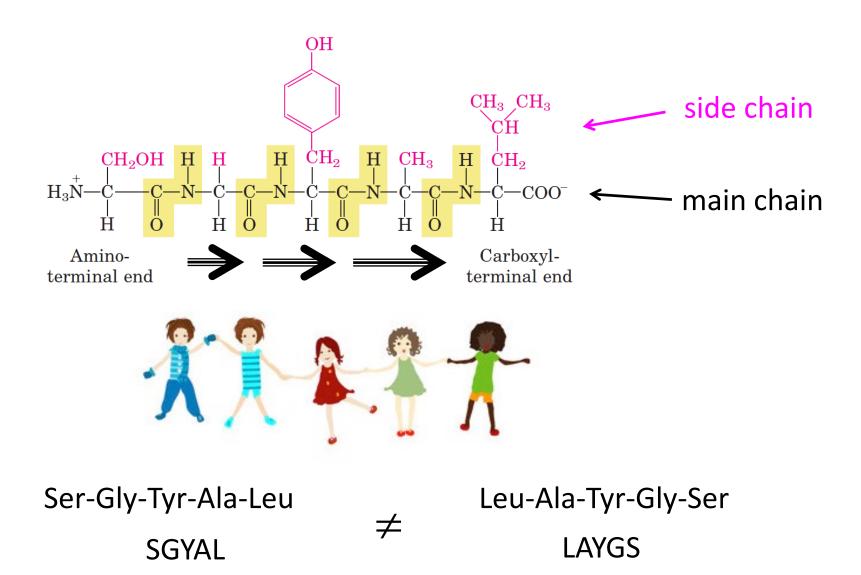
$$HSe-CH_2-CH-COO^ ^+NH_3$$
Selenocysteine

$$m CH_3-NH-CH_2-CH_2-CH_2-CH_2-CH-COO^ ^+NH_3$$
 $^+NH_3$ 

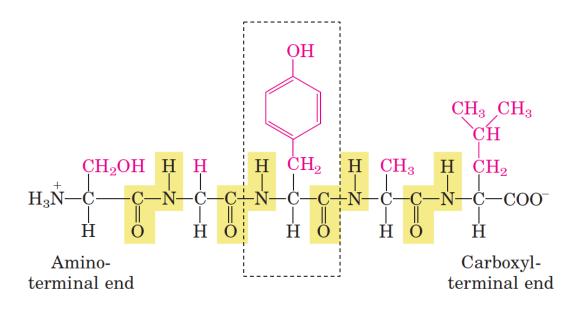
$${
m H_3}{
m N}^+$$
 —  ${
m CH_2}$  —  ${
m CH_2}$  —  ${
m CH}$  —  ${
m COO}^ {
m NH_3}$  Ornithine

### Peptide bond 肽键

### Polypeptide chain

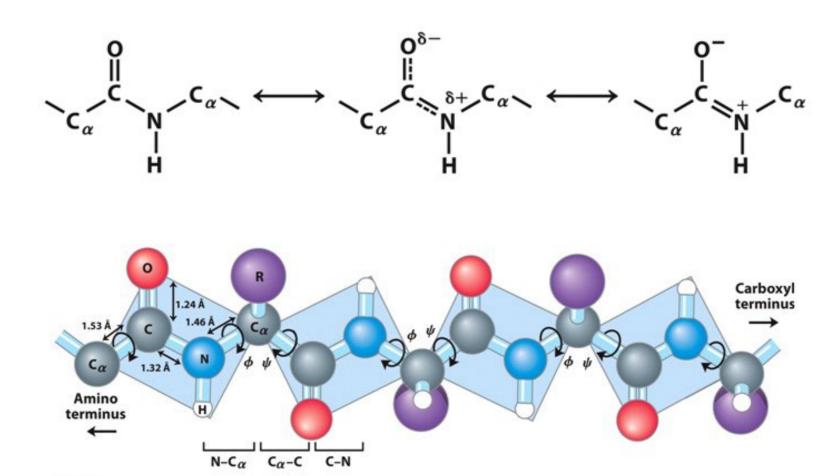


### Amino acid vs. residue (残基).

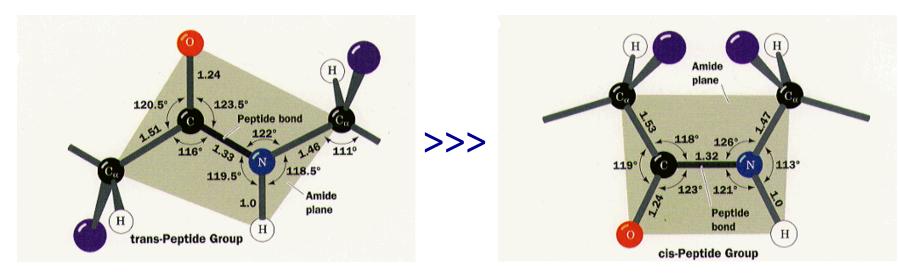


$$\begin{array}{c|c} \text{OH} \\ \text{H} & \text{CH}_2 \\ \text{H-N--C--C-OH} \\ \text{H} & \text{O} \end{array}$$

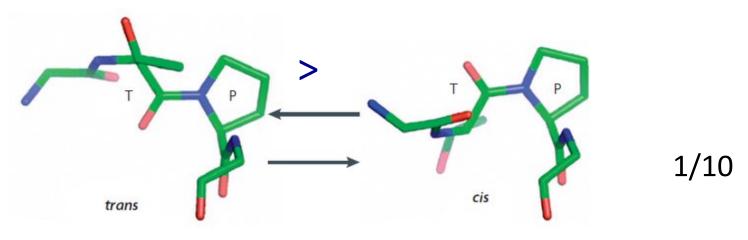
#### Peptide bond has some double-bond character.



## Trans vs. cis configuration (构型)



1/1000



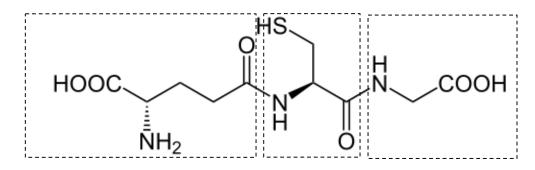
#### Some small peptides of physiological interest

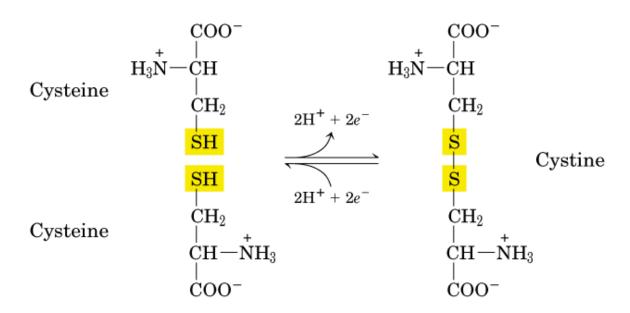
**Aspartame**: methyl ester derivative of L-Aspartyl-L-phenylalanine; 200x sweeter than sugar.



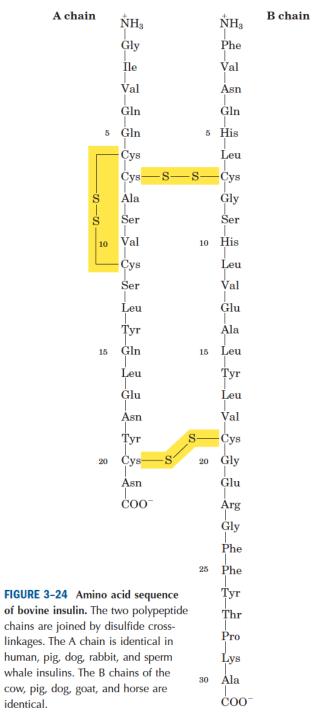
#### Some small peptides of physiological interest

**Glutathione (GSH)**(谷胱甘肽): tripeptide scavenger of oxidizing agents; oxidized form consists of two glutathione molecules joined by disulfide bridge.

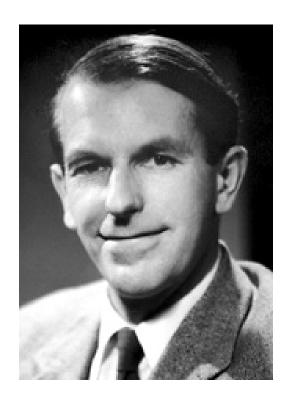




# insulin 胰岛素



#### **Frederick Sanger**



**The Nobel Prize in Chemistry 1958** 

"for his work on the structure of proteins, especially that of insulin"



The Nobel Prize in Chemistry 1980

"for their contributions concerning the determination of base sequences in nucleic acids"

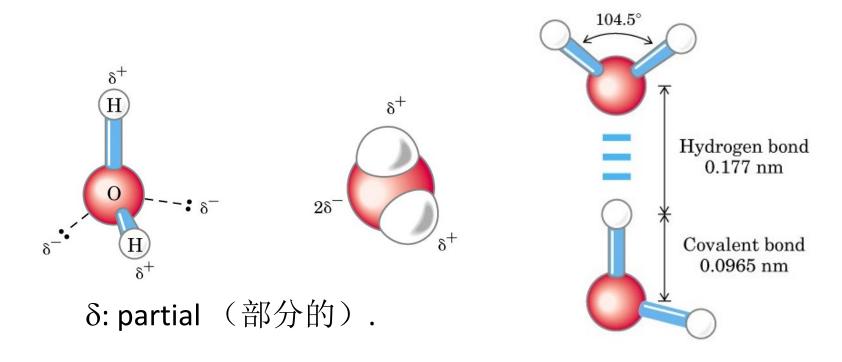
#### 我国首次人工合成牛胰岛素







## hydrogen bond (氢键)



A hydrogen bond is the attractive force between the hydrogen attached to an electronegative atom of one molecule and an electronegative atom of a different molecule.

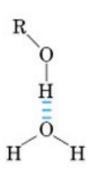
## hydrogen bond (氢键)

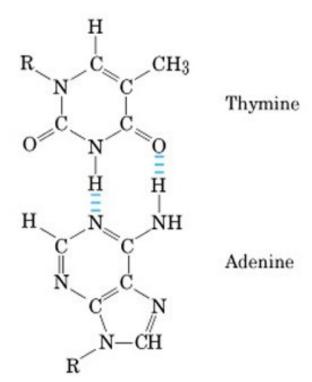
Hydrogen bond ≈ 5% covalent bond (共价键).

Hydrogen bonds, often in a large amount, make significant contribution for maintaining the protein structure.

### Some biologically important hydrogen bonds

Between the hydroxyl group of an alcohol and water Between the carbonyl group of a ketone and water Between peptide groups in polypeptides Between complementary bases of DNA

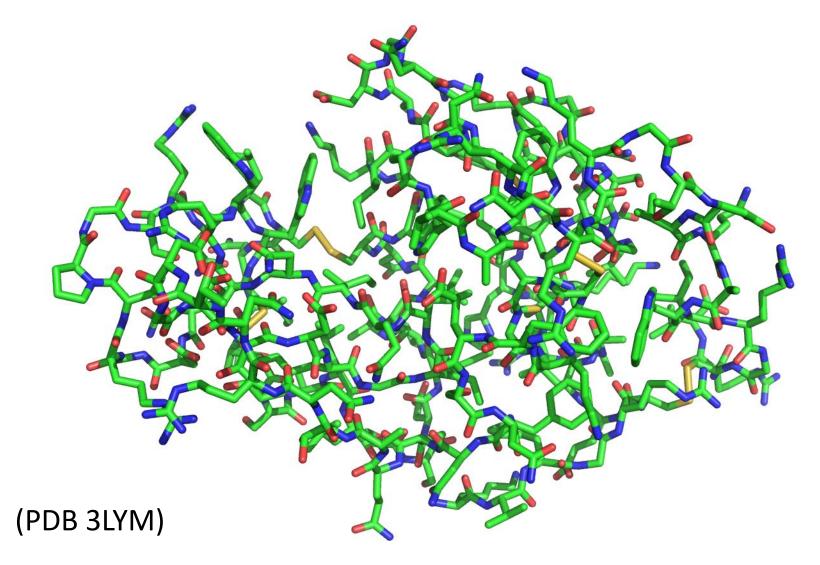


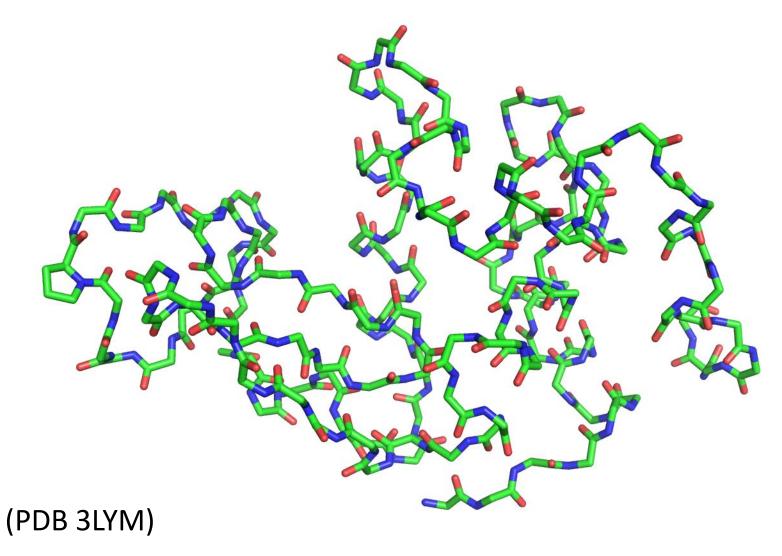


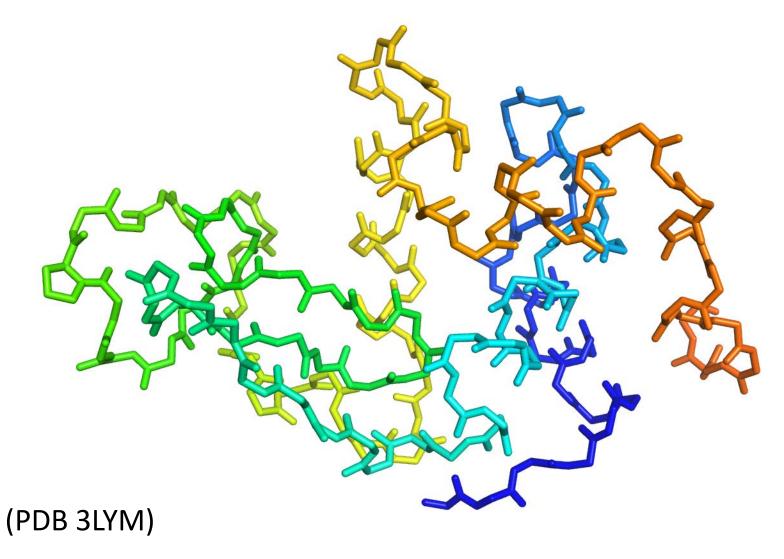
KVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAK FESNFNTQATNRNTDGSTDYGILQINSRWWCND GRTPGSRNLCNIPCSALLSSDITASVNCAKKIV SDGNGMNAWVAWRNRCKGTDVQAWIRGCRL

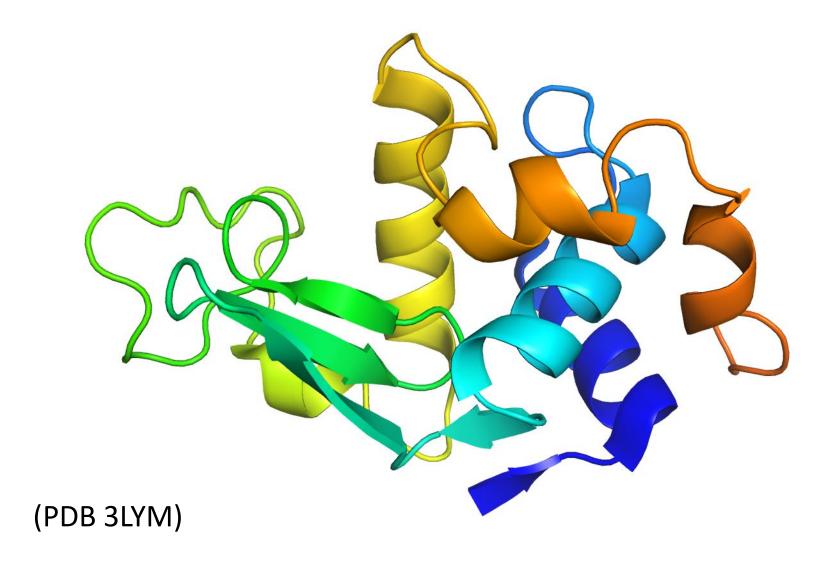
129 residues;

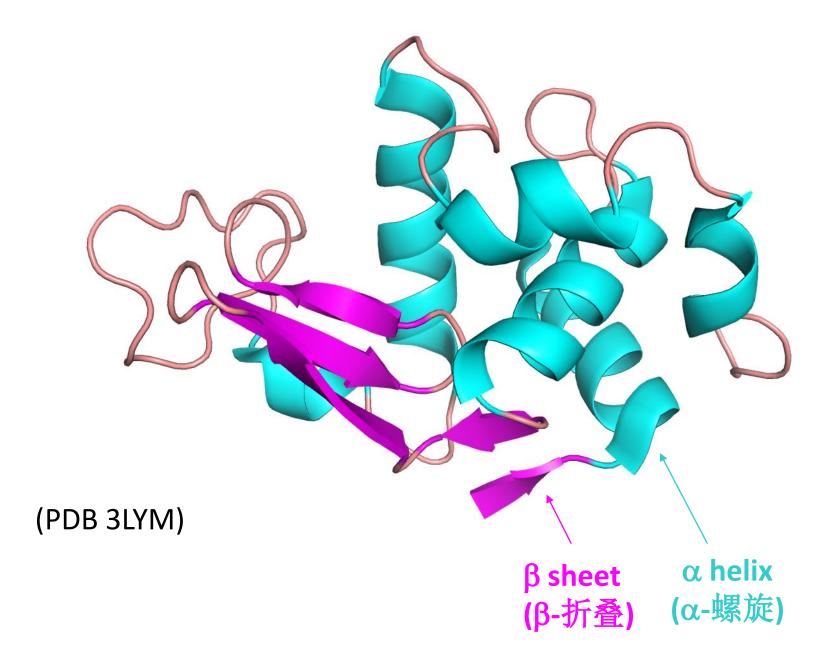
D + E: 9; K + R: 17.

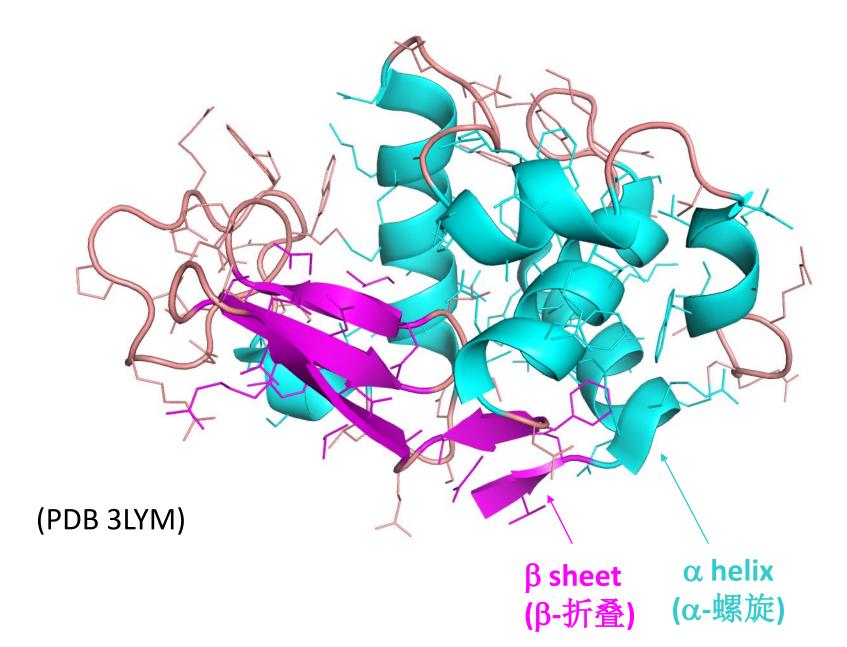




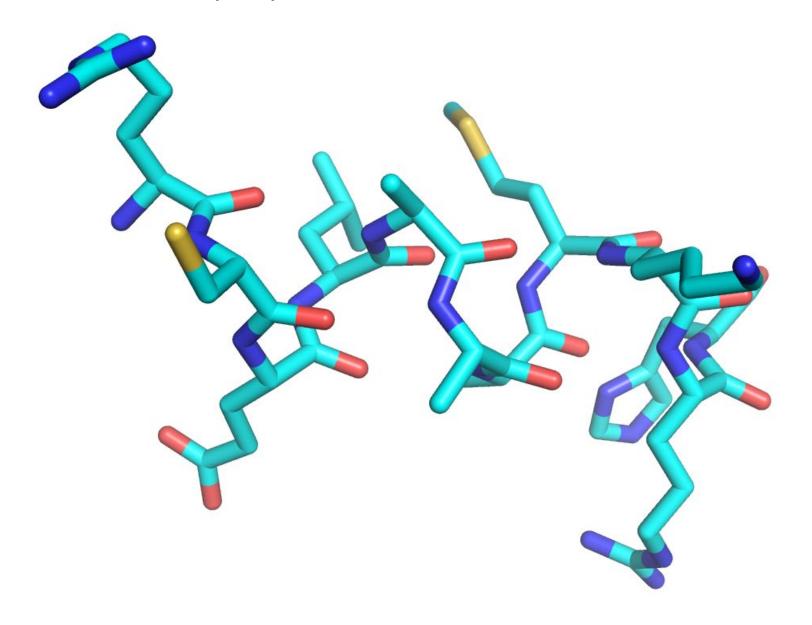




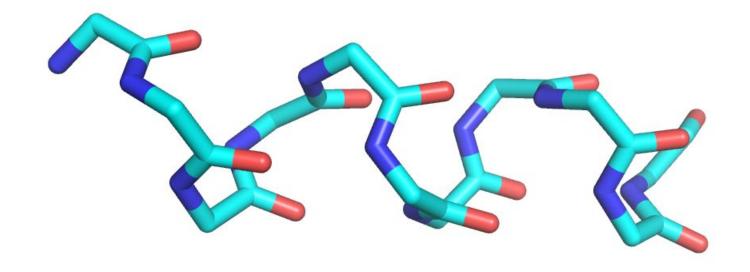




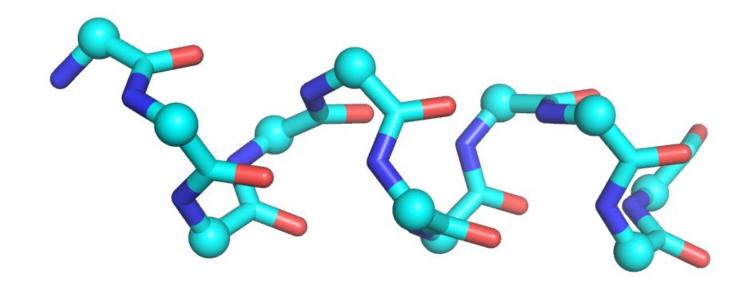
## An $\alpha$ -helix in lysozyme: RCELAAAMKRH (color code: CNOS)



## An $\alpha$ -helix in lysozyme: RCELAAAMKRH (color code: CNOS)

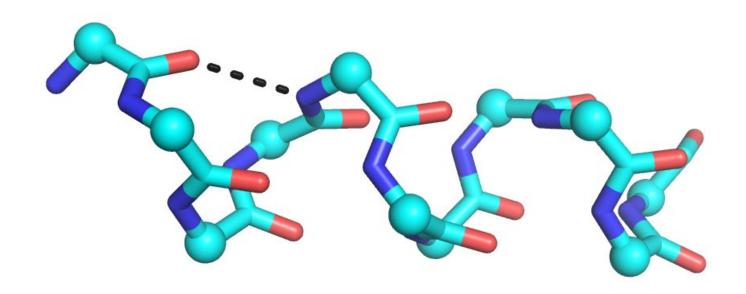


#### Recall the planar trans-peptide group(反式肽平面)

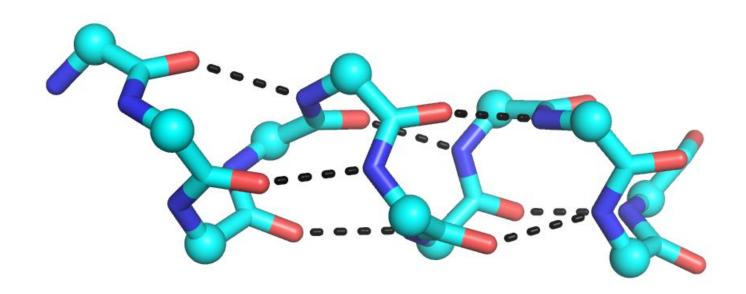


 $C\alpha$  highlighted!

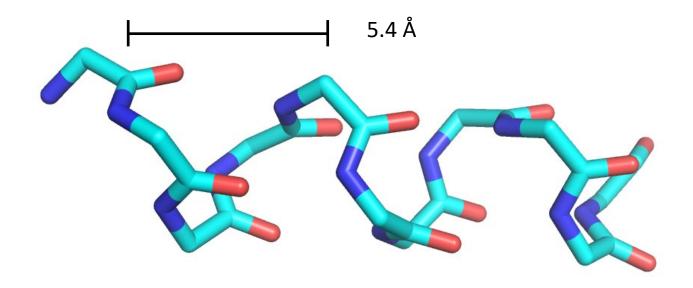
## $\alpha$ helix



## $\alpha$ helix

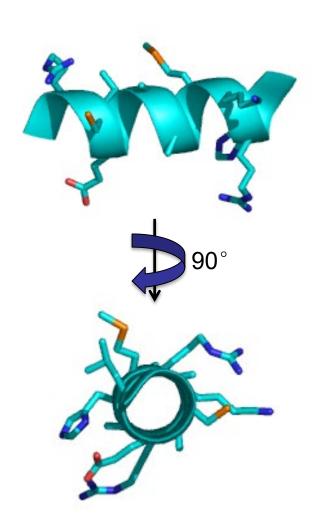


#### The $\alpha$ helix



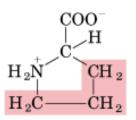
- To make optimal use of internal hydrogen bonds.
- Only right-handed helix.
- Every helical turn extends about 5.4 Å along the axis.
- Every helical turn includes 3.6 residues, so that every residue turns 100 degrees.

#### An $\alpha$ helix in lysozyme: RCELAAAMKRH



Interaction between side chains of residue i and i+3 or i+4;

Pro rarely appears in  $\boldsymbol{\alpha}$  helix .



#### THE STRUCTURE OF PROTEINS: TWO HYDROGEN-BONDED HELICAL CONFIGURATIONS OF THE POLYPEPTIDE CHAIN

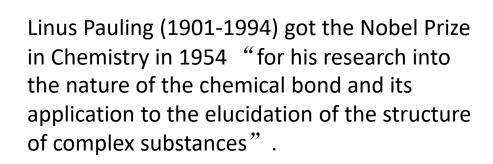
By Linus Pauling, Robert B. Corey, and H. R. Branson\*

GATES AND CRELLIN LABORATORIES OF CHEMISTRY, CALIFORNIA INSTITUTE OF TECHNOLOGY, PASADENA, CALIFORNIA†

Communicated February 28, 1951

During the past fifteen years we have been attacking the problem of the structure of proteins in several ways. One of these ways is the complete and accurate determination of the crystal structure of amino acids, peptides, and other simple substances related to proteins, in order that information about interatomic distances, bond angles, and other configurational parameters might be obtained that would permit the reliable prediction of reasonable configurations for the polypeptide chain. We have now used

nstruct two reasonable hydrogen-bonded helical conypeptide chain; we think that it is likely that these ite an important part of the structure of both fibrous as well as of synthetic polypeptides. A letter anry was published last year.<sup>1</sup>



#### Next time:

Protein structure.