

# The Chemical Nature of Enzyme Reaction

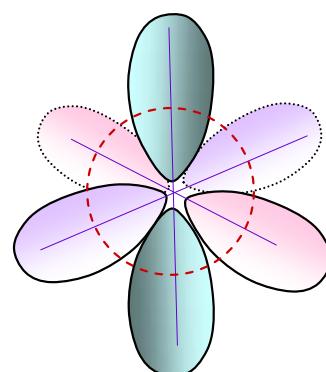
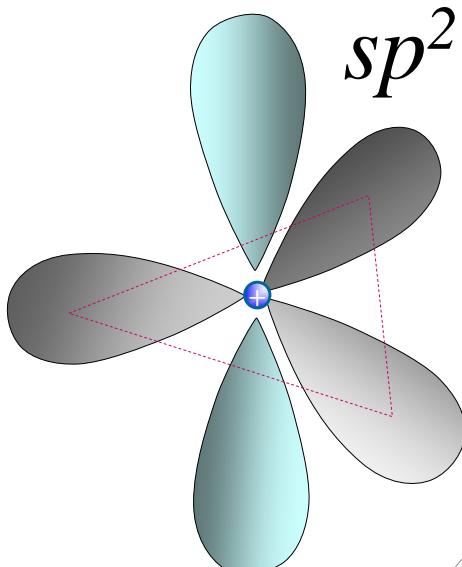
C<sup>6</sup>

I Chemical reactions

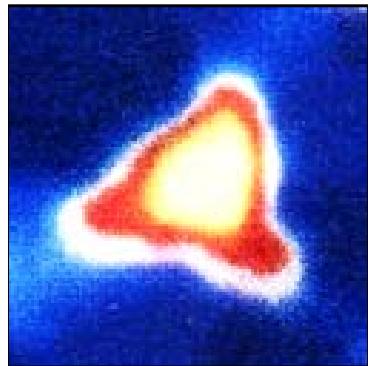
II Enzyme catalytic mechanism

III Identification of catalytic sites

*sp<sup>3</sup> hybrid*



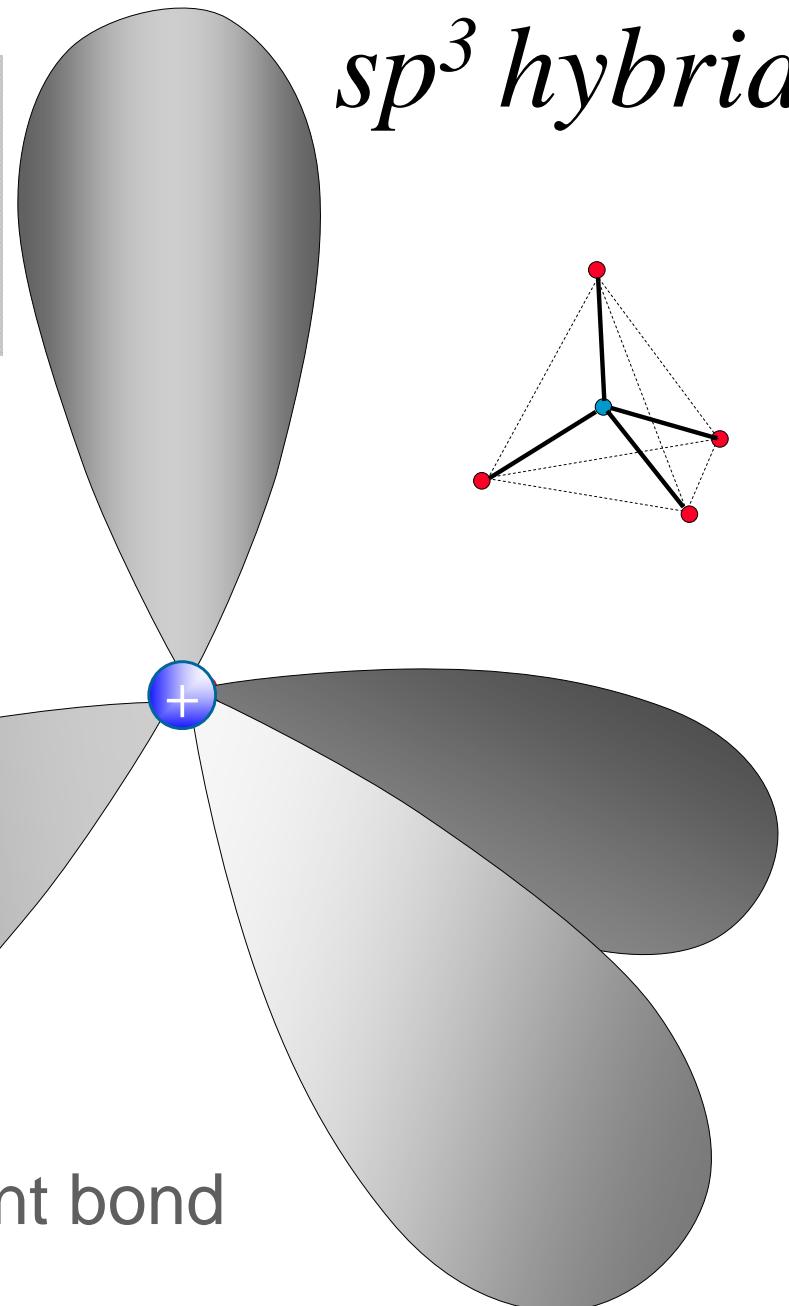
矽的  $sp^3$  四面體



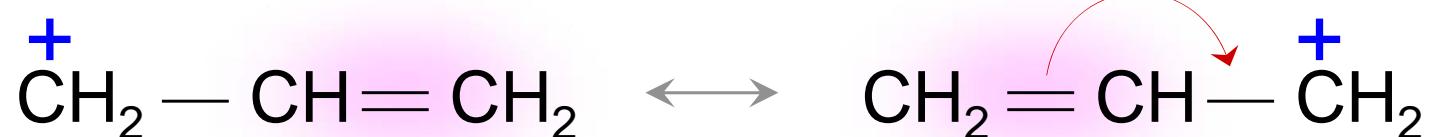
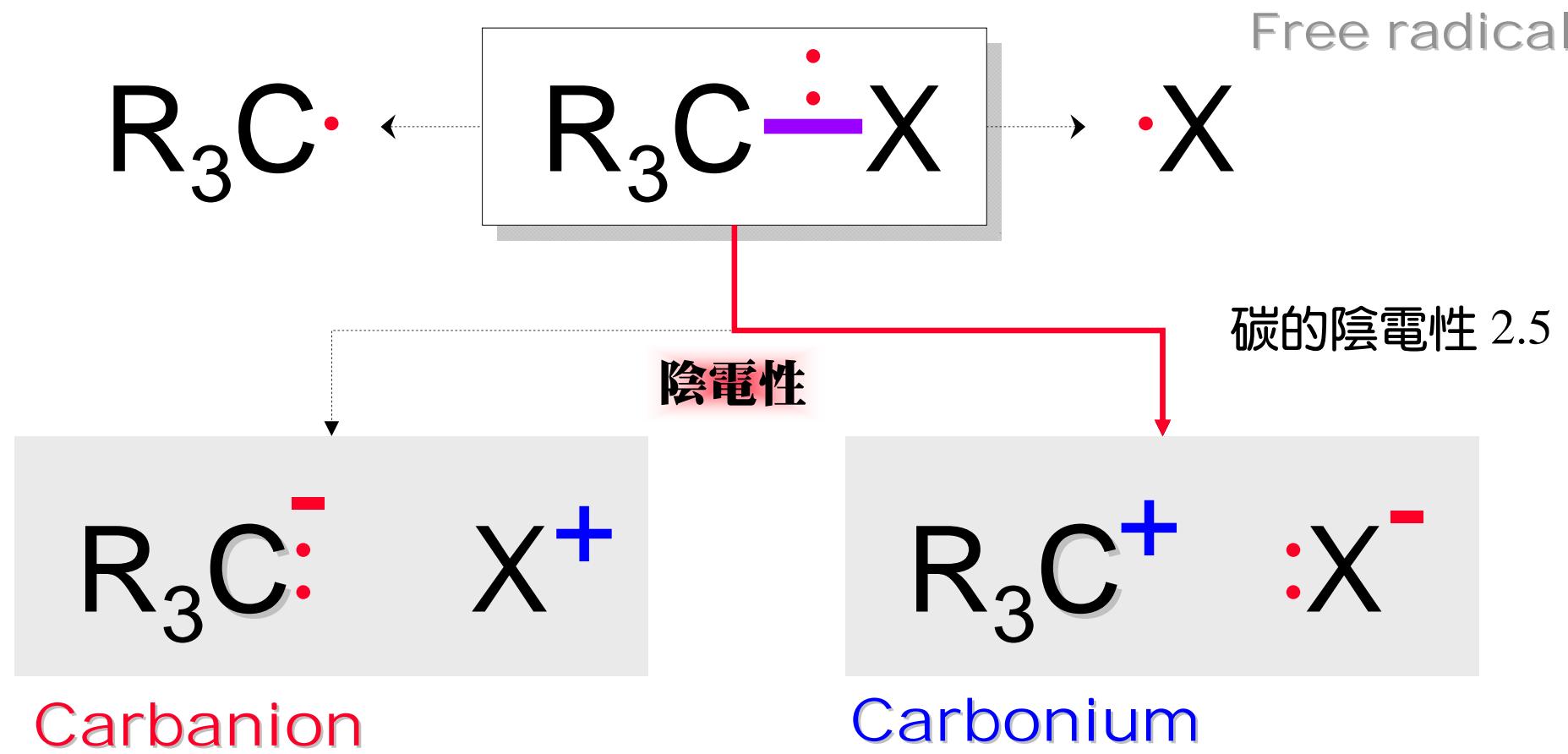
H

Campbell (1990) Biology (2e) p.23

Covalent bond



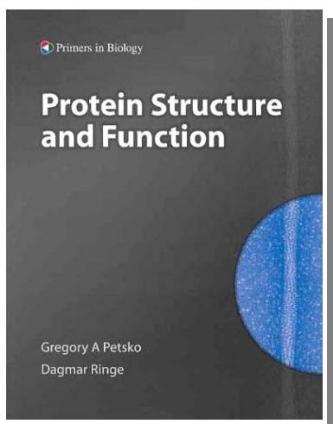
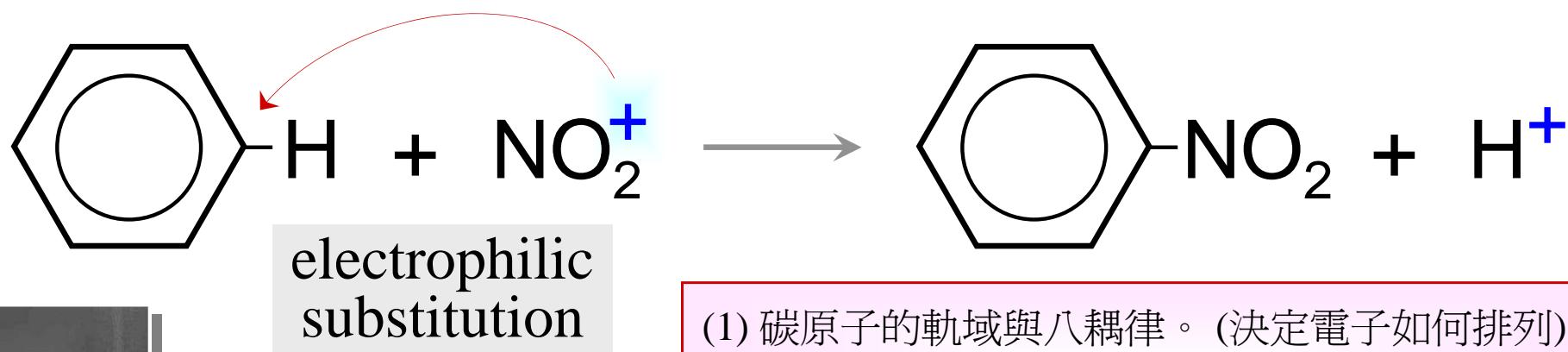
# I The basic mechanism of chemical reaction



stabilized by resonance

# Four main types of reactions

Oxidation/reduction  
Addition/elimination  
Hydrolysis  
Decarboxylation



- (1) 碳原子的軌域與八耦律。(決定電子如何排列)
  - (2) 相鄰原子陰電性之大小。(決定何者搶奪電子)
  - (3) 反應物與生成物之穩定。(穩定者較容易形成)

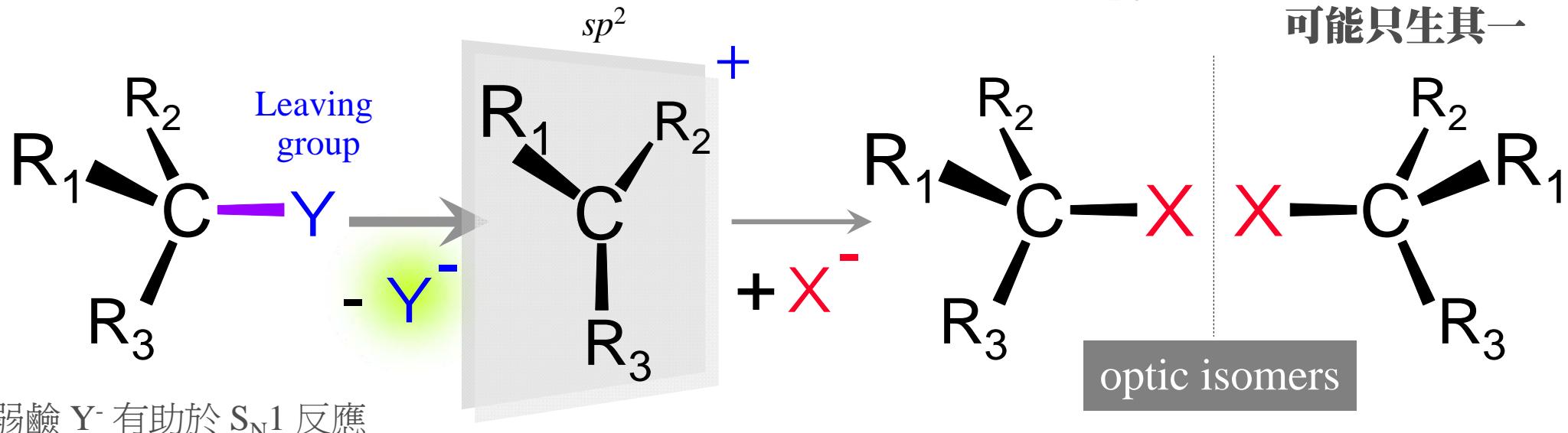
# *It's a matter of electrons!*

Palmer T (1991) *Understanding Enzymes*, Chap. 10, 11 (Ellis Horwood, England)

Petsko GA, Ringe D (2004) ***Protein Structure and Function*** (New Science Press, London)

# Nucleophilic substitution reactions

## Unimolecular nucleophilic substitution ( $S_N1$ )



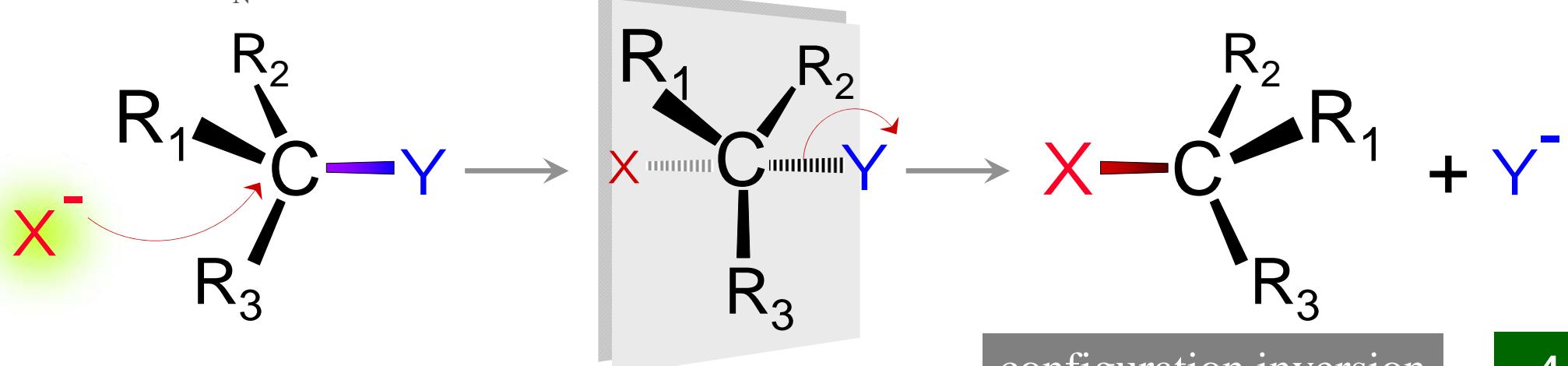
弱鹼  $Y^-$  有助於  $S_N1$  反應

若經酵素催化  
可能只生其一

## Bimolecular nucleophilic substitution ( $S_N2$ )

注意  $sp^3 - sp^2$  變化

強鹼  $X^-$  有助於  $S_N2$  反應

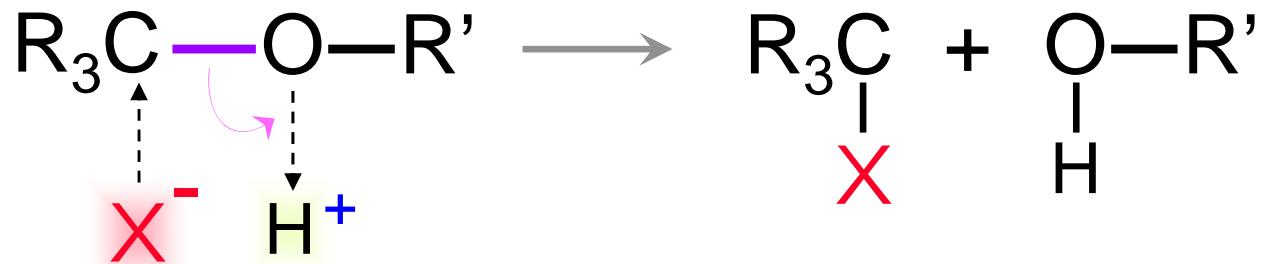


反應速率決定於形成過渡狀態的難易

## II Mechanisms of enzyme catalytic reactions

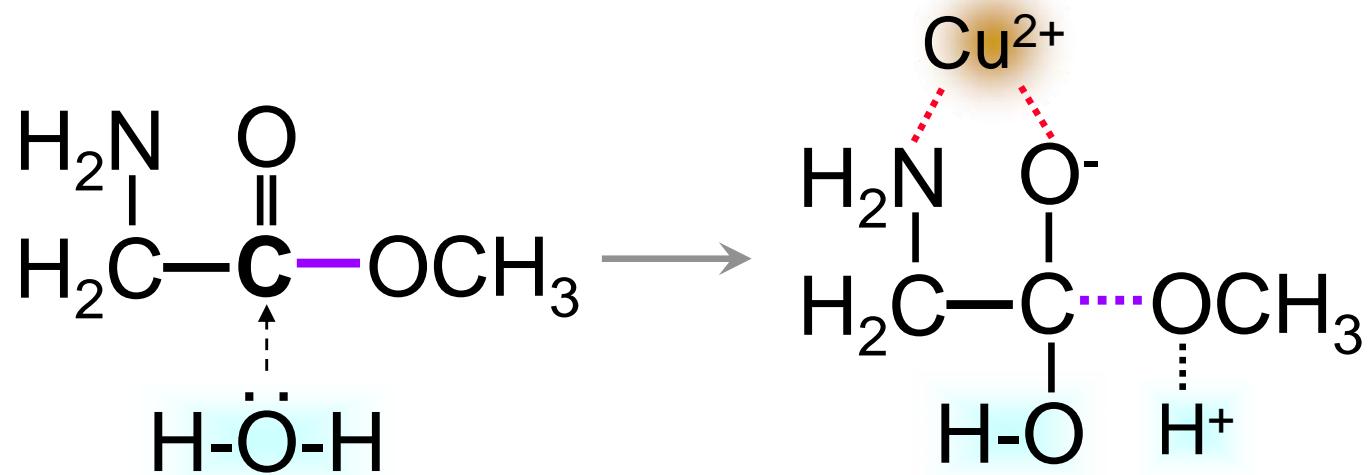
### (1) Acid-base catalysis

反應速率受環境 pH 影響  
(要注意 buffer 的 pH)

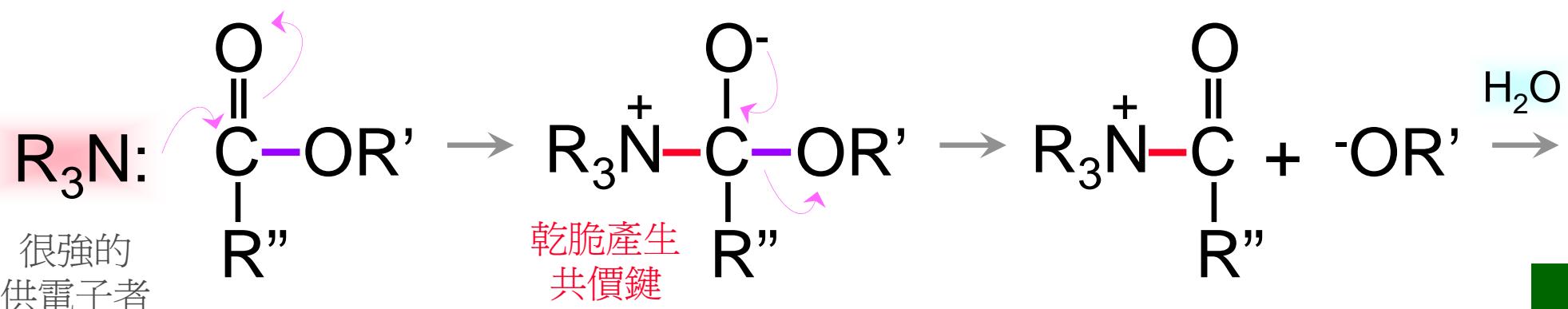


### (2) Electrostatic catalysis

以中和電荷穩定過渡狀態

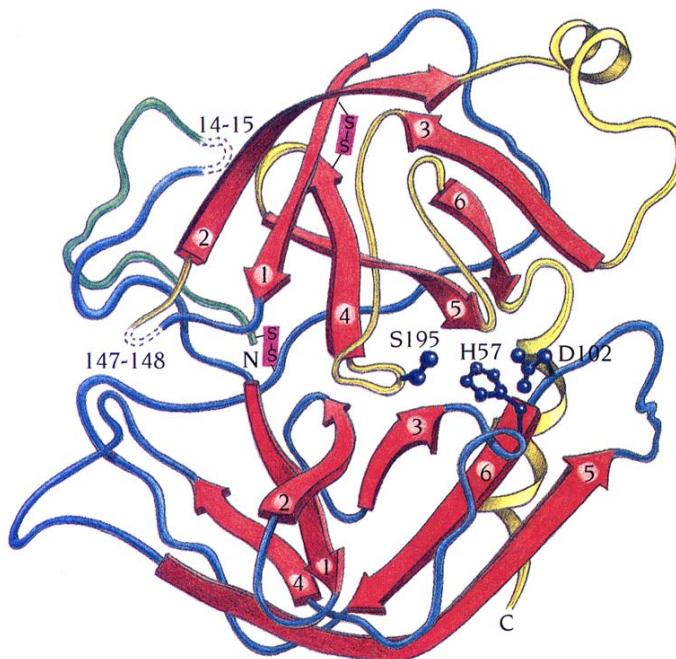
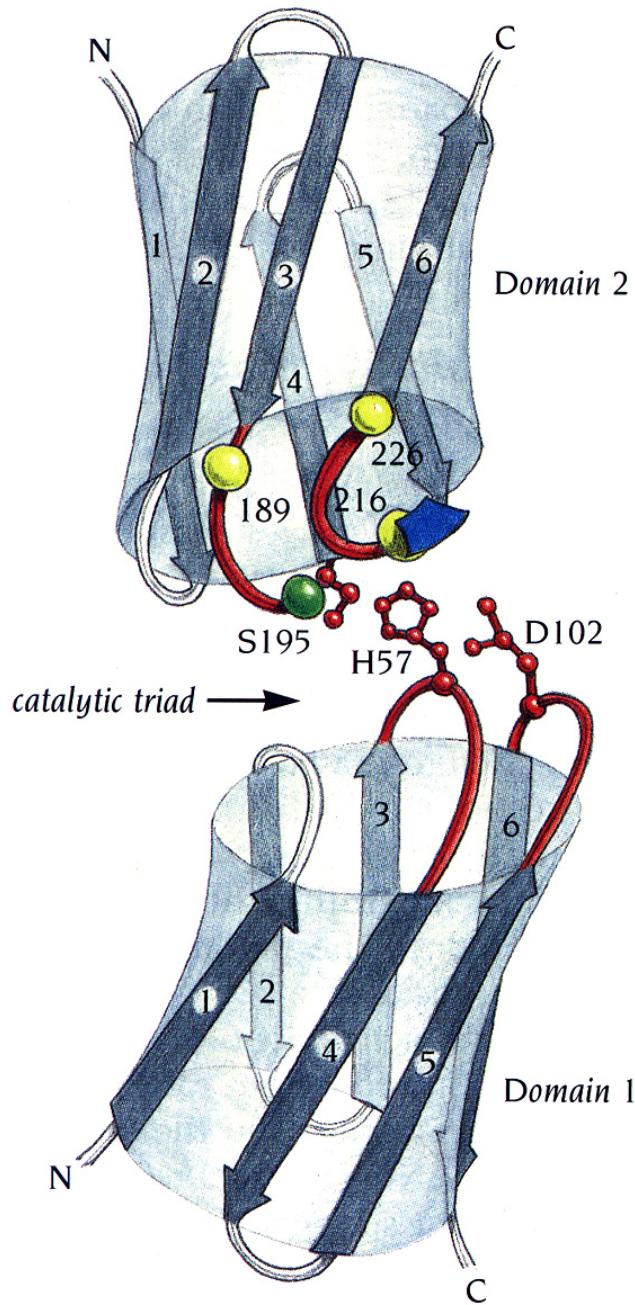


### (3) Covalent catalysis



Chymotrypsin 催化過程利用以上三種機制

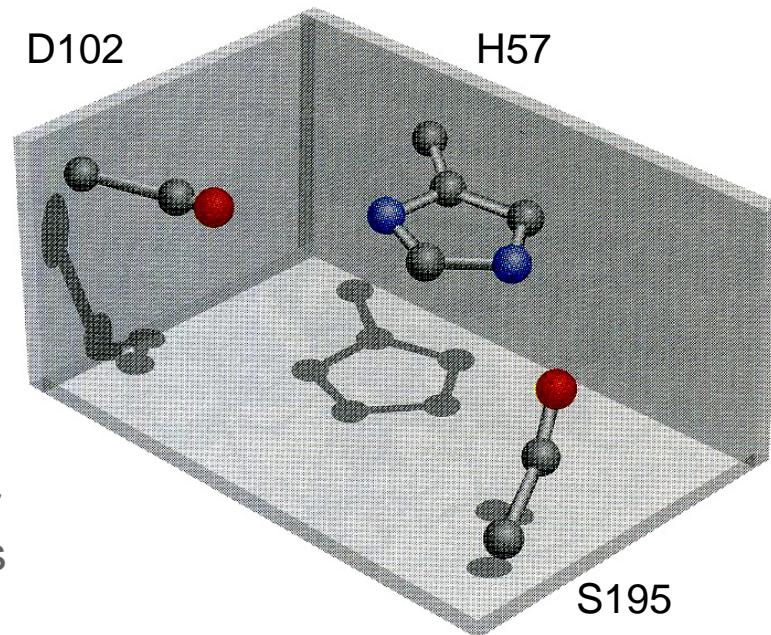
# Chymotrypsin



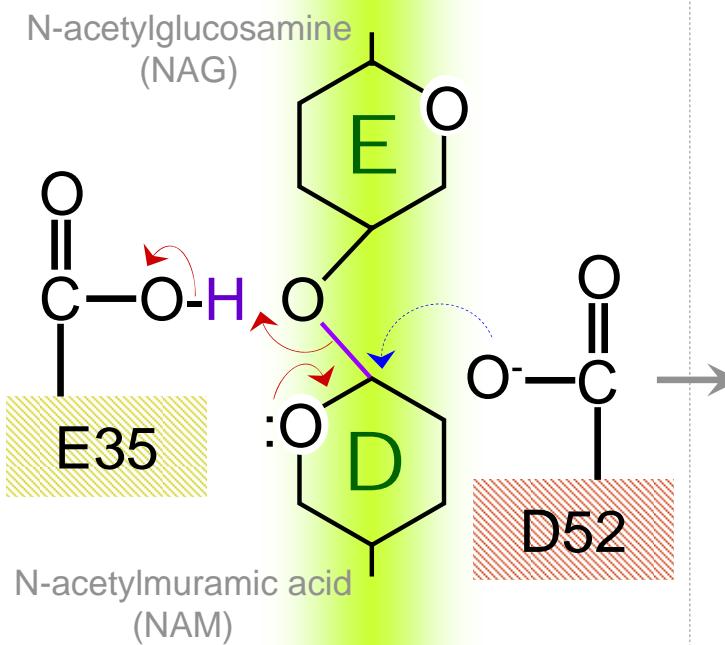
←  
Active site could be  
created between  
two domains

→  
The geometry of the  
catalytic triad of the  
serine protease as  
used to locate similar  
sites in other proteins

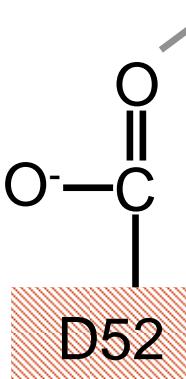
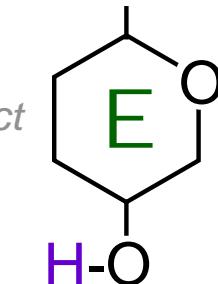
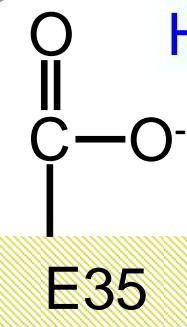
Catalytic triad  
Zymogen activation  
pH dependence  
Transition state  
Two-step mechanism  
Covalent catalysis  
Substrate specificity



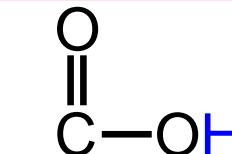
# Lysozyme



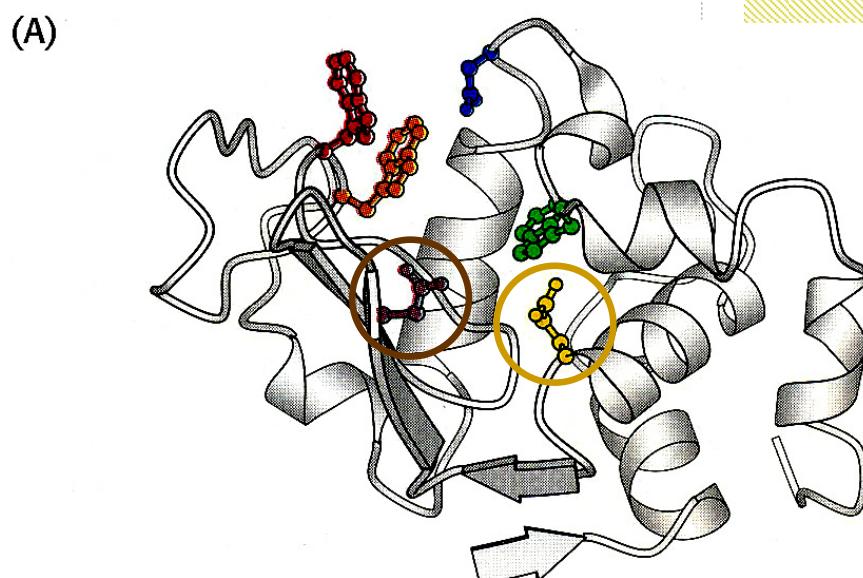
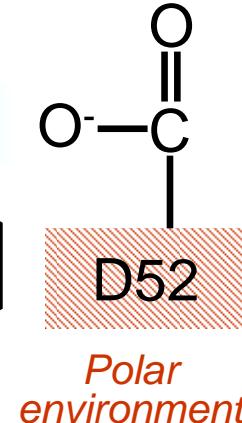
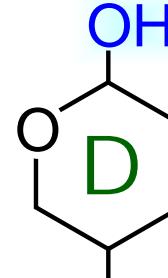
*First product*



兩個酸基在 pH 5 有不同形式



Non-polar environment



(B) N ————— 35 ————— 52 ————— 62,63 ————— 101 ————— 108 ————— 129 ————— C

Electrostatic catalysis

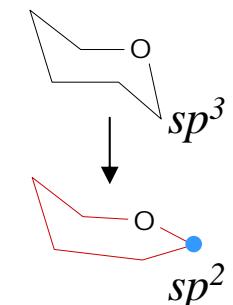
Chair → Half-chair

NAG-NAM-NAG-NAM-NAG-NAM-

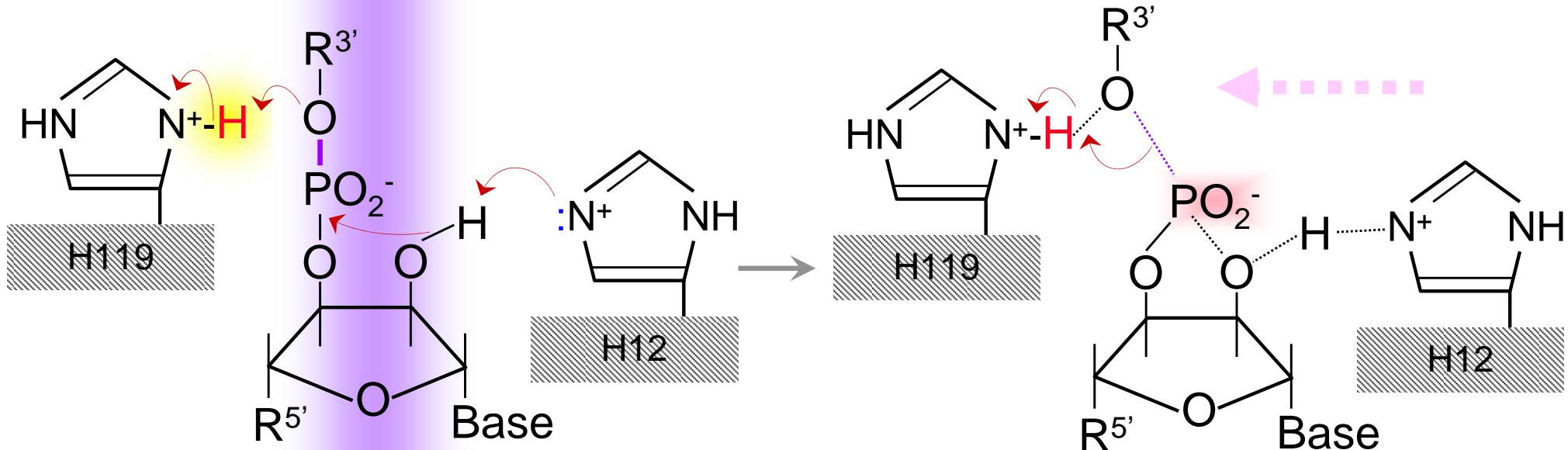
A ————— B ————— C ————— D ————— E ————— F

H-bonds

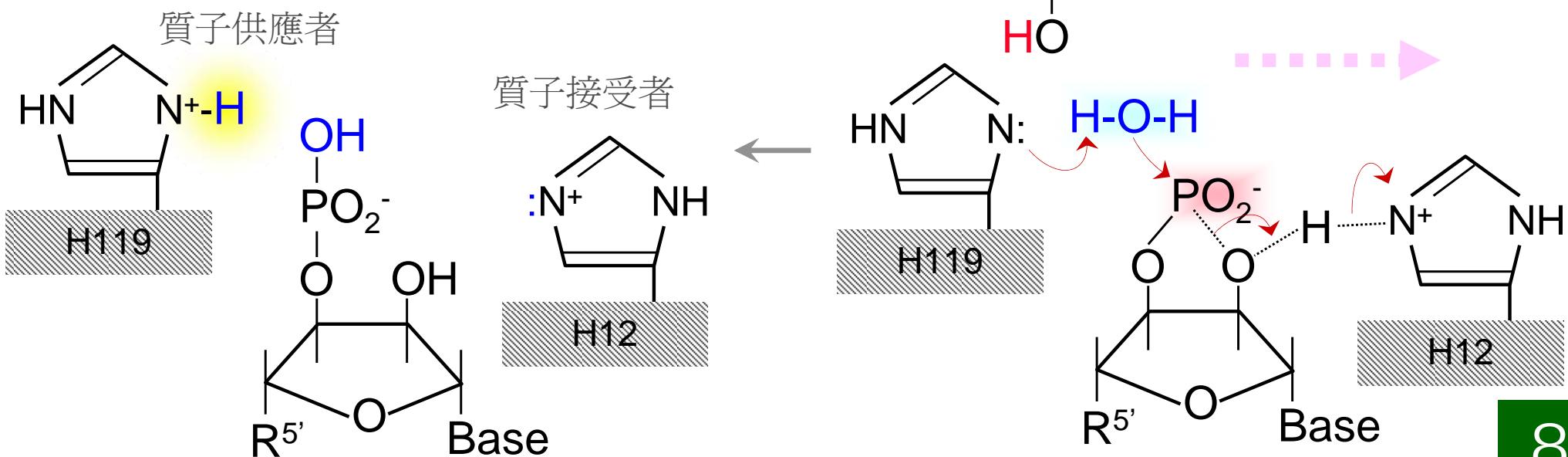
Substrate binding site



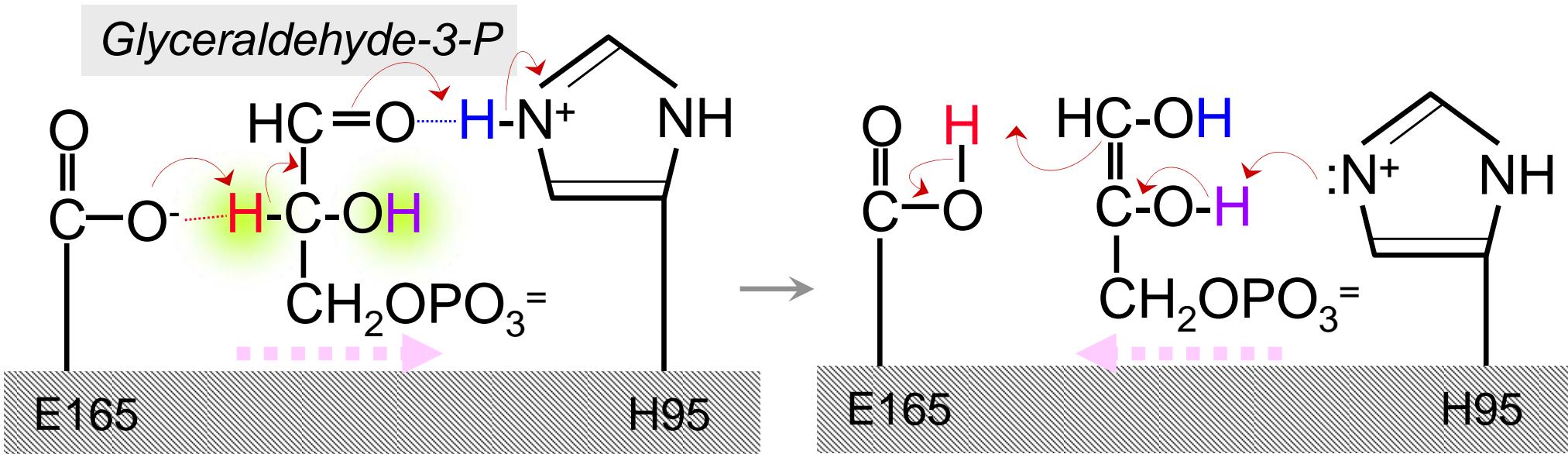
# Ribonuclease



## Histidine proton shuffle



# Triose phosphate isomerase

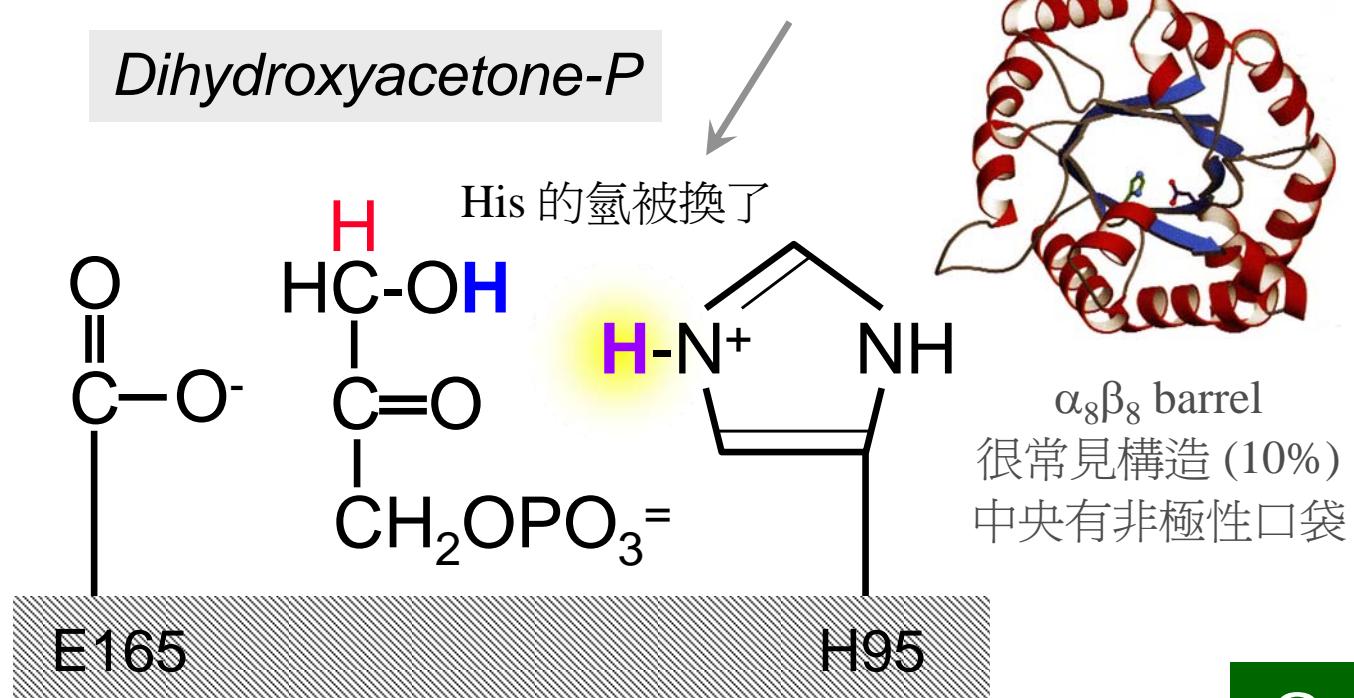


# Histidine in an enzyme

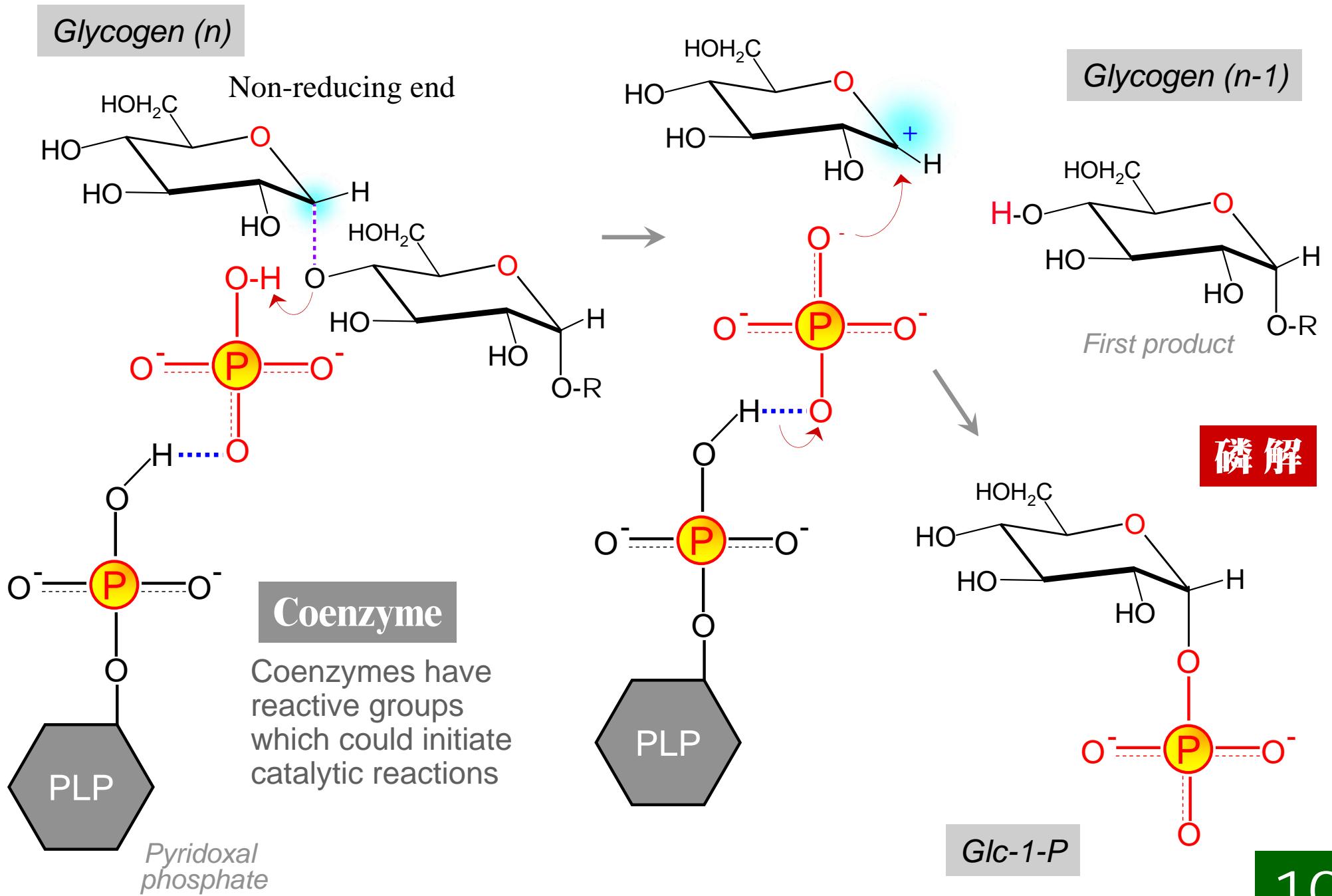
- (1) Imidazole has neutral pKa
  - (2) Proton donor & acceptor
  - (3) Nucleophile & electrophile
  - (4) Stabilize charged groups
  - (5) Could be phosphorylated

## *G3P formula unchanged*

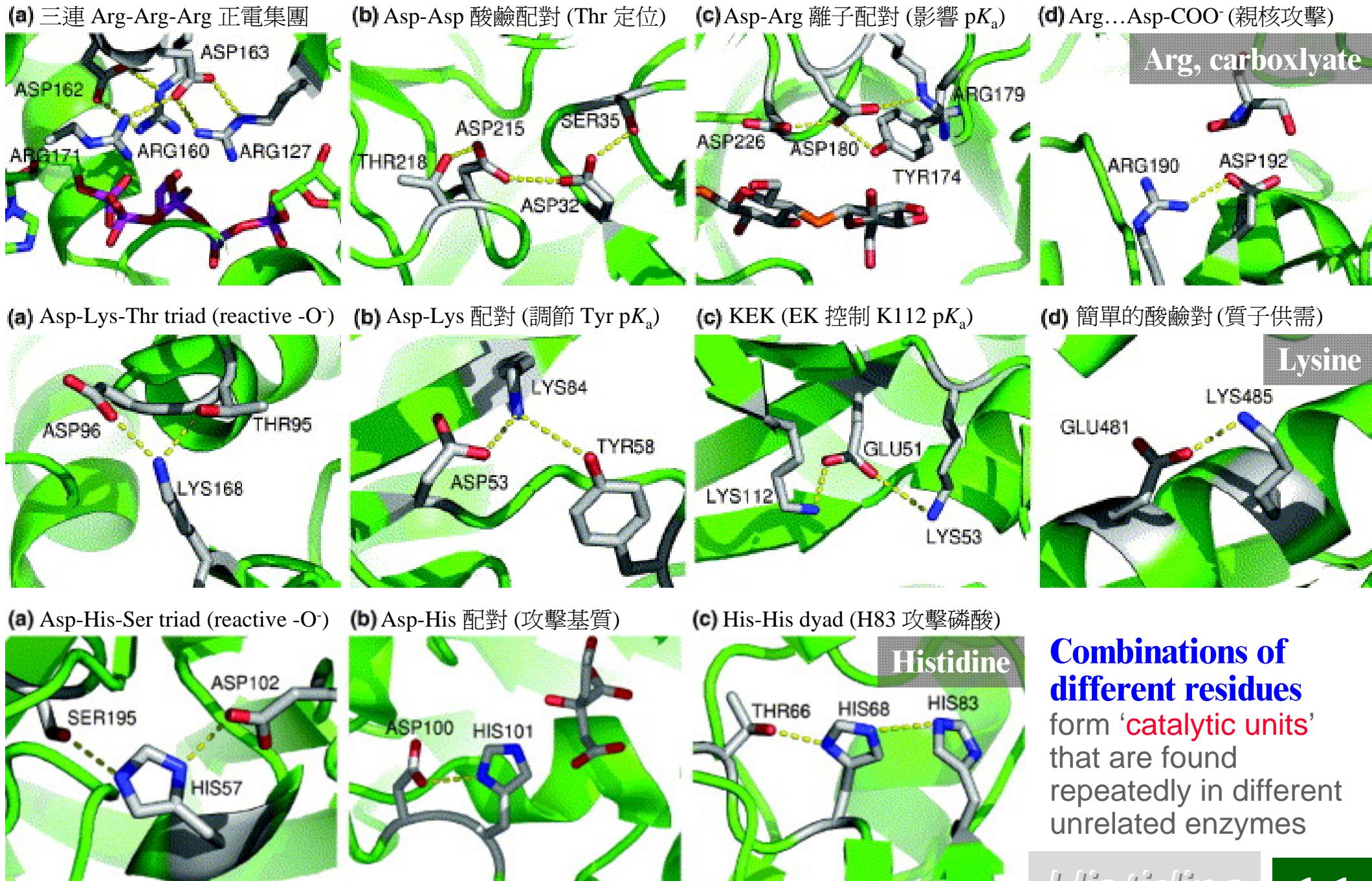
# 此酵素的最佳作用 pH？



# Glycogen phosphorylase



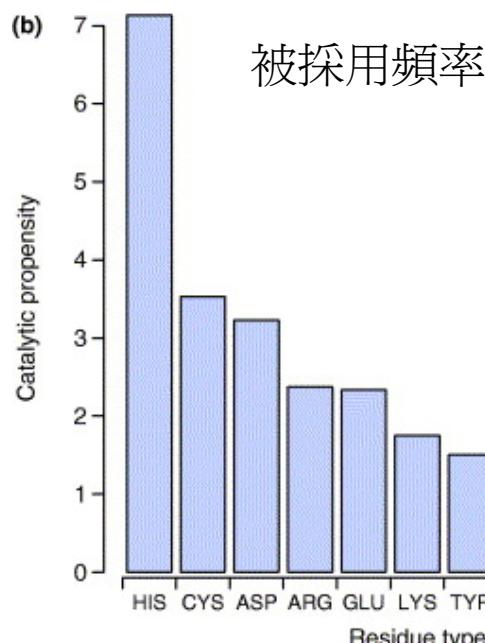
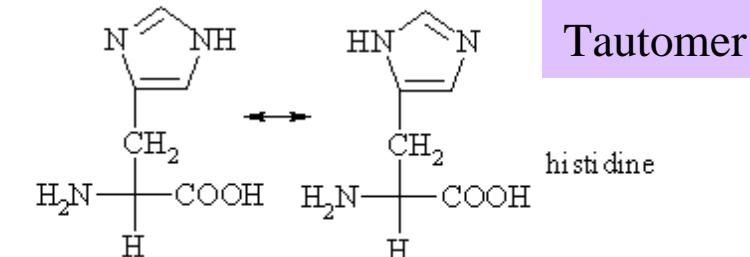
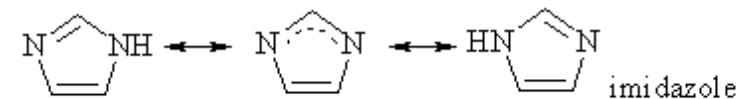
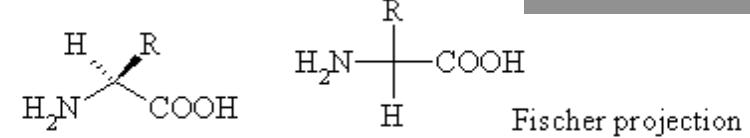
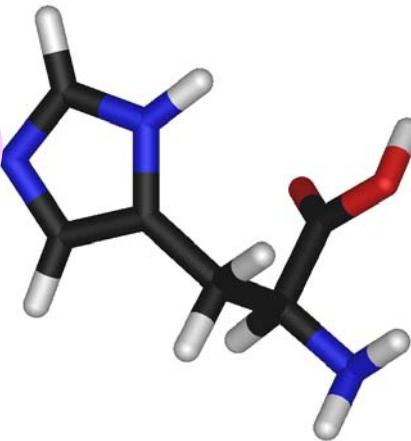
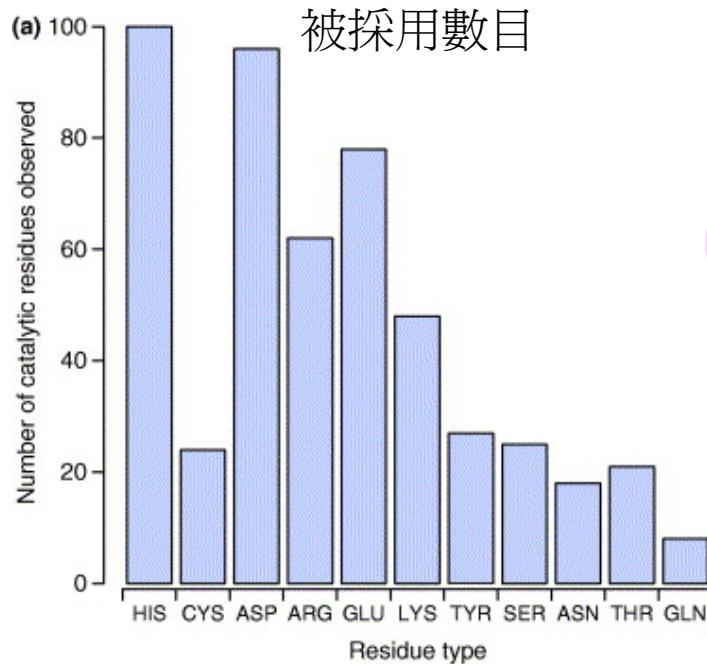
# Catalytic toolkit for active sites



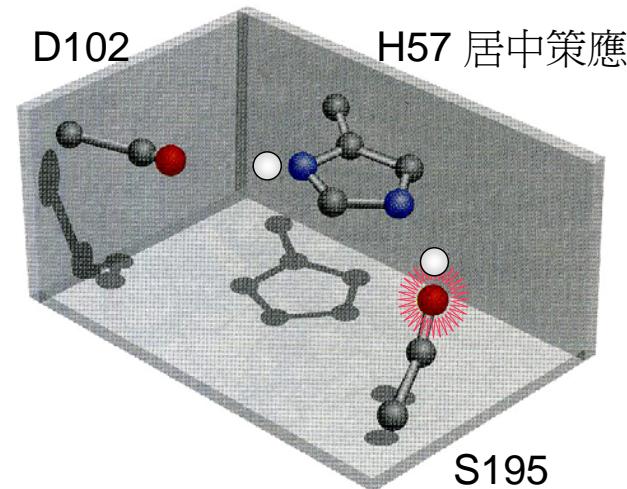
Combinations of different residues form 'catalytic units' that are found repeatedly in different unrelated enzymes

# Amazing histidine

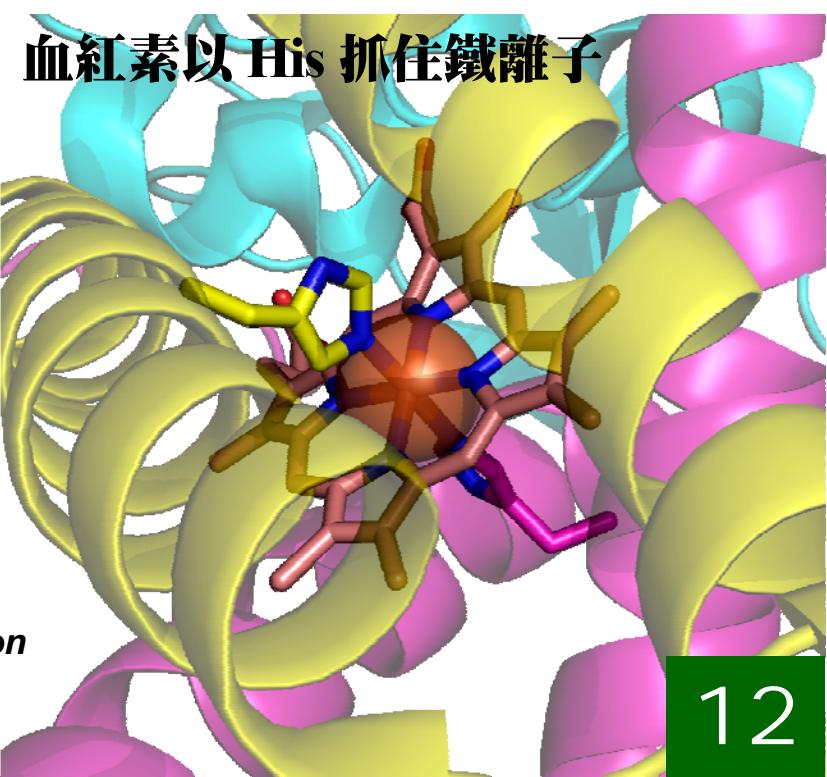
WIKIPEDIA



Catalytic triad



Petsko GA, Ringe D (2004)  
**Protein Structure and Function**  
F4-35

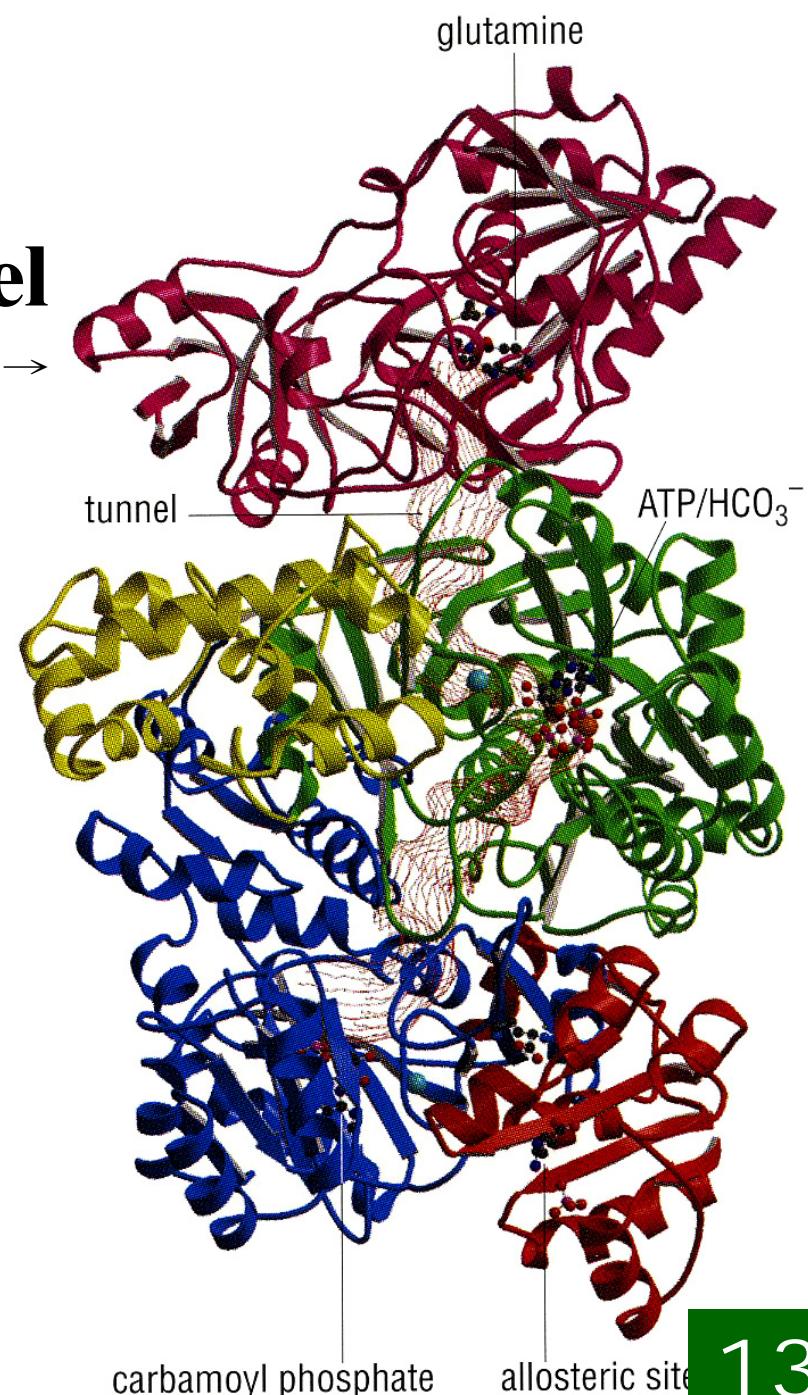
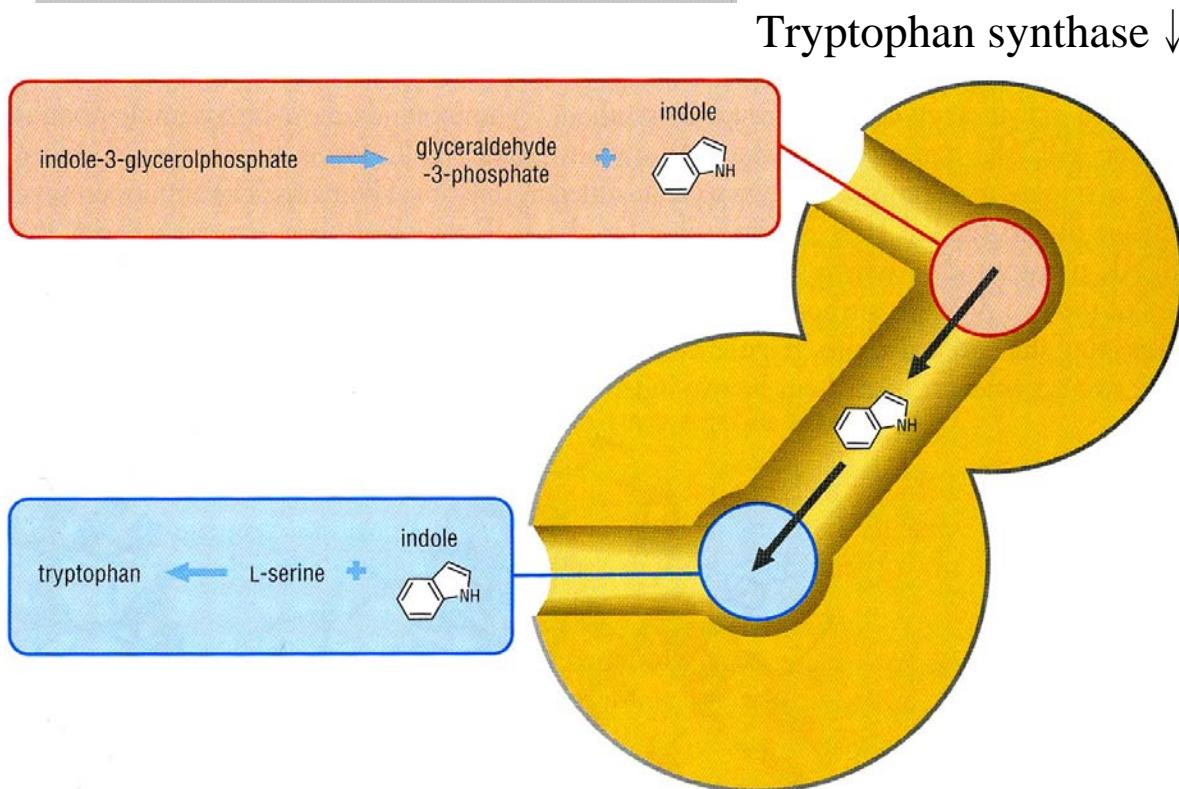


# Multifunctional enzymes

- (1) One active site, two reactions
- (2) Two active sites, two reactions
- (3) Trifunctional enzyme with tunnel

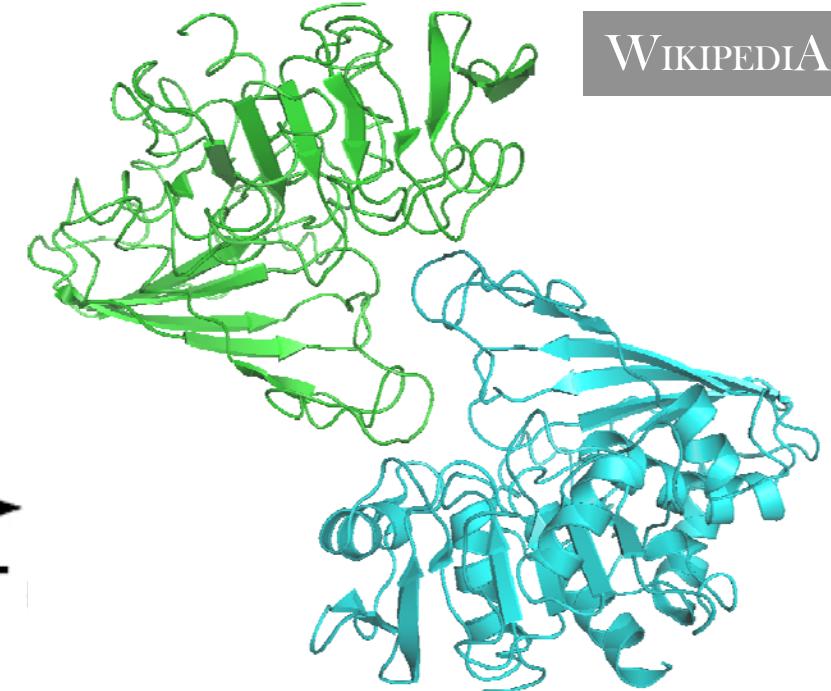
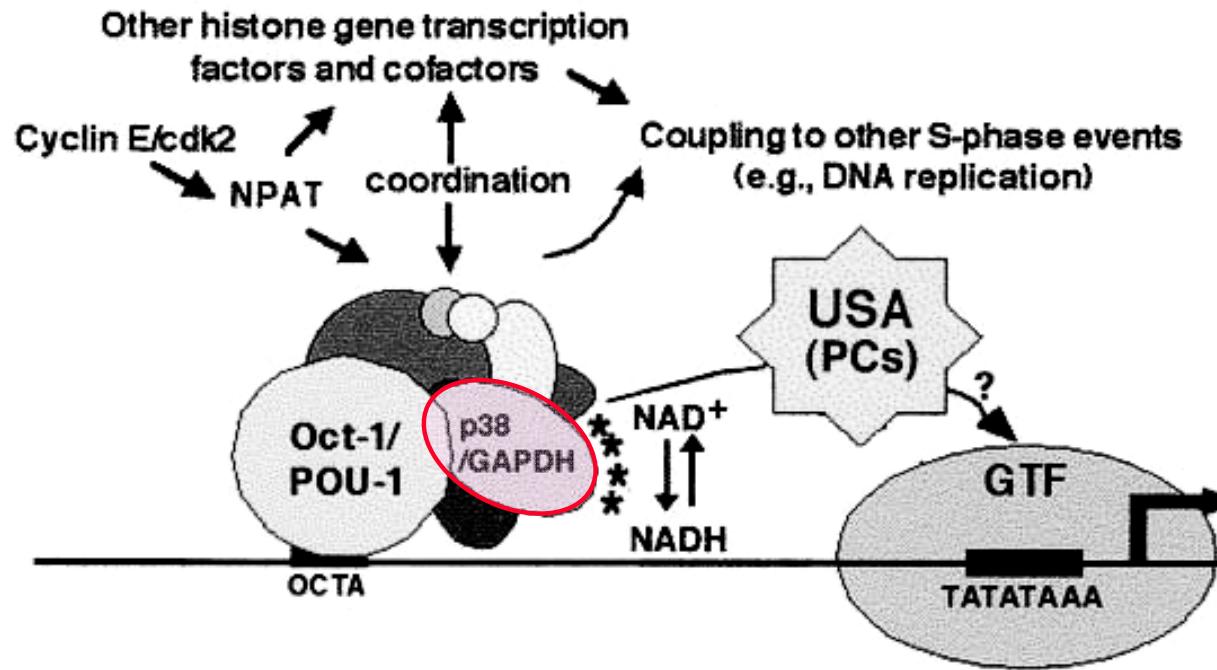
Carbamoyl phosphate synthetase →

演化真是無限可能



# Enzymes also has *non-catalytic* functions

Zheng, L et al (2003) S phase activation of the histone H2B promoter by OCA-S, a coactivator complex that contains **GAPDH** as a key component. *Cell* 114: 255~266



**GAPDH has several functions:**

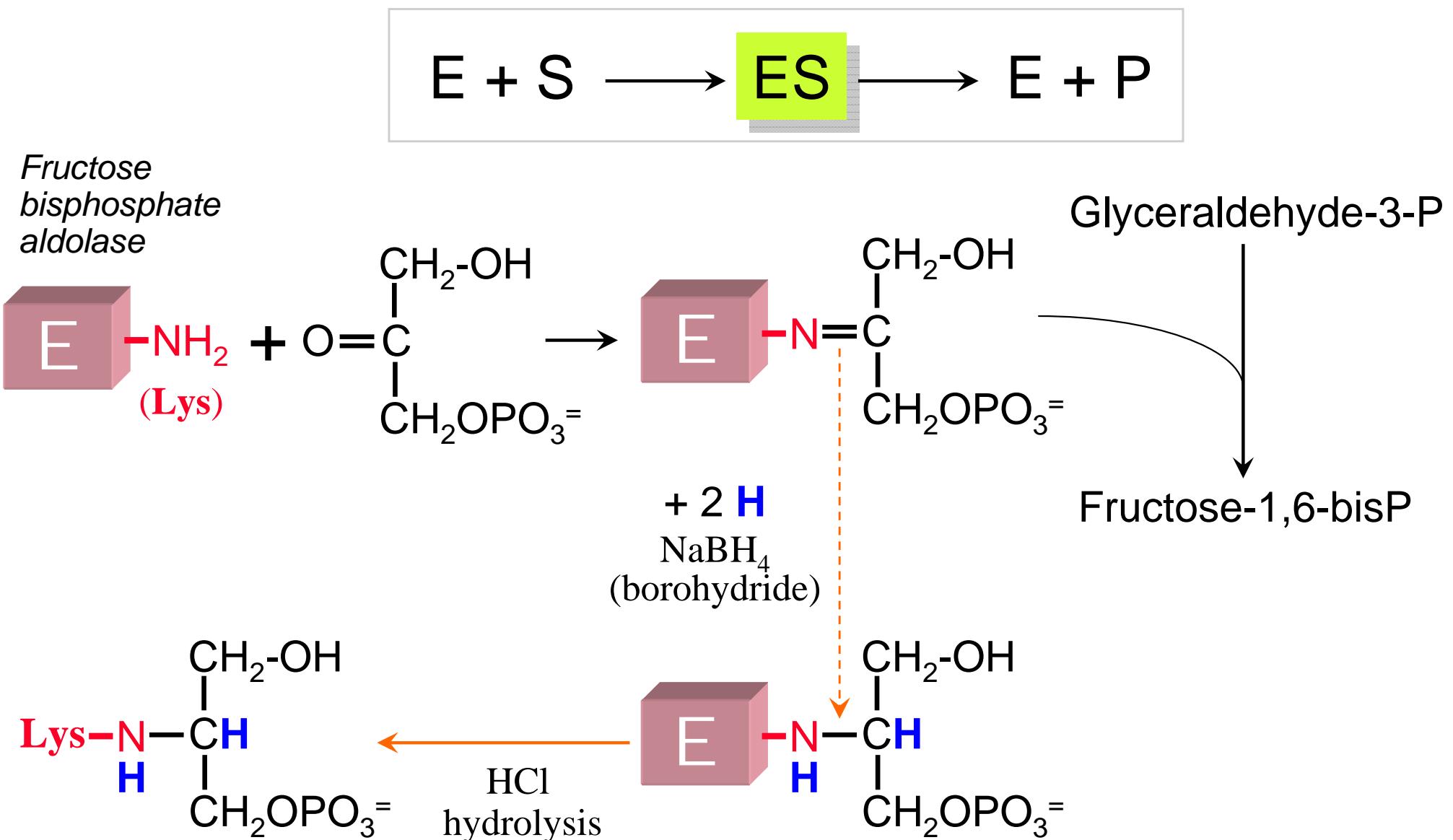
- (0) Glycolysis enzyme**
- (1) Transcription cofactor**
- (2) Initiates apoptosis**
- (3) ER to Golgi transportation**

**Other examples:**

- Phosphoglucose isomerase**  
**(Glycolysis & Cytokine)**
- LON** (Mitochondrial protease & Chaperone protein)

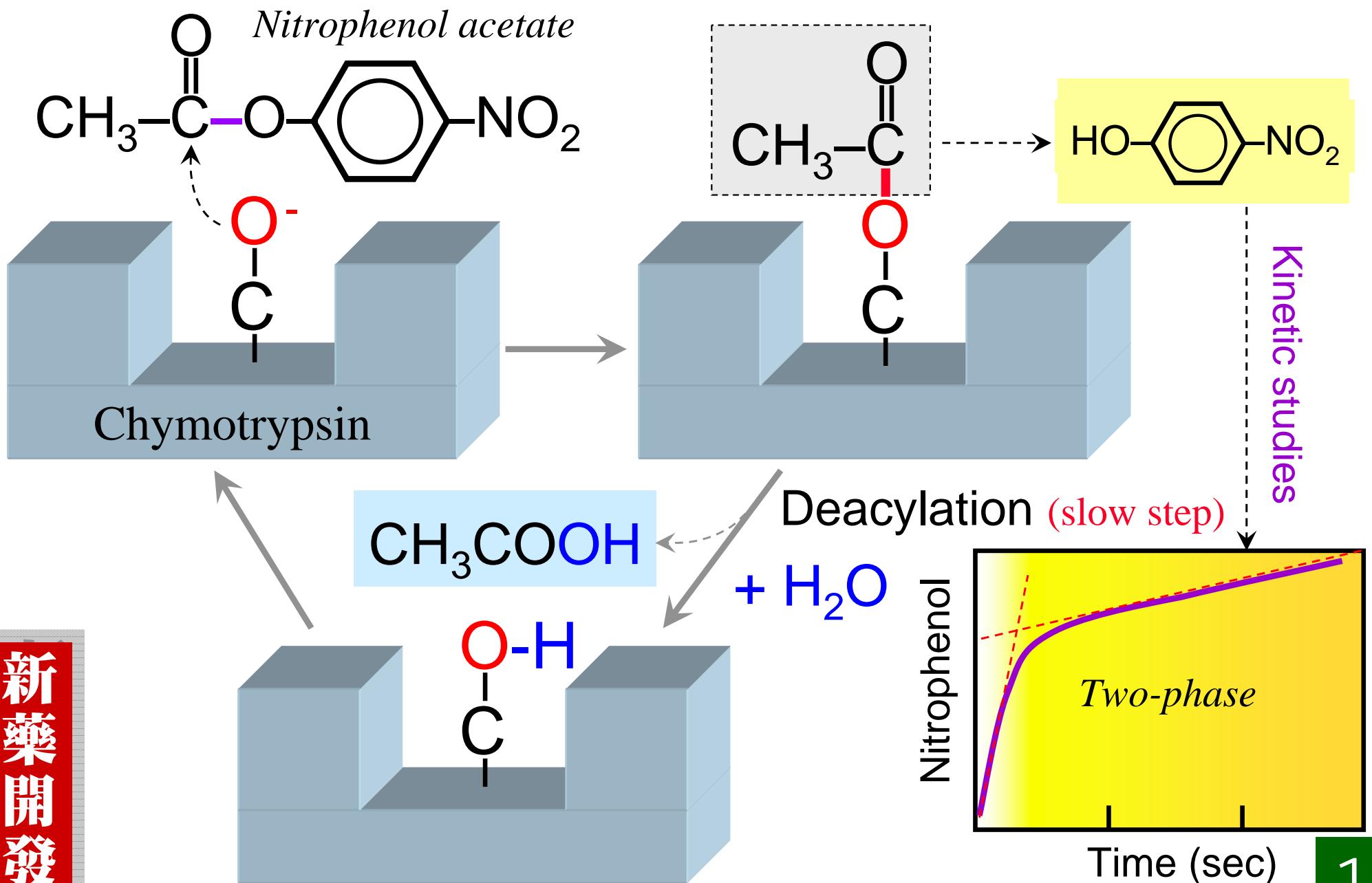
### III Identification of enzyme catalytic sites

#### (1) Trapping the enzyme-substrate complex (classical)



# Identification of enzyme catalytic sites

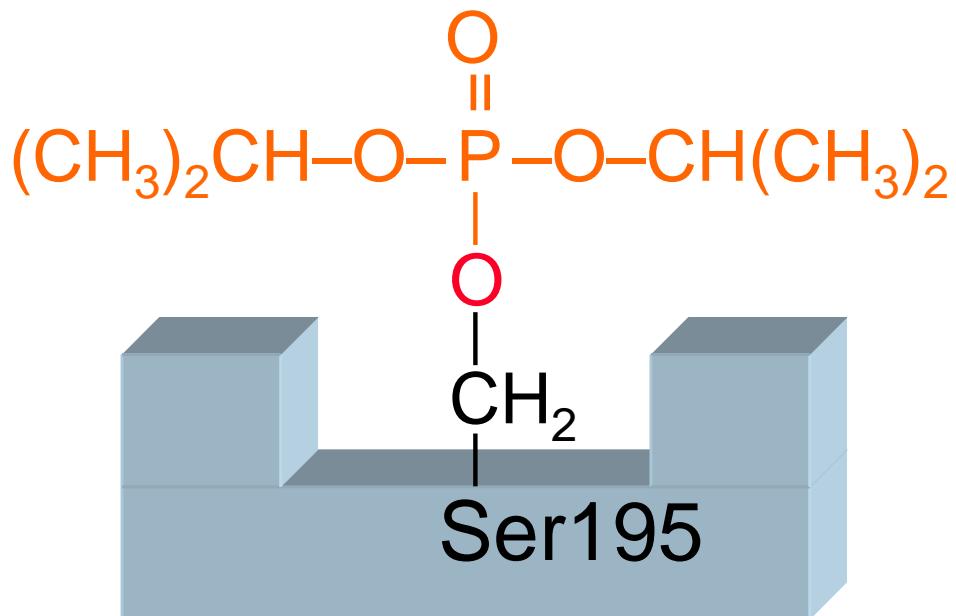
## (2) The use of substrate analogues or rapid-reaction tech



# Identification of enzyme catalytic sites

## (3) Chemical modification protected by substrate (classical)

DIFP (Diisopropyl-fluorophosphate)

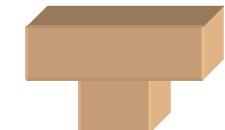
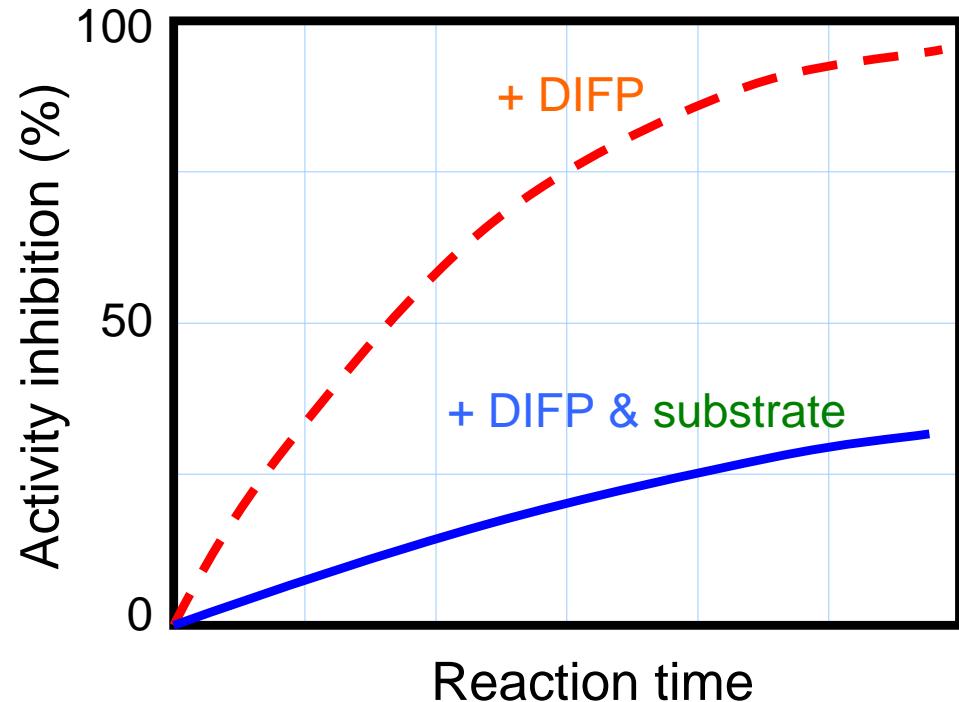


Partial hydrolysis

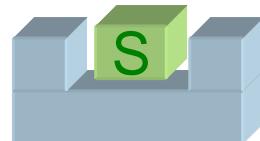
DIFP

Gly-Asp-Ser-Gly-Gly-Pro

以質譜儀分析片段序列可推知活性區重要資訊



$K_m$  increased

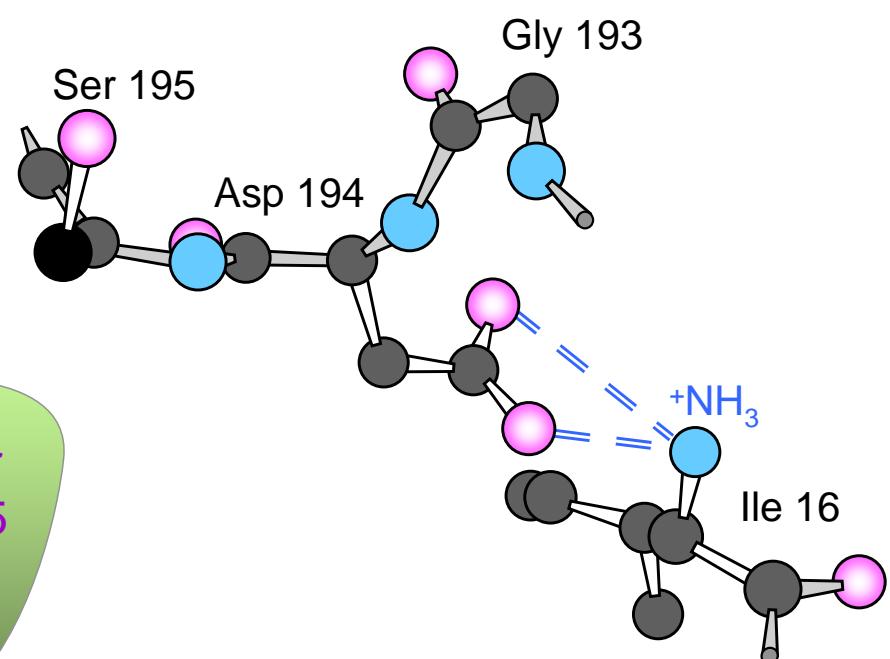
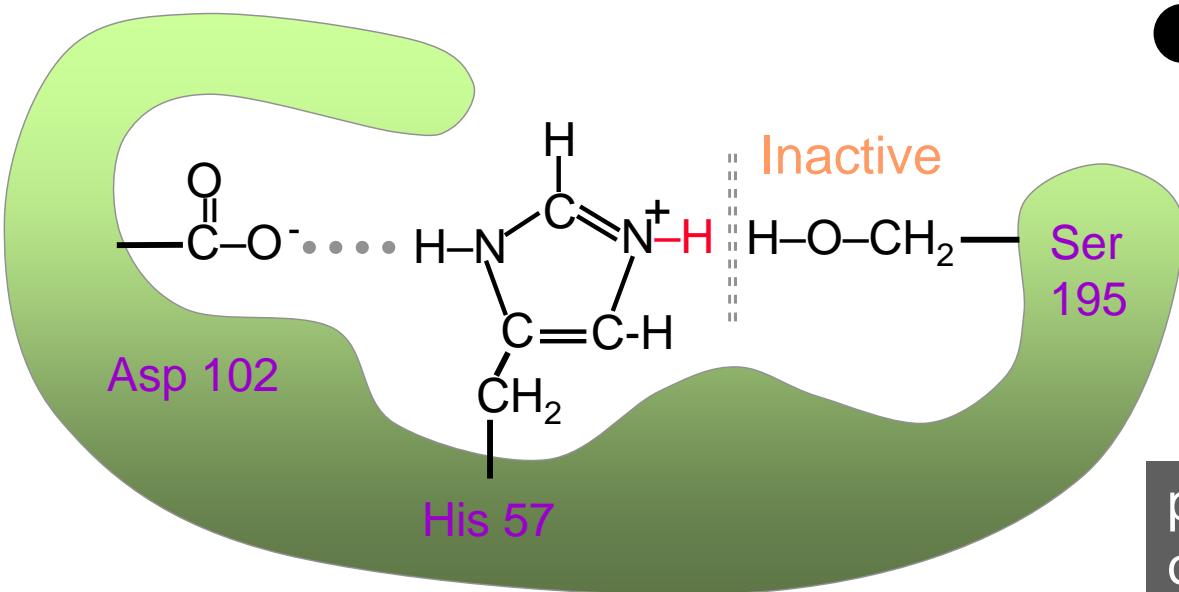
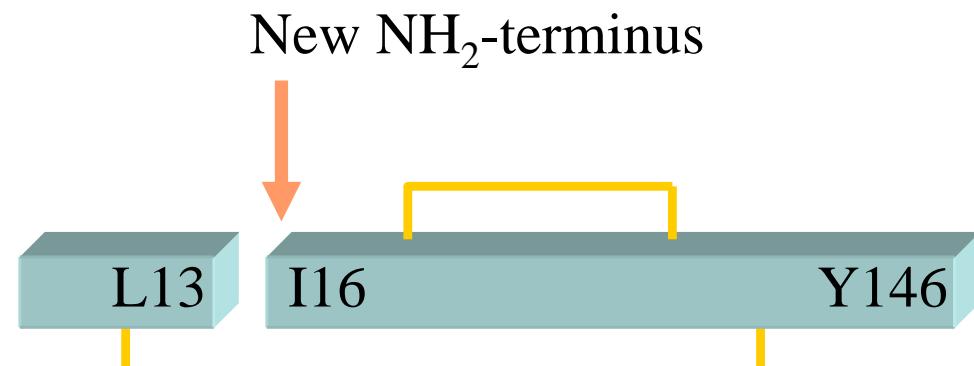
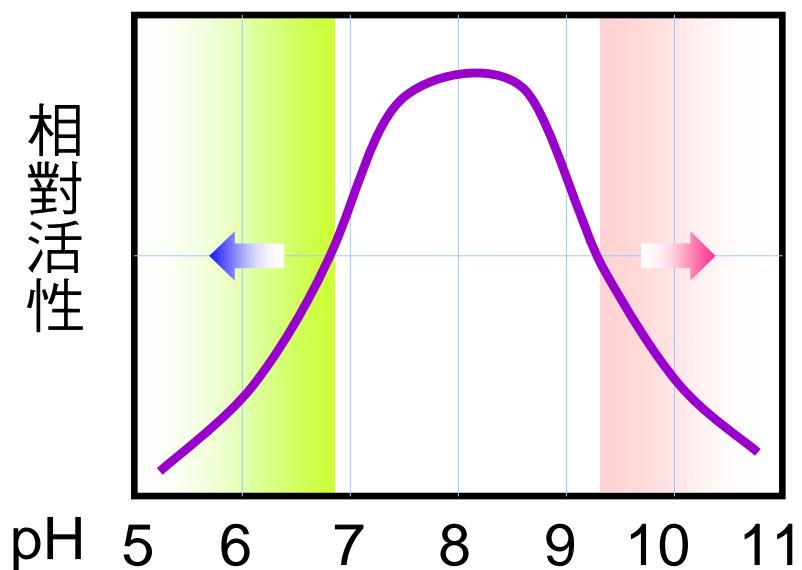


$V_{max}$  unchanged

Active site protected  
by substrate

# Identification of enzyme catalytic sites

## (4) The effect of changing pH (classical but useful)



$pK_a$  changes depending  
on microenvironment

# Identification of enzyme catalytic sites

## (5) Enzyme modified by site-directed mutagenesis (hot!)

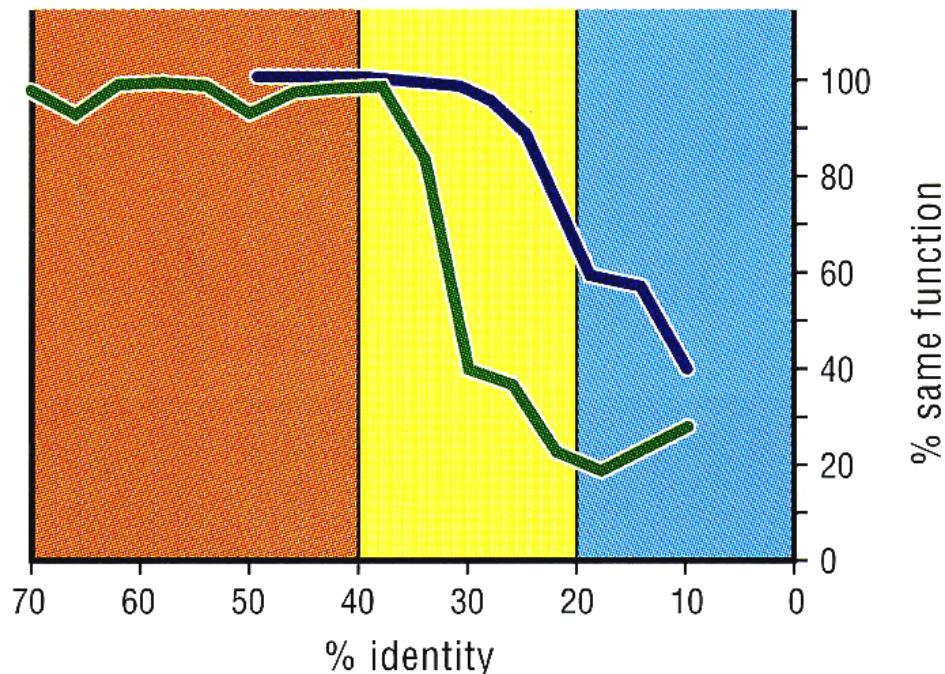
Mutations	<i>Triad:</i>	<i>Amino acids in active site</i>			Relative activity
		Ser	His	Asp	
<i>No enzyme</i>	-				1
<b>Subtilisin</b>		●	●	●	10,000,000,000
Ser, His & Asp → Ala		○	○	○	4,000
His & Asp → Ala		●	○	○	37,000
Ser → Ala		○	●	●	5,000
Asp → Ala		●	●	○	330,000
Asn <sup>155</sup> → Leu		●	●	●	10,000,000
(Asn <sup>155</sup> stabilizes transition state)					

# Identification of enzyme catalytic sites

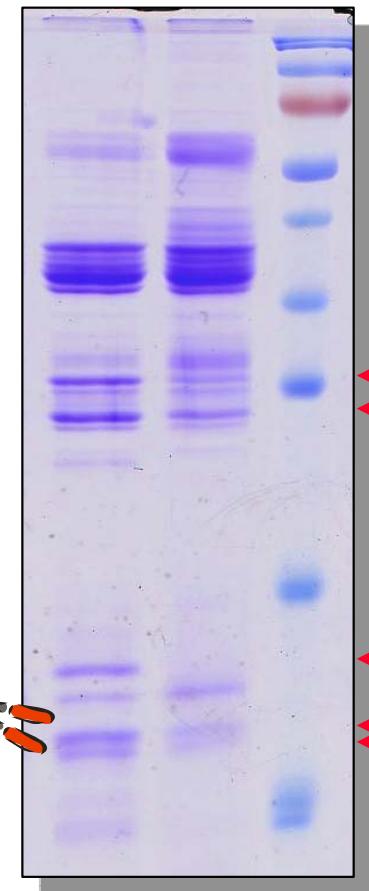
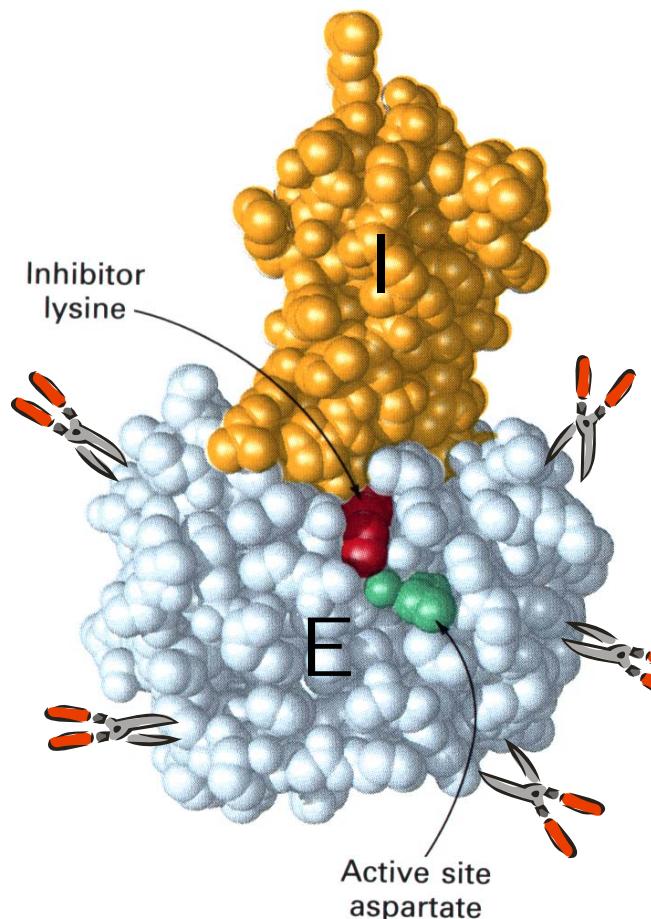
- (6) Enzyme kinetics and inhibition kinetics (real useful)
- (7) Partial proteolysis protected by binding groups
- (8) Prediction from protein sequences (very reliable!)

Mathews et al (2000) Biochemistry (3e) p.208

兩酵素序列若有 30% 相似則功能相同



Relationship of sequence similarity to similarity of function. Enzyme, blue curve; non-enzyme, green curve

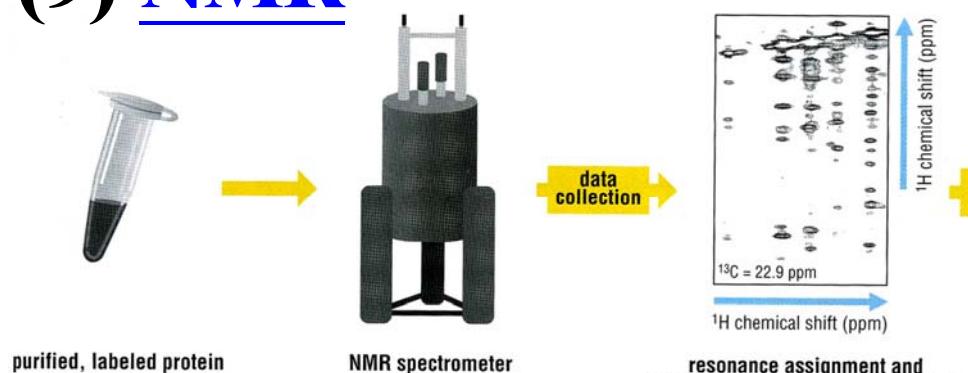


Stryer (1995) Biochemistry (4e) p.252

Petsko GA, Ringe D (2004) *Protein Structure and Function* F4-12

# Identification of enzyme catalytic sites

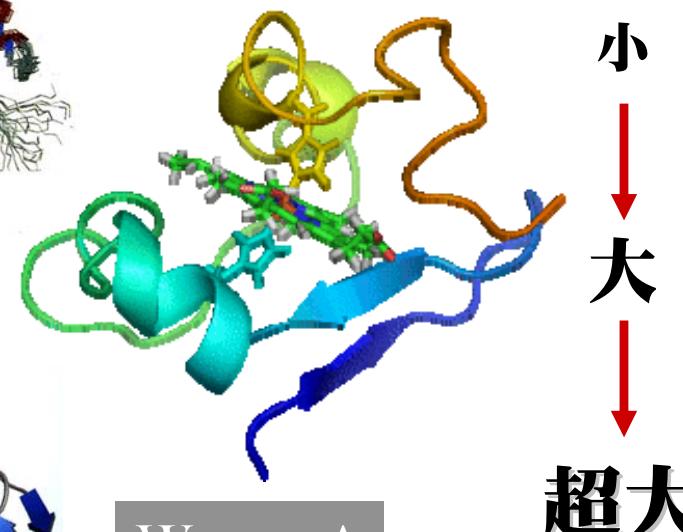
## (9) NMR 核磁共振



Petsko GA, Ringe D (2004) *Protein Structure and Function* F5-3, 5-4

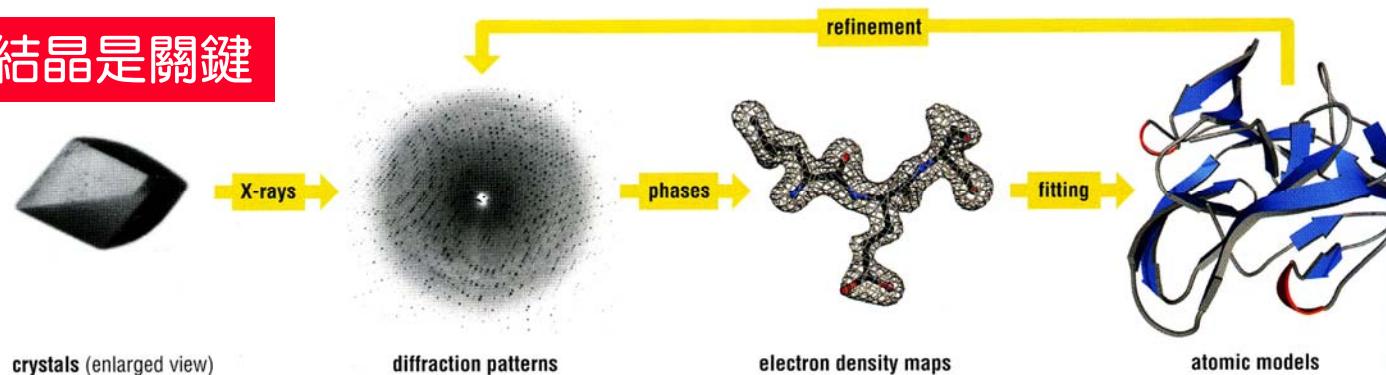
NMR structures of  
*cytochrome c* in solution

分子量



## (10) X-ray crystallography X 光結晶學

結晶是關鍵



WIKIPEDIA

超大

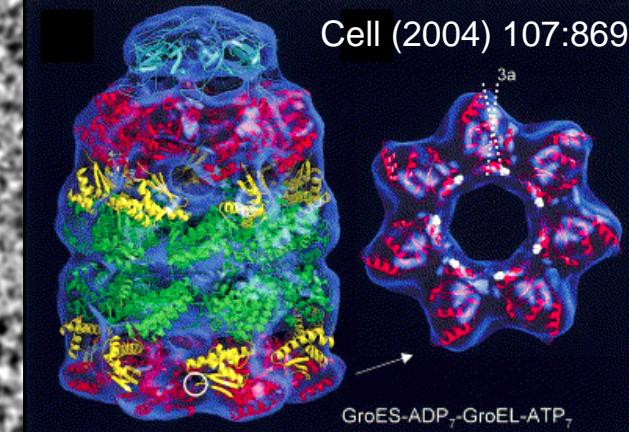
電腦影像科技之貢獻

## (11) Cryo-EM (new)

超低溫電顯

不必用結晶

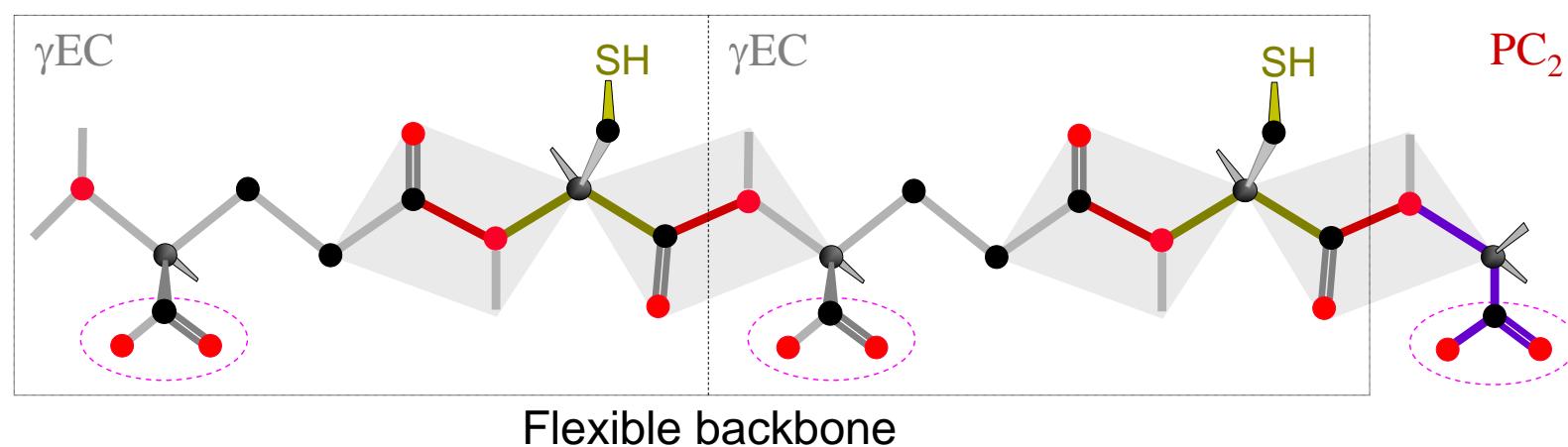
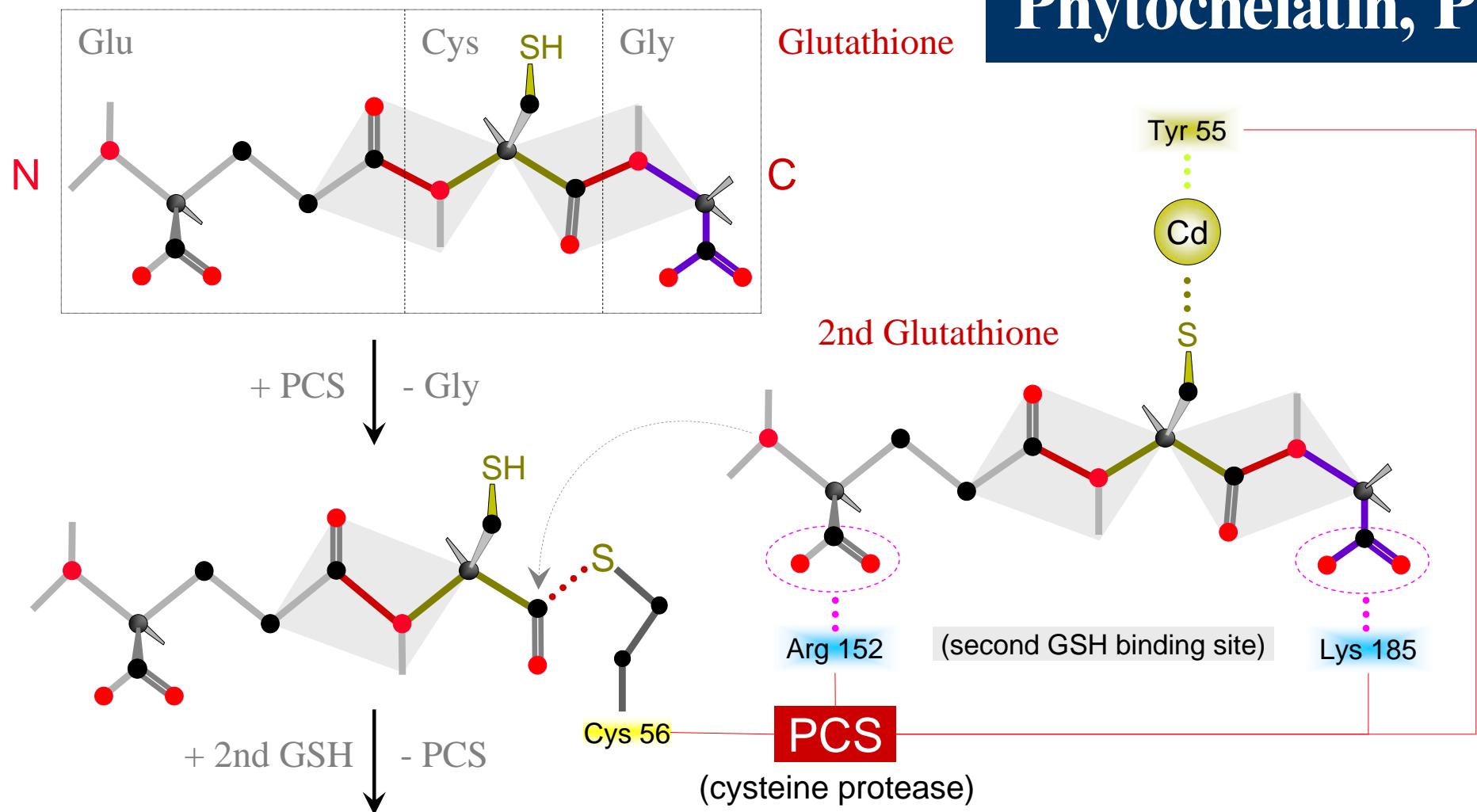
Cell (2004) 107:869



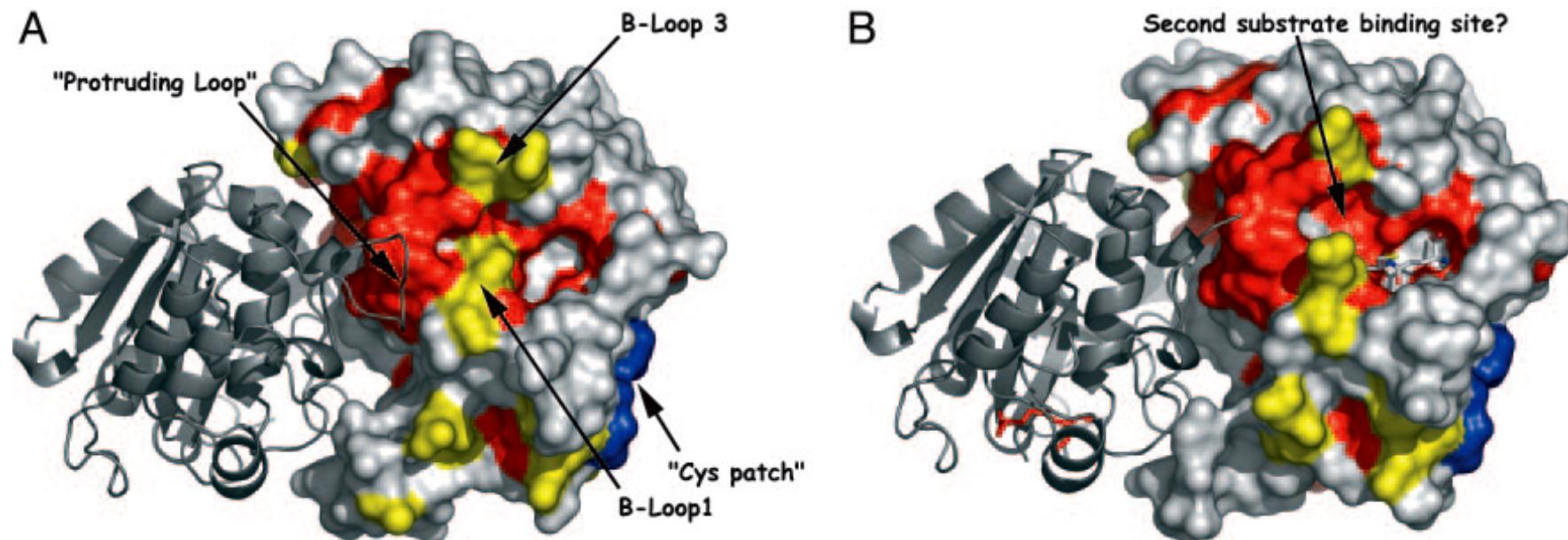
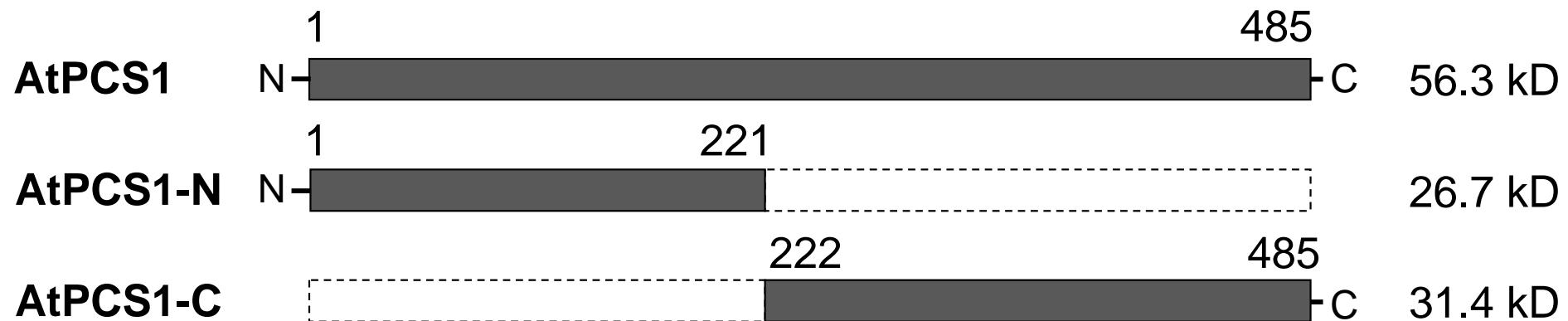
# Structure of Phytochelatin Synthase

GSH + GSH → Phytochelatin ( $PC_2$ )

# Phytochelatin, PC

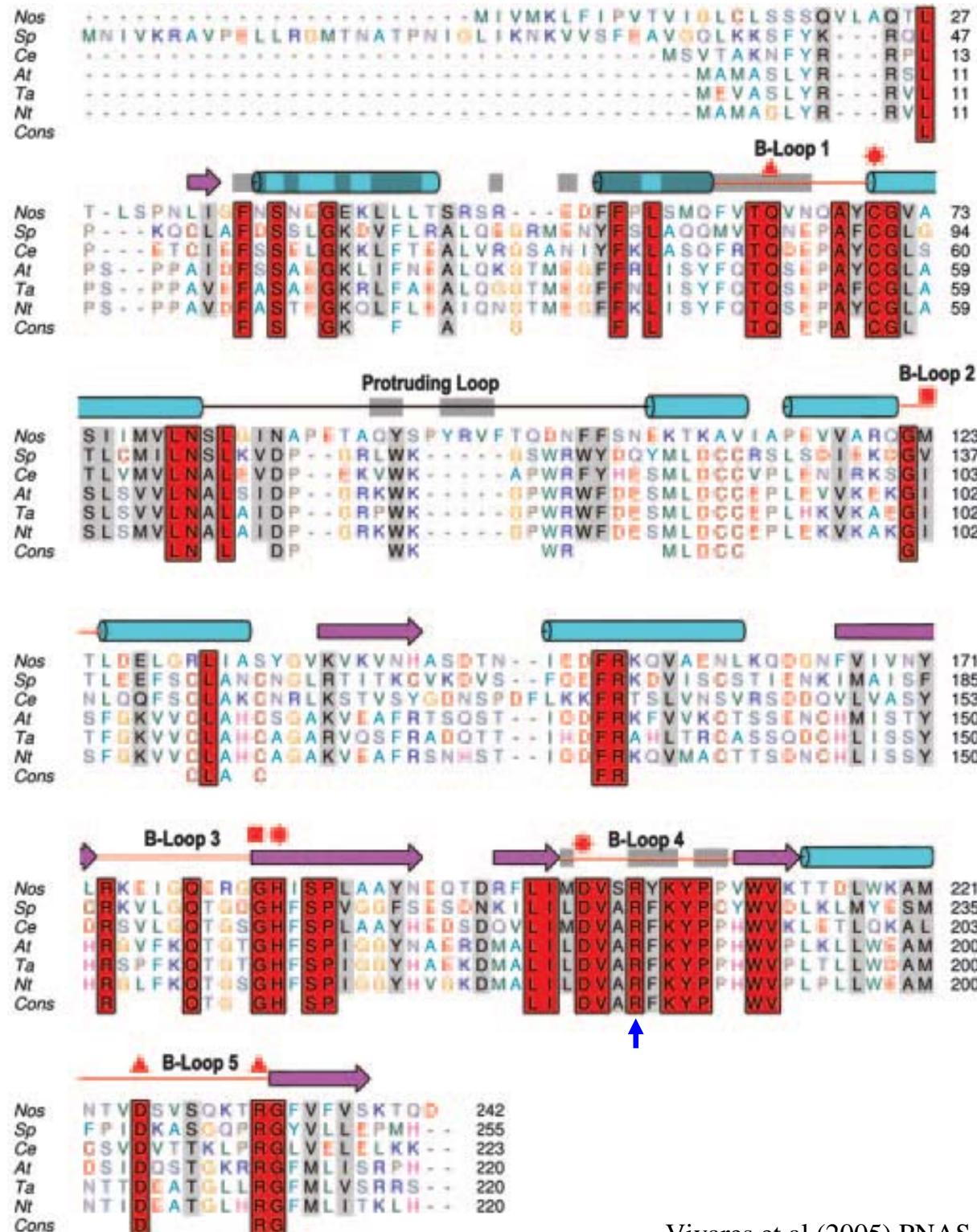


# Phytocochelin synthase molecules



NsPCS is a Cys protease-like enzyme

Vivares et al (2005) PNAS 102:18848-18853



# Motif prediction for PCS phosphorylation

Phosphorylation site  
↓

1 MAMASLYRRSLPSPPAIDF**S**SAEGKLIFNEALQKGTMEGFFRLISYFQT**Q**

Catalytic triad      51 **S**EPA<sup>\*</sup>YCGLASLSVVLNALSIDPGRKWKGPWRWFDE**S**MLDCCPELEVVK<sup>\*</sup>EK

101 GISFGKVVCLAHCSGAKVEAFRTS**Q**<sup>\*</sup>**T**I<sup>\*</sup>DDFRKFVVK**C**<sup>\*</sup>**T**SENCHMISTY

151 HRSVFKQTGN<sup>\*</sup>GHF<sup>\*</sup>SPIGGYNAERDMALILDVARFKYPPHWVPLKLLWEAM

201 DSIDQ**S**<sup>221</sup>**T**GKRRGFMLISRPHREPGLLYTL**S**CKDE**S**WIEIAKYLKEDVPRL

251 VSSQHVDSVEKIISVVFKSLPSNFNQFIRWVAEIRITEDSNQNL**S**AEEKS

301 RLKLKQLVLKEVHETELFKHINKFLSTVGYEDSLTYAAAKACCQGAEILS

351 GSPSKEFCCRETCVKCIKG**P**DDSEGTVVTGVVVRDGNEQKV**D**LLVPS**T**<sup>\*</sup>**Q**<sup>\*</sup>**T**

401 ECECGPEATYPAGNDVFTALLLALPPQTWSGIKDQALMHEMKQLISMASL

451 PTLLQEEVLHLRRQLQLLKRCQENKEEDDLAAPAY

485

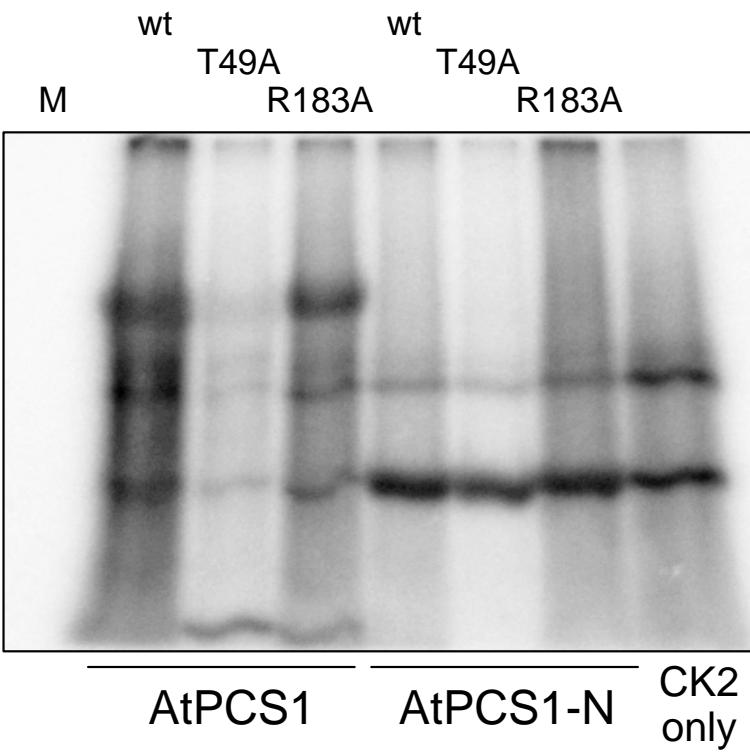
CKII\_PHOSPHO\_SITE  
[ST]-x(2)-[DE] —————

PKC\_PHOSPHO\_SITE  
[ST]-x-[RK] ······

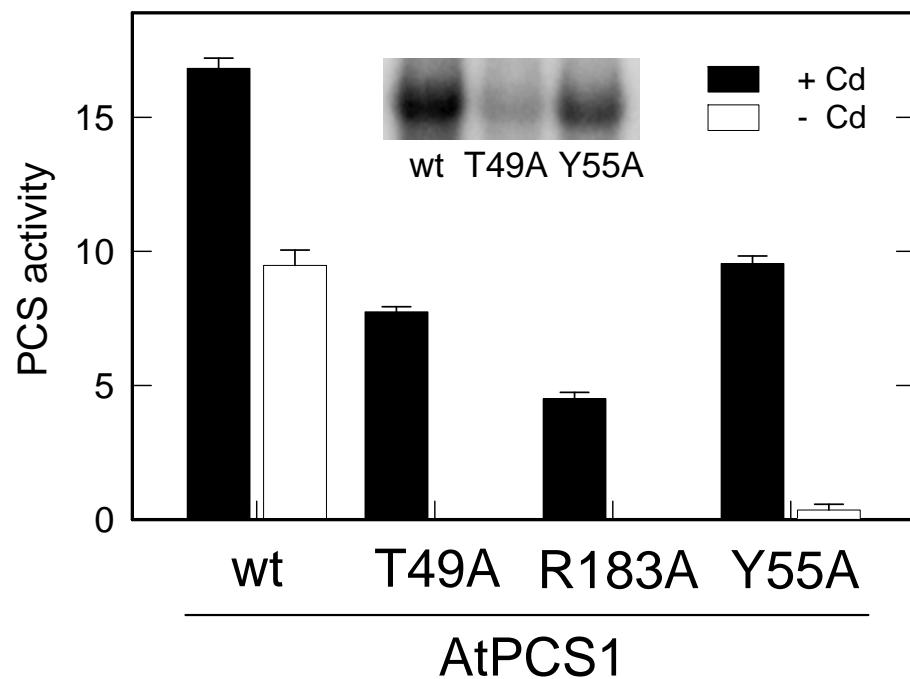
TQSE

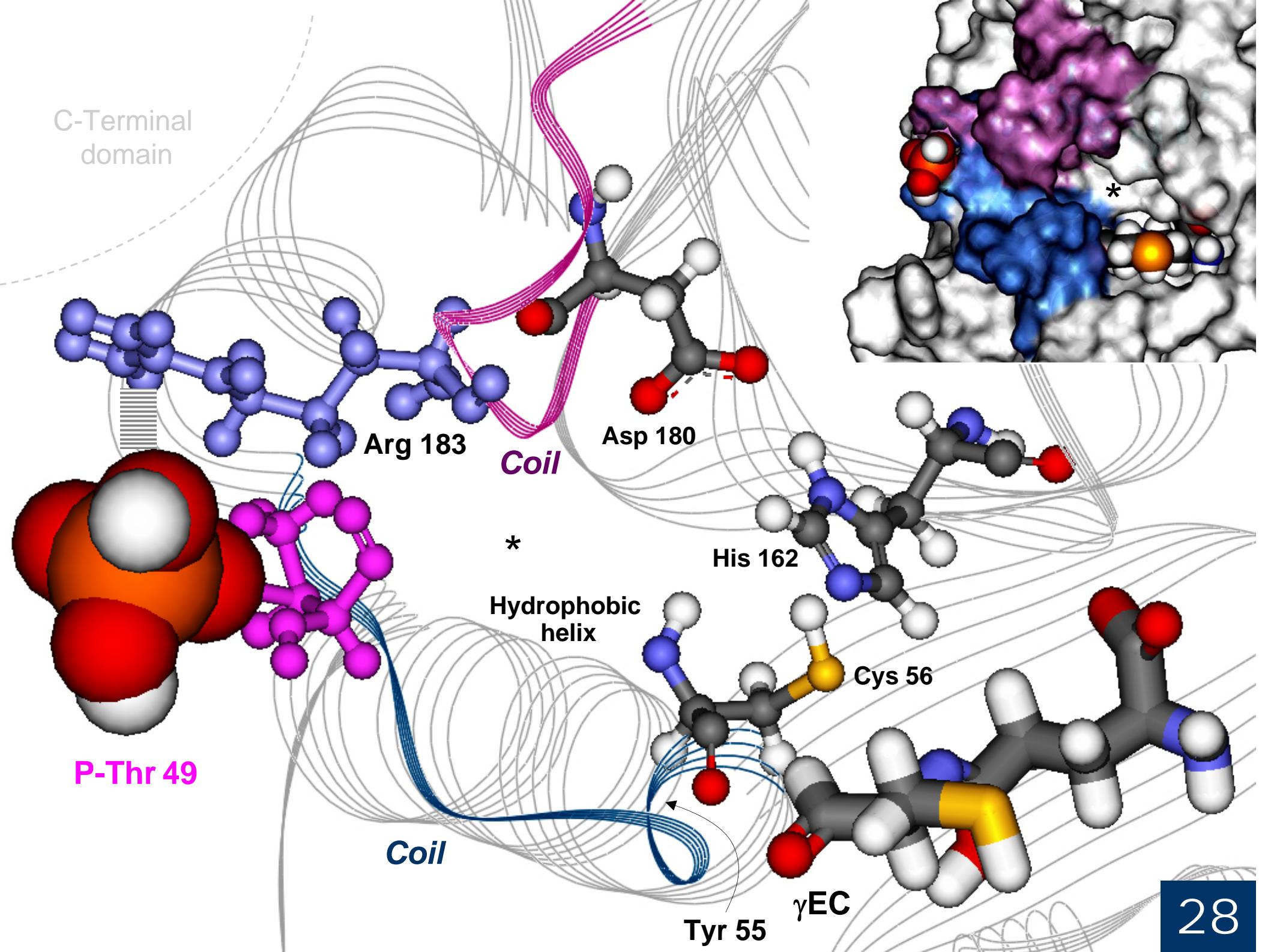
# PCS is phosphorylated on Thr 49

Autoradiograph

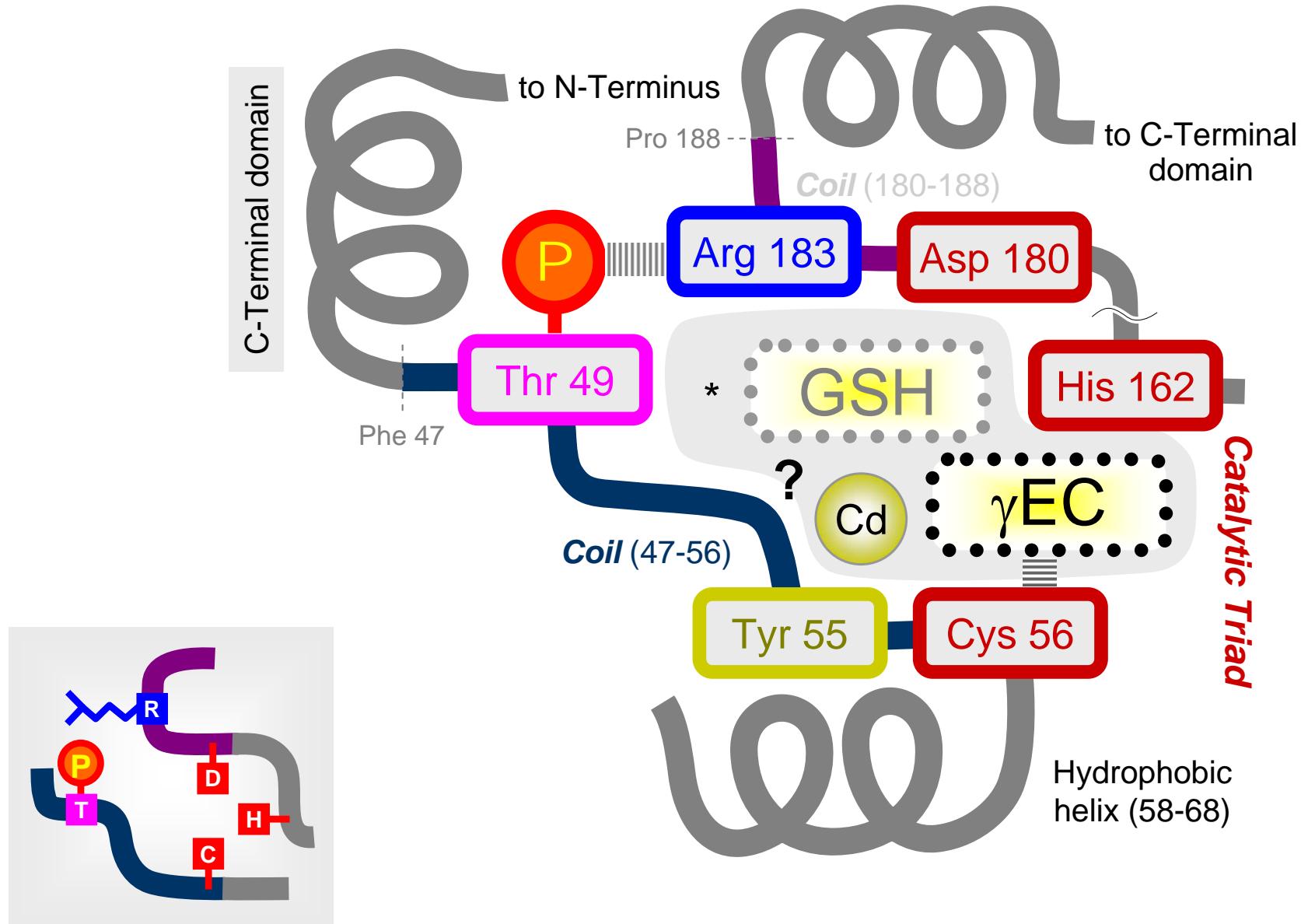


GSH + GSH → Phytochelatin ( $PC_2$ )





# The active site of PCS



# 3-Dimensional structure prediction

## Phytochelatin synthase 融合素合成酶

\*Catalytic triad

Phosphorylation site ↓

1 MAMASLYRRSLPSPPAIDF **S**SAEGKLIFNEALQKGTMEGFFRLISYFQTQ

51 SEPAYCGLASLSVVLNALSIDPGRKWKGWPWRWFDES**M**LDCCEPLEVVKEK \*

101 GISFGKVVC LAHCSGAKVEAFRTS**Q**STIDDFRKFVVKCT**T**SENCHMISTY

151 HRSVFKQTGN GHFSPIGGYNAERDMALILDVARFKYPPHWVPLKLLWEAM \*

201 DSIDQ**S**TGKRRGFMLISRPHREPGLLYTL**S**C KDES WIEIAKYLKEDVPRL 221 \*\*\*

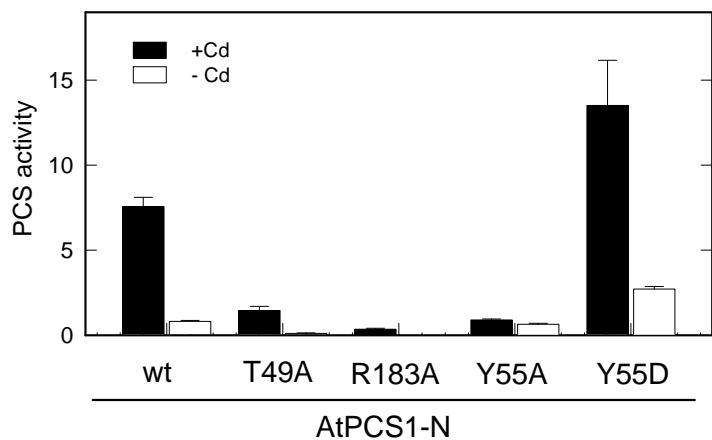
251 VSSQHVDSVEKIISVVFKSLPSNFNQFIRWVAEIRITEDSNQNL**S**AEEKS

301 RLKLKQLVLKEVHETELFKHINKFLSTVGYEDSLTYAAAKACCQGAEL S

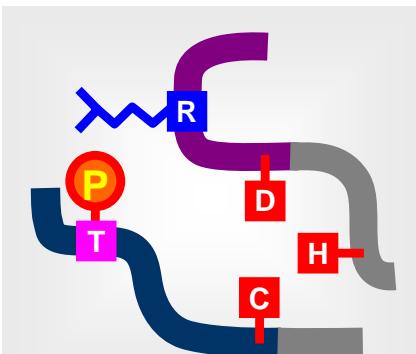
351 GSPSKEFCCRETCVKCIKGPD**D**SEGTVVTGVVVRDGNEQKV DLLVPS**TQ**T

401 ECECGPEATYPAGNDVFTALLLALPPQTWSGIKDQALMHEMKQLISMASL

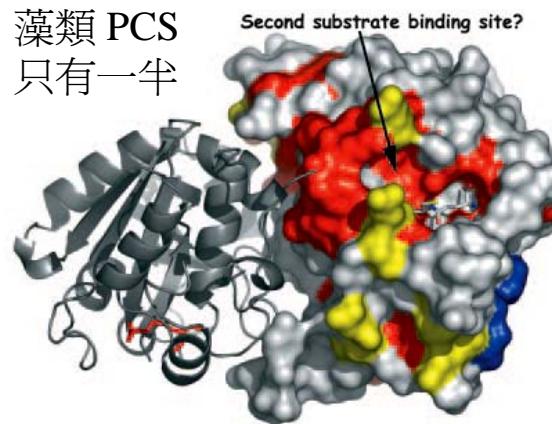
451 PTLLQEEVLHLRRQLQLLKRCQENKEEDDLAAPAY 485



GSH + GSH → Phytochelatin (PC<sub>2</sub>)



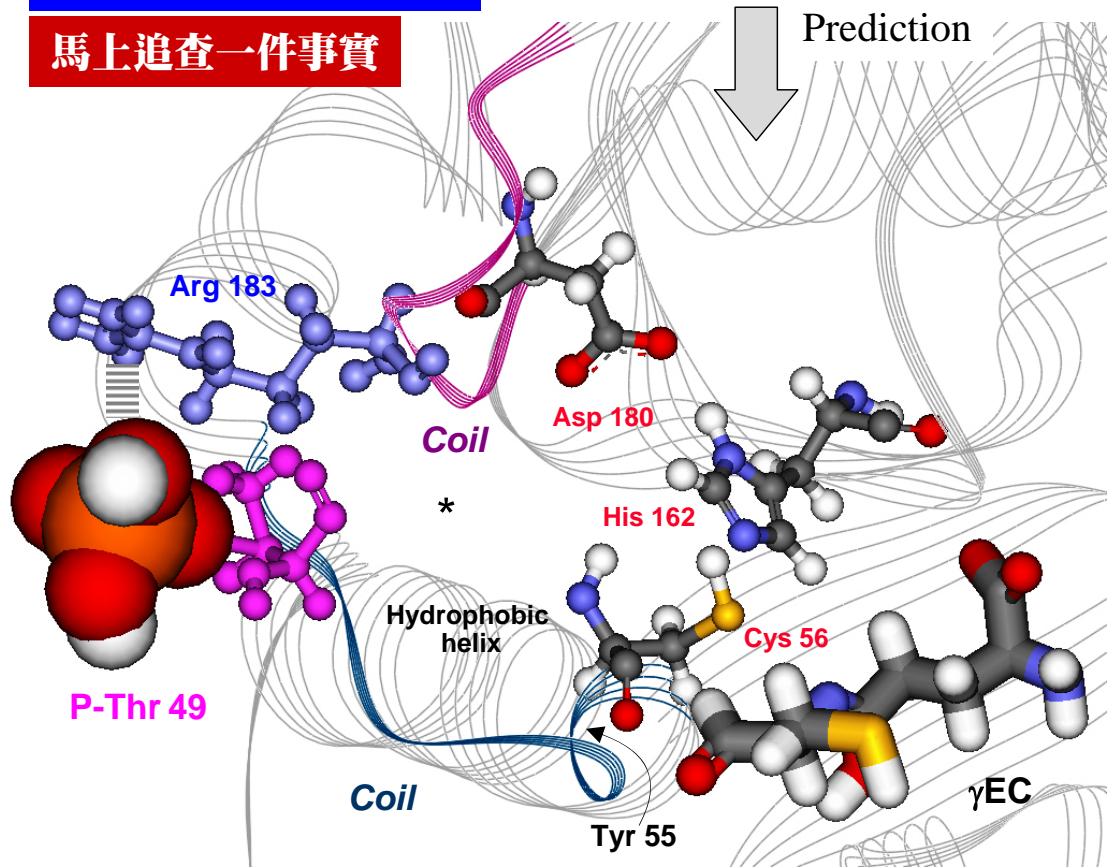
藻類 PCS  
只有一半



預測 Arg 183 可能角色

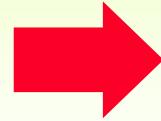
馬上追查一件事實

Prediction



到任何搜尋引擎以  
『上課演講』搜尋  
即可在首行找到

## 講義部份



## 指定閱讀

## 參考資料

上課演講下載 - Microsoft Internet Explorer						
檔案(F) 編輯(E) 檢視(V) 我的最愛(A) 工具(T) 說明(H)						
上一頁	下一個	X	3	家	搜尋	我的最愛
網址(D)	http://juang.bst.ntu.edu.tw/JRH/talks.htm#酵素學				移至	連結
基因表現	[2004 EPA.PPT]	純化與電泳	11.3 M	52	pdf	1.5 h
酵素學	2010/03/08, 15 兩次					
醫學院生化所	Short Course	Chapters	Size	Pages	下載	
講義(0)	[Enzymology 0.pdf]	基本酵素學原理(參考)	3.07 M	28	pdf	0 h
講義(1)	[Enzymology1 Ten.pdf]	酵素學十誡 (Kornberg)	4.74 M	15	pdf	0 h
講義(2)	[Enzymology2 chem nature.pdf]	酵素的化學本質	1.60 M	17	pdf	0 h
講義(3)	[Enzymology3 reaction.pdf]	酵素反應機制	7.07 M	28	pdf	2 h
講義(4)	[Enzymology4 L-SP.pdf]	澱粉磷解酶	7.00 M	48	pdf	2 h
講義(5)	[Enzymology5 Biotech.pdf]	酵素在生物技術應用	0.86 M	14	pdf	0 h
↓ 指定閱讀 ↓	↓ Original journal	↓ PubMed				
指定閱讀(1)	TiBS (2003) 28:515-517	Ten commandments	82 K	3		
指定閱讀(2)	TiBS (2005) 30:622-629	Nature's catalytic toolkit	298 K	8		
指定閱讀(3)	Science (2006) 311:535-538	Design catalytic activity	299 K	5		
指定閱讀(3)	Perspectives (Science)	(上篇報告的評論)	681 K	2		
指定閱讀(3)	JAFC (2009) 57:7348-7355	Phytochelatin synthase	988 K	8		
指定閱讀(4)	Phyiol Plant (2002) 114:506	Proteolytic regulation	293 K	10	pdf	
指定閱讀(4)	Planta (2006) 223:468	Starch phosphorylase	655 K	11	pdf	
↓ 參考資料 ↓						
科學哲學	科學之路	科學的哲學思考			pdf	
酵素基礎	Enzyme (生物化學課程)	BC basics 2008			pdf	
純化分析	Enzyme purification & analysis	酵素化學實驗			pdf	
參考動畫	Chymotrypsin	(更多動畫)				