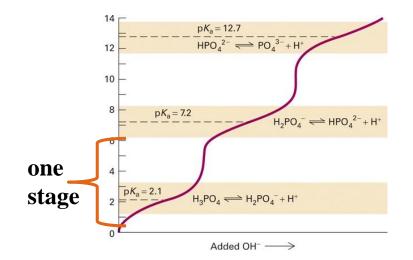
BCH312 [Practical]

## Titration curve of amino acids

# **Titration Curves :**

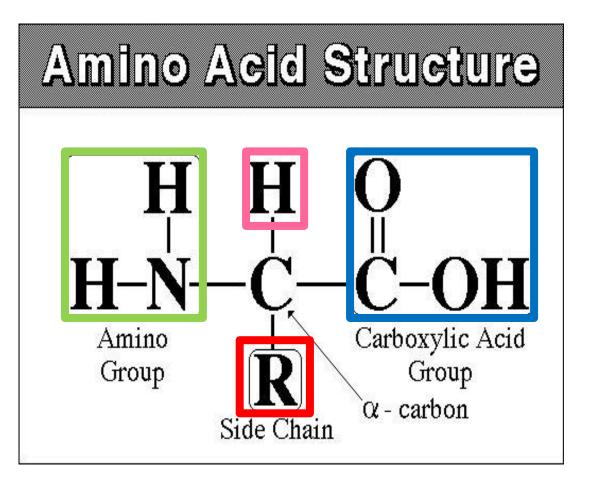
- □ Titration Curves are produced by <u>monitoring the pH</u> of a <u>given volume</u> of a sample solution after successive **addition of acid or alkali**.
- The curves are usually plots of pH against the volume of <u>titrant</u> added (acid or base).
- □ Each dissociation group represent one stage in the titration curve.



# Amino acid general formula:

## Amino acids consist of:

- A basic amino group (  $-NH_2$  )
- An acidic carboxyl group ( —COOH)
- ► A hydrogen atom ( —H)
- > A distinctive side chain ( --R).



# Amphoteric nature of amino acid:

- When an amino acid is dissolved in water it exists predominantly in the zwitterion form.
- □ Amino acid is an <u>amphoteric</u> compound → It act as either an <u>acid</u> or a base:
  - > Upon titration with acid  $\rightarrow$  it acts as a <u>BASE</u> (accept a proton).
  - > Upon titration with base  $\rightarrow$  it acts as an <u>ACID</u> (donate a proton)

# Amino acid as weak acids:

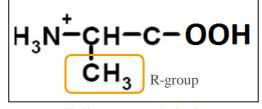
□ Amino acids are example of weak acid which contain more than one dissociate group.

### **Examples:**

### (1) <u>Alanine:</u>

-Contain COOH ( $pKa_1 = 2.34$ ) and  $NH_3^+$  ( $pKa_2 = 9.69$ ) groups (it has one pI value =6.010). [Diprotic]

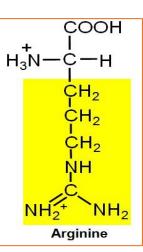
-The COOH will dissociate first then  $NH_3^+$  dissociate later . (Because pKa1<pKa2)



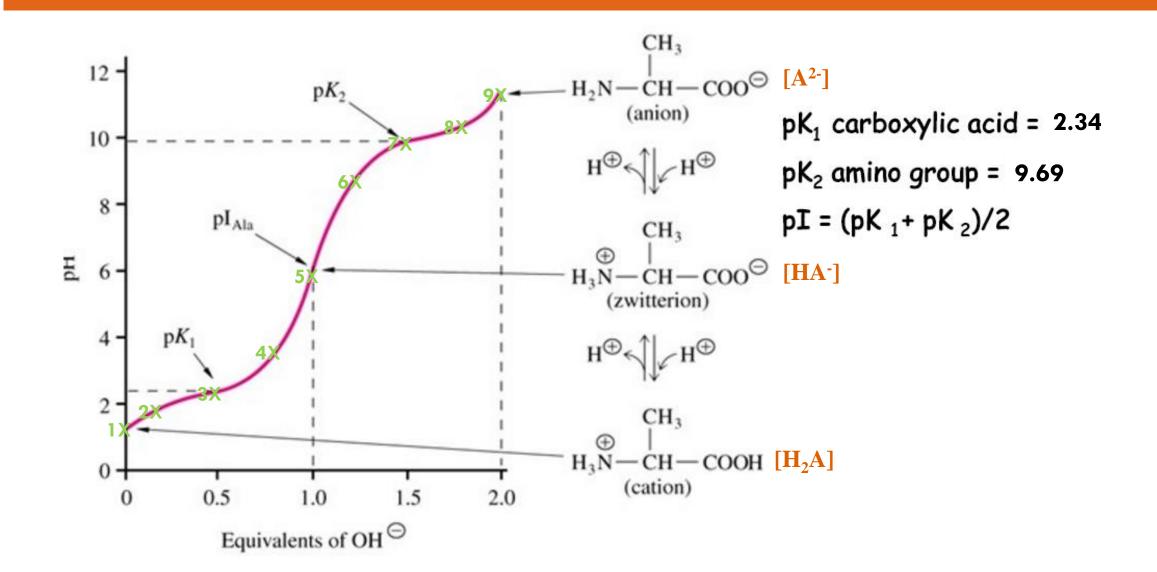
Full protonated alanine

### (2) <u>Arginine:</u>

-Contain COOH ( $pKa_1 = 2.34$ ),  $NH_3^+$  ( $pKa_2 = 9.69$ ) groups and basic group ( $pKa_3 = 12.5$ ) (it has one pI value=11). [Triprotic]



## **Titration curve of Alanine**



## **Titration curve of alanine [diprotic]:**

### [1] In starting point:

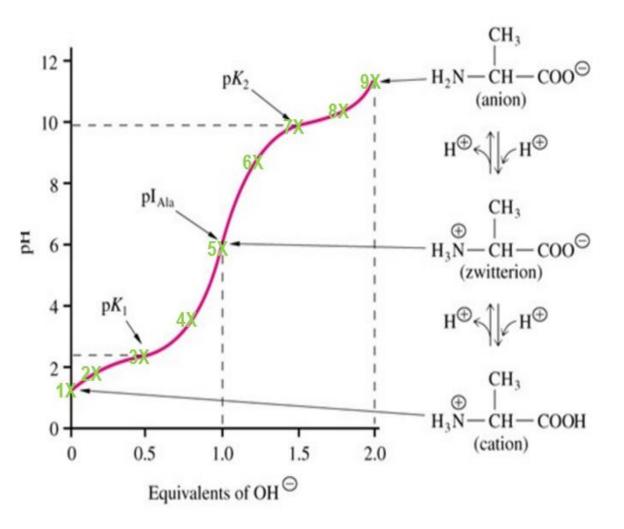
- □ Alanine is full protonated.
- $\square [NH_3^+-CH-CH_3-COOH].$

### [2] COOH will <u>dissociate</u> first:

 $[NH_3^+-CH-CH_3-COOH] > [NH3+-CH-CH3-COO^-]$  $pH < pKa_1.$ 

# [3] In this point the component of alanine act as **buffer**:

□  $[NH_3^+-CH-CH_3-COOH] = [NH_3^+-CH-CH_3-COO^-].$ □  $pH = pKa_1$ 



## **Titration curve of alanine or glycine [diprotic]:**

#### [4] In this point:

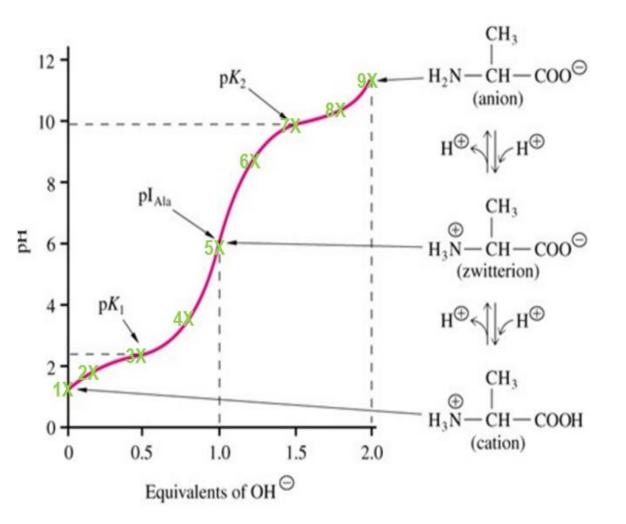
- $\square [NH_3^+-CH-CH_3-COOH] < [NH_3^+-CH-CH_3-COO^-].$
- $\square \quad pH > pKa_{1.}$

#### [5] Isoelectric point:

- □ The COOH is full dissociate to COO<sup>-</sup>.
- $\square [NH_3^+-CH-CH_3^-COO^-].$
- $\Box$  -ve charge = +ve charge.
- □ The amino acid present as Zwetter ion (neutral form).
- Remember that :pI (isoelectric point) is the pH value at which the net charge of amino acid equal to zero.
- □  $pI = (pKa_1 + pKa_2) / 2 = (2.32 + 9.96) / 2 = 6.01$

#### [6] The NH<sub>3</sub><sup>+</sup> start <u>dissociate</u>:

- $\square \qquad [\mathrm{NH}_3^+-\mathrm{CH}-\mathrm{CH}_3-\mathrm{COO}^-] > [\mathrm{NH}_2-\mathrm{CH}-\mathrm{CH}_3-\mathrm{COO}^-].$
- $\square \quad pH < pKa_2.$



## **Titration curve of alanine or glycine [diprotic]:**

[7] In this point the component of alanine act as **buffer**:

 $\square [NH_3^+-CH-CH_3-COO^-] = [NH_2-CH-CH_3-COO^-].$ 

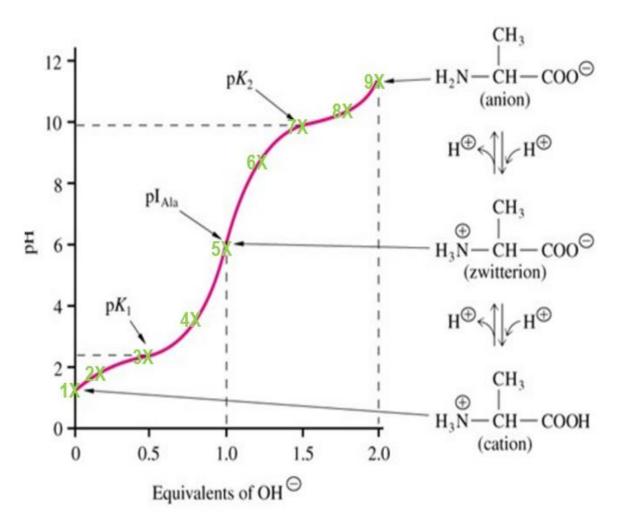
 $\square$  pH=pKa<sub>2</sub>.

### [8] In this point:

 $[NH_3^+-CH-CH_3-COO^-] < [NH_2-CH-CH_3-COO^-] .$  $pH > pKa_2$ 

### [9] End point:

- □ The alanine is full dissociated.
- $\square [NH_2-CH-CH_3-COO^-]$
- $\square \quad pOH=(pkb+P[A-])/2$
- $\Rightarrow pKb = pKw pKa2$



## **Calculating the pH at different point of the titration curve :**

The pH calculated by different way :

[1] at starting point :

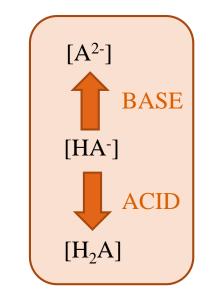
pH=(pka1+p[HA])/2

[2] At any point within the curve (except start and end points):

 $pH=pka1+log([HA^-]/[H_2A])$  and  $pH=pka2+log([A^2-]/[HA^-])$ 

[3] At end point:

pOH=(pKb+p[A-])/2 pH=pKw - pOH pKb = pKw - pKa2





Determine the pH value of 100 ml of alanine (0.2M), titrated with 0.2M KOH and 0.2M HCl, (pKa1=2.34 and pKa2=9.69), after addition of: (1) 50 ml of HCL. (2) 30 ml of KOH.

### [1] pH after addition of 40 ml of HCL?

HCL (acid) → amino acid act as base → COO<sup>-</sup> to COOH

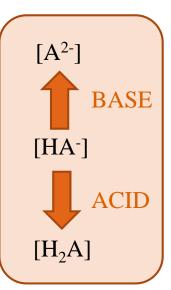
 $pH=pka1+log([HA^-]/[H_2A]) \ ,$ 

HA = Mole of HA [original] – mole of HCl [added] = mole of HA remaining. H<sub>2</sub>A = mole of HCL [added]

-No. of HCL [H<sub>2</sub>A] mole =  $0.2 \times 0.04 \text{ L} = 0.008$  mole -No. of HA mole originally =  $0.2 \times 0.1 \text{ L} = 0.02$  mole -No. of HA mole remaining = 0.02 - 0.008 = 0.012 mole

So, pH=pka1+log([remaining]/[added]) pH = 2.34 + log [0.012]/[0.008] pH = 2.52

#### [2] pH after addition of 30 ml of KOH?



NaOH (base)  $\rightarrow$  amino acid act as acid  $\rightarrow$  NH<sub>3</sub><sup>+</sup> to NH<sub>2</sub>

 $pH=pka2+log([A^{2-}]/[HA^{-}])$ 

HA<sup>-=</sup> Mole of HA [original] – mole of KOH [added] = mole of HA remaining. A<sup>2</sup>-= mole of KOH [added]

-No. of KOH [ $A^{2-}$ ] mole = 0.2 X 0.03 L = 0.006 mole -No. of HA mole originally = 0.2 X 0.1 L =0.02 mole -No. of HA mole remaining = 0.02 - 0.006 = 0.014 mole

So, pH=pka2+log([added]/[remaining]) pH = 9.69 + log [0.006] / [0.014] pH=9.32

## Preisticel Pert



- □ To study titration curves of amino acid.
- To use this curve to estimate the pKa values of the ionizable groups of the amino acid.
- □ To determine pI.
- □ To determine the buffering region.
- □ To understand the acid base behaviour of an amino acid.



a) You are provided with 10 ml of a 0.1M alanine solution, titrate it with 0.1M NaOH adding the base drop wise mixing, and recording the pH after each 0.5 ml NaOH added until you reach a pH=11.

Measured pH value	Amount of 0.1M NaOH added [ml]

b) Take another 10 ml of a 0.1M alanine solution, titrate it with 0.1 M HCL adding the acid drop wise mixing, and recording the pH after each 0.5 ml HCL added until you reach a pH=2.17.

Measured pH value	Amount of 0.1M HCl added [ml]



- □ Record the titration table and plot a curve of pH versus ml of titrant added.
- Calculate the pH of the alanine solution after the addition of 0 ml, 5ml, of 0.1M NaOH, and calculate pH after addition of 0.5 ml, 2ml of HCl.
- Determine the pKa of ionizable groups of amino acids.
- □ Compare your calculated pH values with those obtained from Curve.
- Determine the pI value from your result .

