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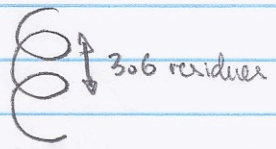
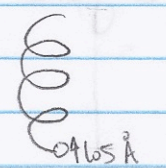
Problem Set 2

1. a.  3.6 residues

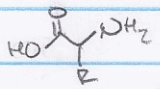
$\frac{15 \text{ residues}}{3.6}$

b.  1.5 Å

Each amino acid moves up 1.5 Å

$(15)(1.5) = 22.5$ Å

c. Q-E-A-N-I-K-Q-R-L-S-T-E-K-W



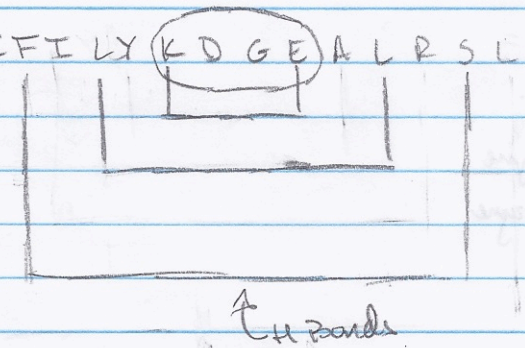
Each amino acid can donate and accept a hydrogen bond.
4 Amino acids at the ends can only donate or accept a hydrogen bond.

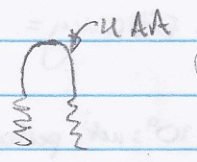
$\frac{(15 \times 2) - (2 \times 4)}{2} = \frac{22}{2} =$ **11 H Bonds**

2. a) Arginine & Lysine right next to each other
b) Glycine & Proline near each other
c) Lysine, Glutamic Acid, Arginine

- Glycine and proline not likely to form α-helix (Table 6.1)
- C) QKASVEMAURNSG will likely form an α-helix because the side chains of Lysine and Arginine are alternating. This allows both side chains to be on the inside of the α-helix

3. I F I L Y (K D G E) A L R S L





K-D-G-E will make the β-turn

b) D G
K ⟷ E

D —H-Bond→ C

Y A
L ⟷ L
I R
F ⟷ S
I L

Hydrogen bonds occur every other amino acid

4. $A + E \underset{K_{-1}}{\overset{K_1}{\rightleftharpoons}} A\text{-}E \overset{K_2}{\rightleftharpoons} E + B$ Look up in book for equation

a) $A + E \overset{K_{cat}}{\rightleftharpoons} A\text{-}E \rightleftharpoons E + B$

4 nM — 4 nM [E_T]

$[E_T] = 4$ nM

$v_{max} = 66 \frac{nM}{s}$

*K_{cat} stays constant

$v_{max} = K_{cat}[E_T] \rightarrow K_{cat} = \frac{v_{max}}{[E_T]}$ *Lowest units

b) $A + E \underset{K_{-1}}{\overset{K_1}{\rightleftharpoons}} A\text{-}E \overset{K_2}{\rightleftharpoons} E + B$

$K_M = \frac{K_{-1} + K_2}{K_1}$

*K_M = affinity for enzyme of substrate

*If K_M is small, then high affinity for substrate

$v = \frac{v_{max}[S]}{K_M + [S]}$

$K_M = \frac{v_{max}[S]}{v} - [S]$

c) Catalytic Efficiency = $\frac{K_{cat}}{K_M}$ =

$< 10^8 - 10^9$: not perfect enzyme

if between 10^8-10^9: perfect enzyme

*H_2O slows down enzymes

5. a. $y = v \qquad x = \left(\frac{v}{[S]}\right)$

$$v = \frac{v_{max}[S]}{K_m + [S]}$$

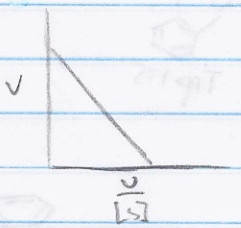
$$\left(\frac{1}{v} = \frac{K_m + [S]}{v_{max}[S]}\right) v_{max}$$

$$\frac{v_{max}}{v} = \frac{K_m + [S]}{[S]} \rightarrow \left(\frac{v_{max}}{v} = \frac{K_m}{[S]} + 1\right) v$$

$$\downarrow$$

$$v_{max} = \frac{K_m v}{[S]} + v$$

$$\boxed{v = -K_m\left(\frac{v}{[S]}\right) + v_{max}}$$



slope $= -K_m$

y-intercept $= v_{max}$

x-intercept $= \frac{v_{max}}{K_m}$

6. a. $\frac{1}{v} = \frac{K_m}{v_{max}}\left(\frac{1}{[S]}\right) + \frac{1}{v_{max}}$ ← spinagosine

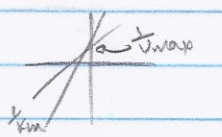
x	v
$\frac{1}{\#}$	$\frac{1}{\#}$

*Plot in excel

y-intercept $= \frac{1}{v_{max}}$

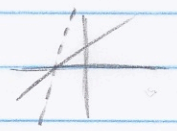
slope $= \frac{K_m}{v_{max}}$

b. competitive inhibitor *answer — noncompetitive inhibitor



v_{max} stays same

K_m changes

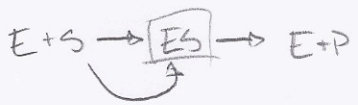


v_{max} changes

K_m stays same

1) line test shows competitive inhibitor because y-intercepts are fairly similar

2) Because spinagosine has a stereoisomer, it will have a competitive inhibitor



7. Low [S] | High [S]

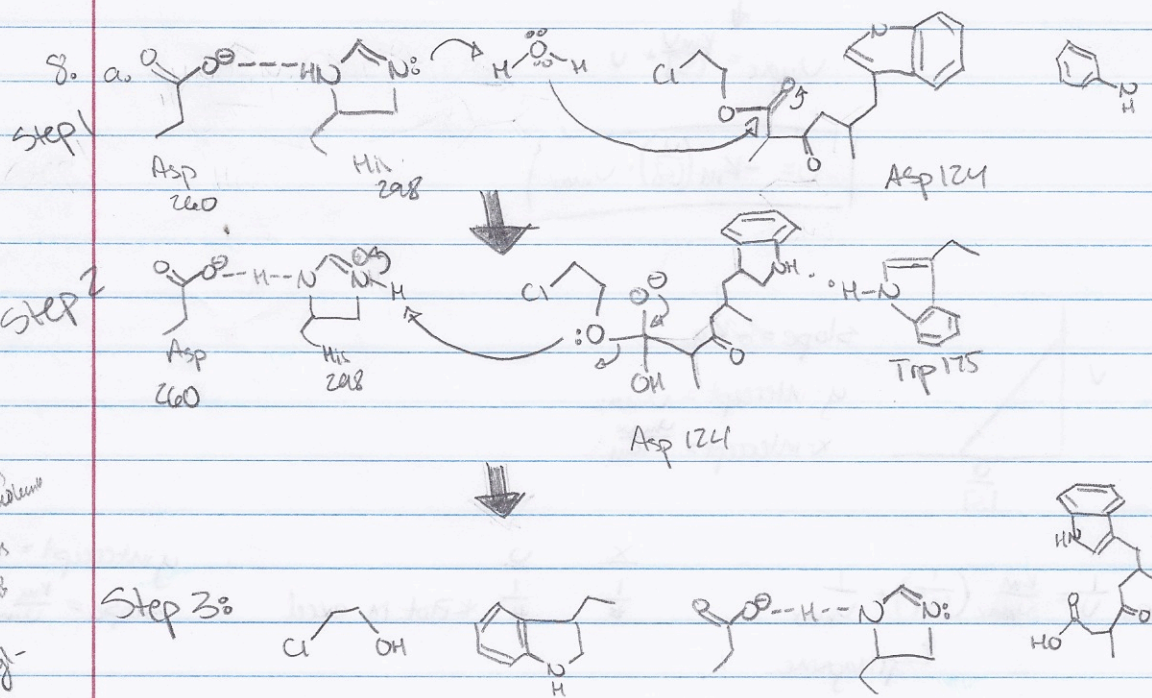
No inhibitor: $v = .0364$ | No inhibitor: $v = .2$

Inhibitor: $v = .0308$ | Inhibitor: $v = .1$

Low [S]: $\frac{\text{Inhibitor}}{\text{No Inhibitor}} = \frac{.0308}{.0364} = .84$ Uncompetitive Inhibitor

High [S]: $\frac{\text{Inhibitor}}{\text{No Inhibitor}} = \frac{.1}{.2} = .5$

8. a.



5) accept H+ from attacking H2O molecule

6) His acts as A-B

chloroethyl-enzyme-ester-intermediate