

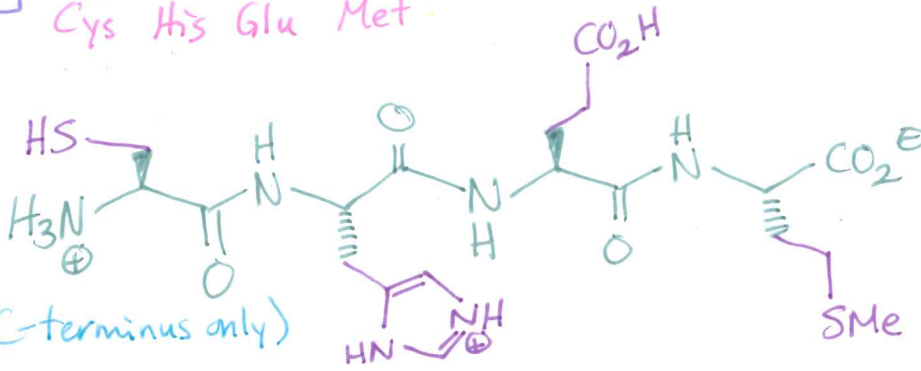
Lecture 6 HW Key

Uo
HW Key
PI 0

26.38 (a) C-H-E-M
Cys His Glu Met

pH 3

past pK_a
Met
(effects C-terminus only)

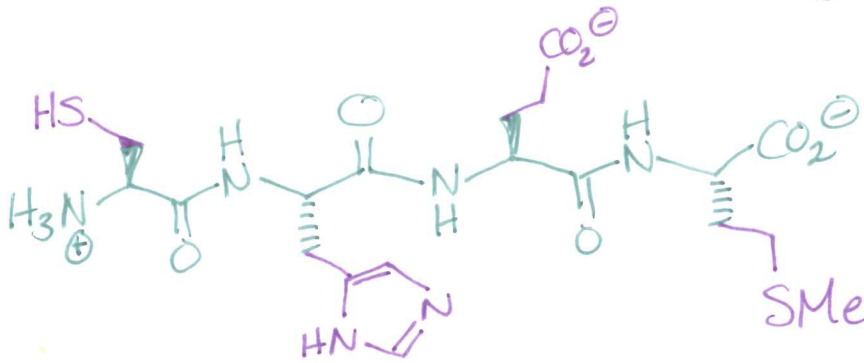


net charge
+1

in case you
were curious,
and you should
be!

pH 7.4

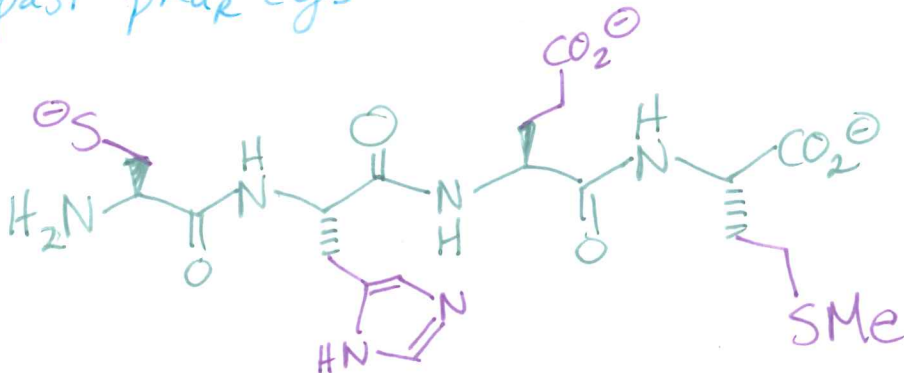
past pK_a Glu
 pK_a His



net charge
-1

pH 10


past pK_a (effects N-terminus only; amide N-H's not acidic)
also past pK_a Cys



net charge
-3

26.44 Where is each aa found inside vs. outside of protein?

L6
Hw Key
p2 d

H_2O  H_2O polar/charged aa side chains found on outside of protein (hydrophilic)

non-polar/noncharged aa side chains buried inside protein (hydrophobic)

Phe ^(c) Val ^(a) - neutral side chain (hydrocarbon) always inside protein, never charged

(b) Asp

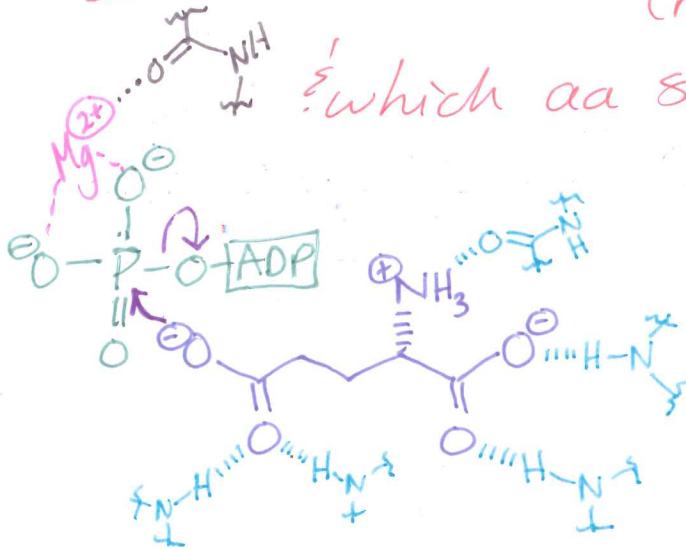
pH 3
side chain polar, not charged likely on outside of protein
could be inside

pH 7.4 side chain deprotonated (charged) more likely on outside of protein

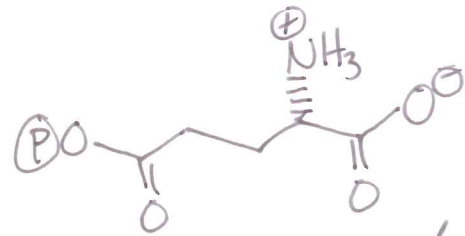
(c) Lys - side chain protonated (charged) @ pH 3, 7.4, 10 found on outside of protein

Enzyme Active Site Design

Consider: how substrates & co-factors are held in place (reagents)

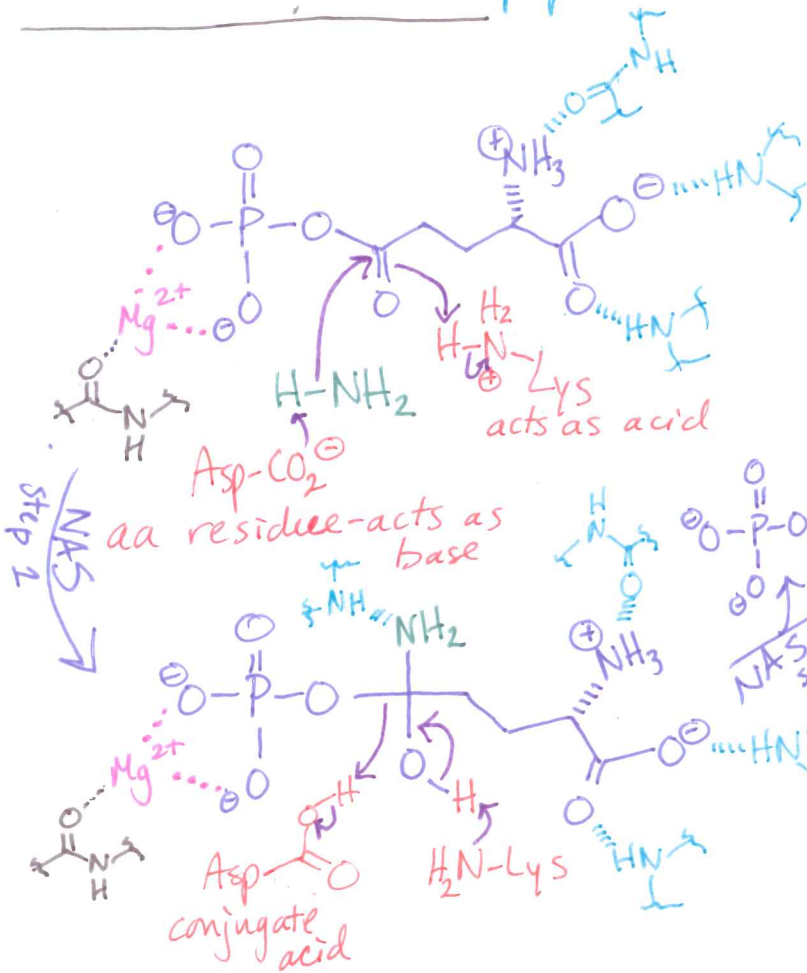


ATP → ATP



no need to show stabilization after rxn, unless it goes through another step...

* H bonding to peptide backbone



* re-use aa's when possible *

Note: arrow-pushing is same as in L5 HW!
Difference is defining H⁺ & :B as aa residues & adding stabilizing factors (H-bonding or metal)