(9) **Today**

Sections 2.3 - 2.4.9: Buffers and Solubility In the Aqueous World

We will refer back to 2.4.10 and 2.4.11 when looking at proteins

Next Class (10)

Chap 3: Amino Acids, Peptides, and Proteins

(11) **Second Class from Today**

Chap 3: Amino Acids, Peptides, and Proteins

Third Class from Today (12)

Chap 3: Amino Acids, Peptides, and Proteins

Biochem Test 1 is being rescheduled to Wed. Feb 26

Buffers: Phosphate

too acidic Section 2.3.2

$H_3PO_4(aq) + H_2O(l) \rightleftharpoons H_2PO_4^-(aq) + H_3O^+(aq)$ pK$_a$ = 2.14 $[A^-] = [HA]$

$H_2PO_4^-(aq) + H_2O(l) \rightleftharpoons HPO_4^{2-}(aq) + H_3O^+(aq)$ pK$_a$ = 7.20 Goldilocks

$HPO_4^{2-}(aq) + H_2O(l) \rightleftharpoons PO_4^{3-}(aq) + H_3O^+(aq)$ pK$_a$ = 12.37 too basic

will this acid-base equilibrium play an important role in maintaining physiological pH at around 7.4? no the require $[A^-]$ to $[HA]$ ratio is too far off

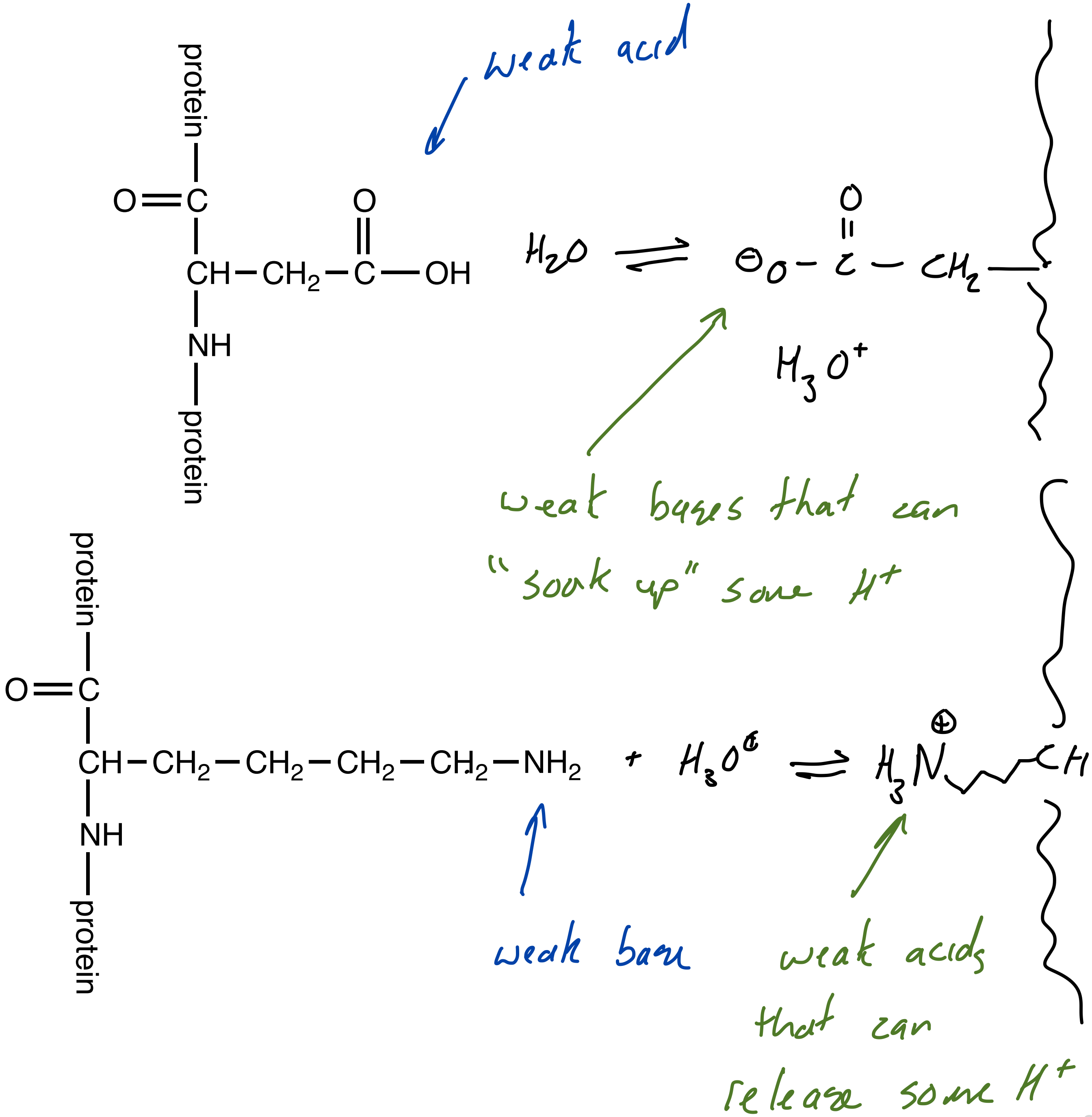
Similarly this one is too far off too.

$H_2PO_4^- + H_2O \rightleftharpoons HPO_4^{2-} + H_3O^+$ is the system that would be best

phosphorylated biomolecules will do the same thing

Buffers: Proteins

weak acids + bases in side chains of amino acids can absorb + release H^+



Buffers

Summary

$[A^-] = [HA]$

$[A^-]/[HA] = 1$

Buffers are best at buffering when [A⁻]/[HA], when pH = pK$_a$

Buffers have to be chosen so that they do not interfere with the system of interest

Buffers have to be made so that they have adequate capacity and the proper osmolarity

enough

A^- + HA to minimize change in pH

too concentrated (more concentrat then inside of cell)

H_2O drawn out

Buffers can made made by

combining solution of weak acid and its conjugate base until the desired pH is achieved

adding a base like NaOH to a solution of a weak acid to generate the weak base

adding a acid like HCl to a solution containing a weak base to generate the weak acid

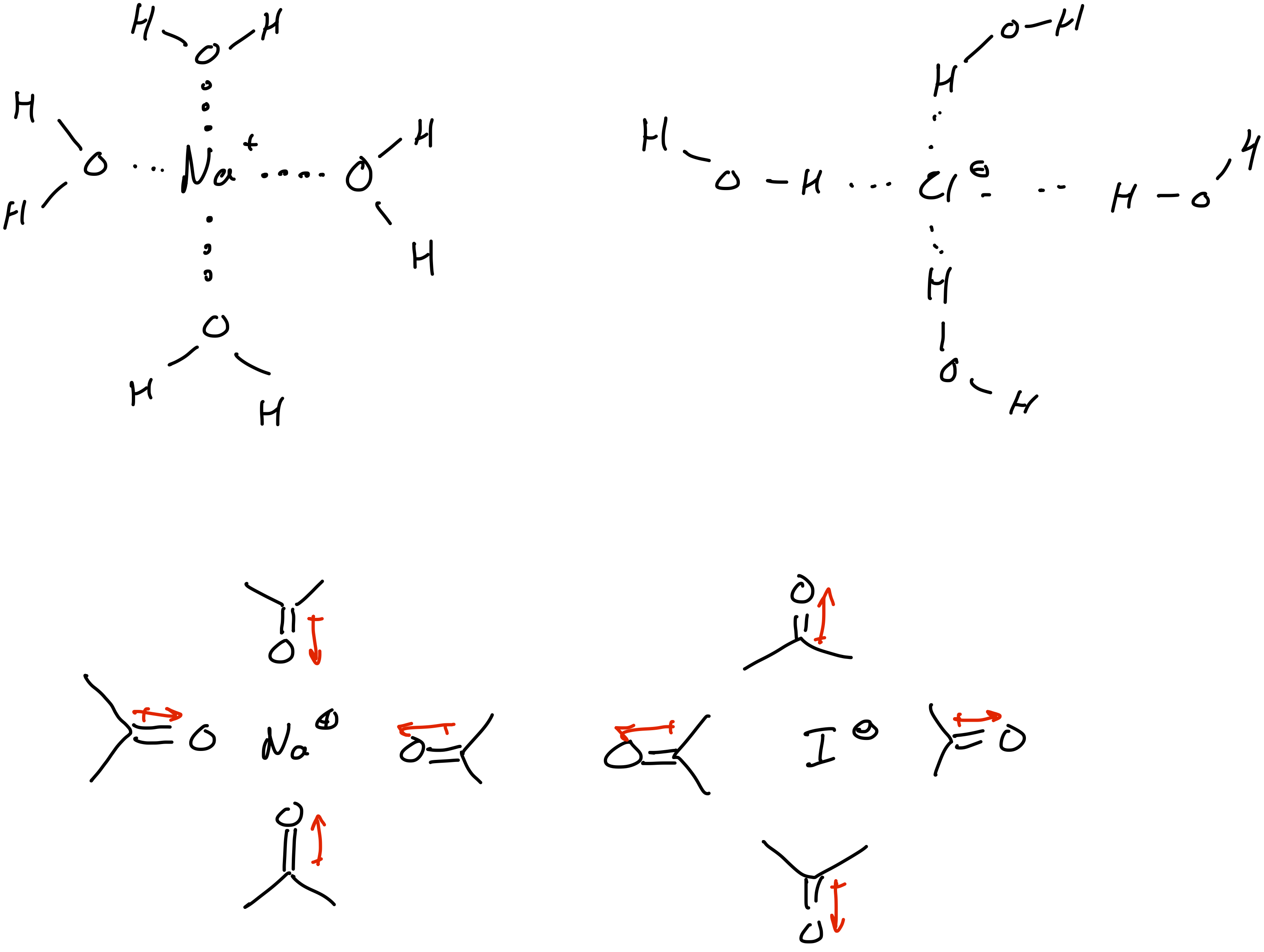
cannot make a buffer with only strong acids + bases

too low a concentration outside cell... H_2O rushes in ... bursts

Noncovalent interactions in depth

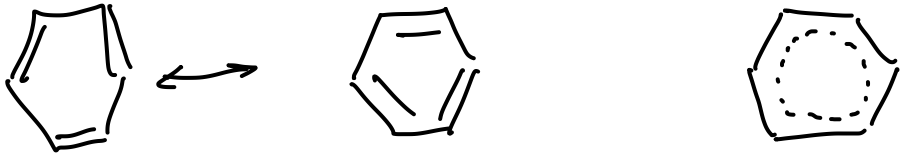
Section 2.41. - 2.4.6

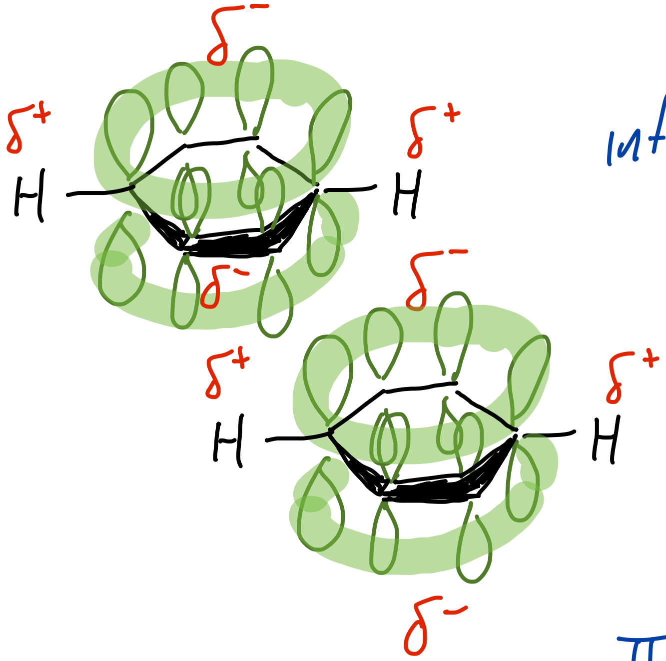
Ionic interactions ✓, H-Bonding ✓, Dipole-Dipole ✓, Ion-Dipole, LDF ✓



Noncovalent interactions in depth: π stacking

aromatic rings stacked one atop the other



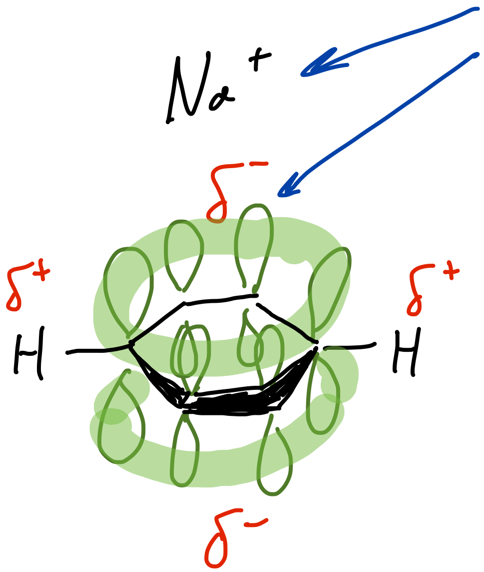


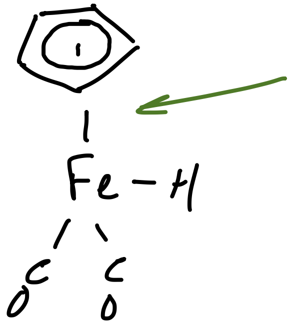
interaction between H of one aromatic ring with the π system of another aromatic ring results in attraction between two rings

π s

Noncovalent interactions in depth: cation π interactions

⊕ attracted to ⊖

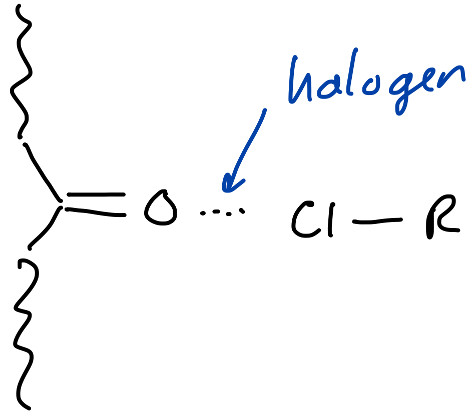


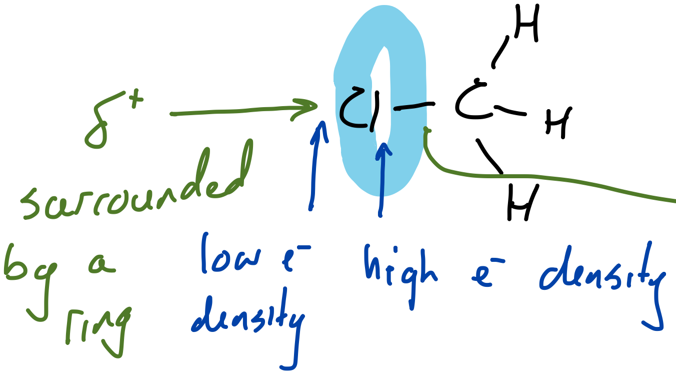


π intraction with a metal forms a covalent bond in this organometallic compond

Noncovalent interactions in depth: The Halogen Bond and the σ-hole

halogen bond between e⁻ rich O and the halogen





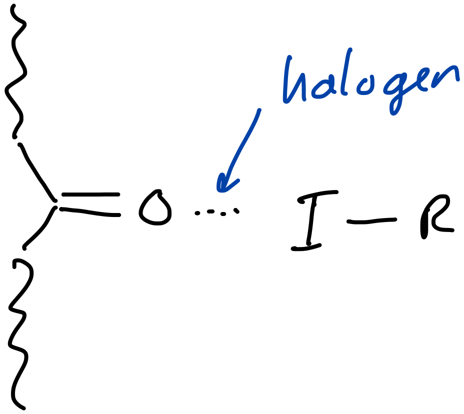
hybridization Model

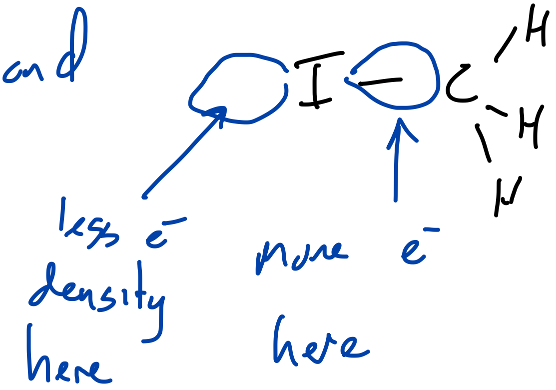
e⁻ in sp³ hybrid are on this side of the Cl

MO model

far side of p orbital used to make σ bond is depleted in e⁻ density

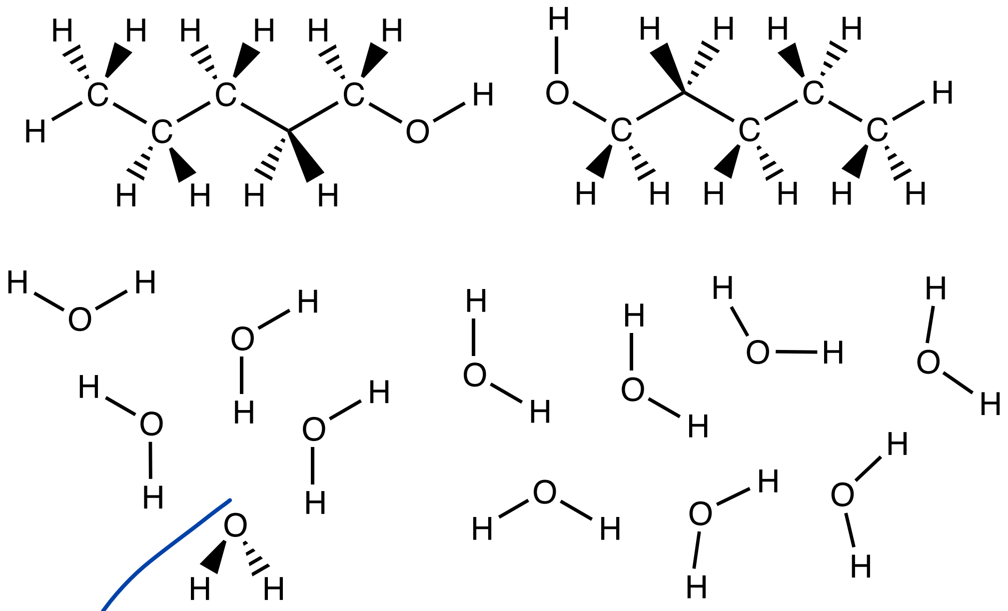
halogen bond

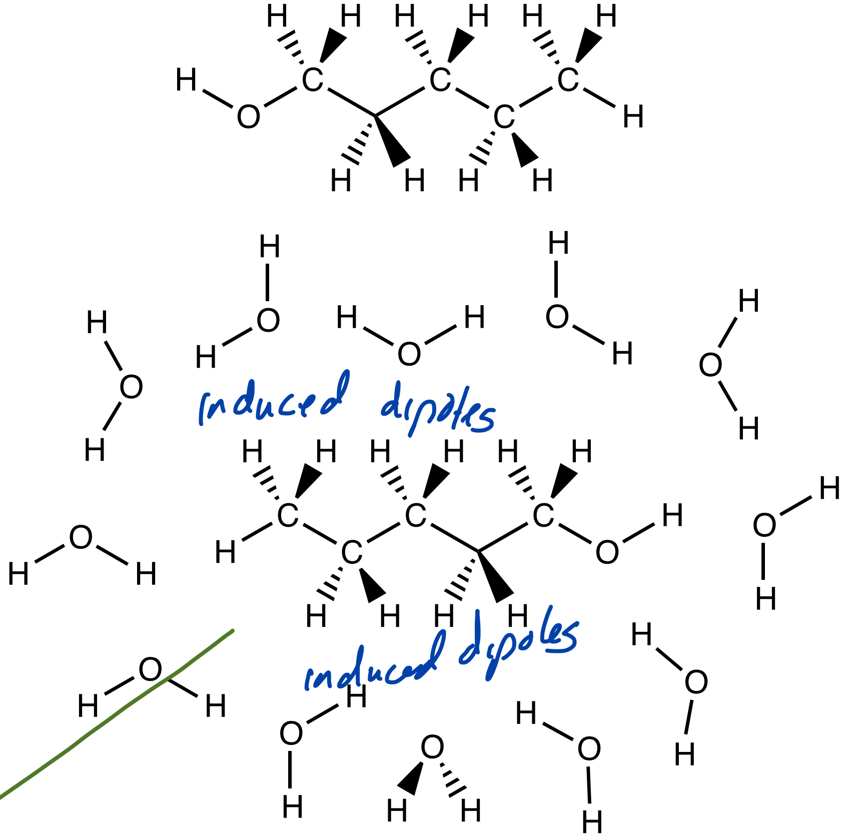




the "σ-hole" is an area of lower e⁻ density opposite the halogen to C bond. This slightly positive area will be attracted to e⁻ rich areas of other molecules

Noncovalent interactions in depth: The Hydrophobic Effect





separation of hydrophobic molecules from water is driven by entropy.

H_2O's can H-bond in any direction

This hole means the H_2O's have to become more ordered to form the same # H-bond interactions entropy would be lost

From an enthalpy point of view induced dipoles between H_2O +  are favorable