EPFL

Master in Electrical and Electronics Engineering

EE-517: Bio-Nano-Chip Design

Lecture #6

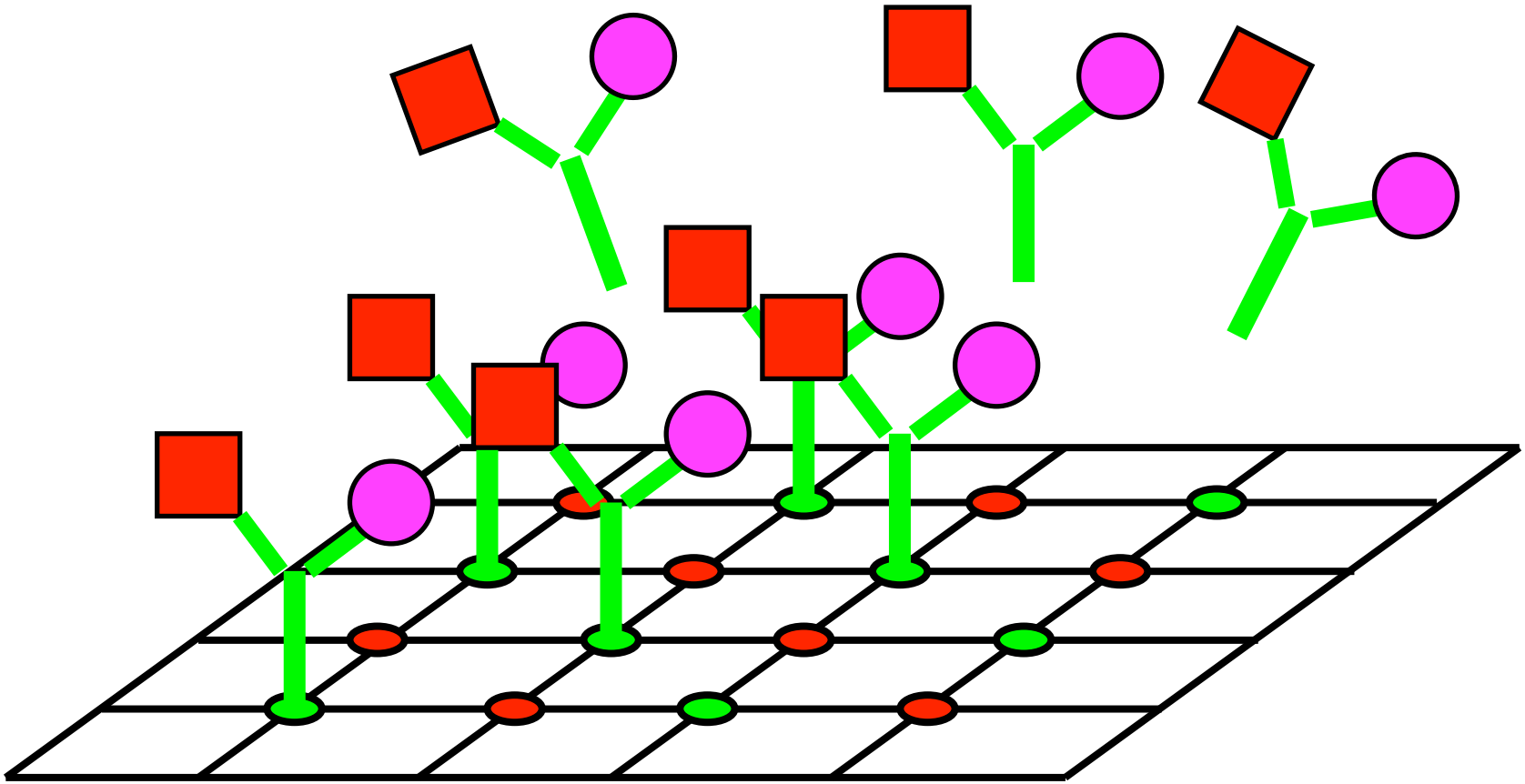
Probes immobilisation

Lecture Outline

(Book Bio/CMOS: Chapter' paragraphs §5.1.1-5)

- Different immobilization methods
- Langmuir Model
- Kisliuk Model
- Steric Hindrance Model
- Spreading Model

Self-assembly on a surface



Absorption methods and mechanisms

Different immobilization methods

- Drop casting
- Covalent bonding:
  peptide bond
- Covalent bonding:
  thiol-groups
- Covalent bonding:
  silane-groups

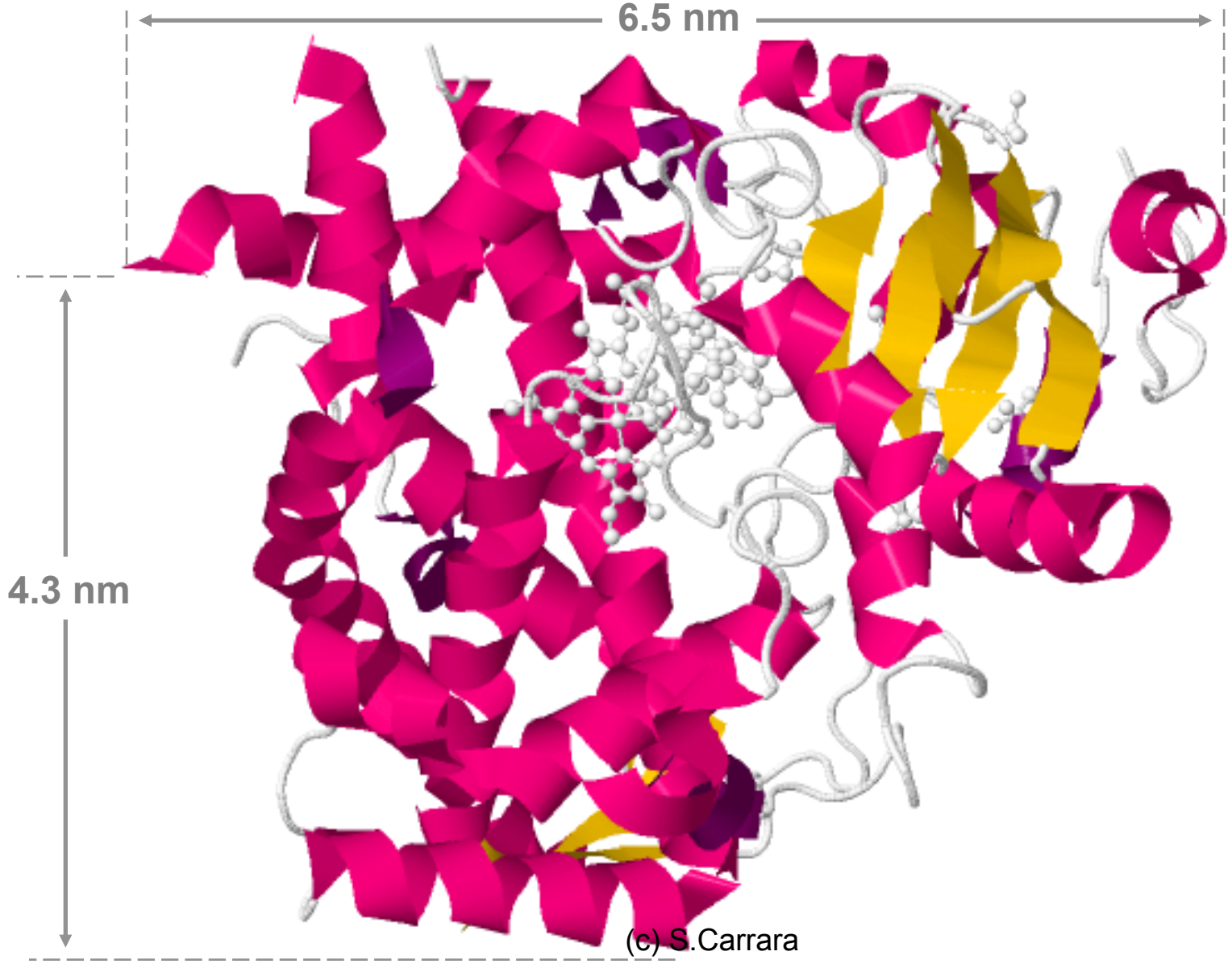
Proteins drop cast onto hydrophobic surfaces

$$\Delta H_{\Phi} = \alpha A_{contact}$$

$$\alpha = -104.5 \frac{kJ}{mol\, nm^2}$$

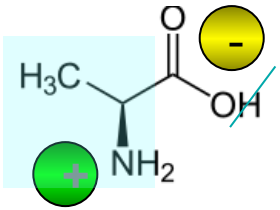
The hydrophobic forces are of the same intensity of the usual ones in Antigen/Antibody interactions

Cytochromes P450

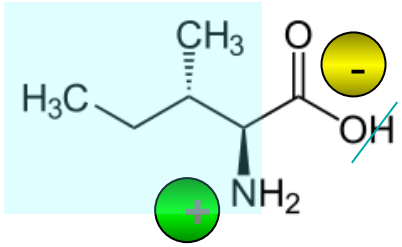


Hydrophobic AA

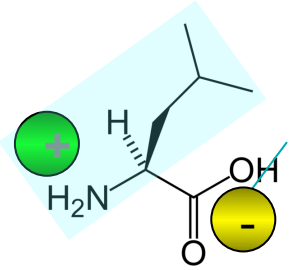
Hydrophobic Side Chains



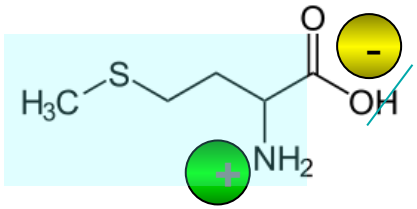
Alanine



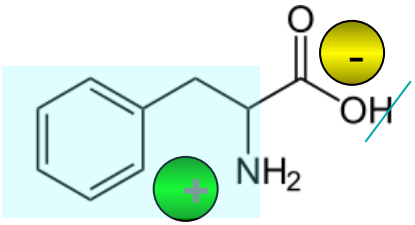
Isoleucine



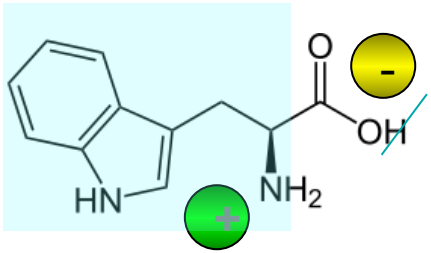
Leucine



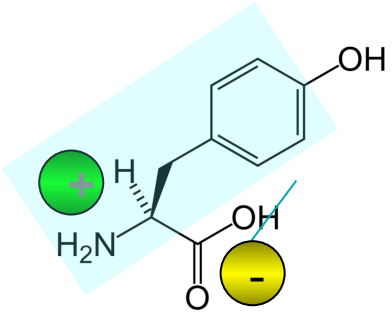
Methionine



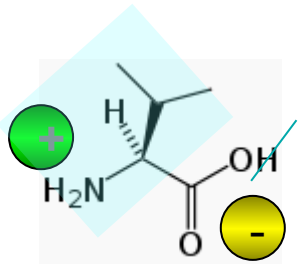
Phenylalanine



Tryptophan

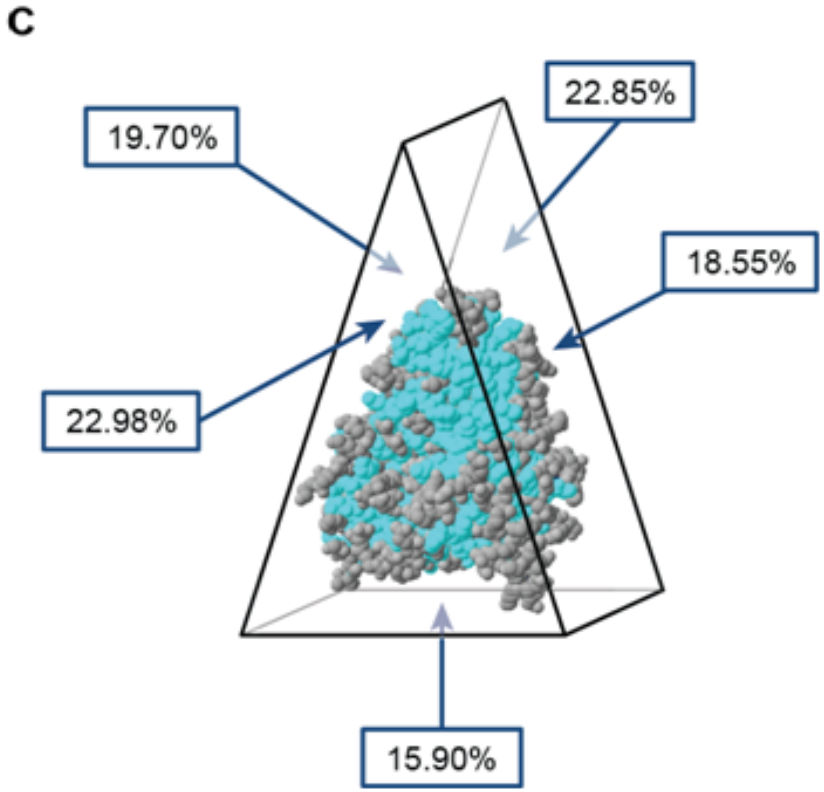


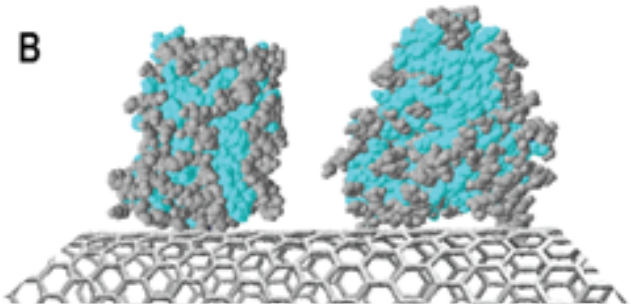
Tyrosine



Valine

Hydrophobic Amino Acids anchor proteins onto carbon surfaces





C - percentage of hydrophobic residues in the different cytochrome' surfaces

B – The cytochromes anchored onto a carbon surface

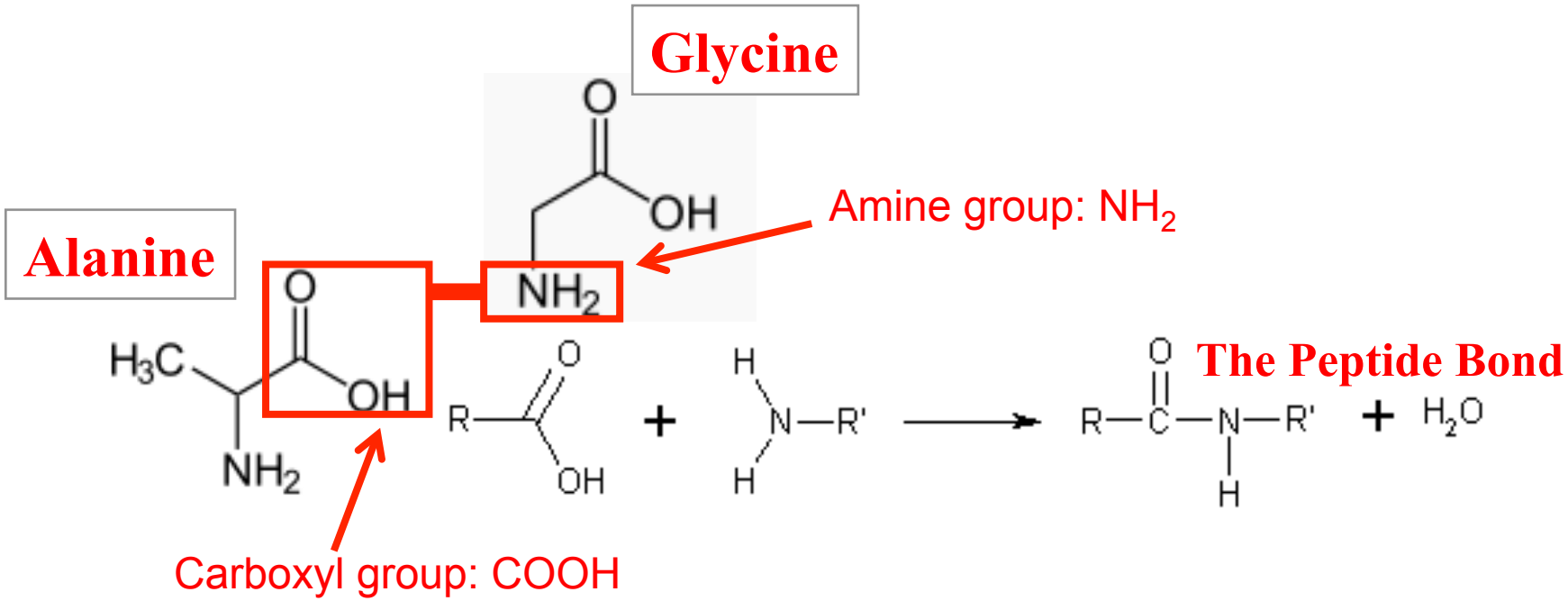
The percentage of hydrophobic residues at the surface of a cytochrome P450

P450 onto carbon surfaces

Complex	**Area [Å^2]**	**Enthalpy [-kJ/mol]**
Ab/Ag	150-690	16-74
P450/CNT	272-378	28-40

The hydrophobic forces are of the same intensity of the usual ones in Antigen/Antibody interactions

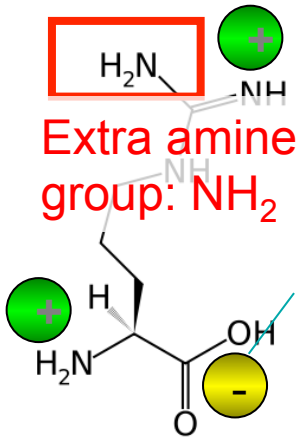
The Peptide Bond



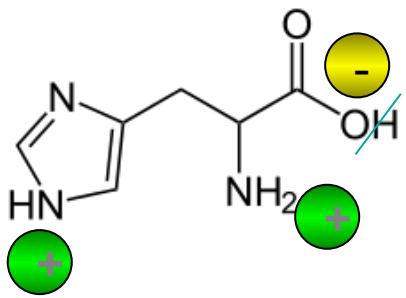
The same mechanism used to form peptides may be used to covalently immobilize probes on surfaces

Charged AA

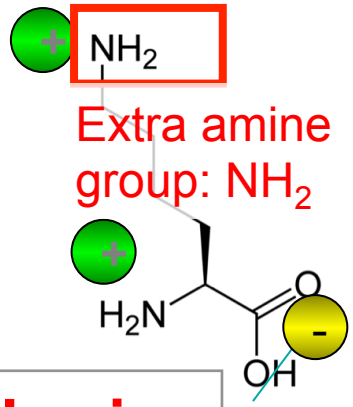
Positively Charged



Arginine

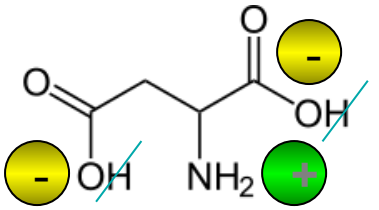


Histidine

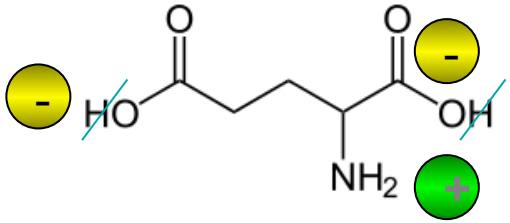


Lysine

Neg. Charged

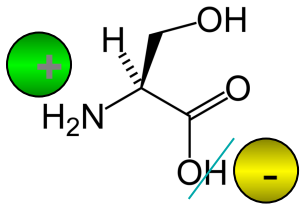


Aspartic Acid

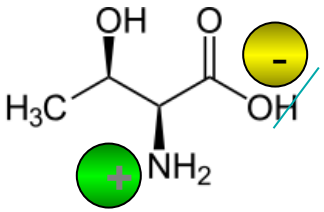


Glutamic Acid

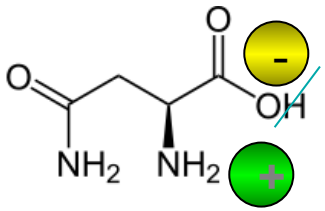
Polar Uncharged



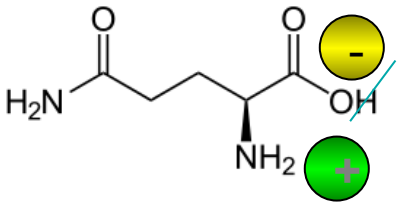
Serine



Threonine

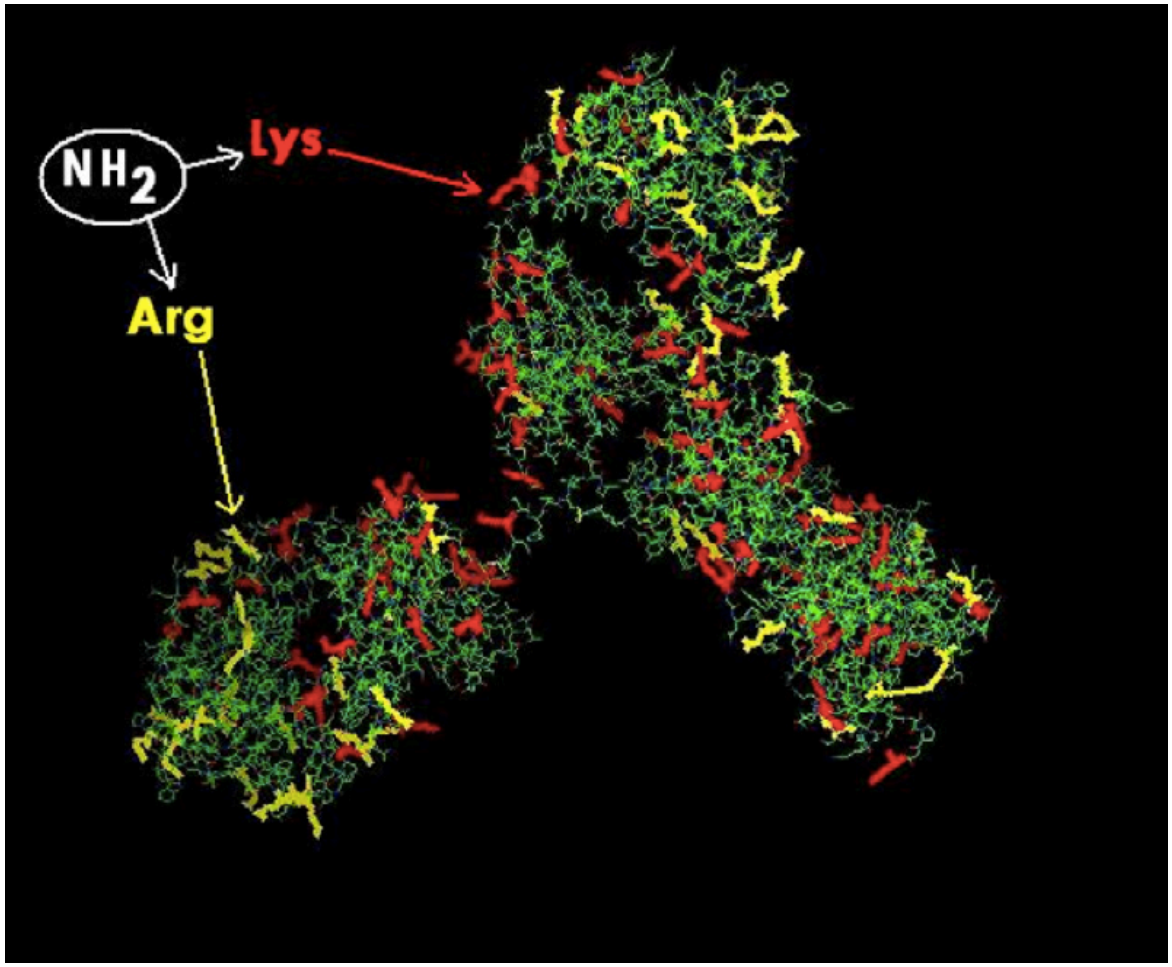


Aspargine



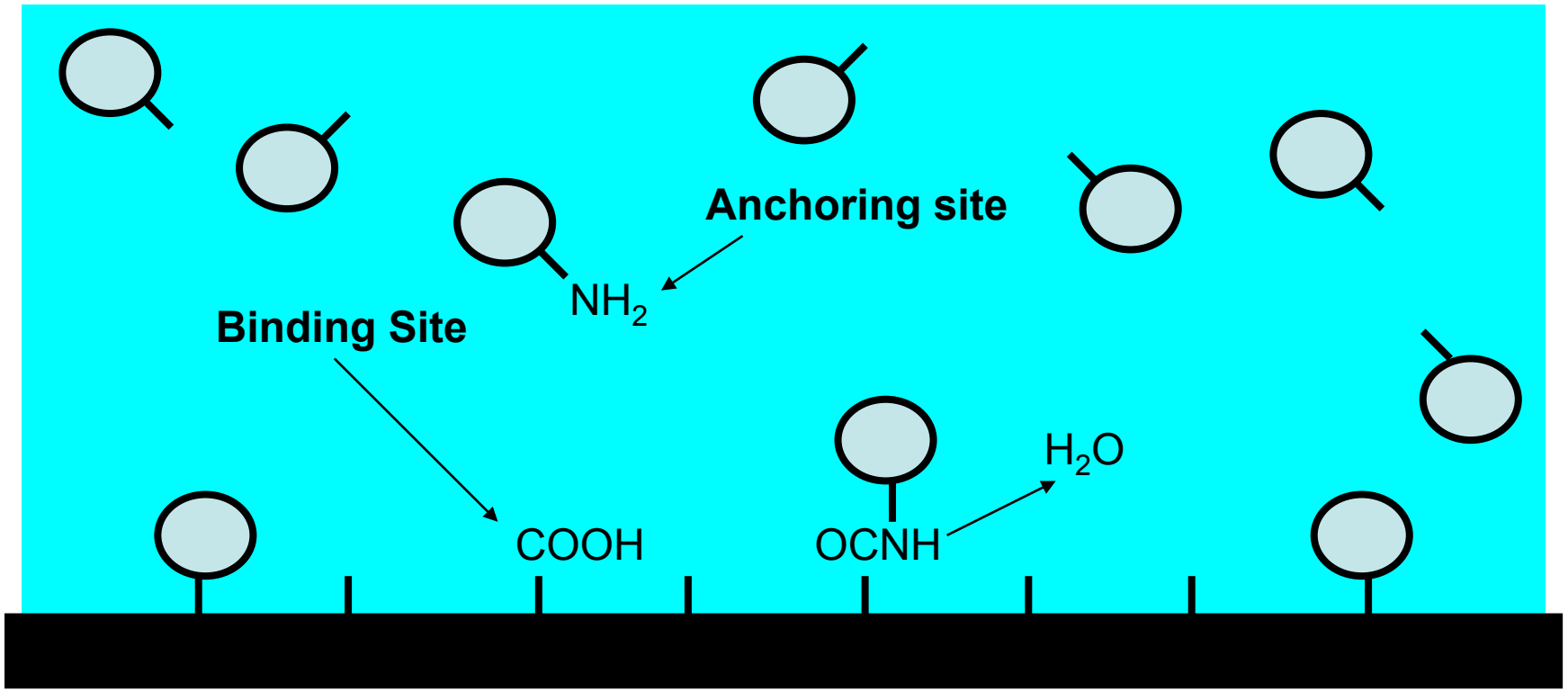
Glutamine

Residues with Amine group



Location of Arginines and Lysines in an antibody

Peptide bond on carbon surface



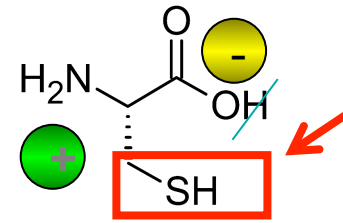
How to obtain COOH groups

- Strong bases (e.g., NaOH) or acids (e.g., H_2SO_4)
- Energy to break the C-C structure (e.g., electrochemical potentials, plasma irradiation, heating, etc…)

Several treatments are possible to create the right functional groups on the sensing surface

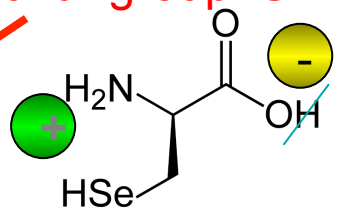
Neutral AA

Special Cases

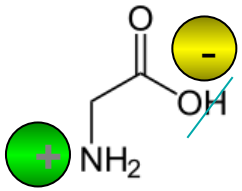


Sulfur group: SH

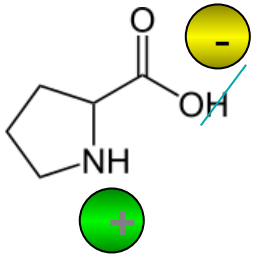
Cysteine



Selenocysteine

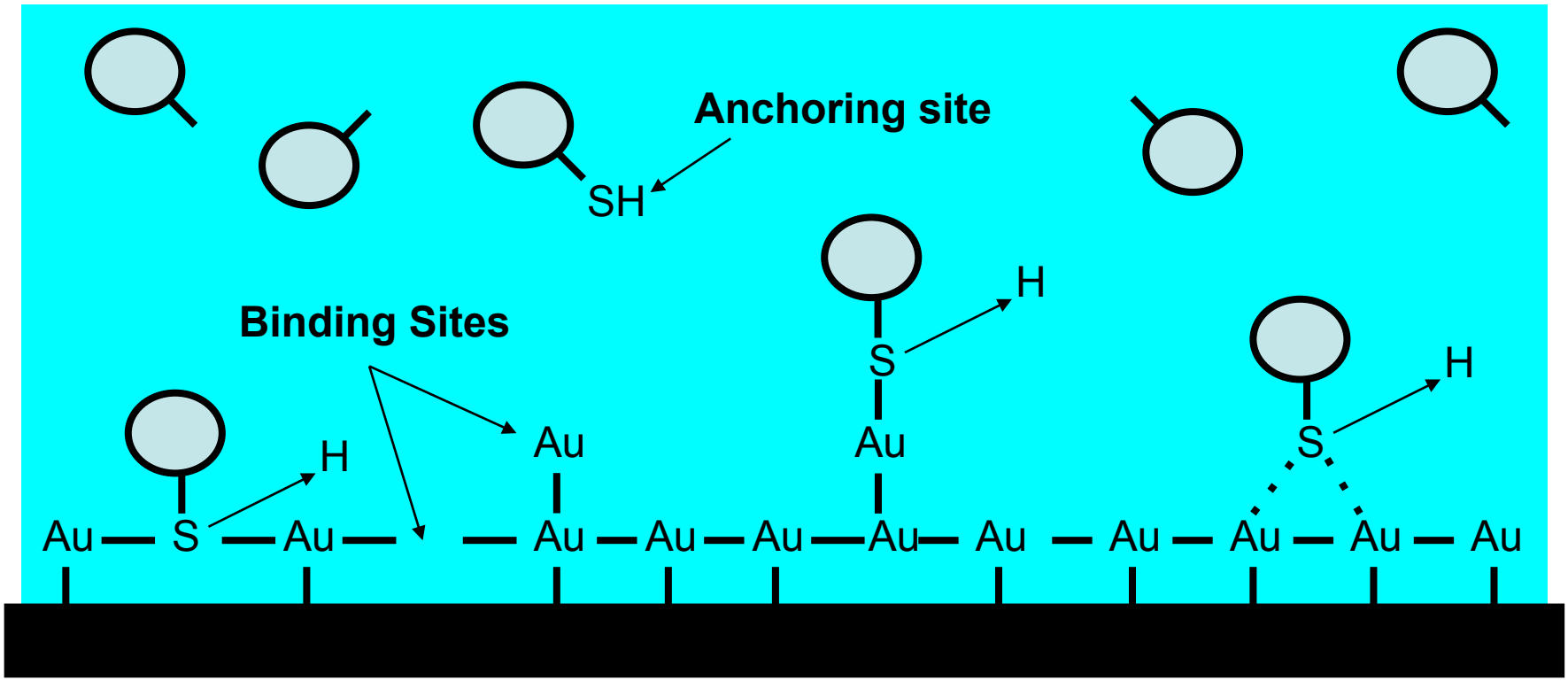


Glycine



Proline

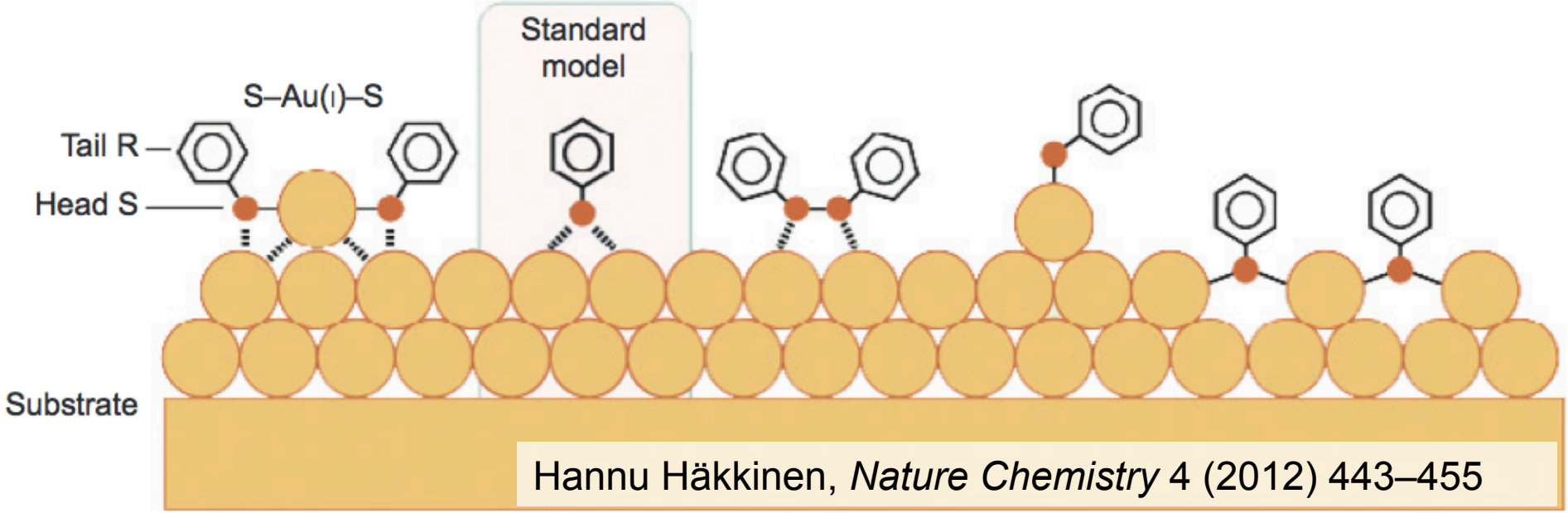
Thiol bond on gold surface



Thiols bond

- Thiols are frequently used on metallic substrates because of the strong affinity of sulfur for noble metals (e.g., for our aim, platinum, gold, silver, copper, …)
- The sulfur gold interaction provides a semi-covalent bond with a strength in the order of **100kJ/mol** (covalent O-H bond in water molecules is about 460 kJ/mol)

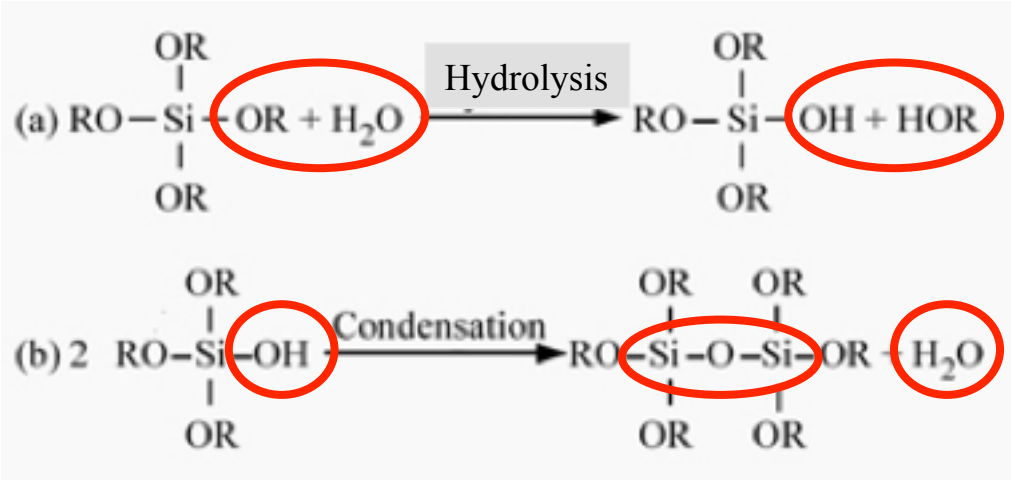
Thiol bond models



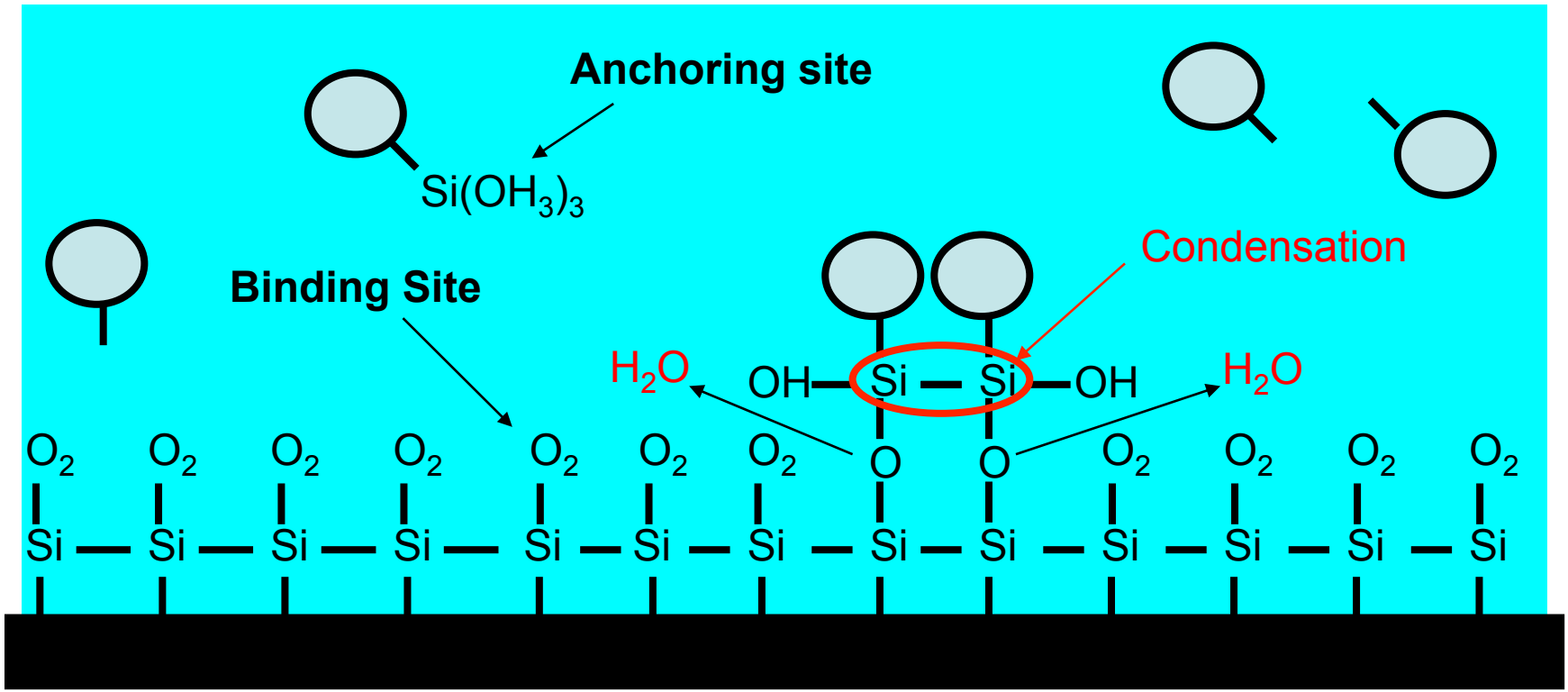
The ‘standard model’ foresees a monothiolate binding at atop, while new experimental evidence shows other key structural with complexes where the bridging gold atom is in a formal oxidation state of +1

Silanes bond

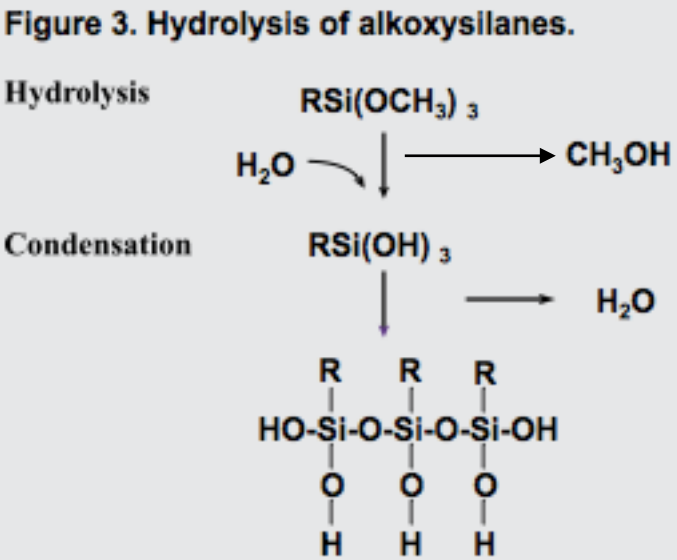
Silanes usually bond well to most inorganic silicon substrates. Typically, the alkoxy groups on silicon hydrolyze to silanols, either through the addition of water or from residual water on the inorganic surface

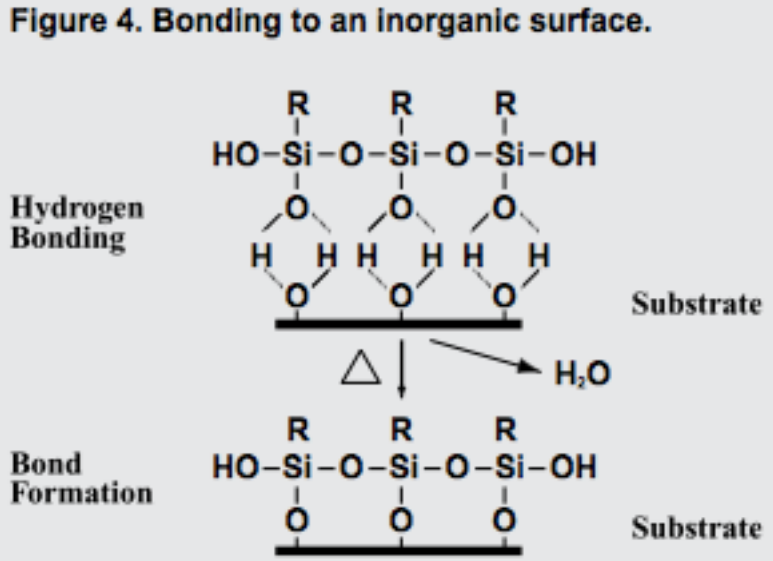


Silanes bond on silicon surface



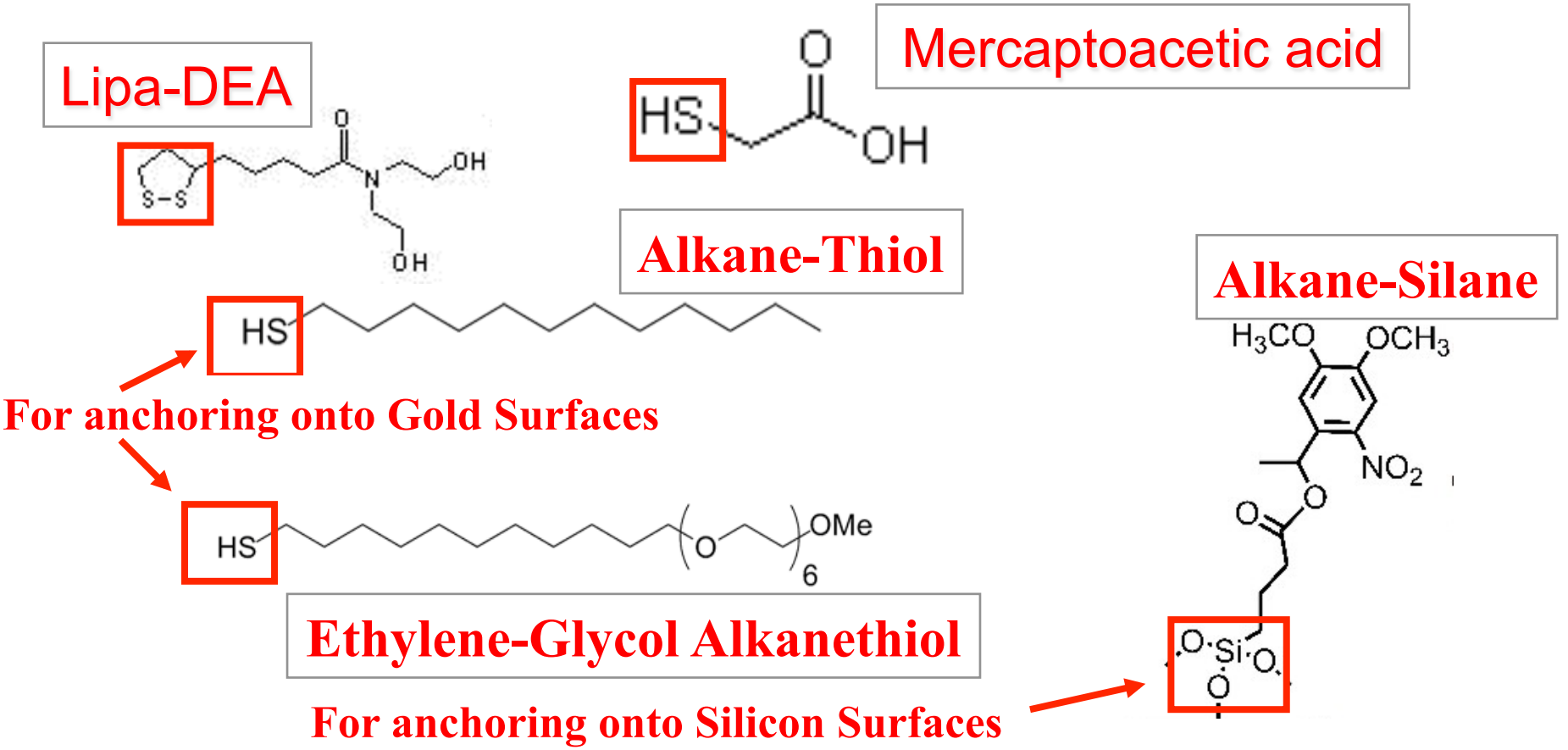
Silanes bond





The formation of silanes film is due to different mechanisms: condensation and hydrolysis

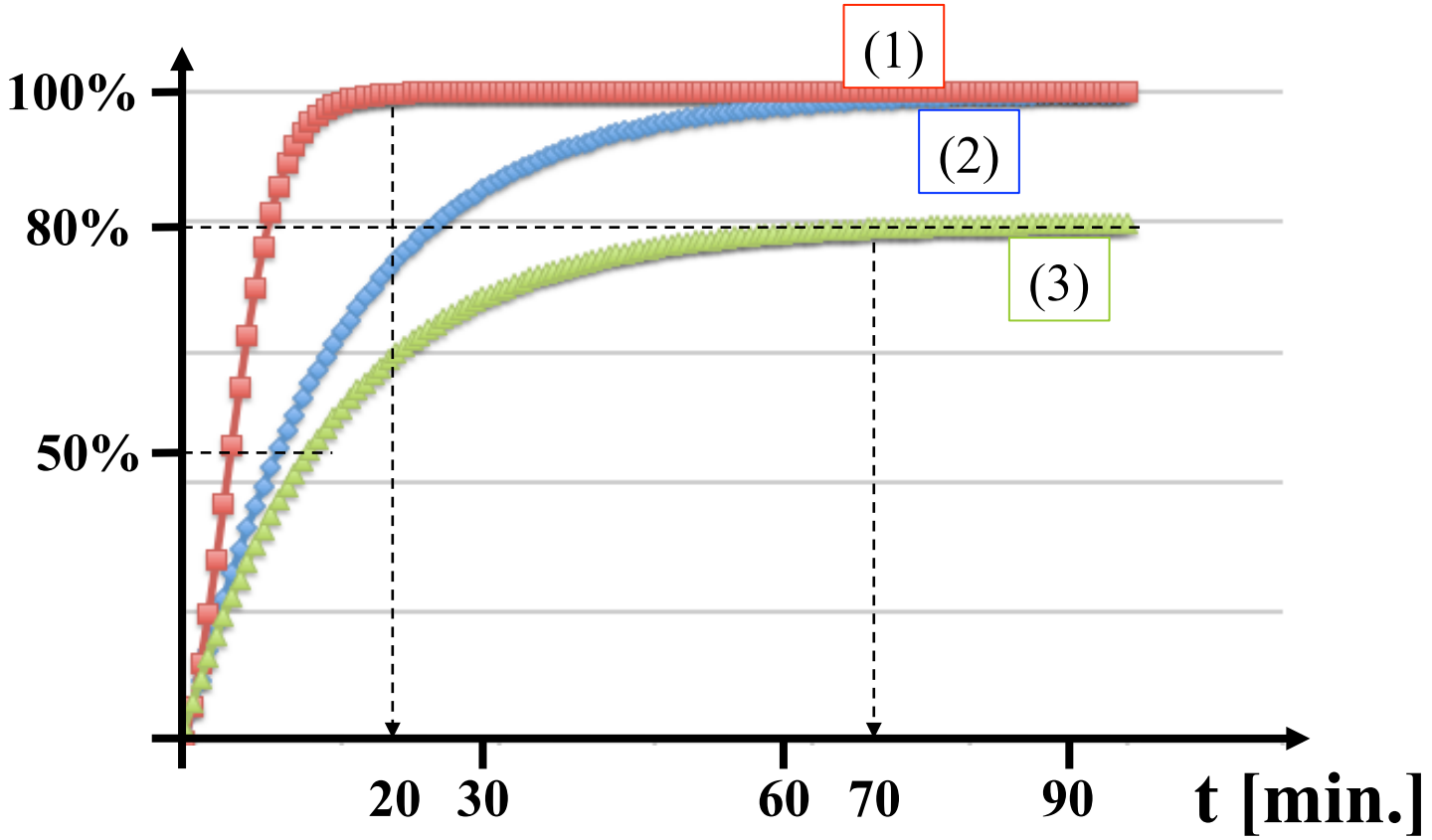
Molecules with alkyl chains



Aliphatic chains may provide thiols or silanes for several aims, including linkers to proteins

Different molecules result in different Yields onto the same surface

Yield = Percentage of covered surface



How to characterize the Probes Immobilization?

What are the mechanisms of self-assembly?

How to monitor the self-assembly process?

How to check the film quality?

Adsorption kinetic models

1. Langmuir Model
2. Kisliuk Model
3. Steric Hindrance Model
4. Spreading Model

The Langmuir Model

Ideal Gas Adsorption.

Four Assumptions:

- The Surface of adsorbent is uniform
- Adsorbed molecules do not interact
- All adsorption occur with the same mechanism
- Only a monolayer is obtained at the maximum adsorption

The Langmuir Model

A molecule L is adsorbed in quantity A onto a surface with an amount BS of free binding sites

$$L + BS_S \Leftrightarrow A$$

$$R_A = k_A p[BS_{free}]$$

$$R_D = k_D[A]$$

$$Equilibrium \rightarrow R_A = R_D \rightarrow K = \frac{k_A}{k_D} = \frac{[A]}{p[BS_{free}]}$$

The Langmuir Model

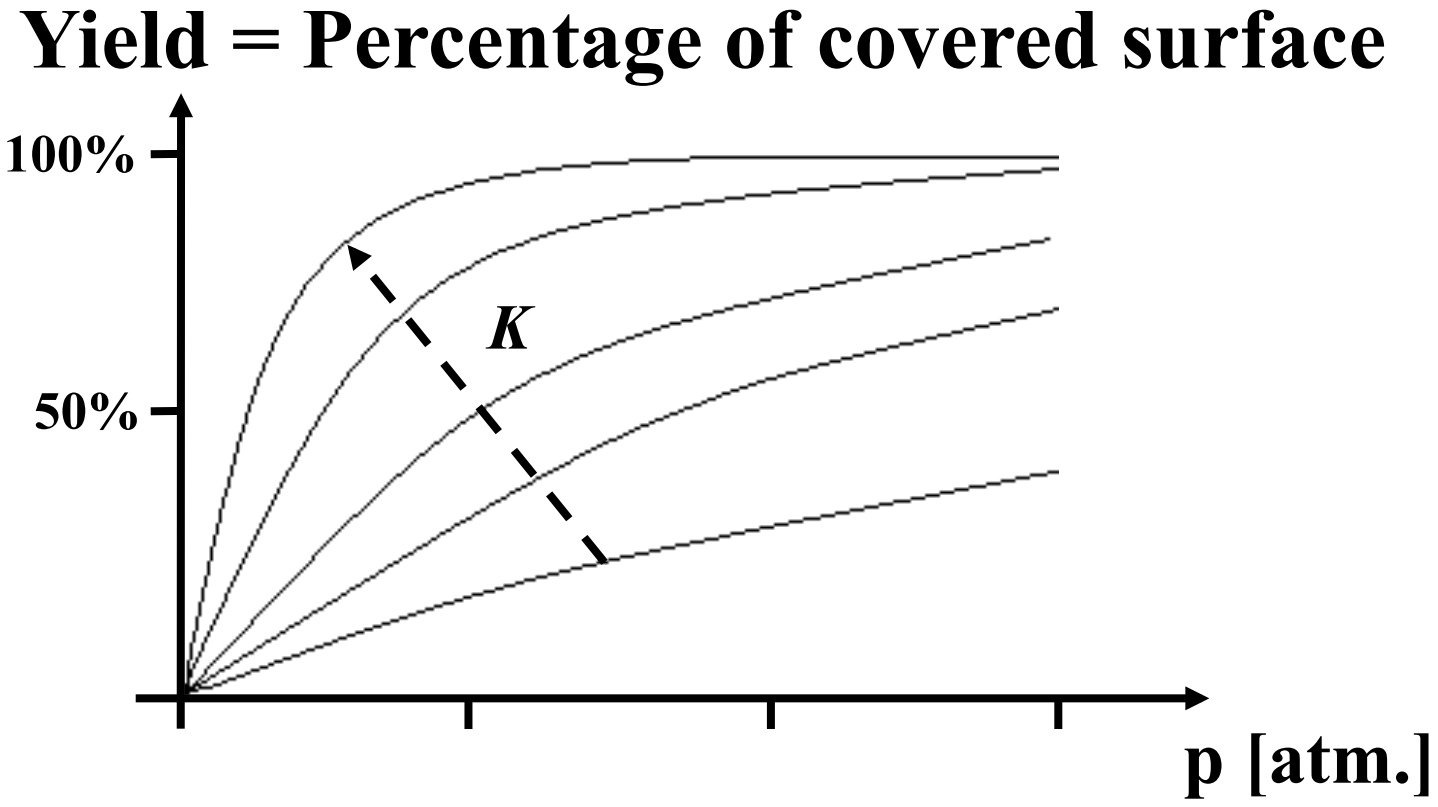
A molecule L is adsorbed in quantity A onto a surface with an amount BS of free binding sites

$$[BS_0] = [BS_{free}] + [A] = \frac{[A]}{pK} + [A] = \frac{1 + pK}{pK}[A]$$

$$Y = \frac{[A]}{[BS_0]} = \frac{pK}{1 + pK}$$

The Yield

The Yield in Langmuir Model



The Langmuir Model

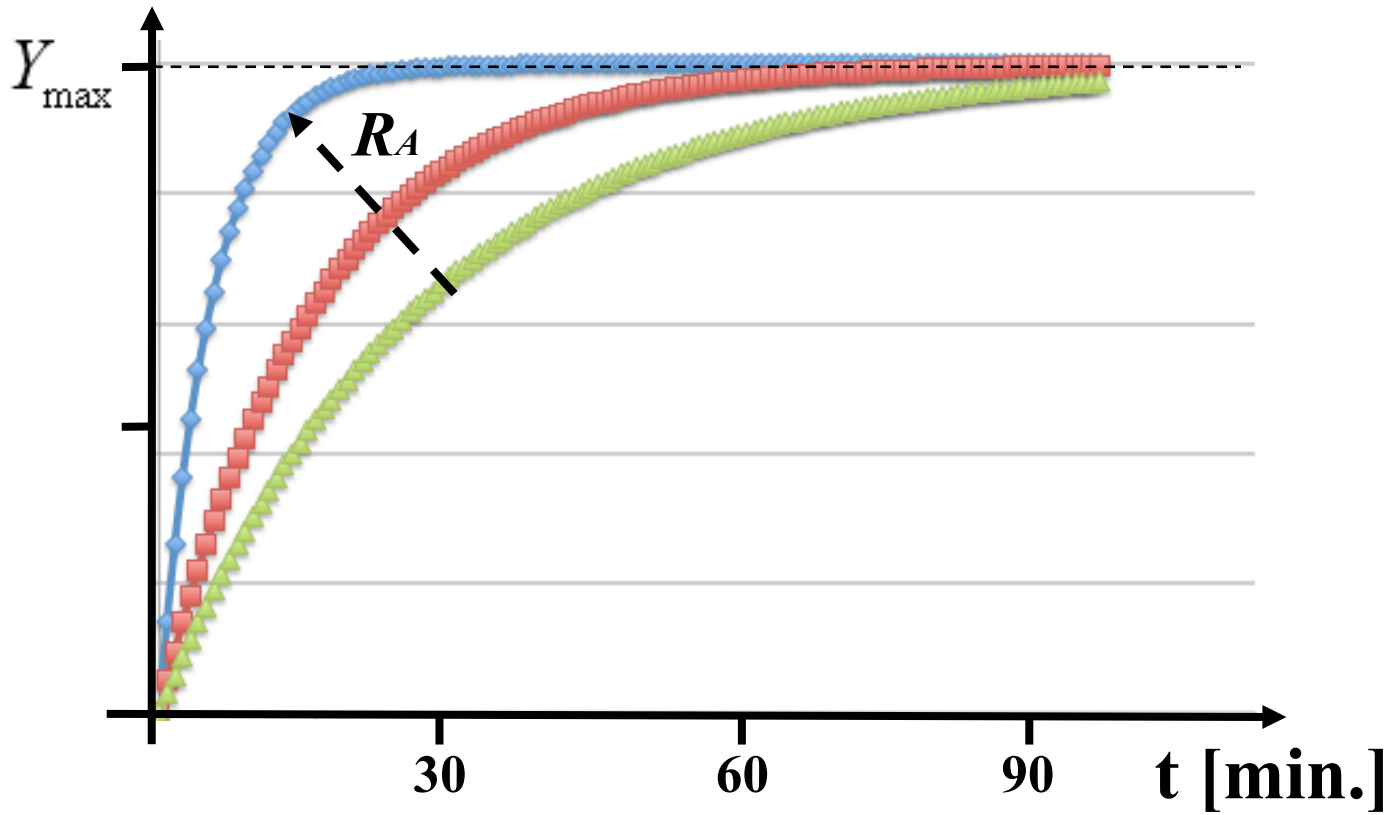
$$\frac{dY}{dt} = R_A - R_D Y \xrightarrow{equilibrium} R_A(1-Y)$$

$$\frac{dY}{dt} = R_A(1-Y)$$

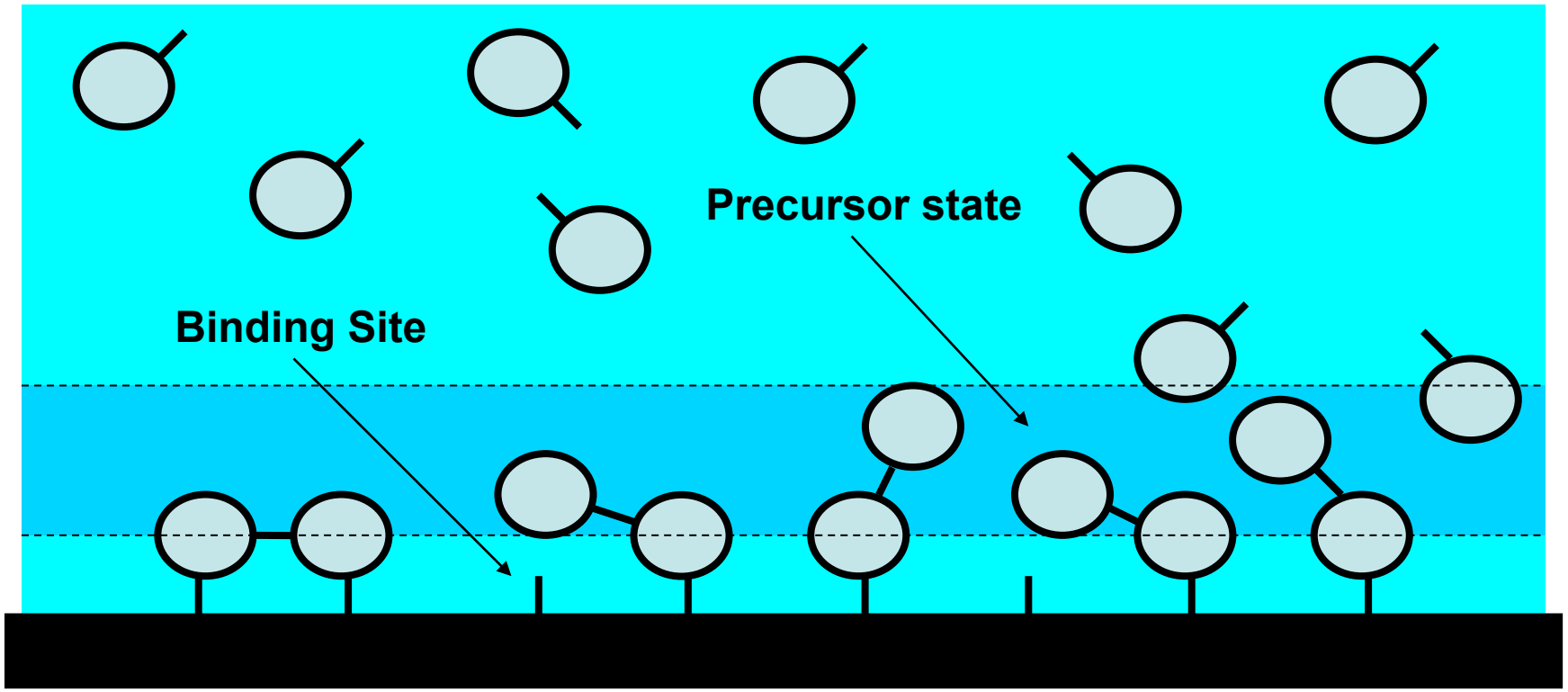
$$Y(t) = 1 - e^{-R_A t}$$

The Yield in Langmuir Model

Yield = Percentage of covered surface



The precursor state



The Kisliuk Model

Langmuir

$$\frac{dY}{dt} = R_A - R_D Y \xrightarrow{equilibrium} R_A(1-Y)$$

Precursor states at equilibrium interacting with gas

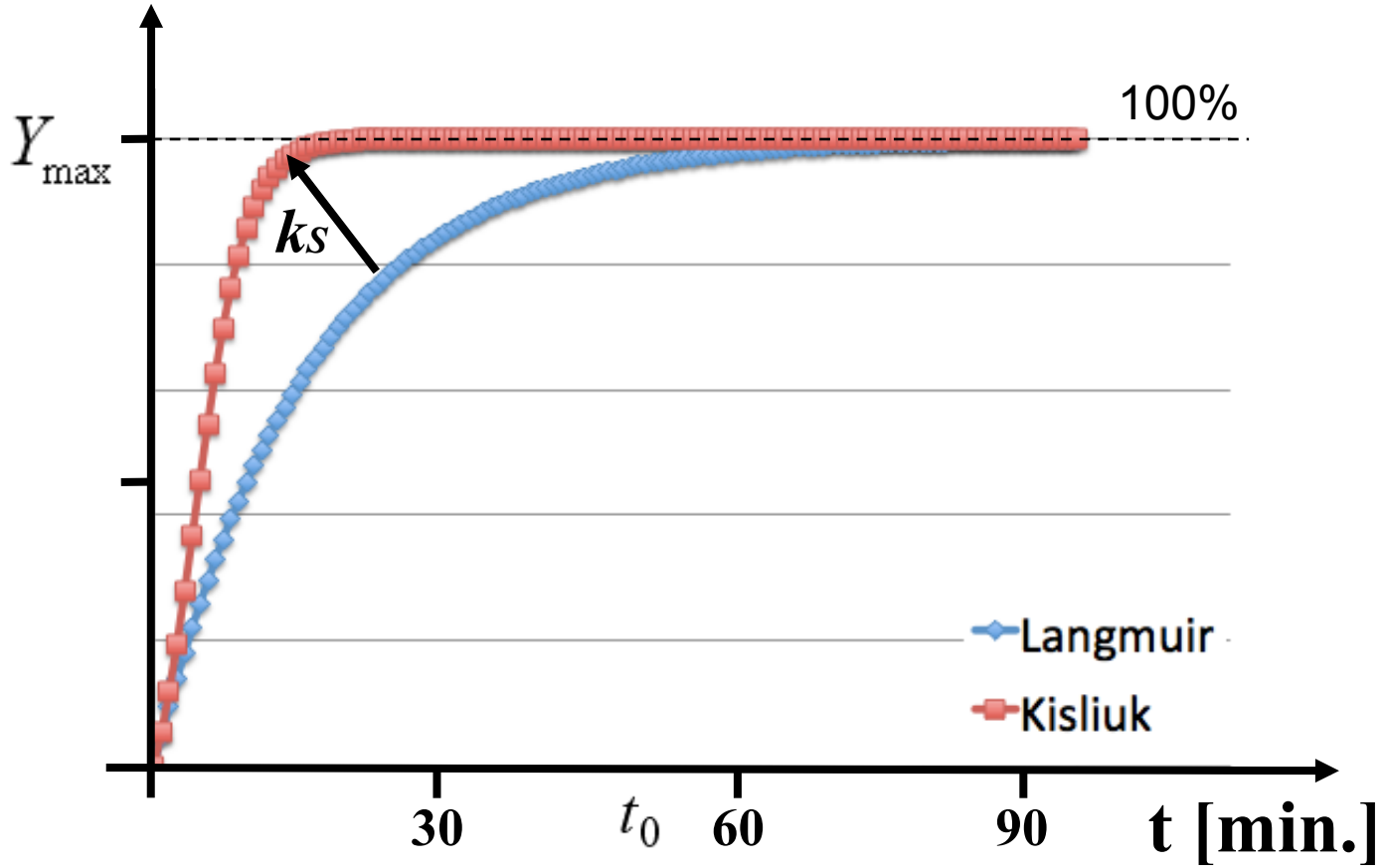
$$\frac{dY}{dt} = R_A(1-Y)(1+k_S Y)$$

The Sticking coefficient

$$Y(t) = \frac{1-e^{-R_A(1+k_S)t}}{1+k_S e^{-R_A(1+k_S)t}}$$

The Yield in Kisliuk Model

Yield = Percentage of covered surface



The Langmuir Model

Four Assumptions

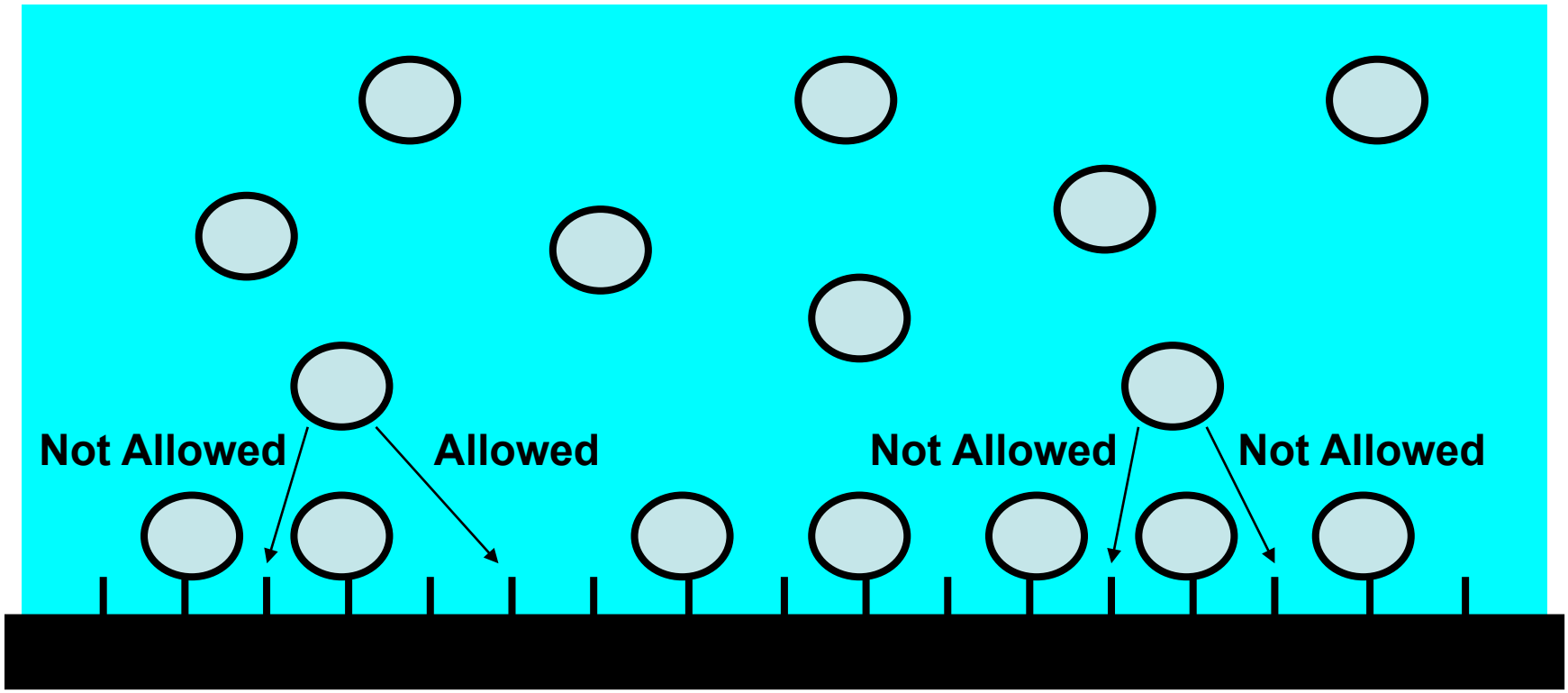
The Surface of adsorbent is uniform

~~**Adsorbed molecules do not interact**~~

All adsorptions occur with simple mechanism

Only a monolayer is obtained at the maximum adsorption

The Steric Hindrance Model



The Steric Hindrance Model

In the steric hindrance model, the previously adsorbed molecules prevent the adsorption of the next incoming ones:

$$\frac{dY}{dt} = R_A(1-Y) - \alpha Y[R_A(1-Y)].$$

A polynomial expansion of the molecular interaction term:

$$\frac{dY}{dt} = R_A(1-Y) - \sum_{\forall n>0} \alpha_n Y^n[R_A(1-Y)].$$

The Steric Hindrance Model

It is easy to show that the first approximation returns the Kisliuk model, while the second returns:

$$\frac{dY}{dt} = R_A(1-Y)[1-\alpha_1 Y - \alpha_2 Y^2].$$

As often written in literature. The fourth approximation gives us instead:

$$\frac{dY}{dt} = R_A(1-Y)[1-\alpha_1 Y - \alpha_2 Y^2 - \alpha_3 Y^3 - \alpha_4 Y^4]$$

Which corresponds to: $\frac{dY}{dt} = R_A(1-Y)[1-AY-BY^2]^2$

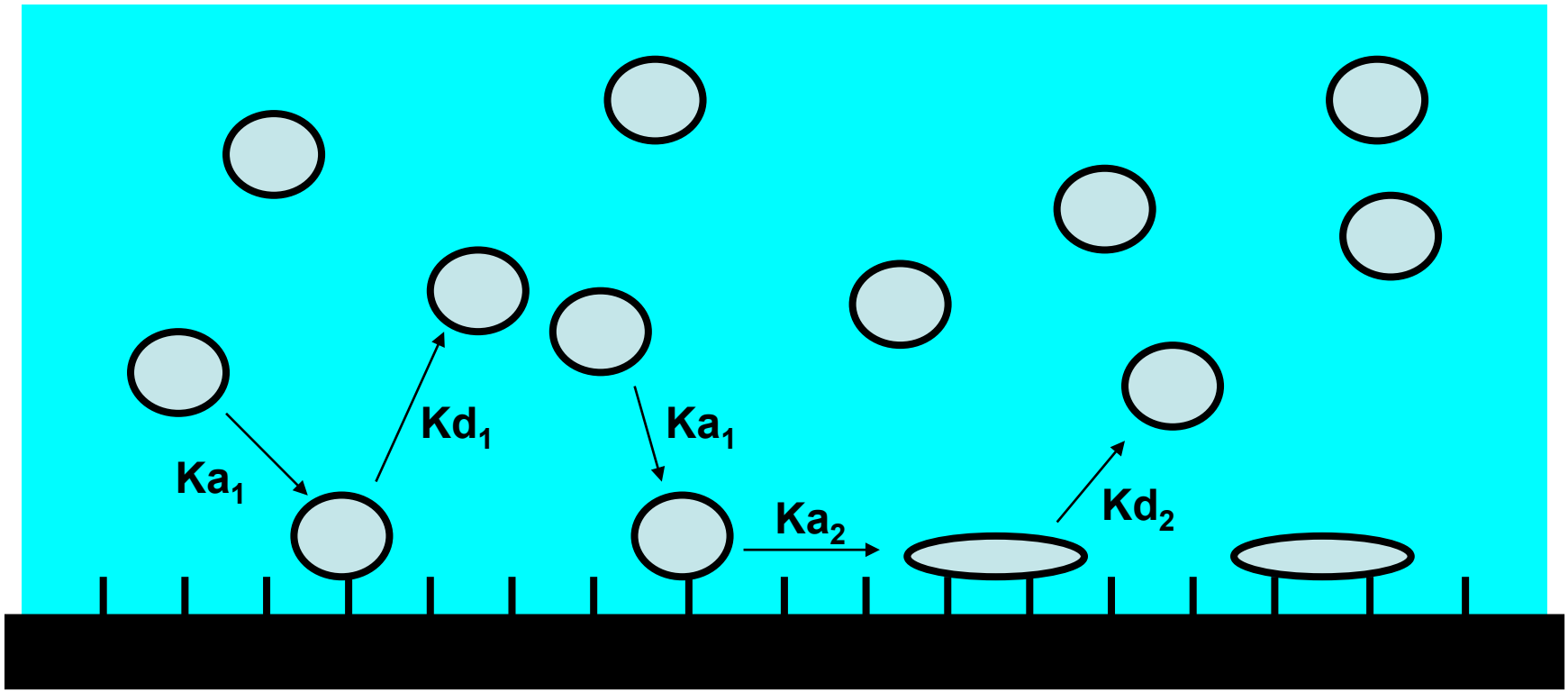
Wei-Dong Chen, Han-Hua Hu, Yan-Dong Wang (2006) Chem Eng Sci 61:7068–7076

The Langmuir Model

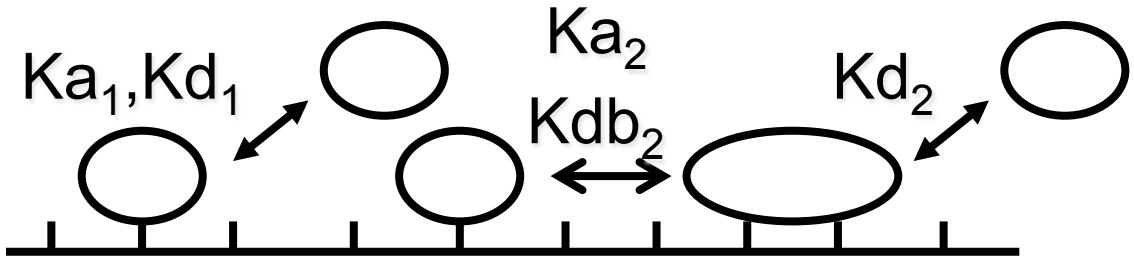
Four Assumptions

- **The Surface of adsorbent is uniform**
- **Adsorbed molecules do not interact**
- ~~**All adsorptions occur with simple mechanism**~~
- **Only a monolayer is obtained at the maximum adsorption**

The Spreading Model



The Spreading Model



If adsorbed molecules anchoring is by thought the Langmuir mechanism

$$\frac{dY_1}{dt} = R_{A1}(1 - Y_1 - \alpha Y_2)$$

$$\frac{dY_2}{dt} = R_{A2}(1 - Y_2 - \beta Y_1)$$

Direct Comparison for several Yields by different models