

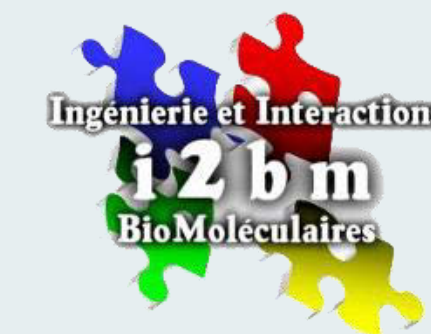
Design and characterization of CD20 antigen surfaces for the selection of rituximab peptide mimics



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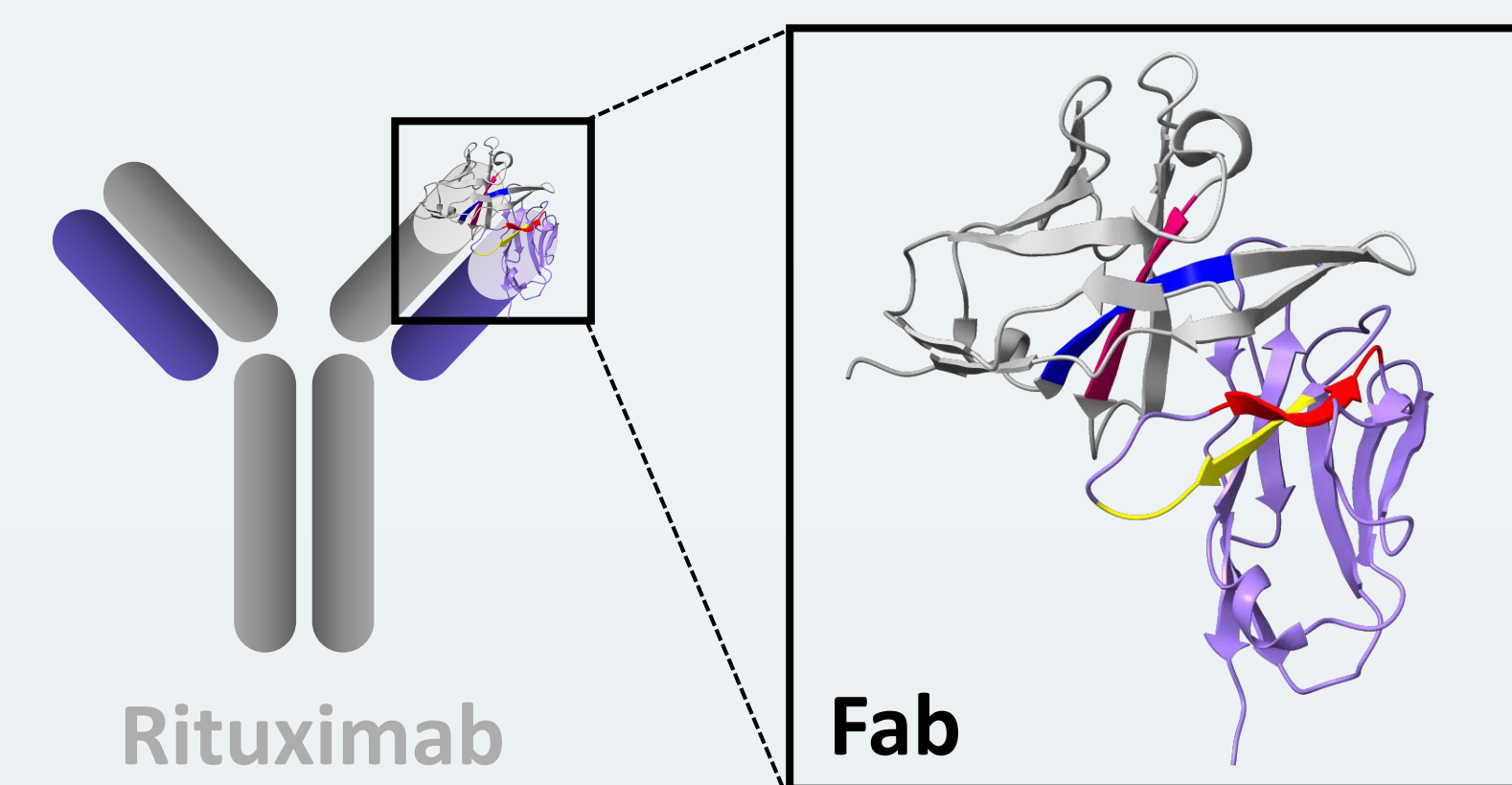
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Introduction

Since the 90s, **monoclonal antibodies** (mAb) have emerged as a promising class of pharmaceuticals and were successfully used for cancer therapy. However, several **limitations** related to the nature of mAbs such as their cost, their low tissue penetration and immunogenicity limits their extensive clinical use. So, **new technological solutions**, as small organic mAb mimics, have to be explored. In this context, we are interested in the **development of mAb mimics** that recognize the CD20 antigen, which is expressed on B cells and is a key target for several cancer and autoimmune diseases. In this context, the **mAb Rituximab (RTX)** that target CD20, is routinely used to treat some Lymphoma. Herein, we propose to **design macromolecular compounds comprising cyclopeptides selected from the RTX Fab as recognition elements for CD20** in combination with a detection element and/or a cytotoxic unit for therapeutic applications. For this purpose, we **developed and characterized biomimetic surfaces** to mimic the surface of B cells in order to **screen and select the RTX mimics** before moving on to cell-based assays.

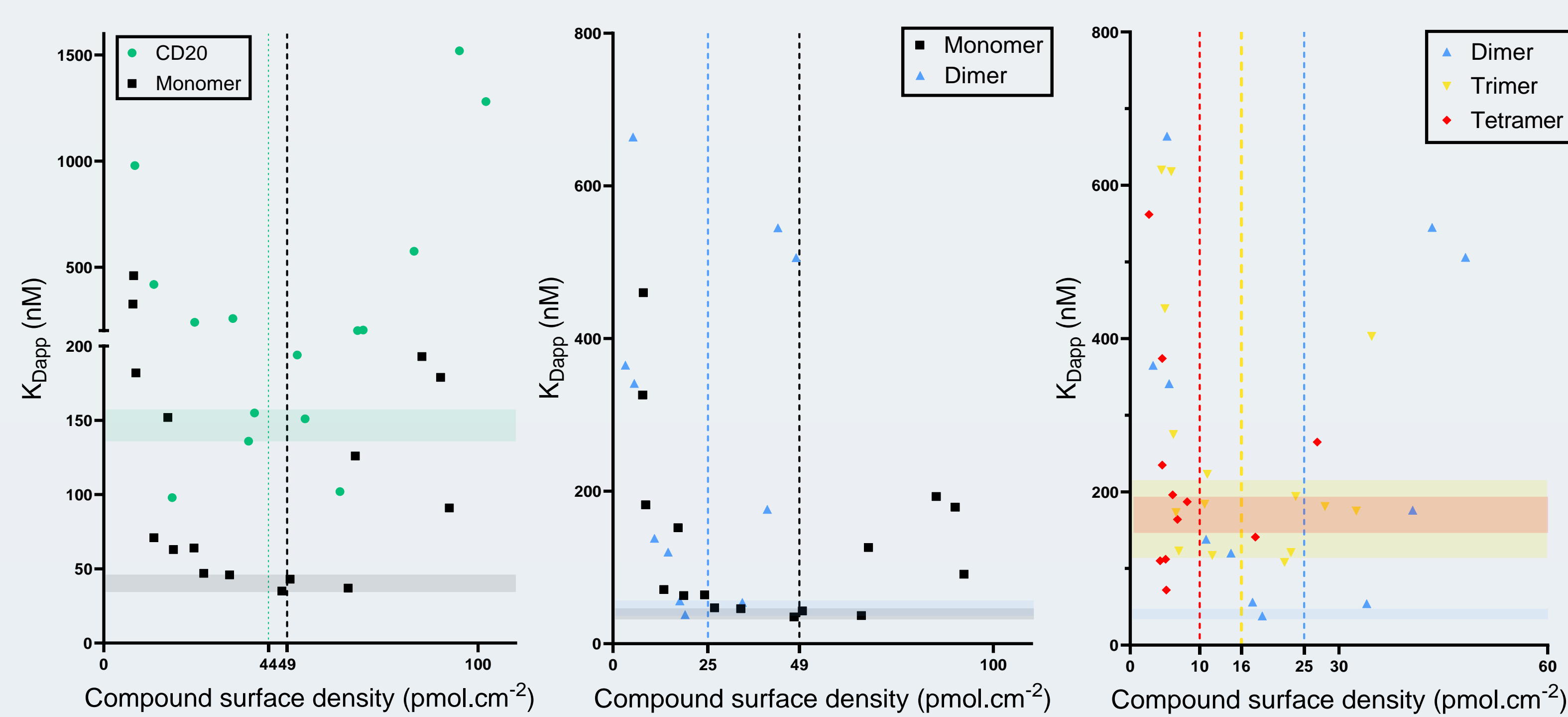


Development of antigenic surfaces for SPR

- The **biomimetic surfaces** were characterized by **Spectroscopic ellipsometry (SE)** coupled with **quartz microbalance (QCM-D)**

Compound	Surface density SE (pmol.cm ⁻²)	Surface density QCM-D (pmol.cm ⁻²)	Hydration (%)
Monomer *	37 ± 1	32 ± 6	66 ± 5
Dimer **	41 ± 4	32 ± 11	47 ± 13

Characterization of CD20 surfaces by SE coupled to QCM-D. SE areal densities were determined by *De Feijter* equation and QCM-D areal densities were extracted from *Sauerbrey* equation. * n = 2, ** n = 3



Impact of epitope surface density and clustering on RTX/CD20 affinity in SPR. KDapp were determined via the Heterogeneous Ligand (HL) model by the koff/kon ratio and areal densities by *Jung's* formula.

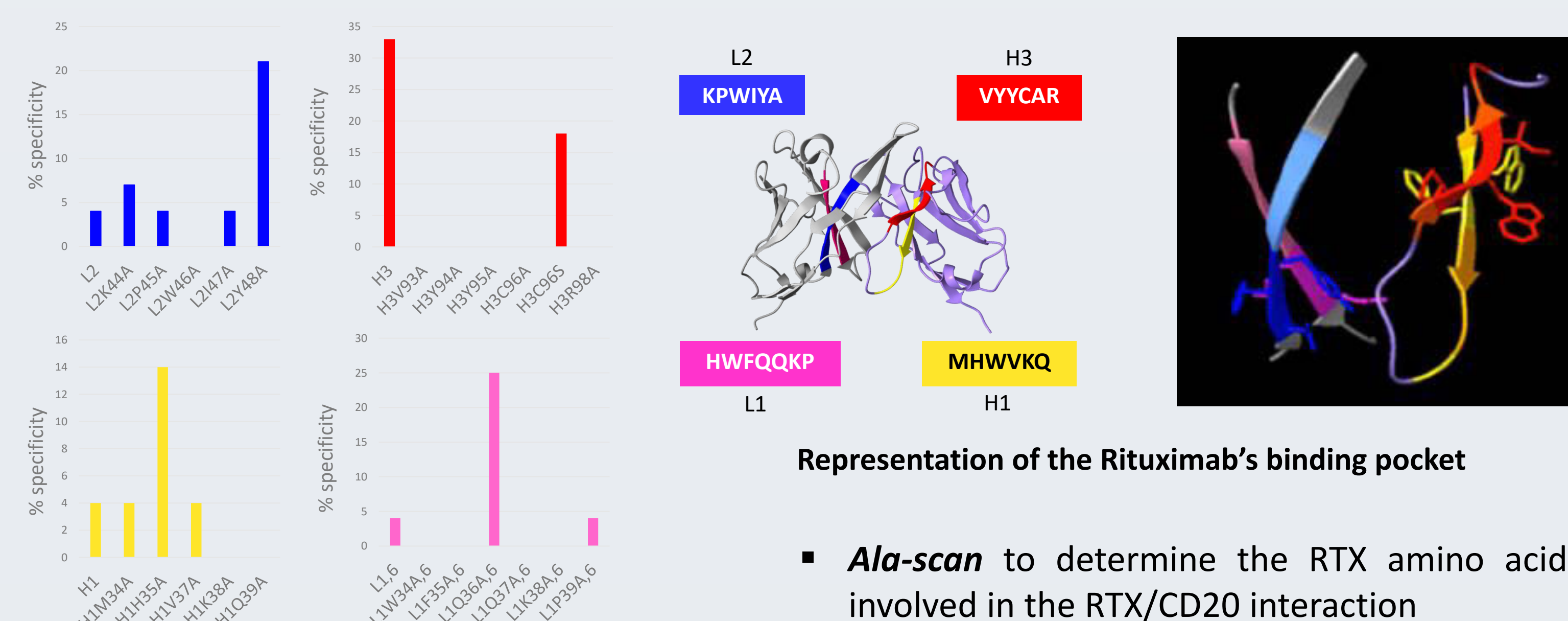
Affinity of rituximab against CD20 at optimal surface density in SPR. KDapp were determined via the Heterogeneous Ligand (HL) model by the koff/kon ratio and areal densities by *Jung's* formula. For the determination of inter-ligand distances, the projected surface of the compounds is considered circular. ^a n = 3, ^b n = 4

Compound	Surface density (pmol.cm ⁻²)	KDapp* (nM)	Inter-ligand spacing (nm)
CD20 ^a	44 ± 8	147 ± 10	2.2 ± 0.2
Monomer ^b	49 ± 13	40 ± 5	2.1 ± 0.3
Dimer ^a	25 ± 11	49 ± 10	3.1 ± 0.6
Trimer ^b	16 ± 6	165 ± 50	3.8 ± 0.7
Tetramer ^b	10 ± 6	172 ± 25	5.0 ± 1.1

* KD values *in vitro* : KDapp ≈ 5 - 19 nM

Study of RTX/CD20 interaction

- Amino acid significance of Rituximab-derived peptide sequences via Ala-scan**



Representation of the Rituximab's binding pocket

- Ala-scan** to determine the RTX amino acids involved in the RTX/CD20 interaction
- Presence of a **binding pocket** in RTX with two interaction areas

Conclusion & Outlooks

- Conclusion**

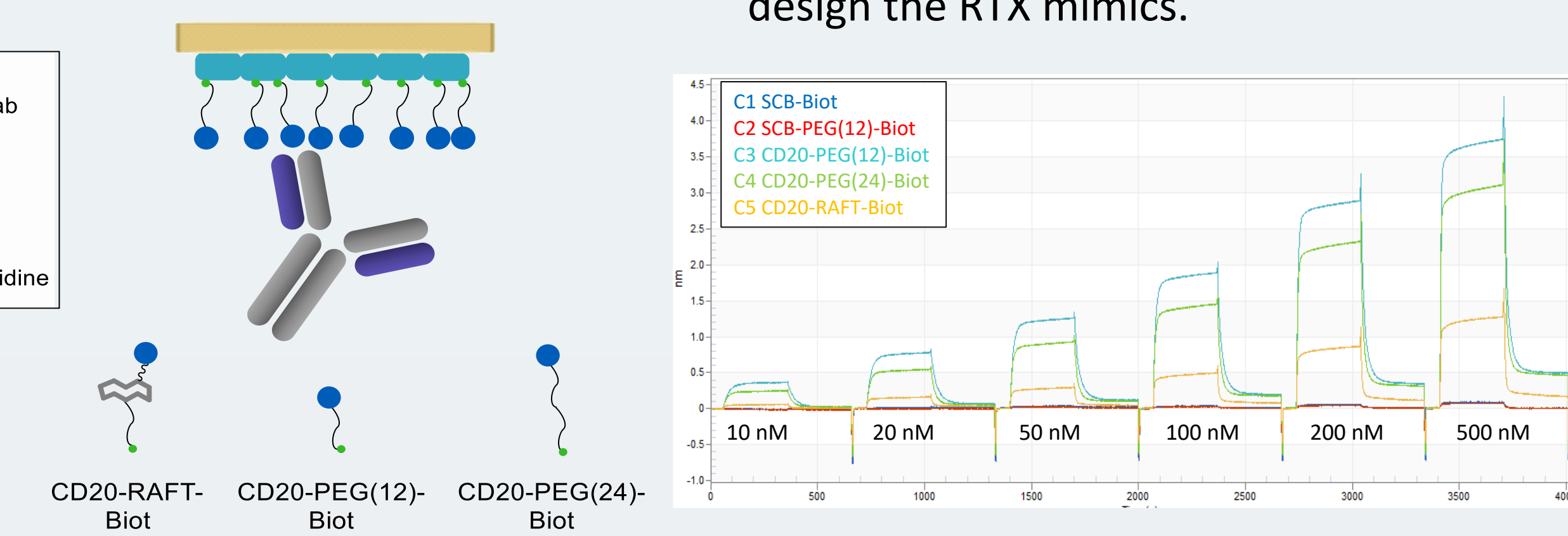
- Design of antigenic surfaces with high specificity and affinity for its antibody
- Design of BLI biosensors for peptide screening
- Determination of the amino acids from RTX binding pocket involved in the interaction
- Design and synthesis of RTX mimics

- And now ?**

- Evaluation of the affinity and the specificity of RTX mimics by BLI and SPR
- Biological assays with the hits

Development of biosensors for BLI

Grafting by **Streptavidin/Biotin** interaction
Antigen density is controlled by the time of grafting



- BioLayer Interferometry (BLI) biosensors** to screen RTX sequences to design the RTX mimics.

Compound	Loading response max (nm)	KDapp (nM)
SCB-Biot	0.8 ± 0.1	> mM
SCB-PEG(12)-Biot	1.3 ± 0.1	> mM
CD20-Biot	1.1 ± 0.1	> mM
CD20-PEG(12)-Biot	1.5 ± 0.1	250 ± 20
CD20-PEG(24)-Biot	1.5 ± 0.1	320 ± 10
CD20-RAFT-Biot	0.9 ± 0.1	560 ± 20

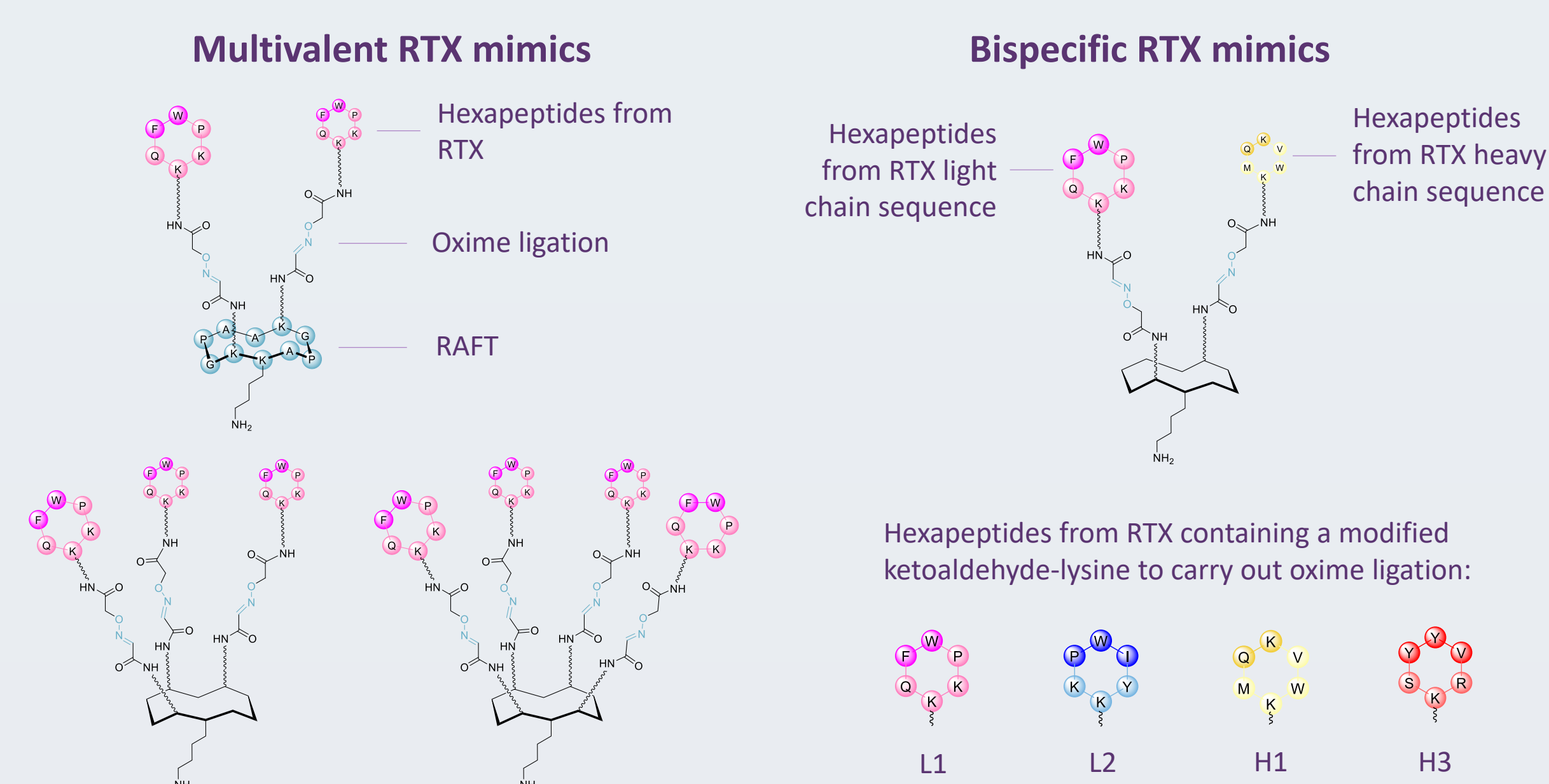
Impact of linker length on RTX/CD20 affinity in BLI. KDapp were determined via the Heterogeneous Ligand (HL) model by the koff/kon ratio.

Design and Evaluation of RTX mimics

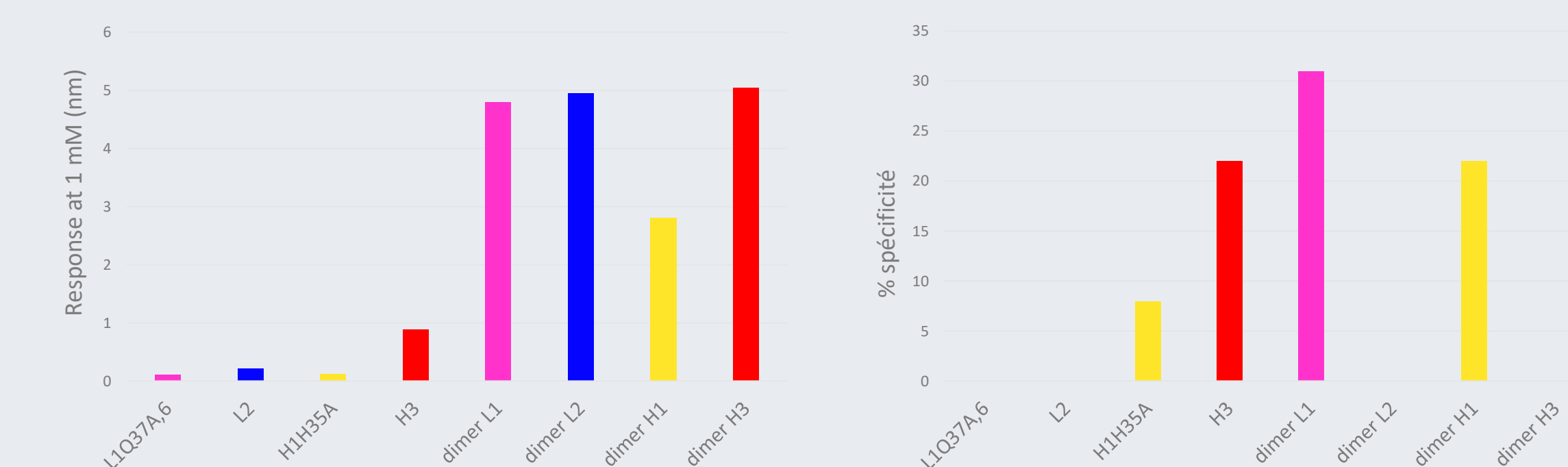
- RTX peptide mimic design**

Two types of RTX mimics :

- **multivalent mimics** displaying 2 to 4 times the same cyclopeptide from RTX consensus sequence
- **Bispecific mimics** displaying 2 different cyclopeptides, one from the heavy chain and one from the light chain sequences.



- Affinity of RTX peptide mimics for CD20**



Impact of dimerization of RTX cyclopeptides on CD20 recognition by BLI model. The specificity percentage was determined by comparison with the "CD20-scramble" response at a concentration of 1 mM.

- **Dimerization induces an increase in response**
- **Dimerization can improve specificity for the target**

References

Bar, L.; Dejeu, J.; Lartia, R.; Bano, F.; Richter, R. P.; Coche-Guerente, L.; Boturyn, D. *Anal. Chem.* **2020**, *92*, 5396–5403.

Bar, L.; Nguyen, C.; Galibert, M.; Santos-Schneider, F.; Aldrian, G.; Dejeu, J.; Lartia, R.; Coche-Guerente, L.; Molina, F.; Boturyn, D. *Anal. Chem.* **2021**, *93*, 6865–6872.