Conformational analysis of sequence defined oligomers by molecular dynamics

<u>Corentin Tonneaux¹, Resat Aksakal², Annemiek Uvyn³, Mathieu Fossépré¹, Bruno G. De Geest³, Filip E. Du Prez², Mathieu Surin¹</u> ¹ Laboratory for Chemistry of Novel Materials, Center of Innovation and Research in Materials and Polymers,

University of Mons – UMONS, 20, Place du Parc B-7000 Mons, Belgium

² Polymer Chemistry Research Group, Centre of Macromolecular Chemistry (CMaC), Department of Organic and Macromolecular Chemistry, Faculty of Sciences, Ghent University, Krijgslaan 281 S4-bis, Ghent, B-9000, Belgium

³ Department of Pharmaceutics, University of Ghent – UGent, Ottergemsesteenweg 460, 9000 Ghent, Belgium

Molecule A

INTRODUCTION

- Antibody-recruiting molecules (ARM)¹ are a promising class of molecules in the field of immunotherapy.
- Combination of anchoring groups (for target cell binding) and haptens (for antibody binding) to trigger response of immune effector cells.
- Aim: increase of the binding affinity by using multivalent ARM².

- **DNP groups** used for antibody-recruitment.
- Modelling of 3 sequence defined antibody-recruiting oligomers with different spacing of DNPs.



Global structure of ARM

DNP accessibility



Figure 3a: Box-and-whisker plots of radius of gyration and SASA of oligomers.

	Median radius of gyration (Å)	Median SASA (Ų)
Molecule A	7.8	1943
Molecule B	8.3	2082
Molecule C	8.2	2069

The size of each molecule was assessed by looking at the radius of gyration and the molecular SASA.

The 3 molecules adopt a globular compact shape in solution (Figure 4).

Size of molecules does not significantly change but molecule A is slightly more compact.





Figure 3b: Box-and-whisker plots of DNPs SASA and DNPs spacing.

	Median SASA (Ų)	Median area (Ų)
Aolecule A	143	19.5
Aolecule B	85	10.3
Aolecule C	100	14.3
Aolecule A Aolecule B Aolecule C	143 85 100	19. 10. 14.

The SASA of each DNP group was measured to evaluate their accessibility. DNPs from oligomer A are in general more accessible than for B and C. This is illustrate by the last snapshots of each MD (Figure 4) where DNPs are located on the edge of the globular structure of oligomer A.

Despite proximity of DNPs in the primary structure of oligomer A (Figure 2), the DNPs are more separated during MD. This leads to a larger area of the triangle formed by the DNPs.

Those results suggest that DNPs (Figure 4, in

blue) are more accessible for molecule A and

could facilitate the binding of antibodies.



Figure 4: Final structures of the sequence defined oligomers. The blue dashed lines represents the distance between the aromatic centers of DNPs (gray spheres). The number in blue is the area of the triangle.

CONCLUSION AND PERSPECTIVES

- The molecular modelling approach allows us to get insight on the conformation of sequence defined antibody-recruiting oligomers.
- Those results highlights the importance of inspecting the 3D structure of molecules as the spacing in 2D does not necessarly reflect a good separation in a globular structure.
- Avidity measurements and antibody recruitments have been measured experimentally and showed better results for oligomer A.

ACKNOWLEDGMENTS

The collaboration between Mons and Gent is supported by FNRS-FWO under the Excellence of Science EOS grant No. 30650939 (PRECISION). Computational resources have been provided by the Consortium des Équipements de Calcul Intensif (CÉCI), funded by the F.R.S.-FNRS under Grant No. 2.5020.11.

REFERENCES

- McEnaney, P.J., et al. ACS Chem Biol. 2012, 7, 1139-1151.
- Uvyn, A., De Geest, B.G. *ChemBioChem*. 2020, 21, 3036-3043.
- Wang, J., et al. J. Comput. Chem. 2004, 25, 1157-1174.
- Jakalian, A., Jack, D.B., Bayly, C.I. J. *Comput. Chem.* 2002, 23, 1623-1641











