









New Insights on the Structural Features of the Different Interleukin 15/Receptor Interfaces Using Molecular Dynamics Simulations Rui P. Sousa(1)*, Agnès Quéméner (2), Jean-Yves Le Questel (1), Adèle D. Laurent (1)

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Introduction

- Interleukin 15 (IL-15): a tightly regulated pleiotropic cytokine involved in a plethora of different cellular functions. (1)
- IL15 structure: based on a quaternary complex between IL-15 and its α (IL-15R α), β (IL-15R β) and γ (IL-15R γ) receptors. (2, 3)

The design of ligands targeting IL-15 interfaces requires a deep knowledge of their structure and behavior

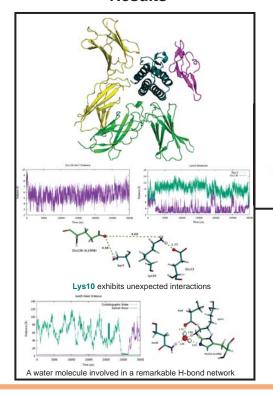
Objectives

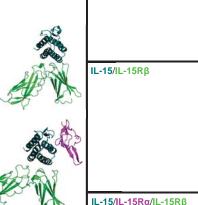
- o Investigate the time related behavior of the IL-15/IL-15Rβ interface through MD simulations
- Determine the key amino acid components of the interface and their interactions.

Methods

- MD simulations NAMD (CHARMM3)
- 200 ps equilibration (NVT) followed by 30 ns production (NPT), on the different multimeric models

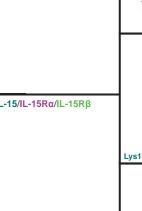
Results

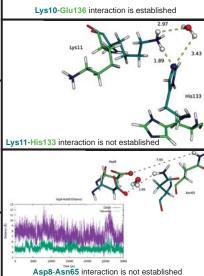




IL-15/IL-15Ra

IL-15





ys11-Asp8 interaction is not kept

Conclusions

- MD simulations allow the identification of key features not previously observed.
- The presence/absence of receptor chains directly or indirectly influences the structural features of the IL-15/IL-15RB interface.

Work in progress

- Analyses of the other IL-15/receptor interfaces.
- Study of relevant mutants to probe the influence of key residues in the features of the different interfaces.

References