## **Poster Presentation**

## Netrin4 and laminin gamma-1 interacts via their N-terminal globular domains

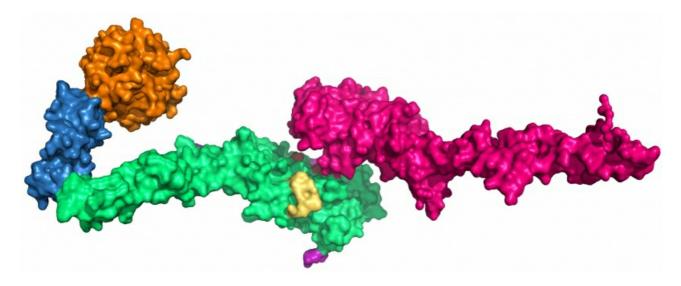
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Laminin is a heterotrimeric molecule composed of an alpha, a beta and a gamma chain. It interacts with various ligands at the extracellular matrix and plays a pivotal role in many biological processes. Netrin4, one of the four secreted netrins, specifically interacts with the laminin gamma-1 chain (Schneiders et al. 2007). We recently highlighted the biological significance of this complex using ex vivo and in vivo studies (Reuten et al. 2016). Furthermore, we also solved a structure of netrin4 at 3.1 Å that allowed us to reason why netrin4 and our previously reported structure of netrin1 (Grandin et al. 2016) interact with different binding partners. To implicate the structure of netrin4/laminin gamma-1 complex and its biological functions, we employed a multidisciplinary approach where we combined the low-resolution shape information of netrin4/laminin gamma-1 complex. This approach revealed that the N-terminal globular domains of netrin4 and laminin gamma-1 are required for the interaction (Reuten et al. 2016). The interaction sites were validated using structure-guided mutations that provided detailed insights on the biological relevance of this complex (Reuten et al. 2016). The high-resolution model of the netrin4/laminin gamma-1 complex was validated by comparing the experimentally derived hydrodynamic properties with those calculated from the structures.

1, Schneiders, F.I. and Maertens, B. et al. (2007) J. Biol. Chem. 282, 23750–23758

2, Reuten R. and Patel, T. R. et al. (2016) Nat. Commun. 7, 13515, 1-17

3, Grandin, M. and Meier, M. et al. (2016) Cancer Cell. 29, 175-185



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