Poster Presentation

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Domain swapping in structure of mNKR-P1A: unique feature with unknown function

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Natural killer (NK) cells, large granular lymphocytes, play an important role in the innate immune response against viruses, parasites and tumour cells. NK cells use a wide repertoire of surface receptors to modulate their activity [1]. The family of NKR-P1 surface receptors of NK cells belong to proteins with C-type lectin-like (CTL) fold. The overall architecture of other known CTL receptors (e.g. members of Ly49 family, NKG2D, CD94, mouse CLRg) is conserved [2]. The mechanism of ligand binding has been revealed by the crystal structure of Nkp65 bound to its keratinocyte ligand [3]. However, observation of domain swapping in crystal structure of mouse (m) NKR-P1A represents an unusual structural feature that might be involved in a new mechanism of ligand binding that would be specific for some members of NKR-P1 family. Nevertheless, our crystal structure of mNKR-P1A represents a unique structural observation that demands careful analysis. Even the latest structural studies do not answer the question of function or role of swapped domain of the receptor in potential ligand binding. We have generated new variants of mNKR-P1A of varied chain length that undergo biochemical and structural analysis including mass spectrometry.

[1] *P. Kolenko et al., J. Struct. Biol., 2011, 175, 434-441.,* ***[2]*** *T. Skálová et al., J. Immunol., 2012, 189, 4881-4889.,* ***[3]*** *Y. Li et al., PNAS, 2013, 110, 11505-11510.*

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