MS06-1-6 Examples of the functional and structural diversity of NYN nucleases
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Abstract
RNA maturations and modifications play a crucial role in the living by enabling a variety of RNAs to fulfil their functions. These include the cleavages carried out by ribonucleases, which are characterised by binding domains enabling them to interact with RNAs (RBDs) or other partners and catalytic domains responsible for their cleavage function. In 2006, a new globular domain associated with RBDs was identified in several eukaryotic and prokaryotic proteins including YacP and N4BP1. Structural predictions suggested an α/β domain with 5 strands (S) and 4 helices (H), perfectly congruent with secondary structures observed in the PIN (PilT N-terminal) and FLAP catalytic domains. The presence of 2 conserved Asp (D) at the end of S1 and S4 as well as 2 acidic residues in the N-terminal part of H2 and H4 suggests a potential nuclease function for this new domain, which was then named NYN for N4BP1, YacP-like Nuclease domain[1]. Subsequently, this PIN-like domain superfamily was split into 5 major structural subclasses including “NYN” (true NYN) and “PRORP” (Protein only RNase P[2])[3]. Although several proteins with NYN domains have already been identified, the huge diversity of domains associated with NYN suggests a variety of functions and targets, from which very little is known at present.
The structural (X-ray crystallography, SAXS), biophysical (DLS, NanoDSF) and functional (*in vitro* cleavages, RNA-seq) study of these proteins can lead to a better understanding of their role *in vivo* and, in the longer term, to the possibility of diverting their function to solve agronomic[4] or health problems.

References
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