Poster Presentation

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Structural and biophysical characterization of human RNase 6

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Human members of the RNase A superfamily include eight rapidly evolving homologous enzymes with varying ribonucleolytic activity. All eight canonical members are characterized by the presence of two histidines and a lysine forming the catalytic triad, in addition to strictly conserved cysteines involved in the formation of 3 or 4 disulfide bridges essential for structural integrity. Despite these architectural and catalytic similarities, human RNases are functionally diverse and their biological activities remain elusive. Apart from degrading RNA with varying degrees of efficiency, these structural homologues have acquired a variety of distinct biological functions, including anti-bactericidal, cytotoxic, angiogenic, immunosuppressive, anti-tumoral and/or anti-viral activities. Among human members of this vertebrate-specific family, RNase 6 and RNase 8 have never been structurally resolved. To better understand its biological function and to characterize its molecular interactions with RNA and/or potential unknown ligands, we present the three-dimensional structure of human RNase 6 in its apo form. While the enzyme shares similar structural features with other members of the RNase A superfamily, we emphasize interesting differences unique to RNase 6 that may be pertaining to its unique biological function. Additional NMR, CD and ITC biophysical characterization in presence of RNA ligands will also be presented.

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