Structural and Functional Insight into Celldefending Non-specific Nucleases

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The bacterial toxin ColE7 bears an H-N-H motif that has been identified in hundreds of prokaryotic and eukaryotic endonucleases, involved in DNA homing, restriction, repair or chromosome degradation. The crystal structures of the nuclease domain of ColE7 in complex with an 8-bp [1], 12-bp and 18-bp duplex DNA have been determined respectively by X-ray diffraction methods. In each of the structure, the H-N-H motif is bound at the minor groove primarily to DNA phosphate groups, with little interaction to ribose groups and bases. This result provides a structural basis for sugar and sequence independent DNA recognition. Structural comparison shows that several families of endonucleases bind and bend DNA in a similar way to that of the H-N-H ColE7, indicating that endonucleases containing a similar His-metal finger fold of active site possess a universal mode for protein-DNA interactions [2].

[1] Hsia K.-C., Chak K.-F., Liang P.-H., Cheng Y.-S., Ku W.-Y., Yuan H. S., *Structure,* 2004, **12**, 205-214. [2] Hsia K.-C., Li C.-L., Yuan H. S., *Curr. Opin. Struct. Biol.,* 2005, **15**, 126–134.

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