Poster Presentation

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Structural-Functional Analysis of USP7

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Ubiquitin Specific Protease 7 (USP7) catalyzes the deubiquitination of several substrate proteins including p53, Mdm2 and UbE2E1. Deubiquitination results in their rescue from 26S proteasome mediated degradation thus USP7 is critical in maintaining the cellular steady state levels of its substrates. USP7 is also known to interact with several viral proteins including herpes simplex virus Infected Cell Protein 0 (ICP0), Epstein Barr Nuclear Antigen 1 (EBNA1) and Kaposi's sarcoma-associated viral interferon regulatory factor 4 (vIRF4). USP7 possesses several domains including an N-terminal TRAF, a catalytic and five ubiquitin-like domains. The crystal structures of several complexes revealed that most substrate proteins interact with the N-terminal domain of USP7 which folds into an eight-stranded antiparallel beta sandwich. EBNA1 and MCM-BP also interact with USP7 through its N-terminal domain in an identical manner to its substrates p53, Mdm2 and UbE2E1 however these proteins are not deubiquitinated by USP7. Substrates that interact with USP7 through its N-terminal domain possess a P/AxxS binding motif. The identification, characterization and structure determination of novel USP7 substrates is ongoing.

[1] *J. Biol. Chem. 2013 Jun 7;288(23):16975-85. doi: 10.1074/jbc.M113.469262. Epub 2013 Apr 19,* ***[2]*** *Mol. Cell. Biol. 2014 Jan;34(1):132-45. doi: 10.1128/MCB.00639-13. Epub 2013 Nov 4*

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