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Volume 12

Washington University
Undergraduate Research Digest

Spring 2017

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Recommended Citation

Gupta, Harshath, "The Potential Role of ER-Associated Degradation Protein DERL3 in Multiple Myeloma" (2017). *Volume 12*. 73.

https://openscholarship.wustl.edu/wuurd_vol12/73

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THE POTENTIAL ROLE OF ER-ASSOCIATED
DEGRADATION PROTEIN DERL3 IN
MULTIPLE MYELOMA

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Multiple myeloma (MM) accounts for 13% of hematologic cancers and is characterized by a diversity of genetic lesions—translocations, copy number alterations, and single nucleotide variants. We designed a single-platform targeted sequencing approach capable of detecting all three variant types. Here, we focused on the translocations. We performed targeted sequencing of myeloma cells from MM patients (n=96) and detected novel IgH translocations with partners near *DERL3* (n=2) and observed outlying expression of *DERL3* from RNA-seq data. Since *DERL3* regulates protein misfolding, we hypothesized that knockdown of *DERL3* in MM would lead to increased apoptosis. After validating the translocation via PCR, we knocked down *DERL3* with shRNA constructs in MM cell lines and observed increased cell death in one of two MM cell lines. This study provided some evidence suggesting *DERL3* may play a role in regulating MM progression and may be a target of IgH-induced overexpression. Identifying *DERL3* as a tumor suppressor gene for MM could lead to increased understanding of MM development and potential use for therapy.