

## Supplementary Material

# **SUMO-Modification of Human Nrf2 at K<sup>110</sup> and K<sup>533</sup> Regulates Its Nucleocytoplasmic Localization, Stability and Transcriptional Activity**

Treniqka S. Walters<sup>a</sup> Deneshia J. McIntosh<sup>a</sup> Shalonda M. Ingram<sup>b</sup>  
Lakeisha Tillery<sup>b</sup> Evangeline D. Motley<sup>b</sup> Ifeanyi J. Arinze<sup>a</sup> Smita Misra<sup>b,c,d</sup>

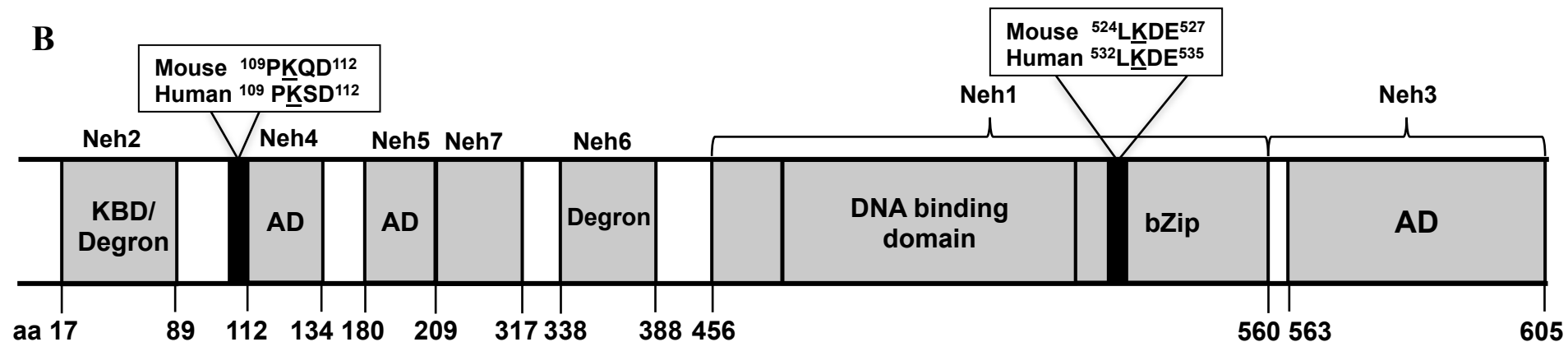
<sup>a</sup>Department of Biochemistry, Cancer Biology, Neuroscience and Pharmacology, School of Medicine, Meharry Medical College, Nashville, TN, USA, <sup>b</sup>Department of Microbiology, Immunology and Physiology, School of Medicine, Meharry Medical College, Nashville, TN, USA, <sup>c</sup>School of Graduate Studies and Research, Meharry Medical College, Nashville TN, USA, <sup>d</sup>Center for Women's Health, Meharry Medical College, Nashville TN, USA

**Supplemental Figure 1: Putative SUMO-conjugation motifs in Nrf2.** *A.* NIH's COBALT: Multiple Alignment Tool comparing amino acid sequences of Nrf2 from mouse (Accession # NP\_035032.1) and human Nrf2 (Accession # NP\_006155.2) Putative SUMO-conjugation motifs as predicated by SUMOplot are bold and italicized. Top two SUMO-conjugation motifs are underlined. *B.* Map of the Nrf2 domain structures showing the location of top two putative SUMO-acceptor Lysine residues predicted by SUMOplot in Nrf2 protein.

# Supplemental Figure 1

**A**

Human	1	MMDLELPPPGLPSQQDMDLIDILWRQDIDLGVSRVDFDSQRRKEYELEKQKKLEKERQEQLQKEQEKAFFAQLQLDEET	80
Mouse	1	MMDLELPPPGLQSQQDMDLIDILWRQDIDLGVSRVDFDSQRQKDYELEKQKKLEKERQEQLQKEQEKAFFAQFQLDEET	80
Human	81	GEFLPIQPAQHIQSETSGSANYSQVAHI <b>PKSD</b> ALYFDDCMQLLAQTFFVDDNEVSSATFQSLVPDIPGHIESPVFIATN	160
Mouse	81	GEFLPIQPAQHIQTDTSGSASYSQVAHI <b>PKQD</b> ALYFEDCMQLLAETFFVDDHE-----SLALDIPSHAESSVFTAPH	153
Human	161	QAQSPETSVAQVAPVDLDGMQQDIEQVWEELLSIPELQCLNIENDKLVETTMVPSPEAKLTEVD-NYHFYSSIPSMEKEV	239
Mouse	154	QAQSLNSSL-EAAMTDLSSIEQDMEQVWQELFSIPELQCLNTENKQLADTTAVPSPEATLTEMDSNYHFYSSISSLEKEV	232
Human	240	GNCSPHFLNAFEDSFSSILSTEDPNQLTVNSLNSDATVNTDFGDEFYSAFIAEPSISNSMPSPATLSHSLSELLNGPIDV	319
Mouse	233	GNCGPHFLHGFEDSFSSILSTDDASQLT--SLDSNPTLNTDFGDEFYSAFIAEPSDGGSMPSAAISQSLSELLDGTIEG	310
Human	320	SDLSLCKAFNQNHPESTAEFNDSDSGISLNTSPSVASPEHSVESSSYGDTLLGLSDSEVEELDSAPGSVKQNGPKT-PVH	398
Mouse	311	CDLSLCKAFNPKHAEGTMEFNDSDSGISLNTSPSRASPEHSVESSIYGDPPPFGSDSEMEELDSAPGSVKQNGPKAQPAH	390
Human	399	SSGDMVQPLSPSQGQSTHVHDAQCENTPEKELPVSPGHRKTPFTKDKHSSRLEAHLTRDELRAKALHIPFPVEKIINLPV	478
Mouse	391	SPGDTVQPLSPAQGHSAPMRESQCENNTKKEVPVSPGHRKAPFTKDKHSSRLEAHLTRDELRAKALHIPFPVEKIINLPV	470
Human	479	VDFNEMMSKEQFNEAQLALIRDIRRRGKNKVAQAQNCRRKLENIIVELEQDLHLKDEKEKLLKEKGENDKSLHLLKKQLS	558
Mouse	471	DDFNEMMSKEQFNEAQLALIRDIRRRGKNKVAQAQNCRRKLENIIVELEQDLGHLKDEREKLLREKGENDRNLHLLKRRLS	550
Human	559	TLYLEVFSMLRDEDGKPYSPSEYSLQQTRDGNVFLVPKSKKPDVKKN	605
Mouse	551	TLYLEVFSMLRDEDGKPYSPSEYSLQQTRDGNVFLVPKSKKPDTKKN	597



**Supplemental Figure 2: SUMO-acceptor K residues are needed for transactivation of the hNrf2 and stability of HO1 protein.** HEK293T cells were transfected with plasmid for either FLAG-tagged WT or mutant hNrf2 (K<sup>110</sup>R, K<sup>533</sup>R, or 2K) for 24 hrs. The transfected cells were treated with 100  $\mu$ M Cycloheximide (CHX) for 0, 5, 15, 30, and 60 min. Total cell lysates were resolved on a 7.5% SDS-PAGE gel and analyzed by western blotting using anti-FLAG and anti- $\beta$ -actin antibodies. *A.* Representative HO1 and Histone-H3 blots are shown. *B.* Densitometric quantitation of the blots in *A.* The levels of HO1 were normalized to those of Histone-H3. The normalized values at 0 min were designated as 100%. Subsequent normalized values were calculated as percentages of those at 0 min. ImageJ software was used for quantitation. The values plotted are means  $\pm$  S.E (n=3).

# Supplemental Figure 2

