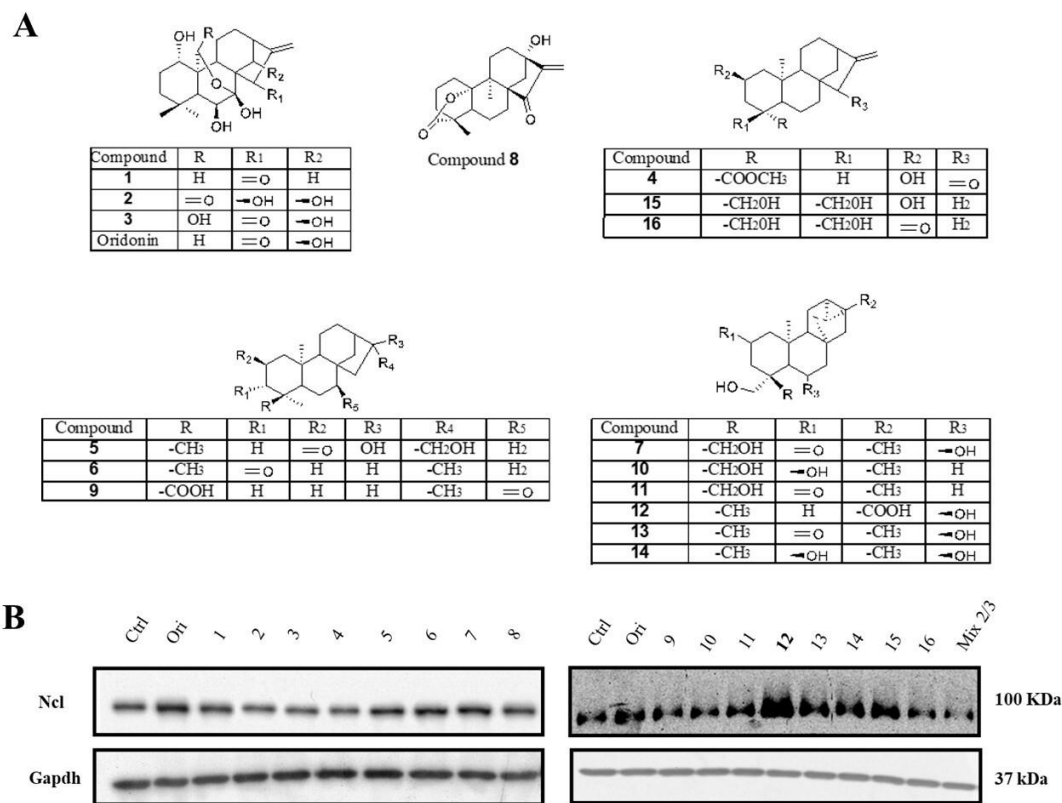


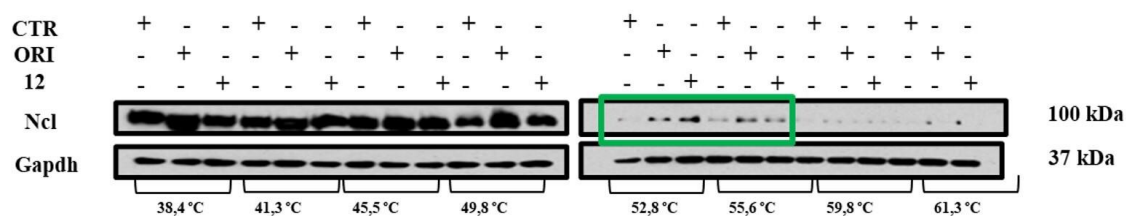
## Supporting Information

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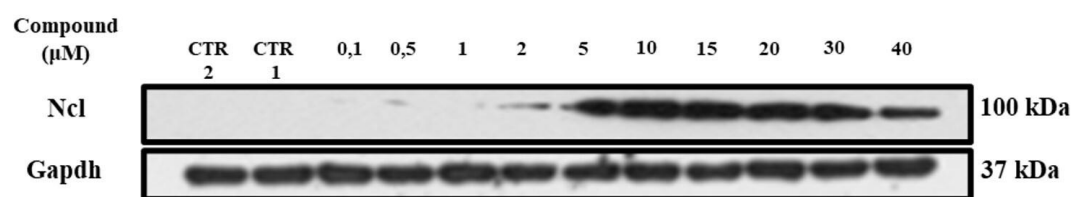
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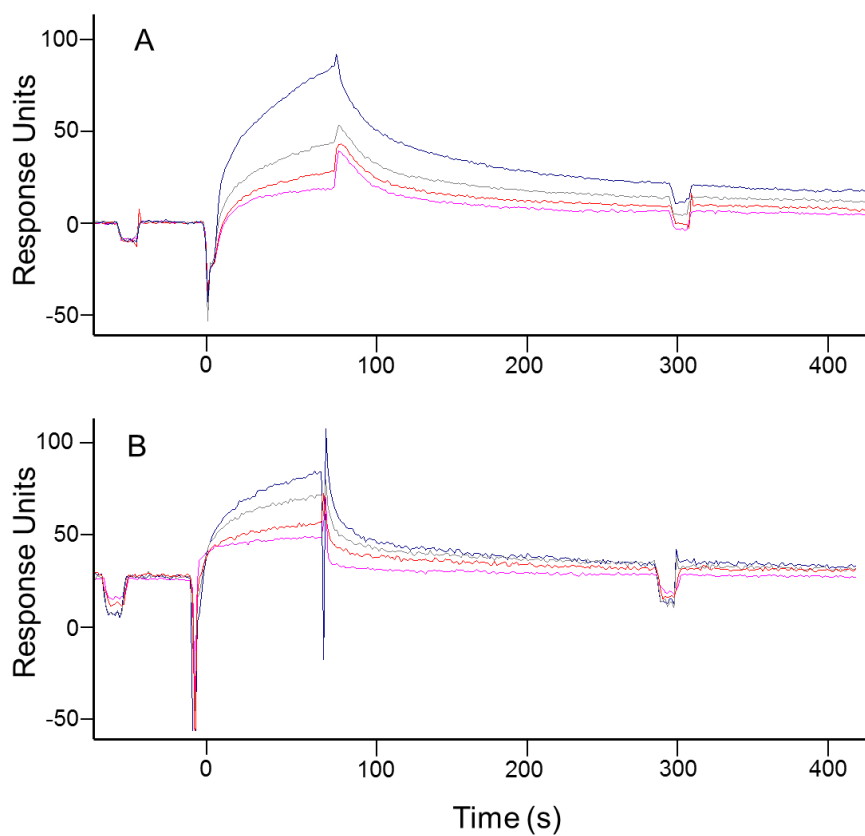
**Figure S1.** (A) Chemical structure of compounds **1-16** and Oridonin. (B) Representative western blot analysis of nucleolin level in the CETSA-based screening performed in Jurkat cell line



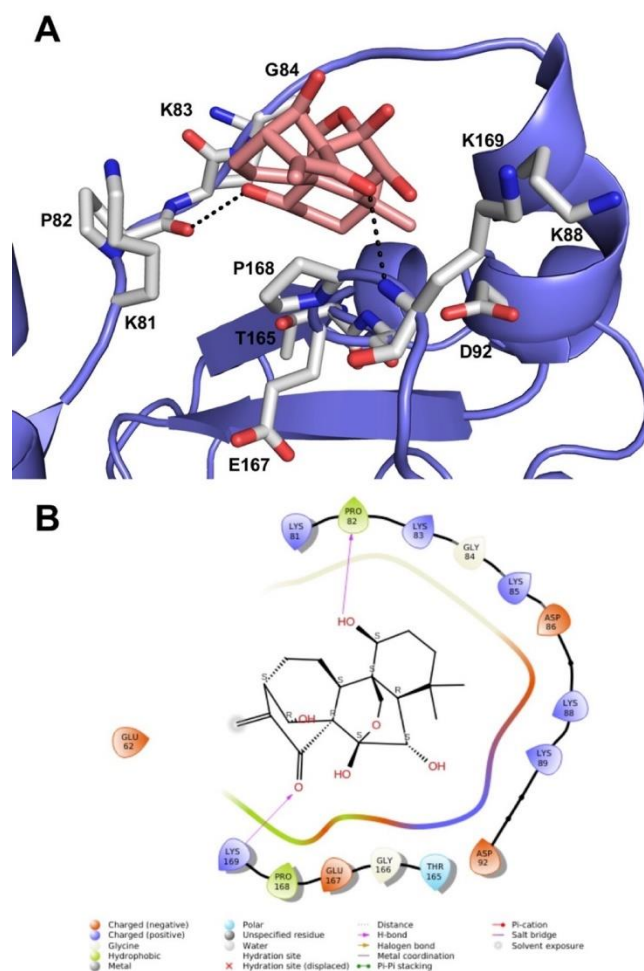
**Figure S2.** Representative western blot analysis of Nucleolin level in CETSA experiment of **12** on HeLa cells to different temperatures



**Figure S3.** Representative western blot analysis of Nucleolin level in CETSA performed using various concentrations of **12**



**Figure S4.** SPR sensorgrams obtained for the interaction of **12** with hNCL (A) and RBD 1,2 (B)



**Figure S5.** (A) Docked pose of oridonin (salmon sticks) within RBD1,2 represented as a slate ribbon model. Only amino acids located within 4 Å of the bound ligand are displayed (white sticks) and labelled. H-bonds are depicted as dashed black lines (B) Two-dimensional ligand interaction diagram of oridonin docked pose. Positively charged amino acids are represented with dark-blue drops, negatively charged amino acids are represented with red drops, polar amino acids are represented with light-blue drops and hydrophobic amino acids are represented with green drops. H-bonds are depicted with purple arrows.