
Supplemental Information

An aptamer-based antagonist against the receptor for advanced glycation end-products (RAGE) blocks development of colorectal cancer

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Supplemental Table 1 Primers sequences for plasmids construction

Primer name	Sequence (5'-3')
RAGE-pc DNA3.1 forward	TGCTGGATATCTGCAGAATTCATGGCTGCCGGAACAGC
RAGE-pc DNA3.1 reverse	TTCGGGCCCAAGCTTGGTACCAGGCCCTCCAGTACTACTCT

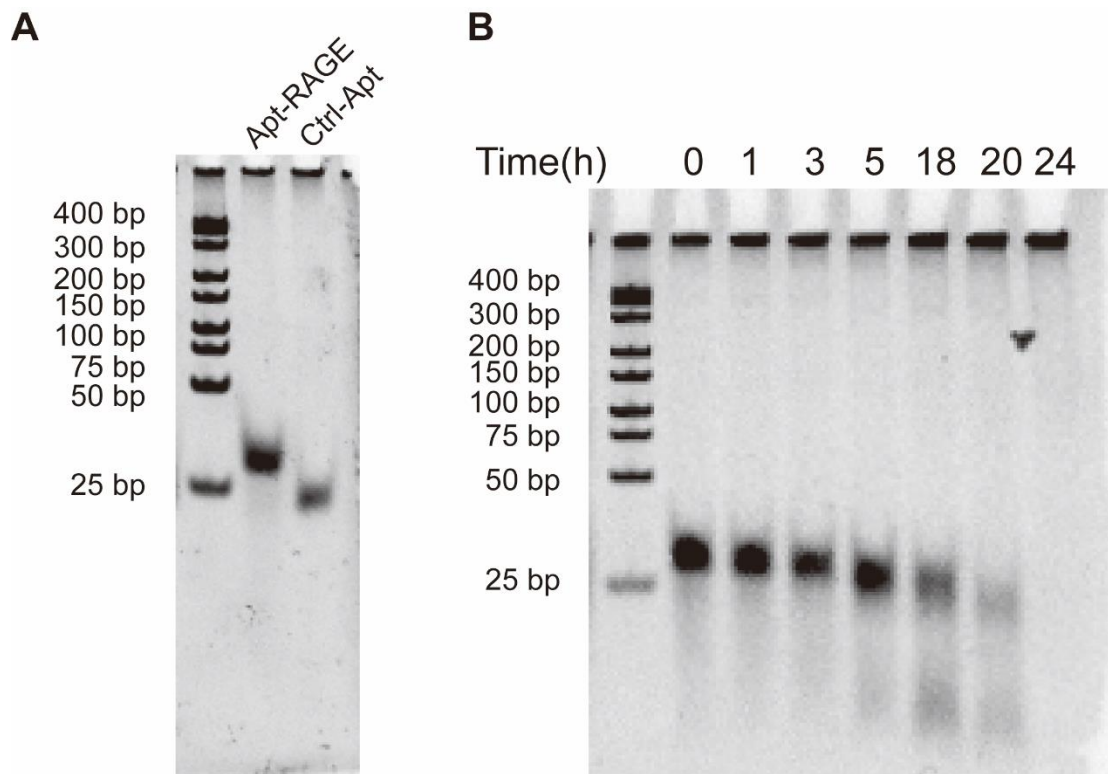


Fig. S1. The characterization of Apt-RAGE. (A) The molecular size of Apt-RAGE (Apt-RAGE) and Ctrl-Aptamer (Ctrl-Apt). (B) The serum stability of Apt-RAGE.

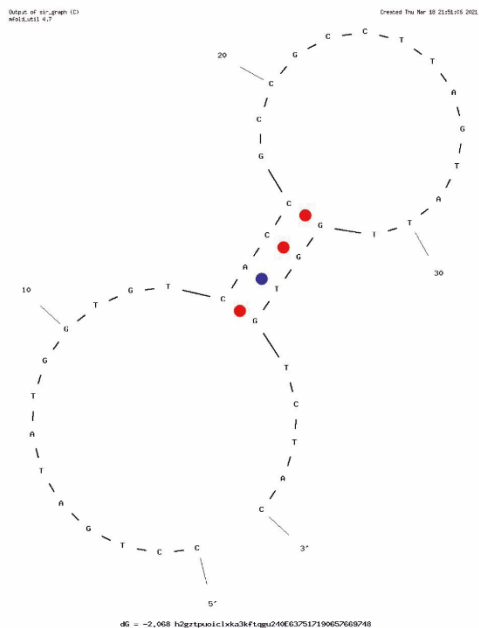
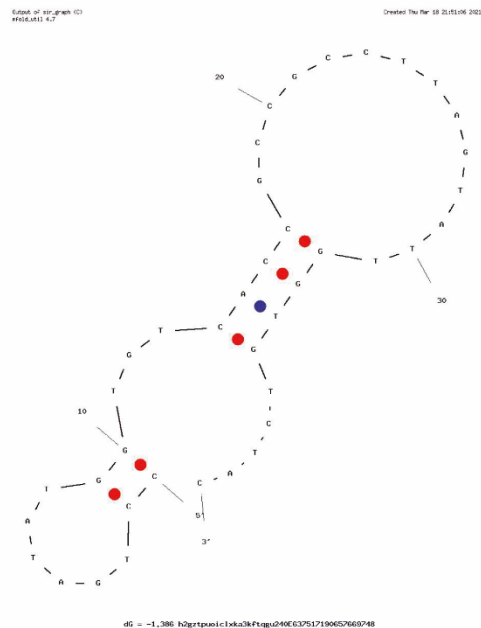
A**B**

Fig. S2. Schematic representations of the secondary structures of the Apt-RAGE. Predicted secondary structures were generated by free energy minimization using the RNA folding algorithm Mfold (calculated free energy for each aptamer: $\Delta G_A = -2.07$ kcal/mol, $\Delta G_B = -1.39$ kcal/mol).

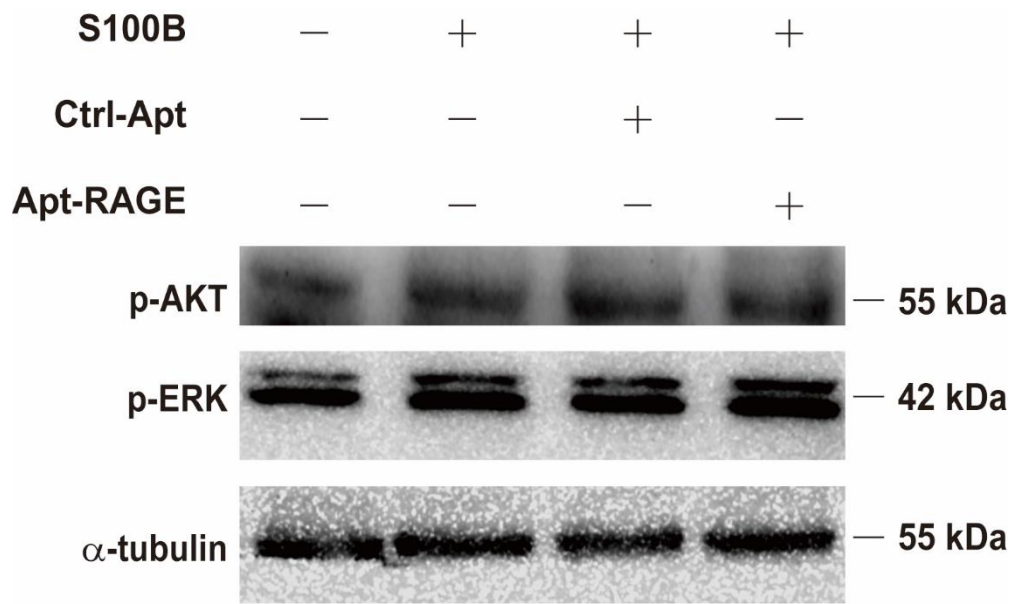


Fig. S3. Effect of Apt-RAGE on AKT and ERK signaling pathway in cultured HCT116 cells.

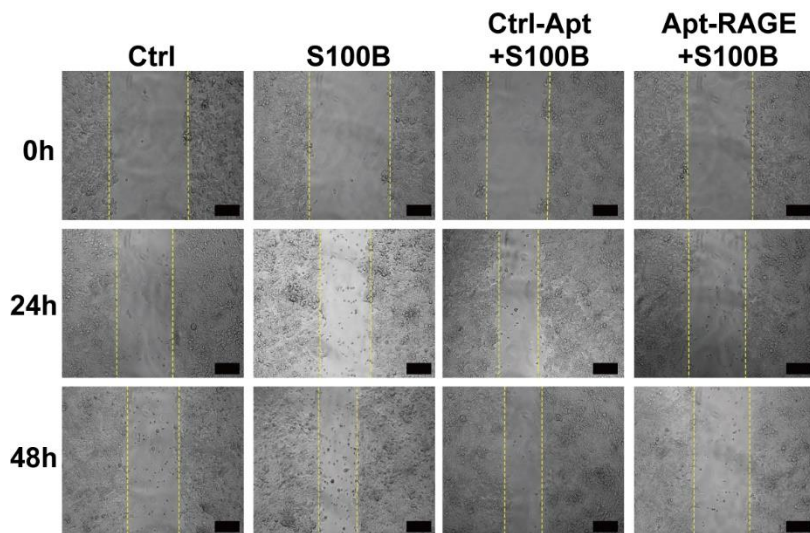


Fig. S4. Effect of Apt-RAGE (100 nM) on the migration induced by S100B (2 $\mu\text{g/mL}$) were detected by wound healing assay at 24 h or 48 h. Scale bar: 50 μm .