



Publisher Correction: Mapping the protein binding site of the (pro)renin receptor using *in silico* 3D structural analysis

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Correction to: *Hypertension Research* <https://doi.org/10.1038/s41440-022-01094-w>, published online 09 December 2022

Graphical Abstract was missing from this article; the figure should have appeared as shown below.

Mapping the protein binding site of the (pro)renin receptor using *in silico* 3D structural analysis

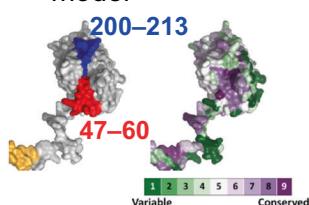
Previous findings

- ✓ The receptor homodimerizes.
- ✓ Antibodies against **47–60** and **200–213** regions show PDAC antiproliferative effect by suppressing Wnt signaling.
- ✓ The receptor is predicted to possess an **intrinsically disordered region**.

Examination **Explanation**

This study (*In silico* approach)

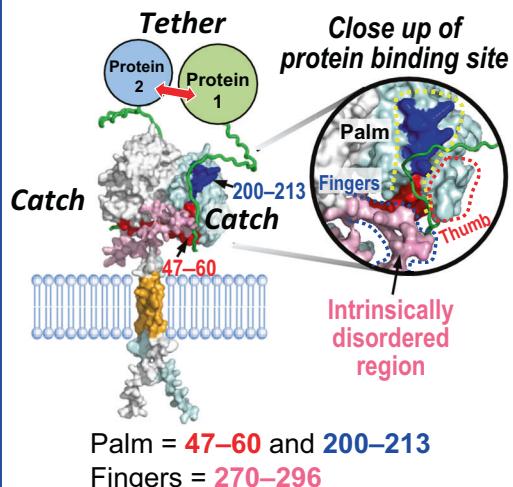
(A) Mapping onto 3D model (B) Analysis of homodimerization



Result: The surface area is comprised of evolutionarily conserved residues.

Result: Structural basis of homodimerization was obtained.

Conclusion



The receptor homodimerizes to generate two protein binding sites important for interaction with Wnt signaling proteins and other protein ligands.

The original article has been corrected.

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