



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

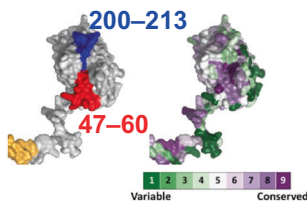
Previous findings

- ✓ 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

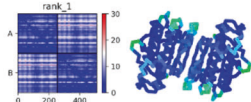
This study (In silico approach)

(A) Mapping onto 3D model



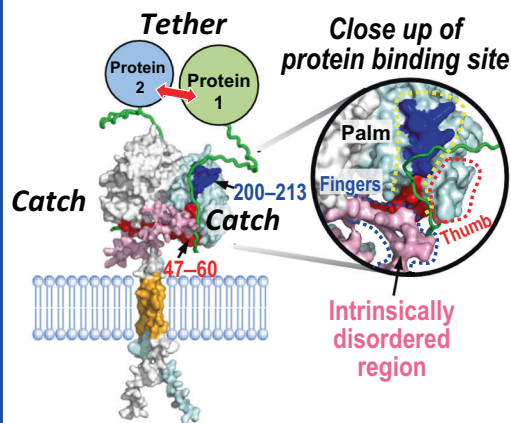
Result: The surface area is comprised of evolutionarily conserved residues.

(B) Analysis of homodimerization



Result: Structural basis of homodimerization was obtained.

Conclusion



Palm = **47–60** and **200–213**
Fingers = **270–296**

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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