

# Mediator is a Transducer of Amyloid Precursor Protein-Dependent Nuclear Signaling

Xuan Xu, Haiying Zhou, and Thomas G. Boyer

## SUPPEMENTARY FIGURES

Figure S1

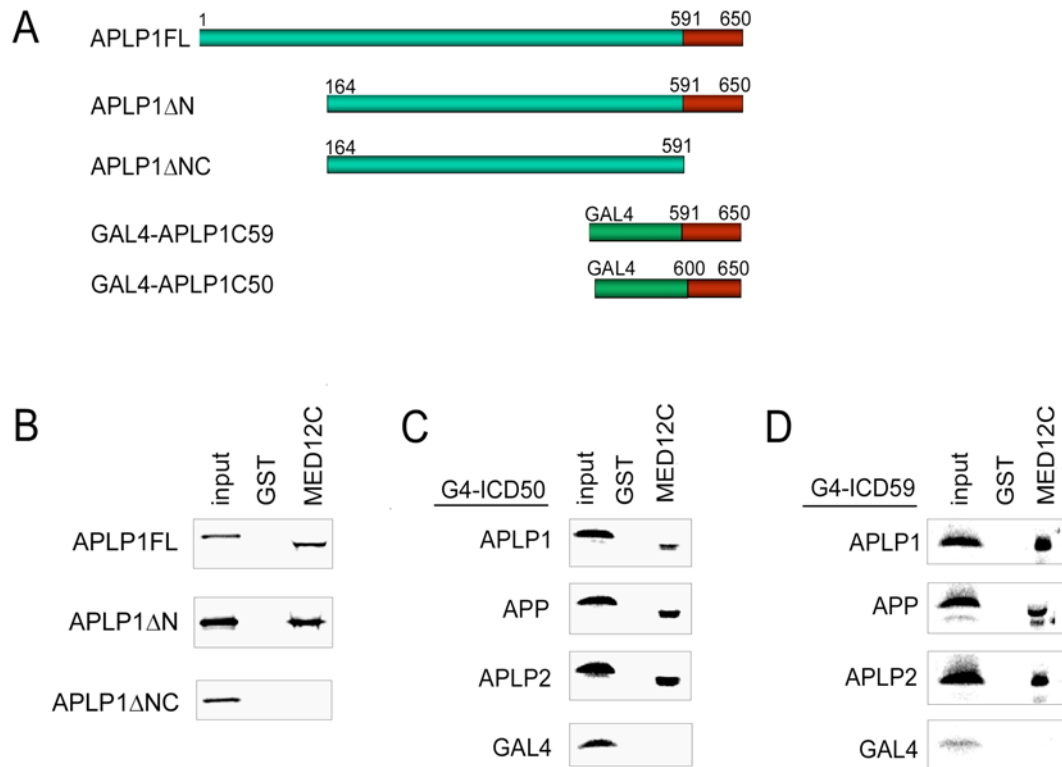


Figure S1. APP/APLP ICDs interact with MED12. (A) Schematic diagram of APLP1 derivatives used for in vitro binding assays. The APLP1 59 amino acid C-terminal intracellular domain (ICD) is highlighted. Numbers refer to amino acid coordinates. (B-D) Recombinant full-length

APLP1 and its specified truncation derivatives were expressed and radiolabeled with [<sup>35</sup>S]methionine by translation in vitro prior to incubation with glutathione-Sepharose-immobilized GST or GST-MED12C (aa 1616-2177) as indicated. Bound proteins were resolved by SDS-PAGE, and visualized by phosphorimager analysis. Input, 10% of in vitro translation product used for binding. GAL4 corresponds to the DNA binding domain (aa 1-147) of the yeast GAL4 protein, to which the APP/APLP ICDs were appended. Note that  $\gamma$ -secretase-mediated cleavage of APP/APLP family members can occur at two positions generating ICDs of 50 and 59 amino acids, both of which were tested for MED12 interaction (C,D); proteomics analyses have revealed that the ICD50 is the predominant intracellular species produced (Gu et al., 2001; Kimberly et al., 2001).

Figure S2

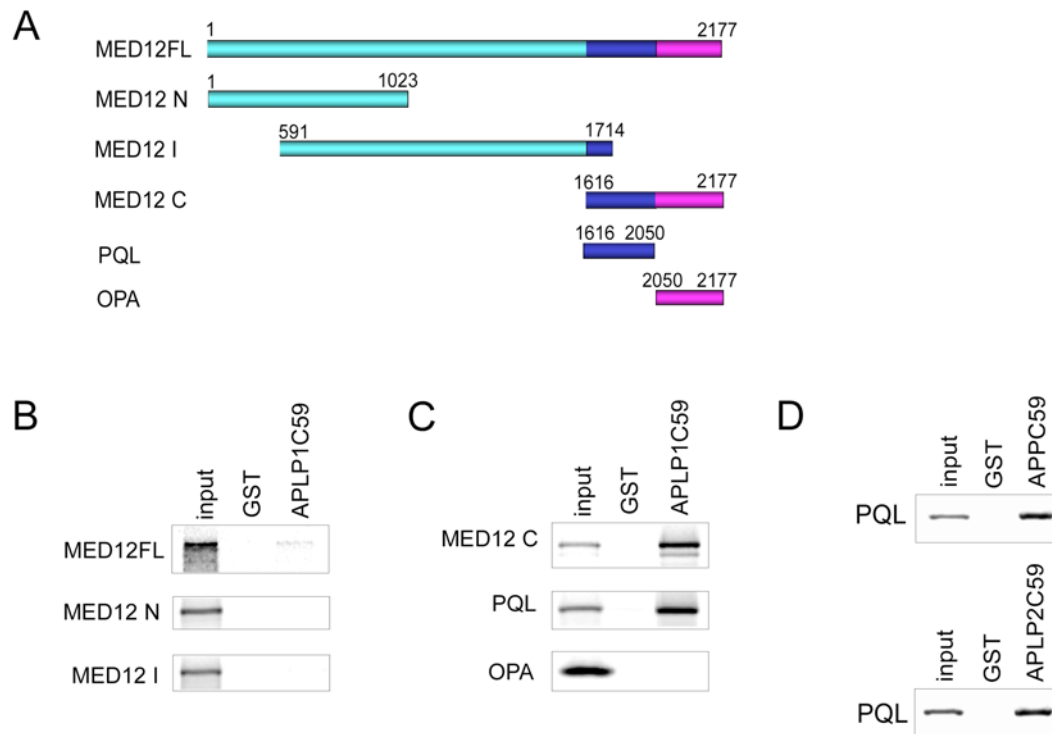


Figure S2. The MED12 PQL domain interacts with the APP/APLP ICDs. (A) Schematic diagram of MED12 derivatives used for in vitro binding assays. The MED12 PQL and OPA domains are highlighted. Numbers refer to amino acid coordinates. (B-D) Recombinant full-length MED12 and its specified truncation derivatives were expressed and radiolabeled with [<sup>35</sup>S]methionine by translation in vitro prior to incubation with glutathione-Sepharose-immobilized GST or GST-APP/APLP ICD59 (C59) as indicated. Bound proteins were resolved by SDS-PAGE, and visualized by phosphorimager analysis. Input, 10% of in vitro translation product used for binding.

## SUPPLEMENTARY MATERIALS AND METHODS

**Plasmids.** Full-length MED12 and truncation fragments used in glutathione S-transferase (GST) pull-down experiments have been described previously (Kim et al., 2006). pCS2+H<sub>6</sub>T<sub>7</sub>-APLP1 (encoding full-length APLP1), pET28C-APLP1<sub>Δ</sub>N (encoding APLP1 aa 164-650), pCS2+H<sub>6</sub>T<sub>7</sub>-APLP1<sub>Δ</sub>NC (aa 164-591), pBind-APLP1C50/59, pBind-APPC50/59 and pBind-APLP2C50/59 were constructed by PCR-based methods using human fetal brain cDNA as template DNA. Human APP/APLP ICD59 cDNA sequences were subcloned into the *E. coli* expression plasmid pGEX-6p-1 for production of GST-fusion proteins used in GST pull-down experiments.

**Glutathione S-Transferase (GST) pull-down assays.** GST-MED12c or GST-APP/APLP ICDs were expressed in *E. coli* strain BL21 (DE3), and soluble lysates were prepared as described previously (Ding et al., 2008; Zhou et al., 2006). Recombinant MED12 and APP/APLPs derivatives were expressed and radiolabeled with [<sup>35</sup>S]methionine by coupled in vitro transcription-translation reactions (TNT sp6/T7 Quickcoupled transcription-translation system; Promega). Radiolabeled recombinant proteins were incubated with GST derivatives immobilized on glutathione-sepharose beads (GE Healthcare Life Sciences), washed, eluted, and bound proteins resolved by 10% or gradient SDS-PAGE followed by Phosphorimager analysis as described previously (Ding et al., 2008; Zhou et al., 2006).

## SUPPLEMENTARY REFERENCES

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