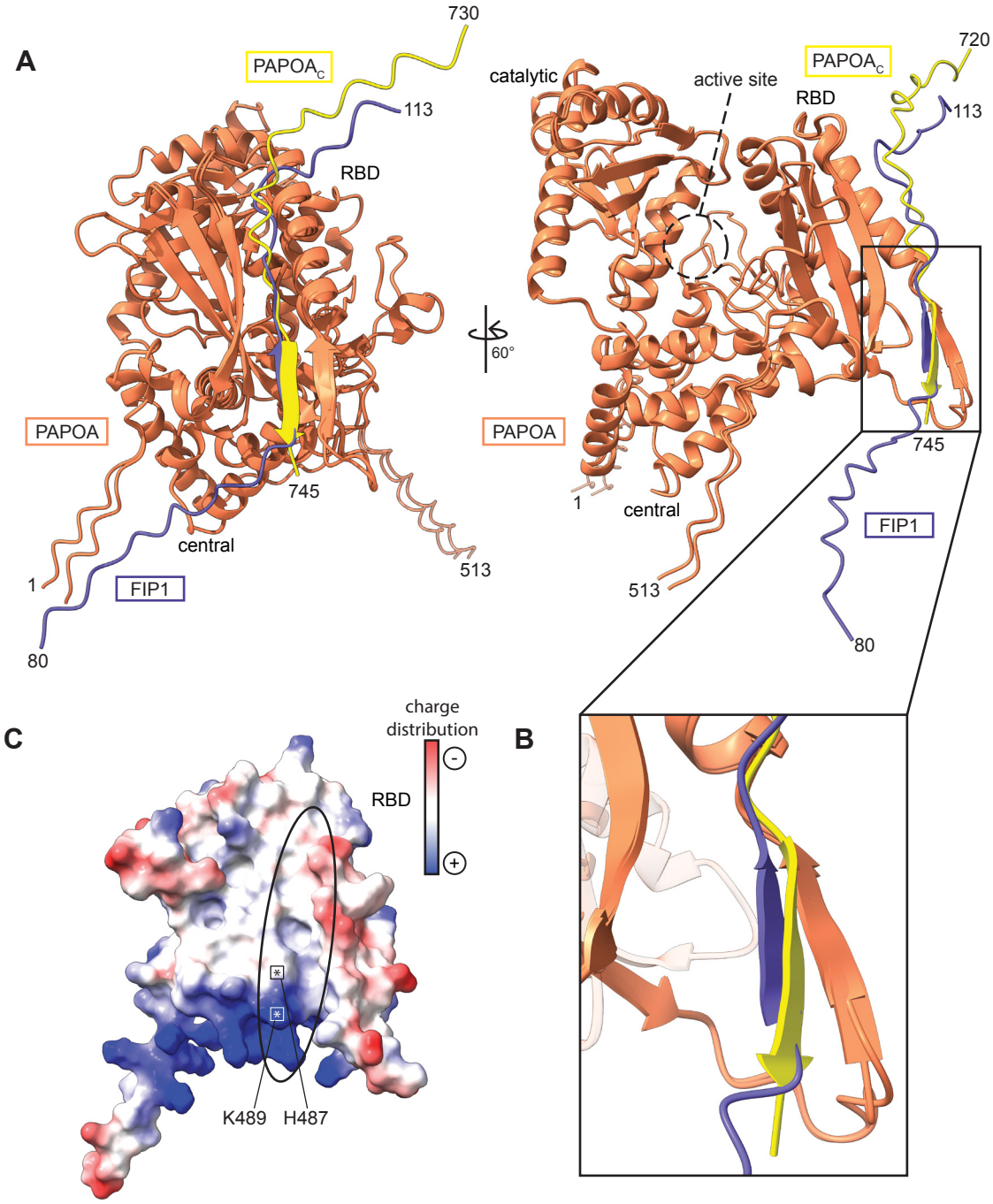
A
730
PAPOA$_C$
113
RBD
PAPOA
745
central
513
1
FIP1
80
catalytic
active site
RBD
720
PAPOA$_C$
113
60°
PAPOA
745
1
central
513
FIP1
80
B
C
charge
distribution
-
+
RBD
K489
H487

Figure S2: Characterization of the PAPOA-PAPOA$_C$ interaction

(A) Overlay of computationally predicted models of PAPOA$_{1-513}$-FIP1$_{80-113}$ and PAPOA$_{1-513}$-PAPOA$_C$. The PAPOA structured domains and active site are indicated.

(B) Close-up of the binding interfaces of PAPOA$_{1-513}$-FIP1$_{80-113}$ overlayed with PAPOA$_{1-513}$-PAPOA$_C$.

(C) The PAPOA RBD shown in surface representation with residues colored by electrostatic properties. The interaction pocket engaged by FIP1 and PAPOA$_C$ is indicated with a black ellipse. Labeled residues were changed to glutamic acid.