

Supplementary

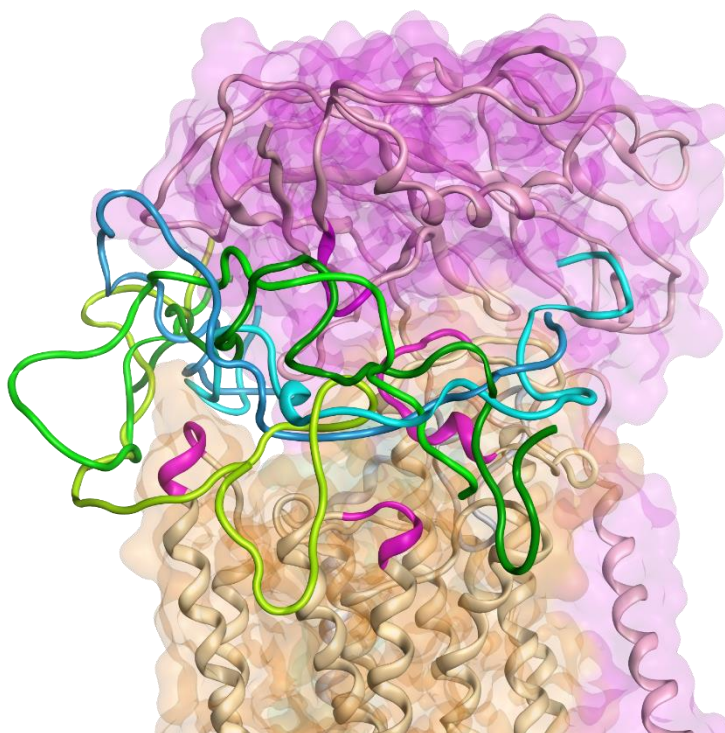


Figure S1. Five complexes of Na,K-ATPase with A β_{42} obtained by fullblind docking as it described in methods section. A β_{42} peptides are colored green and the probable interaction sites are colored magenta.

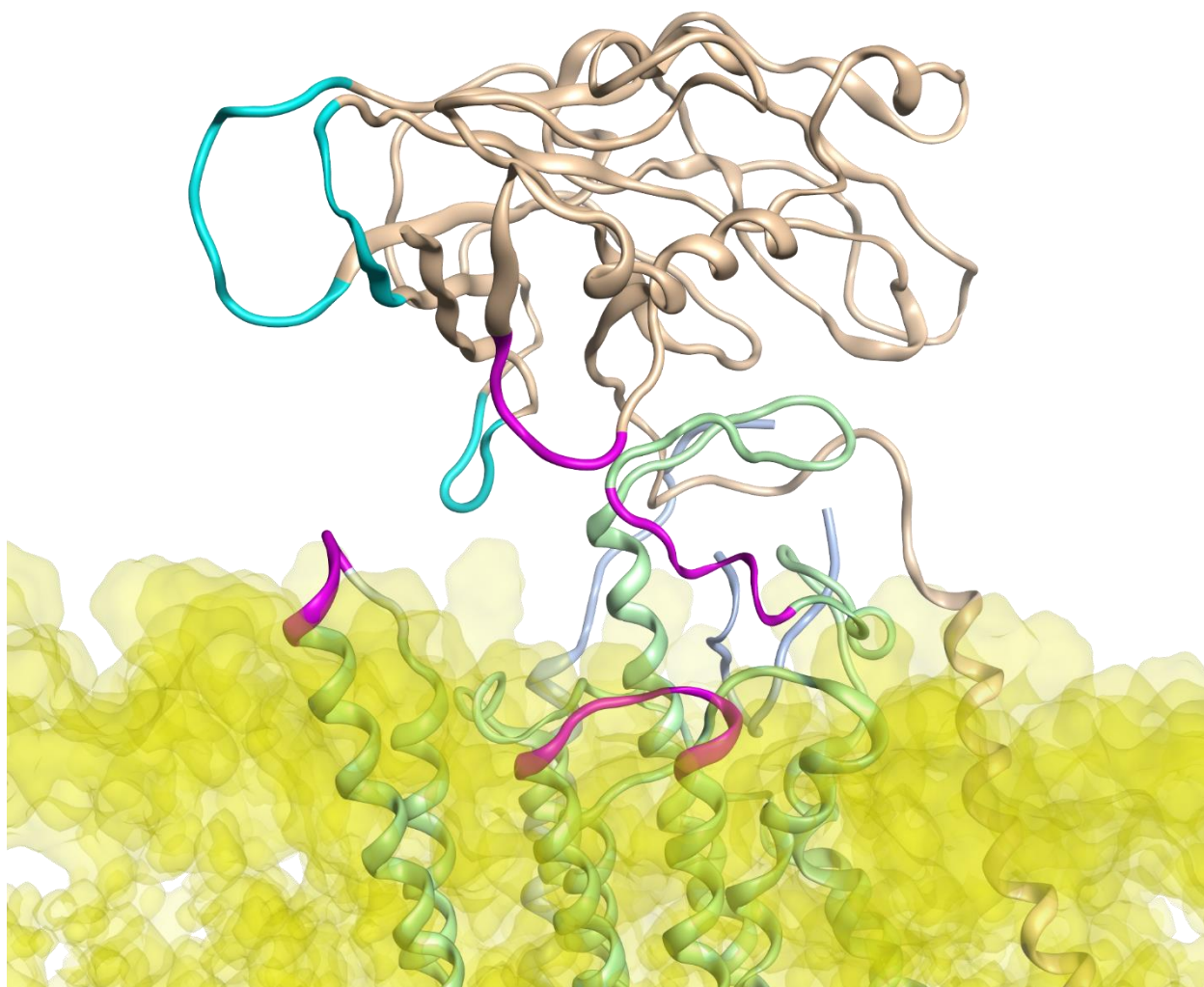


Figure S2. Interaction sites with A β_{42} on E1P Na,K-ATPase after 50 ns MD. Sites 119-AATEE-124, 310-SLILEY-315 and 887-RVDWDDR-893 on α -subunit and site 84-QKTEI-87 on β -subunit are concerned to present the main interaction interface and are colored with magenta. Other interaction sites 216-KRDEKDKVG-226, 267-TMDTEIR-273 and 285-YSEKDR-290 on β -subunit are colored with cyan.

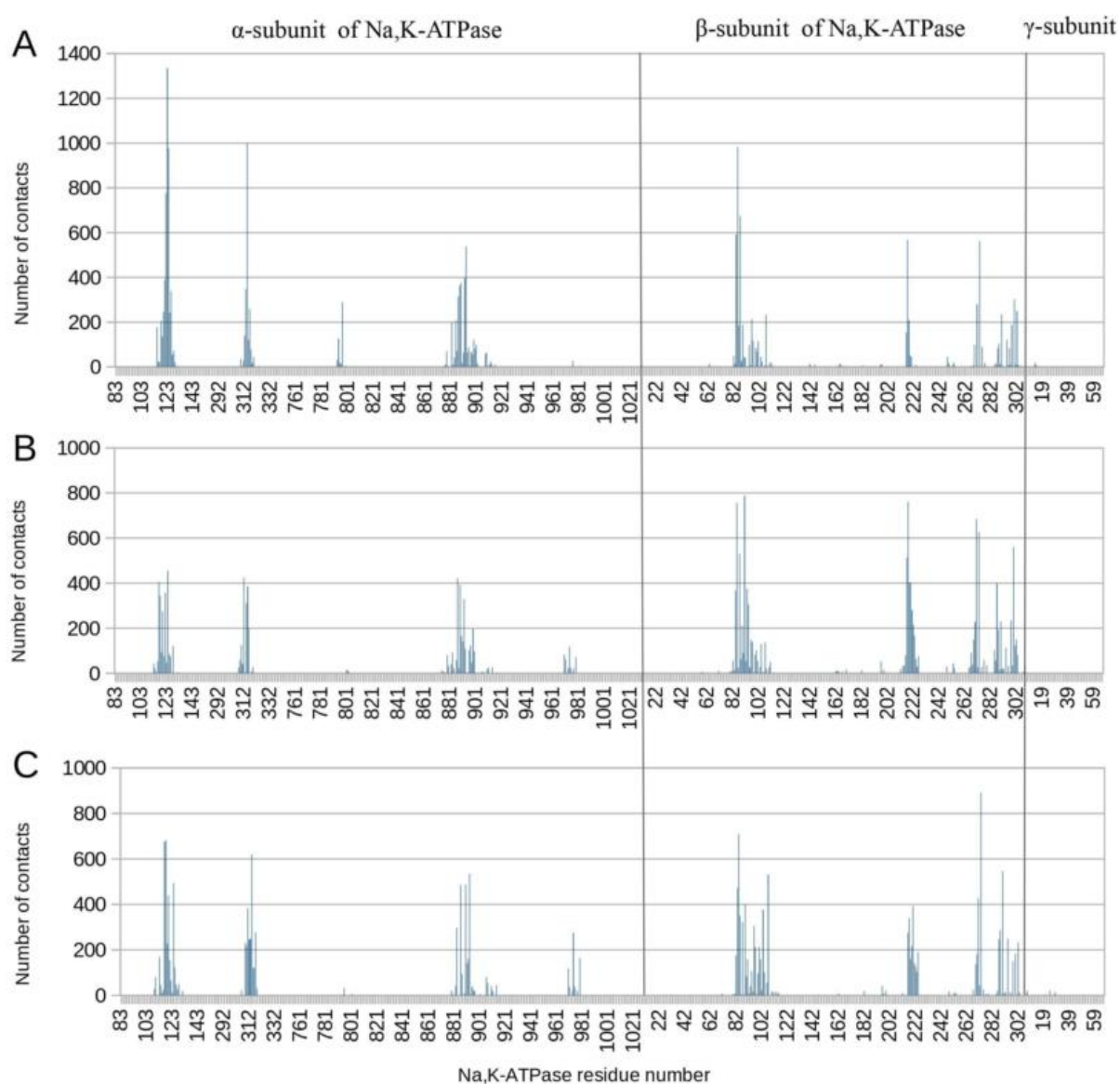


Figure S3. The number of intermolecular contacts with three $A\beta$ isoforms after targeted global docking of E1P (A), E2P (B) and OBN (C) conformations of $\alpha 1$ isoform of human Na, K-ATPase. The data for each conformation are summarized for 3 $A\beta$ isoforms and about 30 complexes from docking.