## Figures/preliminary results

**Figure 1 Initial cryoEM analysis of ACE.** A. SDS page of purified ACE. B. 3D classification of ACE. Extra-densities are mostly from N-linked glycosylations. It is worth noting that ACE-C domains have substantially poor density in comparison to ACE-N, suggesting the denaturation or high structural heterogeneity.

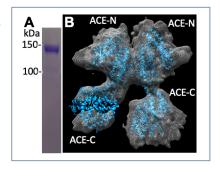
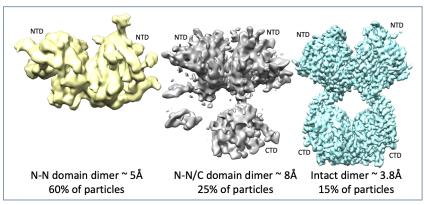


Figure 2 3D classification from the optimized buffer condition that better maintains ACE stability. Of three classes, the most common structure (60% particle) is consistent with that contains only two ACE-N domains. The second (25%) is that contains both ACE-N domains and only one ACE-C. The least one is the dimeric ACE that contains all four



ACE catalytic domains. Our data suggests the preferential denaturation of ACE-C domains.

**Figure 3 Structural heterogeneity analysis of ACE. A.** Overall structure of ACE dimer with Coulomb potential map and structural model in ribbon representation. **B.** Three classes from the

focused refinement that represent ACE monomer. C. Three classes from the focused refinement that represent ACE -N. B. Three classes from the focused refinement that represent ACE-C. Together, this shows the inter-domain variability between ACE-N and ACE-C within each ACE monomer and the structural heterogeneity of individual ACE catalytic domains.

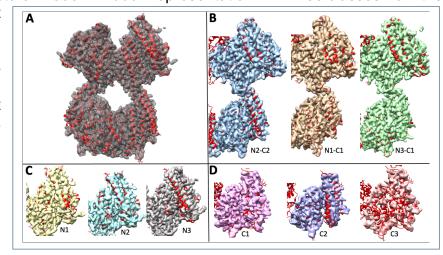
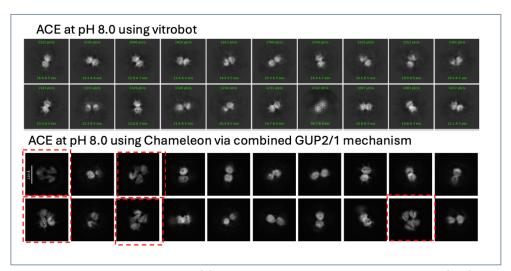


Figure 4 Comparison of classes top 2D of human ACE extracellular region at 8.0 Hq with micrographs prepared by grids using vitrobot versus that by chameleon done by NCCAT via combined GUP 1 & 2 programs. None of 2D classes has the expected four-domain structure from vitrobot



prepared grid, thus we could not obtain 3D structure of four-domain extracellular region of ACE. Under the same condition and using chameleon for grid preparation, we have obtained 2D classes that have four-domain feature marked by red box. At pH 8.0, the physiological relevant substrate, amyloid beta has the reasonable solubility, which should allow us to assess the structure of amyloid beta bound ACE structure.

Figure 5 Coulomb potential map (top) and FSC curves (bottom) of three distinct classes of extracellular region of ACE dimer at pH 8.0 using grid prepared by chameleon.

