

MEETING ABSTRACTS

THE PROTONATION STATE OF Glu197 AND ITS IMPORTANT ROLE IN STABILIZING CATALYTIC TRIAD OF BUTYRYLCHOLINESTERASE

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The Glu197 of butyrylcholinesterase (BChE) has been long considered as deprotonated in various studies, e.g. discovering the dynamical characters, interpreting the binding properties of inhibitors, and proposing hypotheses for BChE-catalyzed reaction mechanism. By performing a series of 100 ns molecular dynamics simulations, we accidentally discovered that Glu197 needed to be protonated to have the structures simulated appropriately, whereas the deprotonated Glu197 eventually caused the collapse of catalytic triad with long enough simulation time.[1] we found that a highly conserved water molecule required Glu197 to be protonated in order to form an important hydrogen bond network, which supported His438 to be preserved within the catalytic triad. Interestingly, catalytic triad and Glu197 have been long recognized for possibly deviating largely from their crystal structure positions, which could be catalytic deficient and is generally considered as the result from difference between crystal and aqueous environment. Here, our results suggest that the large deviations of catalytic triad and Glu197 from crystal structure are caused by inappropriate protonation state of Glu197. This finding of the unexpected protonation state of Glu197 shall provide an important clue that has been long missing for the better understanding of BChE related puzzles or even reconsideration of some BChE-catalyzed reaction mechanisms.

Keywords: protonation state; Glu197; butyrylcholinesterase; catalytic triad

References

1. Wan, X.; Yao, Y.; Fang, L. ;Liu, J., *Unexpected protonation state of Glu197 discovered from simulations of tacrine in butyrylcholinesterase*. PCCP **2018**, 10.1039/c8cp01566j.