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Drug-protein interaction: Ultra Accelerated Quantum Chemical Molecular Dynamics study

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【Introduction】Protein-ligand interactions play a central role in biochemistry and one of the interactions of this kind is that between a pharmaceutically important chemical moiety and its target enzyme. The objective of current work was to study drug-protein interactions using ultra accelerated quantum chemical molecular dynamics method (UAQCMD). For the first time, the drug protein interactions are studied using this method.

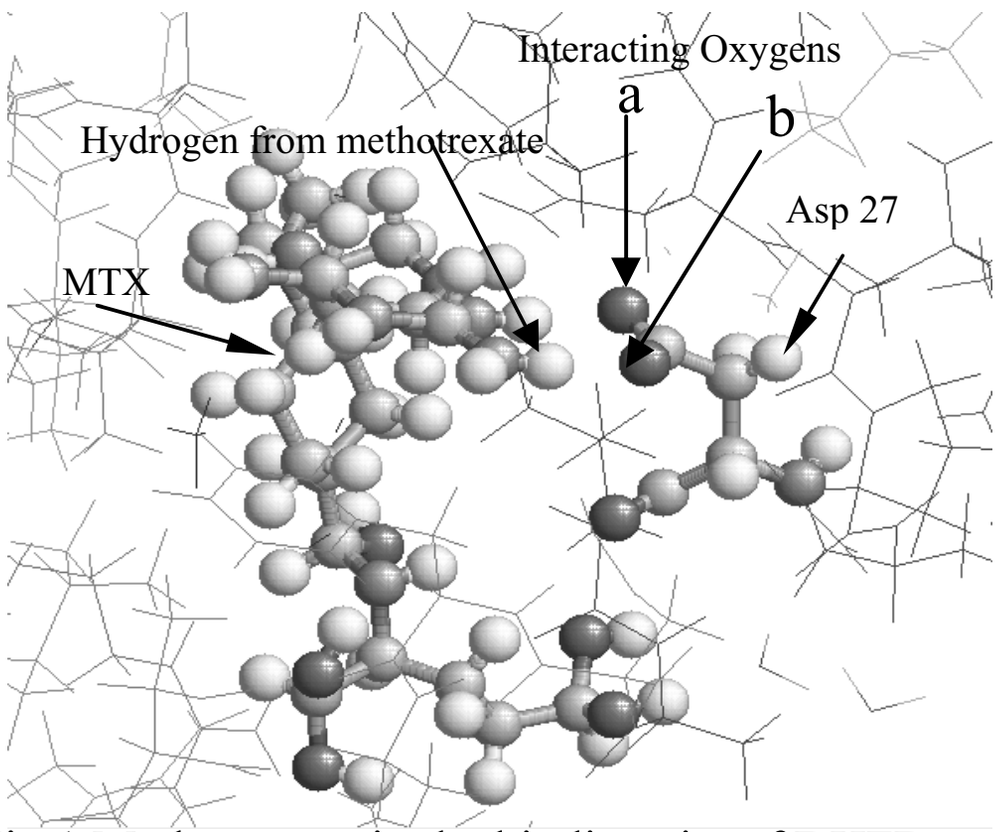

Fig.1 Methotrexate in the binding site of DHFR

【 Method 】 We have used UAQCMD method. We derived potentials from quantum chemical calculations and used for MD simulations.

【Result and discussion】Fig. 1 shows the methotrexate (MTX) in binding site of dihydrofolate reductase (DHFR) enzyme where Asp27 is the closest amino acid whose oxygen atoms interact with hydrogen of MTX. Oxygen atoms a and b from Asp27 were found to be interacting with hydrogen atom of MTX and this was confirmed by QC calculation in which a bond population of 0.4 was obtained for oxygen a and b with MTX-hydrogen. The comparatively lesser charges of –0.422 and –0.514 on oxygen a and b respectively indicate the shift of electron pairs towards hydrogen.