

APPLICATION of X-RAY SPECTROMETRY at X-RAY ABSORPTION EDGES for INVESTIGATION of HUMAN ALBUMIN

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Human albumin demands precise experiment investigation of composition and mostly needed configuration of structural coordination of interatomic distances, oxidation state, and electron structure of Cu–O connections.

This albumin plays a dramatically great role for immunity ability of a human and suppressing of an infection. The supposed mechanism of suppressing is as follows: Cu atoms are the effective oxidant for killing of hazardous bacteria and viruses. In this aspect, it is important that energy binding of Cu should be easily destroyed in order that Cu atoms become free and oxidize hazardous elements and neutralize their effect on spoilt cells.

Typically the albumin molecule consists of 128 atoms and contains only 8 atoms of Cu. If a human is sick then Cu atoms that are delivered by blood stream may be freed from their positions and actively oxidize a bacterium membrane. Our task is to estimate the ability of albumin to lose active Cu oxidation particle. Thus it is important at which state Cu was captured in initial albumin as it defines the probability of injection of active Cu.

One of the most sensitive methods of chemical binding control independently of an aggregate state of a sample (liquid, gas, condensed state) is XANES spectroscopy (registration and evaluation of x-ray absorption fine structure at absorption edges).

We present our results of XANES research of Cu oxidation and binding state in human albumin. Especially underlined is new method for correct interpretation of small signals from only 8 atoms within a molecule of 128 atoms.

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