

MS07-P18 | HIGH-RESOLUTION DIMERIC CRYSTAL STRUCTURES OF WILD-TYPE AND MUTANT ASPERGILLUS NIGER GLUCOSE OXIDASE

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Glucose oxidase (GOx) is an enzyme that catalyzes the oxidation of β -D-glucose to hydrogen peroxide (H_2O_2) and δ -glucono lactone using molecular O_2 . It is a homodimeric glycoprotein non-covalently bound to a flavin adenine dinucleotide (FAD) cofactor. GOx is used for commercial applications and it is among the most important enzymes used in pharmaceutical, clinical chemistry, biotechnology, and other industries. Its most important application is in biosensors for the detection and estimation of glucose in blood and urine. Our goal in this project is better understand the reaction mechanism and dynamics of glucose oxidase.

Here, we describe a 1.63 and 2.0 Å crystal structures of *Aspergillus niger* wt-GOx and its mutant G513S bound to FAD. The enzyme crystallized in the $P2_1$ monoclinic space group with unit-cell dimensions 84.549, 81.920, and 103.190 Å and $\beta=106.30^\circ$. The asymmetric unit contained one GOx homodimer, making it the first structure to have a complete dimer in the asymmetric unit. The current R factor and R_{free} are 18.29 and 21.43 %. The refined model includes 580 amino acid residues for each subunit, two FAD cofactors, fifteen N-acetylglucosamine residues, ten mannose residues, and five bromide anions.

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