

COUPLED SECOND SPHERE RESIDUES BOOST H₂O₂ PRODUCTION IN LYTIC POLYSACCHARIDE MONOOXYGENASES: A COMPUTATIONAL STUDY IN AA11 LPMO

Ashish Tamhankar^a, Synnøve Elisa Rønnekleiv^b, Zarah Forsberg^b, Åsmund K. Røhr^b, Vincent G. H. Eijssink^b, Sergio A. V. Jannuzzi^{a*} and Serena DeBeer^{a*}

^aMax Planck Institute for Chemical Energy Conversion, Stiftstraße 34-36, 45470 Mülheim an der Ruhr, Germany

^bFaculty of Chemistry, Biotechnology and Food Science, Norwegian University of Life Sciences, Ås, Norway

Lytic polysaccharide monooxygenases (LPMOs) are copper-dependent enzymes that catalyze oxidative degradation of recalcitrant polysaccharides and are central to sustainable biofuel production. LPMOs utilize O₂ or H₂O₂ as co-substrate, with experimental evidence identifying H₂O₂ as the preferred oxidant. Under typical experimental conditions, H₂O₂ is generated *in situ* via LPMO oxidase activity, which may constitute the rate-limiting step of LPMO function. Across LPMO families AA9, AA10, and AA11, elevated H₂O₂ production rates show consistent correlation with the presence of a Glu–Tyr motif in the secondary coordination sphere, suggesting a mechanistic role, though the origin and impact of the interplay between these two residues remains unexplored.

Here, we rationalize the structural basis for high H₂O₂ production by an AA11 LPMO with a unique Glu–Tyr pair in the secondary coordination sphere, using QM/MM calculations. We systematically evaluate multiple pathways for proton and electron transfer, focusing on the roles of key secondary sphere residues (Glu–Tyr) and the water molecule coordinated to the copper center together with the dioxygen species. Our analysis highlights the previously underappreciated relative significance of the Cu(I) oxidation by O₂ versus subsequent proton transfer steps. We further assess the potential dissociation of all reaction intermediates from the Cu center (*e.g.*, superoxo, hydroperoxo) using thermodynamics by fully accounting for the reorganization of the first solvation shell of all species, offering a more accurate picture of the dissociation energetics. Additionally, we apply Local Energy Decomposition (LED) analysis to dissect non-covalent interactions, revealing the specific contributions of individual amino acid residues (both stabilizing and destabilizing) throughout the catalytic cycle. Collectively, our findings provide a deeper mechanistic understanding of LPMO oxidase activity, focusing on the involvement of the secondary sphere residues. These findings offer valuable design principles for engineering improved LPMOs and bio-inspired catalysts, emphasizing the strategic integration of secondary sphere residues and dynamic solvation effects.