Lytic polysaccharide monooxygenases and their friends

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We have been working for some years on lytic polysaccharide monooxygenases, a new class of copper enzymes particularly relevant for the degradation of recalcitrant polysaccharides (recently reviewed in [1]). These enzymes are classified in Auxiliary activity families AA9-AA11 and AA13-AA16 in the Cazy database and contain a characteristic histidine brace copper binding site. Recent work has taken us in slightly unexpected directions, since structural and functional studies have revealed that proteins closely related structurally to LPMOs may have evolved completely different molecular or even biological function. Two main unpublished examples where the structural information partly results from data collected at Biomax, MAX IV, will be presented: 1) a group of proteins classified in the AA9 LPMO family, but devoid of the His brace motif; 2) a group of proteins (referred as X325 family) distinct in sequence from known LPMO families, but very similar in structure, including the His-brace copper binding site. X325 have an additional ligand to the copper (Asp); are devoid of LPMO activity, and play important roles in biological functions distinct from biomass degradation and probably linked to copper homeostasis. Thus the cases presented are fascinating examples of evolution of different functions from a common structural scaffold.

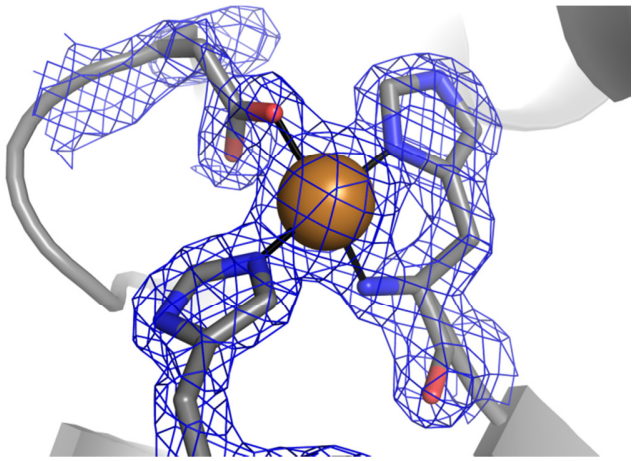

Figure – Electron density (2Fo-Fc contoured at 2 σ) at the Cu-binding site of *L. arvalis* X325 (*P*21 crystal form collected at Biomax, at a maximum resolution of 1.82 Å)

References:

[1] Tandrup T., Frandsen K.E.H., Johansen K.S., Berrin J.-G., Lo Leggio L., Recent insights into lytic polysaccharide monooxygenases (LPMOs), *Biochemical Society Transactions*, 2018, **46**, 1431-1447.