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A structural overview of GH61 proteins – fungal cellulose degrading polysaccharide monooxygenases

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Abstract: Recent years have witnessed a spurt of activities in the elucidation of the molecular function of a class of proteins with great potential in biomass degradation, GH61 proteins are of fungal origin and were originally classified in family 61 of the glycoside hydrolases. From the beginning they were strongly suspected to be involved in cellulose degradation because of their expression profiles, despite very low detectable endoglucanase activities. A major breakthrough came from structure determination of the first members, establishing the presence of a divalent metal binding site and a similarity to bacterial proteins involved in chitin degradation. A second breakthrough came from the identification of cellulase boosting activity dependent on the integrity of the metal binding site. Finally very recently GH61 proteins were demonstrated to oxidatively cleave crystalline cellulose in a Cu and reductant dependant manner. This mini-review in particular focuses on the contribution that structure elucidation has made in the understanding of GH61 molecular function and reviews the currently known structures and the challenges remaining ahead for exploiting this new class of enzymes to the full.

Mini Review Article

Introduction

Decades of research on plant polysaccharide degrading enzymes for the exploitation of biomass have mostly focused on glycoside hydrolases, which have been classified in sequence-based families in the CAZY (Carbohydrate Active enZymes) database [1]. Glycoside hydrolases (GH) and other carbohydrate active catalytic domains are often coupled to non-catalytic carbohydrate binding modules (CBMs, reviewed in [2]), also classified in CAZY, which have the function of binding to eg crystalline or complex substrates and have in some cases been shown to act in synergy with the catalytic domains.

In view of the world energy crisis, bioethanol production has become a rather hot topic. While ethanol can be feasibly produced from starch rich crops, a much more renewable and sustainable solution would be the production from (ligno)cellulosic biomass, which constitutes a large proportion of agricultural and forestry byproducts. Thus a lot of attention has been devoted to enzymes able to degrade cellulose to sugars fermentable by S. cerevisiae. In particular the Trichoderma reesei/Hypocrea jecorina system has received much attention in terms of commercial exploitation. Cellulose breakdown (see [3] for a classic review) has been viewed for many years as carried out mainly by endoglucanases and processive exoglucanases (cellobiohydrolases) acting in synergy, often with the aid of cellulose binding domains assisting attachment to cellulose. β-glucosidases are also often part of cellulosytic systems, where they relieve the product inhibition of cellobiohydrolases by cellobiose, and they are often added to commercial preparations. However, the mechanism by which some microorganisms are able to efficiently degrade crystalline cellulose has remained in many ways a mystery. In the last few years a new class of fungal proteins with huge potential for the degradation of cellulose has received much attention, the GH61 proteins. Initially classified as family 61 among the glycoside hydrolases they are now recognized to be Cu-dependent oxidases [4, 5, 6], calling for a reclassification of these enzymes. As such a reclassification is yet to be implemented in the CAZY database, we choose in this review to keep the somewhat inappropriate GH61 designation, which allows retrieval of most of the earlier literature. This family has puzzled carbohydrate active enzyme experts since its discovery, and to some extent continues to do so. Structure determination by X-ray crystallography was a crucial step towards understanding the significance and mechanism of action of these enzymes. This short review briefly summarizes the progress up to now, and focuses on the structures currently known.

A brief history of GH61

The first GH61 protein to be identified was probably CelII from Agaricus bisporus the sequence of which was described in 1992 after cloning of the gene [7]. Although no activity could be described, the gene was induced on growth on cellulose, and the presence of a sequence typical of a cellulose binding domain implicated the protein in cellulose degradation. The GH61 family was first created in 1997, when it was referred to at least twice in the literature [8, 9]. The evolution of the family in terms of number of members can be seen in Figure 1a.

The first papers on characterization of GH61 family members reported very low cellulose degrading activity if any. For example T. reesei Cel61A [10], showed some degrading activity on polymeric cellulotic substrates, but at levels 5-6 orders of magnitude lower than a conventional cellulase, Cel7B, making it difficult even by use of sensible controls to totally rule out the possibility of contamination by canonical cellulases. In hindsight, the low activity can be explained...
by the lack of essential cofactors, which at the time were unknown. However the identification of GH61 members in cellulosytic organisms such as T. reesei, A. bisporus, Aspergilli species and Neurospora crassa together with their co-induction with classical cellulases upon growth on cellulose [7] [11], already early on suggested the GH61 family involvement in lignocellulose degradation. This was further supported by the fact that several of the first GH61 domains were found to be associated with family I CBMs, which are crystalline cellulose binders.

A first breakthrough in the molecular understanding of GH61 function came from the structures of two family members which were communicated at conferences and in peer-reviewed journals in 2008 [12] [13]. The first publication [13] revealed the 3D structure of Hypocrea jecorina (Trichoderma reesei) Cel61B (from now on referred to as HjGH61B), solved by Single-wavelength Anomalous Diffraction utilizing Ni ions from the crystallization conditions. HjGH61B has an immunoglobulin-like ¿sandwich fold, and very atypically if it were a true GH, lacks a clear substrate binding groove and an appropriately positioned and exposed active site carboxylate pair, which is, with few exceptions, ubiquitous in GHs mechanisms. The authors concluded that based on the structure this was an unlikely GH. Most interestingly, a clear metal binding site was proven by other means to be present in the mixture. Thus the identity of the metal binding site in its native environment remained unclear.

The demonstration that GH61 could boost the activity of hydrolytic cellulases established a biological justification for the coexistence and co-expression of GH61 with the more conventional cellulose-degrading enzymes and underpinned the biotechnological potential of GH61. It is noteworthy that these first structural publications included authors from two large world enzyme producers, Novozymes A/S and Genencor. As can be seen from Figure 1b, after the publication of the TrGH61E article the literature on GH61 was significantly boosted.

Another very important link emerging from these first two structures was the structural similarity to chitin binding protein CBP21 from Serratia marcescens [17] at that point thought to non-enzymatically disrupt chitin and classified as a carbohydrate binding module belonging to family 33 (CBM33). Not only the overall structure of CBP21 was similar to the two GH61 structures, but
CBP21 had also a very similar arrangement of residues as in the identified metal binding site, although no divalent metal was modeled in this structure (a sodium ion is though modeled at this site in one of the molecules in the asymmetric unit, see PDB code 2BEM). Furthermore mutagenesis of the conserved non-terminal His at this site was shown to affect the boosting effect of CBP21 on chitinase C [18]. There is however an important difference at the metal binding site since CBP21 has a conserved Phe instead of Tyr, while a Tyr to Phe substitution is detrimental to the activity of TtGH61E.

![Figure 2. Metal binding site of TtGH61E (PDB code 3EJA, chain A) highlighting the mutated residues [14]. In red residues whose replacement resulted in complete abollishment of activity. In orange Gin151 whose replacement resulted in complete abolishment or severe impairment of activity (depending on the replacement residue). In yellow Tyr153 whose replacement resulted in impairment of activity.](image)

Given the functional and structural similarities and their complementary phylogenetic distribution (GH61 are predominantly fungal – see also the phylogenetic analyses in [14] and [19] - while CBM33 are predominantly bacterial and viral), it was already suspected at this time that the two families maybe distantly related. More details on the CBM33 family can be found in a recent publication which reviews the two families’ (CBM33 and GH61) biotechnological potential [20].

Although this review strictly focuses on GH61, the progress in the understanding of the two families has been so linked that CBM33 cannot be completely ignored. A key paper in the understanding of the two families has been so linked that CBM33 proteins oxidatively degrade crystalline cellulose with production of oxidized (aldonic acids) and unoxidized products, again with dominance of even-numbered DP [22]. Similarly to previous work, divalent metal ions were shown to be necessary, but no clear preference could be shown.

Not long after researchers began to report oxidative activity also for GH61 proteins, resulting in a mixture of non-oxidized and oxidized cellodextrins after crystalline cellulose degradation [4, 23, 5]. In [4], it was clearly shown that at pH 5 a GH61 protein from Thermus aquaticus, TgGH61A, is highly selective for binding of Cu²⁺ ions and that the Cu-loaded TaGH61A oxidatively degrades crystalline cellulose in the presence of small molecule redox active agents such as galate and ascorbate. Electron paramagnetic resonance spectroscopy showed clearly a signal for Cu(II) similar to the one observed in type II copper oxygenases. More or less at the same time [24], it was also shown that the combination of GH61 and cellobiose dehydrogenases (CDH) from same or different organisms could oxidatively degrade highly crystalline cellulose without added small molecule reductants. Later in 2011, reports in [5] and [6] confirmed that GH61 are cellulose degrading Cu metalloenzymes. In [5] the important role of cellobiose dehydrogenases (CDH) in cellulose degradation by GH61 was underpinned by genetic and biochemical experiments, and it was suggested that in nature reduced CDHs may reduce Cu(II) to Cu(I) in the catalytic mechanism of GH61s. Furthermore it was suggested that polysaccharide monooxygenases, as GH61 are referred to in this publication, can be of two types depending on whether oxidation is introduced on one side or the other of the broken glycosidic bond. The mechanisms of the type 1 and type 2 GH61s have been investigated in more detail in [25] and by isotope labelling GH61s of type 1 were shown to incorporate one oxygen atom from molecular oxygen into the product and therefore to be monoxygenases. Two crystal structures for Neutropora crassa GH61s have recently been published [26], where the authors claim to have isolated oxygen species, which however are difficult to unequivocally establish purely by crystallography, despite high resolution and careful refinement. As a final remark, after the very recent elucidation of the chitinolytic system of Enterococcus faecalis V583 and structure determination of a new CBM33 enzyme, Cu has after some dispute been recognized to be the active metal also for these enzymes [27]. Thus there seems to be general consensus that both GH61 and CBM33 are Cu dependent monoxygenases.

Structural biology has thus made an essential contribution to the understanding of the molecular mechanism of GH61 function, especially by the discovery of the similarity between GH61 and CBM33 and the metal binding site, its functional importance (by guiding mutagenesis) and its clarification as a Cu(II) binding site. The structures known so far for GH61 and some of their features are reviewed below.

**Known structures of GH61 family members**

To date, five structures of GH61 proteins have been determined, all by X-ray crystallography. Table 1 summarizes some of the characteristics of the structures, while Table 2 summarizes the sequence and structural similarity between them. Two of the structures (TrGH61E and HjGH61B) have already been discussed in some detail above and are in fact the two most dissimilar (Dali-Lite [28] aligns 200 residues with 1.9 Å Cα rmsd and 29% structure based sequence identity). Three additional structures have since been determined [4] [26]. The dendrogram in Figure 3 illustrates graphically the relationship between the different proteins. TrGH61E (code 3EJA) and NcPMO2 (code 4EIR) are distant from each other and the other sequences, while NcPMO3 (code 4EIS), HjGH61A (code 2VTQ) and TaGH61A (code 3ZUD) form a more closely related group. This is also highlighted in Figure 4, where differences in loop structures as well as presumed functional residues are clearly visible between TrGH61E, NcPMO2 and NcPMO3.
Table 1. Overview of known structures. The Tyr conserved at the aromatic surface in all structures is in bold.

<table>
<thead>
<tr>
<th>Abbreviation</th>
<th>Organism</th>
<th>PDB code(s)</th>
<th>Resolution (Å)</th>
<th>Associated with CBM1</th>
<th>'Flat' surface aromatics</th>
<th>Ref</th>
</tr>
</thead>
<tbody>
<tr>
<td>TtGH61E</td>
<td>Thielavia terrestris</td>
<td>3EII</td>
<td>2.25</td>
<td>No</td>
<td>Tyr67, Tyr191, Tyr192</td>
<td>[14]</td>
</tr>
<tr>
<td></td>
<td></td>
<td>3EJA</td>
<td>1.90</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NcPMO2</td>
<td>Neurospora crassa</td>
<td>4EIR</td>
<td>1.10</td>
<td>No</td>
<td>Tyr67, Tyr206, Trp207</td>
<td>[26]</td>
</tr>
<tr>
<td>TaGH61A</td>
<td>Thermoaecus aurantiuscous</td>
<td>3ZUD</td>
<td>1.25</td>
<td>No</td>
<td>Tyr24,</td>
<td>[4]</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2YET</td>
<td>1.50</td>
<td></td>
<td>Tyr212</td>
<td></td>
</tr>
<tr>
<td>HjGH61B</td>
<td>Hypocreja jecorina</td>
<td>2VTC</td>
<td>1.60</td>
<td>No</td>
<td>Tyr23,</td>
<td>[13]</td>
</tr>
<tr>
<td></td>
<td>(Trichoderma reesei)</td>
<td></td>
<td></td>
<td></td>
<td>Tyr20,</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Tyr24,</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Tyr163,</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Tyr212</td>
<td></td>
</tr>
<tr>
<td>NcPMO3</td>
<td>Neurospora crassa</td>
<td>4EIS</td>
<td>1.37</td>
<td>No</td>
<td></td>
<td>[26]</td>
</tr>
</tbody>
</table>

Association of GH61 catalytic domain with Carbohydrate Binding Modules (CBMs)

As noted also in the early reports on GH61 gene cloning and sequences, these catalytic domains are often associated with CBMs [2], and in particular with CBM1. In [14] about 20% of GH61 sequences were estimated to be associated with a C-terminal CBM1 (an N-terminal CBM would interfere with the N-terminal His metal-binding function). CBM1s are A-type CBM, typically presenting a flat surface which binds to a crystalline polysaccharide, for CBM1 usually cellulose [2]. A recent search using the Cazymes Analysis Toolkit (CAT [32]) shows that 37 out of 143 (26%) of GH61s in CAT are associated with CBM1, indicating that the estimate in [14] is holding up as new sequences come into CAZY. It seems that in organisms having multiple GH61 genes some are associated with a CBM1 and some are not, for example in Heterbasidion irregularare, three out of ten GH61 genes have an associated CBM1 sequence [33]. Two of the CAZY entries are interestingly associated with CBM18s, which are typically chitin fragment binding. Interestingly, the CBM33 CelS2 protein shown to be active on cellulose [22] has a CBM2 associated with it (CBM2s are A-type binders usually binding to cellulose, but also to chitin or xylan).

None of the structurally characterized GH61 proteins has naturally a CBM attached. This is not surprising as successful crystallization is strongly biased towards single domain, compact proteins.

However for the TtGH61E structure [14], a CBM1-like feature within the catalytic domain was noted, three Tyr forming a flat surface and arranged similarly as the three Tyr in the structure of the CBM1 of T. reesei Cellobiohydrolase I [34]. For TtGH61E, crystalline cellulose binding activity has been qualitatively shown experimentally [35] and it has been shown that substitution of one of the aromatics (Tyr192) to Ala reduces activity [14]. Although this CBM1-like feature is not generally conserved, all of the structures of GH61 determined so far have a ‘flat’ face, to which two or more aromatic residues contribute (see Table 1 and Figure 4 for illustration of three of the most diverse structures) which could be involved in crystalline substrate binding. Tyr191 of TtGH61E has an equivalent Tyr in all other structures determined (in bold in Table 1). The multiple structural alignments were carried out with the server version of Mammoth-Mult [31].

Figure 3. Dendrogram (produced by near joining method in ClustalW2 [29] and displayed with Treeview [30]) graphically showing the similarities between the proteins of known structure, indicated by their PDB codes (the proteins corresponding to each PDB code can be found in Table 1). The multiple structural alignments were carried out with the server version of Mammoth-Mult [31].
Table 2. Structure similarity from Dali-Lite [28] (number of aligned residues, Cα rmsd and structure-based sequence identity are shown).

<table>
<thead>
<tr>
<th></th>
<th>TaGH61A (3ZUD, A)</th>
<th>TtGH61E (3EJA, A)</th>
<th>HjGH61B (2VTC, A)</th>
<th>NcPMO2 (4EIR, A)</th>
<th>NcPMO3 (4EIS, A)</th>
</tr>
</thead>
<tbody>
<tr>
<td>TaGH61A</td>
<td>-</td>
<td>1.7 Å</td>
<td>1.3 Å</td>
<td>1.7 Å</td>
<td>1.5 Å</td>
</tr>
<tr>
<td>(3ZUD, A)</td>
<td>201 res</td>
<td>1.7 Å</td>
<td>1.7 Å</td>
<td>47%</td>
<td>41%</td>
</tr>
<tr>
<td></td>
<td>33%</td>
<td>1.9 Å</td>
<td>1.7 Å</td>
<td>31%</td>
<td>42%</td>
</tr>
<tr>
<td>TtGH61E</td>
<td>-</td>
<td>200 res</td>
<td>198 res</td>
<td>1.9 Å</td>
<td>1.5 Å</td>
</tr>
<tr>
<td>(3EJA, A)</td>
<td></td>
<td>1.7 Å</td>
<td>1.7 Å</td>
<td>29%</td>
<td>42%</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2.0 Å</td>
<td>1.7 Å</td>
<td>28%</td>
<td>39%</td>
</tr>
<tr>
<td>HjGH61B</td>
<td>-</td>
<td>205 res</td>
<td>199 res</td>
<td>1.8 Å</td>
<td>1.7 Å</td>
</tr>
<tr>
<td>(2VTC, A)</td>
<td></td>
<td>1.7 Å</td>
<td>1.7 Å</td>
<td>28%</td>
<td>37%</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2.05 Å</td>
<td>2.1 Å</td>
<td>28%</td>
<td>37%</td>
</tr>
<tr>
<td>NcPMO2</td>
<td>-</td>
<td>204</td>
<td>216</td>
<td>1.7 Å</td>
<td>2.8 Å</td>
</tr>
<tr>
<td>(4EIR, A)</td>
<td></td>
<td></td>
<td></td>
<td>39%</td>
<td>42%</td>
</tr>
<tr>
<td>NcPMO3</td>
<td>(4EIS, A)</td>
<td></td>
<td></td>
<td>1.7 Å</td>
<td>2.8 Å</td>
</tr>
</tbody>
</table>

The metal binding site

As stated above, there is currently reasonable consensus that the active metal in GH61 proteins is copper, however it seems that GH61 (and CBM33) can be sometimes demetallated/substituted for other metals during overexpression and purification despite the high affinities for Cu at active pHs. One possibility is that this is mediated by changes in pH during purification. In table 3, the distances to protein residues for the structures where metal at the active site could be positively identified as Cu (3ZUD, 4EIS, 4EIR) are shown and are very typical and very similar in the three proteins. The Cu(II) is in tetragonal coordination geometry in all structures reported. The protein ligands are highly conserved in GH61 sequences and in all the structures reported so far.

The special spatial arrangement of the two coordinating His (one coordinating both with the N-terminus and its side chain) has been named ‘histidine brace’ [4], and a similar arrangement has also been observed in copper methane monoxygenases, which however differ by having two rather than one Cu atoms at a distance of 2.7 Å from each other, as confirmed by a recent 2.68 Å resolution structure [36]. Other conserved residues around the metal binding site are the Gln hydrogen bonding to the conserved Tyr and a third His residue (His164 in TaGH61A), the function of which is yet unknown. These are interestingly not the same in CBM33. In CBP21 an Asn (185) and an Asp (182) are equivalent to the GH61 Gln and His, respectively, and the two residues are highly conserved as Asn and Asp in the family. Only mutation of Asp182 to Ala affected the combined activity of CBP21 and chitinase C, while mutation of Asn185 had little effect [18]. This correlates well to the fact that the equivalent of the conserved Tyr is in CBM33 a Phe, which could not form a hydrogen bond with a polar residue. Aside from the residues directly coordinating the ligands and the additional Gln and His, there is considerable diversity in the residues immediately surrounding the Cu(II) site among the different GH61 proteins, as illustrated in Figure 5 by the structures of TtGH61E and NcPMO3. This diversity may prove important in modulating the activities of different GH61.

Table 3. Cu-protein distances in TaGH61A (3ZUD), NcPMO2 (4EIR) and NcPMO3 (4EIS). For 3ZUD the distances are to the main conformation of the Cu atom. In 4EIR and 4EIS there are two molecules per asymmetric unit, hence two distances are given.

<table>
<thead>
<tr>
<th></th>
<th>N-terminal His N</th>
<th>N-terminal His ND1</th>
<th>His NE2</th>
<th>Tyr OH</th>
</tr>
</thead>
<tbody>
<tr>
<td>3ZUD</td>
<td>2.2 Å</td>
<td>1.9 Å</td>
<td>2.0 Å</td>
<td>2.9 Å</td>
</tr>
<tr>
<td>4EIR</td>
<td>2.2/2.2 Å</td>
<td>1.9/1.9 Å</td>
<td>2.0/2.0 Å</td>
<td>2.8/2.8 Å</td>
</tr>
<tr>
<td>4EIS</td>
<td>2.3/2.3 Å</td>
<td>1.9/1.9 Å</td>
<td>2.1/2.1 Å</td>
<td>2.7/2.8 Å</td>
</tr>
</tbody>
</table>

The N-terminal His plays a special role in coordinating the metal, as it provides two ligands, a main chain and a side chain nitrogen. In [4] it was first recognized that this N-terminal His is a site of unusual post-translational modification, a methylation at Nε2. This was supported by crystallographic analysis and mass spectrometry for T. aurantiacus. Reanalysis of previously reported structures, and
modelling of methylation in all subsequently reported structures suggests that this may be a feature of all active GH61 proteins. No evidence of such a modification has been presented for the bacterial CBM33s.

Intriguingly, although the N-terminal His is extremely well conserved in GH61, some GH61 members have an Arg at this position, for example HiGH61G from Heterobasidion irregulare [33], which also lacks the other Cu-coordinating His. Even more intriguingly, it seems that some of these proteins (including HiGH61G) are upregulated when fungi are grown on lignocellulosic substrates, as well as GH61s having an integral metal binding site (as judged by sequence). This observation opens the possibility that some GH61 may have additional and metal-independent roles in cellulose degradation.

![Figure 5. Structural diversity around the Cu binding site. TiGH61E is shown in cyan, while NcPMO3 in grey. The conserved Cu-binding residues and additional His and Gln are in green.](image-url)

**Outlook**

One of the areas of interest in terms of exploiting the biotechnological potential is of course discovery of novel GH61 enzymes. In this sense it seems that genome mining and generally ‘omics’ analyses in lignocellulose degrading organisms may prove to be a very fruitful strategy for GH61 as well as other plant cell wall degrading enzymes. Especially white-rot fungi such as Phanerochaete chrysosporium [19], thermophilic biomass degrading fungi where the GH61 family is largely expanded – eg. Thielavia terrestris, boasting 18 GH61 genes compared to 3 in T. reesei [37] - and plant pathogens [38] have been subject of great attention. In the last few years, upregulation of some, but not all, GH61s upon growth on cellulosic substrates has been observed in transcriptome and secretome analyses of P. chrysosporium [19], transcriptome analysis of Phanerochaete carnosa [39], proteomic analysis of of Aspergillus nidulans growing on sorghum stover [40], and qRT-PCR studies on GH61 of the pathogen Heterobasidion irregulare [33], where HiGH61H showed a rather spectacular 17,000 fold increase on spruce heartwood. Since some GH61 genes/proteins are not upregulated by growth on cellulosic substrates, these may have different substrate specificities, which are yet to be explored.

The interplay between CDH and GH61 needs to be explored further. Co-induction of CDH and GH61 upon growth on cellulosic substrates has been reported in several large scale studies and organisms, among others P. chrysosporium [19], Aspergillus nidulans [40] and Thielavia terrestris [24, 23]. It has also been suggested that lignin may be sufficient as a reductant, as no addition of small molecules reductants is needed when lignin is used [41] [42].

Although oxidative enzymes like GH61 and CBM33 act in synergy with glycoside hydrolases, the final oxidised products of the reaction can pose a limit to the final yields that can be obtained. Gluconic acid, which can be a significant proportion of overall reaction products from commercial enzyme preparations [41], is a known inhibitor [43] of β-glucosidase and more inhibitory to β-glucosidase activity than glucose in realistic reaction mixtures [41]. Furthermore it is not fermentable by S. cerevisiae. Cellobionic acid is also a worse substrate than cellobiose for β-glucosidases [41]. A better understanding of the interplay of different components is necessary, to achieve as high as possible yields of conversion.

Many challenges remain also on the fundamental understanding of GH61 action, their interaction with substrate and the electron transfer pathways. Crystallography is expected to continue contributing to the elucidation of GH61 detailed function and diversity. However a true molecular understanding will not come from structural biology alone, but requires combined efforts involving experts from different fields including phylogenetics, transcriptomics and bioinorganic chemistry.

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**References**


Citation


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Competing Interests:
LEDM is an employee of Novozymes A/S, a major enzyme producer.

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