



Cite this: *Green Chem.*, 2025, **27**, 9862

## Advancing lignocellulosic conversion through biosensor-enabled metabolic engineering

Qi Gan, Jianli Zhang, Xinyu Gong, Yusong Zou and Yajun Yan \*

Lignocellulosic biomass holds great potential to produce a wide range of chemicals, including biofuels, biomaterials, and bioactive compounds. Effective utilization of these biomass feedstocks can significantly benefit human well-being while helping to mitigate climate change and reduce the environmental damage associated with fossil fuel use. Microbial synthesis plays a key role in converting biomass into valuable products. However, further optimization of these metabolic pathways is required to improve productivity. The design and optimization of these pathways remain major bottlenecks due to the complexity of biological systems and our limited understanding of them. Biosensors hold significant potential in advancing microbial metabolic engineering and enhancing substrate-to-product bioconversion. In this review, we discuss the major microbial conversion pathways for lignocellulosic biomass, the development and optimization of biosensors, and their applications in efficient biocatalytic processes for lignocellulosic conversion.

Received 15th July 2025,  
 Accepted 23rd July 2025  
 DOI: 10.1039/d5gc03618f  
[rsc.li/greenchem](https://rsc.li/greenchem)

### Green foundation

1. This review highlights recent progress in integrating biosensors with metabolic engineering to enhance the biological conversion of lignocellulosic biomass – a key strategy for sustainable biomanufacturing.
2. Biosensor-enabled metabolic engineering offers precise, real-time control over microbial pathways, allowing systems to adapt dynamically to changing substrates or stress conditions. This makes the approach widely relevant to biotechnology and sustainable industrial bioprocessing.
3. The convergence of biosensor technology, systems biology, and machine learning will drive the next generation of smart, adaptive microbial platforms for biomass valorization. The insights presented in this review provide a foundational framework for designing such systems and will help shape the future of green chemistry by advancing cleaner, more efficient, and more sustainable conversion technologies.

## Introduction

Lignocellulosic biomass, one of the most abundant renewable resources on earth, is sourced from plant materials such as agricultural residues, forestry by-products, and energy crops.<sup>1</sup> Composed primarily of cellulose, hemicellulose, and lignin, its depolymerization yields hexoses, pentoses, and aromatic compounds that serve as crucial substrates for biorefineries.<sup>2</sup> The conversion of these compounds supports the development of sustainable alternatives to fossil-based resources.<sup>3</sup> Lignocellulose holds significant value for producing an extensive array of valuable products, including biofuels, biomaterials, and bioactive compounds.<sup>1,4</sup> For instance, lignocellulosic biomass has been utilized to produce bioethanol, biodiesel, and other valuable products, such as butanol, isoamyl alcohol,

coumarin and terpenes.<sup>5,6</sup> Despite this immense potential, the inherent recalcitrance of lignocellulosic biomass presents a substantial barrier to its efficient bioconversion, ultimately limiting overall productivity.<sup>7,8</sup>

Microbial conversion plays a critical role in transforming lignocellulosic biomass into valuable products, but it faces significant challenges, particularly in the development of lignocellulosic biomass biodegradation and conversion techniques for platform chemicals that can contribute to increased biofuel production while lowering the cost.<sup>9,10</sup> While certain microorganisms can degrade lignin, limitations such as low enzyme activity, slow growth rates, and cultivation difficulties limit their effectiveness. Robust engineered strains with high depolymerization efficiency are therefore essential to overcoming these challenges and maximizing lignin breakdown. For industrial applications, optimal strains must achieve high lignin conversion efficiency, elevated product titers, and consistent performance stability. Recent advancements in synthetic biology have expanded opportunities to produce a

School of Chemical, Materials, and Biomedical Engineering, College of Engineering, The University of Georgia, Athens, GA 30602, USA. E-mail: yajunyan@uga.edu



variety of high-value compounds using microbial cell factories.<sup>11</sup> However, introducing heterologous or novel biosynthetic pathways into microbial hosts often leads to metabolic stress and imbalances in metabolic flux.<sup>12</sup> Therefore, precise pathway design and optimization are crucial to balance achieve metabolic balance, thereby improving both product yield and titer.<sup>6</sup>

To achieve pathway optimization and protein engineering in biocatalysts often requires extensive screening of mutation libraries to identify high-yielding strains and efficient biocatalysts. Biosensors are biological components that detect and respond to specific molecules or conditions in a cell or environment, often producing a measurable output. And they play a vital role in this process by detecting specific metabolites, environmental conditions, or cellular signals, thus enabling precise monitoring of cellular responses.<sup>13,14</sup> This capability facilitates high-throughput phenotypic screening, allowing rapid identification of desired traits. Furthermore, the integration of biosensors with metabolic engineering enables fine-tuning of metabolic activities based on real-time data, enhancing microbial adaptability to fluctuations in fermentation conditions and improving both the efficiency and stability of product formation.

Previous reviews have comprehensively summarized recent advancements, advantages, and limitations of both thermochemical depolymerization and biological conversion processes for the valorization of lignocellulosic biomass into valuable products.<sup>15–17</sup> They have also explored the potential for sustainable industrial application of waste lignin through integrated valorization strategies that combine with artificial intelligence. Here, our review primarily focuses on the application of biosensors in lignocellulosic biomass conversion, with particular emphasis on biological conversion processes. This review is intended for early-stage researchers, graduate students, and interdisciplinary scientists who are entering the fields of synthetic biology, metabolic engineering, and biomass valorization. We first summarized the basic advances in biomass conversion, followed by an overview of the discovery and optimization of biosensors that respond specially to the key intermediates in the lignocellulosic biomass conversion process. We then explore major applications of these biosensors: visualization of metabolite dynamics, dynamic metabolic regulation, and high-throughput screening and evolution. Finally, we provide conclusions and perspectives on the future development of small molecule biosensors and their application in enhancing lignocellulosic biomass conversion.

## Lignocellulosic biomass and its bioconversion pathways

Lignocellulose is mainly composed of three key structural components: lignin, cellulose and hemicellulose, each of which can be converted into valuable products through distinct metabolic pathways.<sup>1</sup> Cellulose is a linear polymer of glucose, hemicellulose is a heteropolysaccharide with various sugar mono-

mers, and lignin is a complex phenolic compound. Due to its high carbon-to-oxygen ratio and aromatic content, lignin holds significant potential as a feedstock for biofuels and high-value chemicals.<sup>18,19</sup> However, the complex structure and recalcitrance of lignocellulosic biomass present considerable challenges for efficient conversion into bioproducts.

The typical process for converting lignocellulose into valuable products involves pretreatment, enzymatic degradation, and fermentation. During pretreatment, lignocellulosic biomass is broken down to increase the accessibility of cellulose and hemicellulose for enzymatic or microbial action, although the intricate structure of lignin can complicate this step.<sup>2,20,21</sup> Following pretreatment, enzymes such as cellulases and hemicellulases are added to degrade cellulose and hemicellulose into fermentable sugars like glucose and xylose. This enzymatic hydrolysis is critical, as the released sugars are required for microbial fermentation. However, enzyme activity must be optimized, as residual lignin and inhibitors generated during pretreatment can impede efficiency. In the fermentation step, specialized microorganisms, including yeasts and bacteria, are used to convert these sugars into desired bioproducts. For instance, *Saccharomyces cerevisiae* is commonly used for ethanol production, while other engineered microbes are tailored for the synthesis of biofuels, bioplastics, and other valuable chemicals.<sup>22</sup>

Microbial deconstruction of lignocellulose depends on enzymatic processes that break down cellulose and hemicellulose, with cellulases converting cellulose into cellobiose and glucose and hemicellulases releasing pentoses (*e.g.*, xylose) and hexoses. These sugars enter central metabolic pathways such as glycolysis and the pentose phosphate pathway, leading to biofuel and chemical production (Fig. 1). However, the breakdown of lignin into aromatic compounds, like vanillin or ferulic acid, requires specialized enzymes (*e.g.*, peroxidases, laccases) and is less efficient, as lignin-derived intermediates can inhibit microbial growth. Additional bottlenecks include substrate inhibition, where the accumulation of sugars or intermediates impedes enzyme function, and metabolic pathway inefficiencies, caused by imbalanced fluxes and slow reaction rates at key steps.<sup>20</sup> To overcome these challenges, innovative approaches in metabolic engineering, enzyme optimization, and dynamic regulation strategies is essential, enabling efficient and sustainable lignocellulosic bioconversion.<sup>18</sup>

## Biosensors in microbial metabolic engineering

Biosensors, such as transcription factor-based, whole cell based, nucleic acid-based, and protein-level biosensors, play a critical role in simplifying the engineering process by providing precise and efficient ways to monitor and control metabolic activities,<sup>23,24</sup> Each type has distinct mechanisms and applications that contribute to advancements in biotechnology and synthetic biology (Fig. 2). Among them, transcription



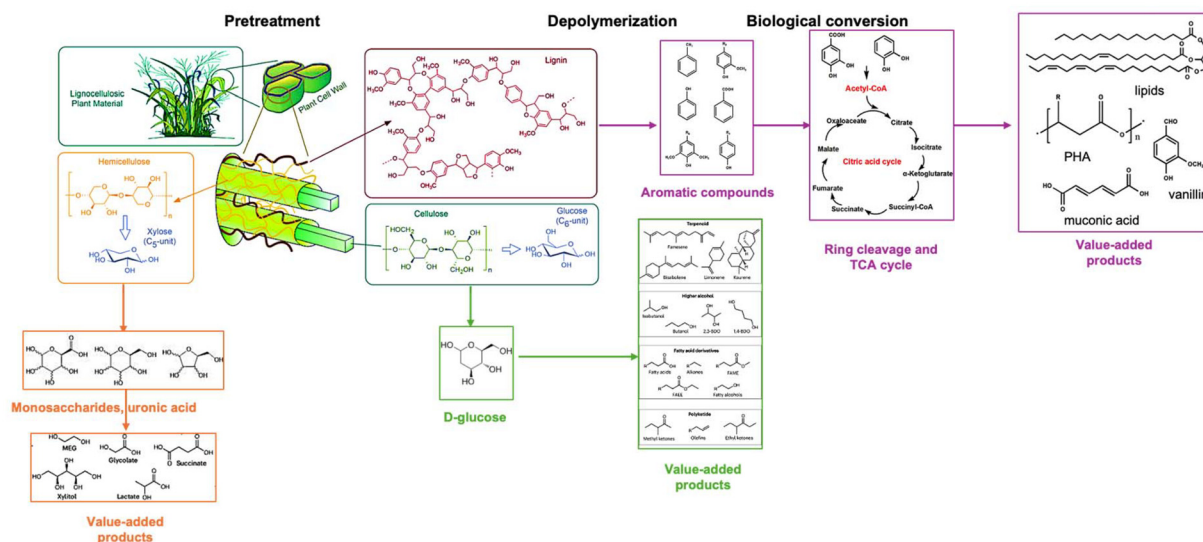


Fig. 1 Key steps in the conversion of lignocellulosic biomass to value-added products.

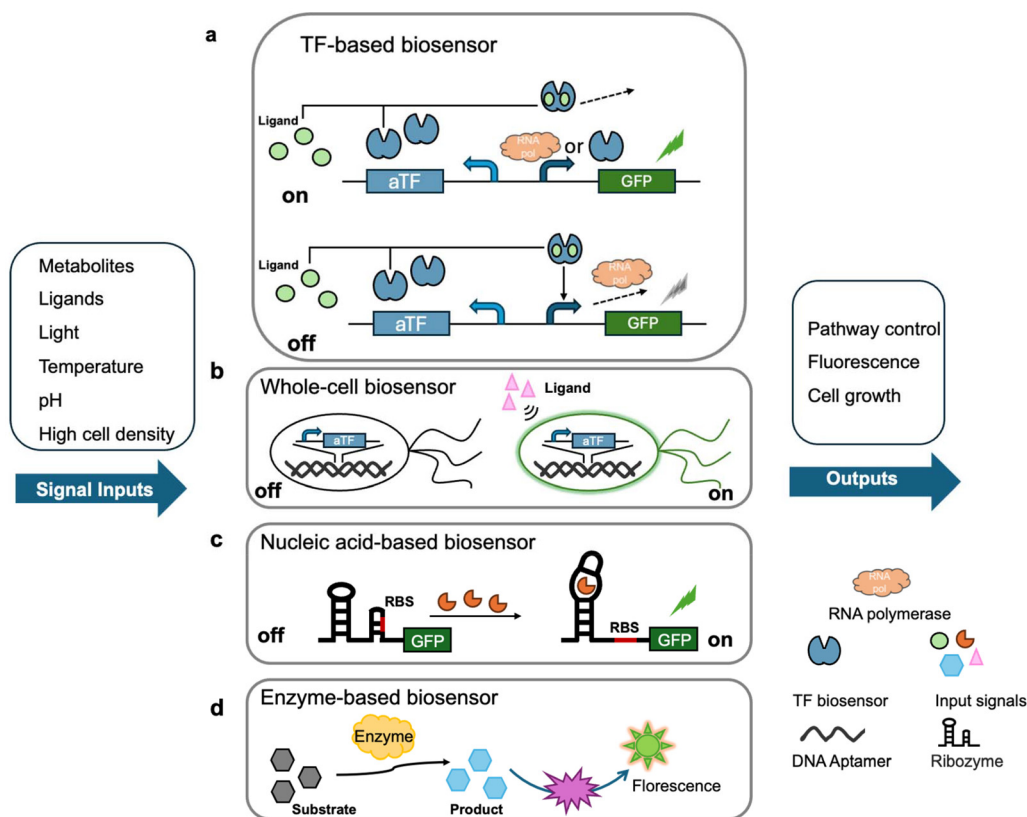
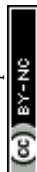


Fig. 2 The major categories of genetically encoded biosensors. (a) Transcriptional Activation via TF-Based Biosensor. Upon signal input, the TF undergoes a conformational change, dissociates from the promoter region, and allows RNA polymerase to initiate transcription. Transcriptional Repression via TF-Based Biosensor, in the presence of the signal, the transcription factor (TF) binds to its target promoter, blocking RNA polymerase binding and repressing gene expression. (b) Whole-cell biosensors are engineered microorganisms that respond to specific environmental or intracellular signals by producing a measurable output, such as fluorescence, colour change, or electrical signal. (c) Nucleic acid-based biosensors, utilize nucleic acids (DNA or RNA) as recognition elements to detect specific biomolecules, pathogens, or other analytes. (d) Enzyme-based biosensors, utilize enzymes as biological recognition elements to detect specific substrates or other analytes. These biosensors capitalize on the catalytic activity of enzymes, which can produce a measurable signal in response to the presence of a target substance.



factor-based biosensor is most widely used in metabolic engineering.<sup>25</sup> These biosensors utilize transcription factors that respond to specific molecules by activating or repressing gene expression. Transcription factor repressor is a molecule that inhibits gene expression by preventing transcription, such as the tetracycline repressor tetR and the tryptophan repressor TrpR. The repressor binds to specific DNA sequences or interacts with transcription factors to block RNA polymerase from transcribing the target genes. In the absence of the target compound, repressor can be used to “switch off” gene expression. When the target metabolite is present, it may interact with the repressor and then change its conformation, thereby relieving repression and allowing gene expression.<sup>26</sup> In contrast, a transcription factor activator is a molecule that binds to a transcription factor or directly to DNA, enhancing gene expression. Activators increase the transcription of specific genes, often in response to the presence of a target metabolite or environmental signal. For instance, in a biosensor designed to detect a particular metabolite, the metabolite itself can act as an activator, binding to the transcription factor and inducing the expression of a reporter gene, such as green fluorescent protein (GFP). To optimize the biosensor performance, various engineering approaches, including modifications to promoters, ribosome binding sites (RBS), and operators, have been employed to fine-tune the expression of biosensor components.<sup>25</sup> Additionally, structural domain exchanges of RNA and proteins have proven effective in altering specificity. Whole-cell biosensors are genetically engineered microbial systems that integrate sensing, signal transduction, and reporting functions within a living cell to detect specific target molecules. The mechanism typically involves three key components: a sensing module, a regulatory circuit, and a reporter output. The sensing module consists of a transcription factor or receptor that selectively recognizes the target analyte, often leading to a conformational change that modulates gene expression. This molecular interaction regulates a synthetic or native promoter that controls the downstream expression of a reporter gene, such as those encoding fluorescent proteins, enzymes, or luminescent markers. Upon activation, the reporter gene generates a quantifiable signal that correlates with the concentration of the target molecule. This design enables dynamic and real-time monitoring of environmental or intracellular conditions, making whole-cell biosensors powerful tools for applications in environmental monitoring, metabolic engineering, and synthetic biology (Fig. 2). Nucleic acid-based biosensors use engineered DNA or RNA elements to detect specific targets with high sensitivity and selectivity. Common designs include aptamers, DNAzymes, and toehold switches. Aptamers fold into defined structures that bind target molecules, triggering measurable outputs such as fluorescence or electrochemical signals. DNAzymes catalyse substrate cleavage in the presence of specific analytes, generating a detectable response. Toehold switches are synthetic RNA structures that block translation until a trigger RNA binds, activating reporter gene expression. Enzyme-based biosensors utilize the catalytic activity of enzymes to detect specific analytes through bio-

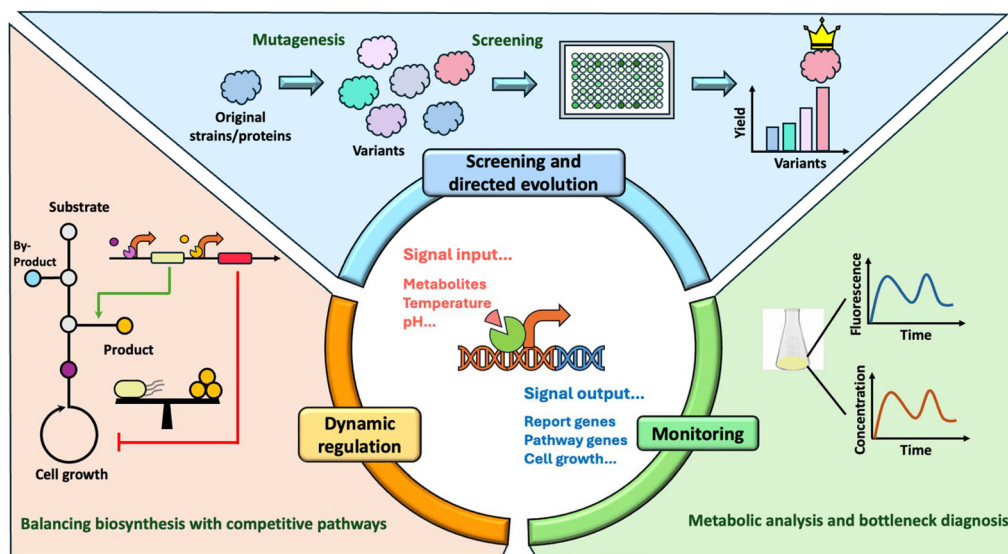
chemical reactions that generate a measurable signal. These biosensors typically consist of an enzyme immobilized on a transducer surface, where the enzyme selectively reacts with the target molecule, producing a product that induces a detectable change—commonly in fluorescence, colour, pH, or electrochemical properties. The signal intensity correlates with analyte concentration, enabling quantitative analysis. Enzyme-based biosensors offer high specificity, fast response times, and sensitivity under mild conditions. They are widely used in clinical diagnostics, environmental monitoring, and food safety applications.

In microbial metabolic engineering, biosensors are employed to monitor and regulate the behavior of engineered microbes by providing real-time feedback on key metabolites or environmental conditions. The biological component, such as enzymes, nucleic acids, or receptors, interacts with the target molecule, and this interaction is converted into a measurable signal by the transducer, which can be optical, electrochemical, or acoustic.<sup>13</sup> Various types of biosensors are used in microbial systems, with optical, electrochemical, and fluorescence-based sensors being the most common. Biosensors have become indispensable tools in microbial metabolic engineering due to their ability to monitor critical parameters in real time. One of their primary applications is tracking metabolite concentrations within microbial cells, providing crucial insights into metabolic flux and the effectiveness of engineered pathways. They are also used to detect environmental changes, such as fluctuations in pH, light, or temperature, which can significantly impact microbial performance and product yields (Fig. 2).<sup>13,27,28</sup> Additionally, biosensors enable real-time feedback for optimizing metabolic pathways, allowing for dynamic adjustments based on immediate cellular responses. This real-time data is vital for fine-tuning metabolic activities, improving overall efficiency in fermentation processes, and reducing waste or by-product accumulation.<sup>29</sup> By continuously monitoring and responding to the internal and external states of microbial systems, biosensors help streamline and enhance the bioconversion of lignocellulosic biomass.

Recent advancements in biosensor technology have significantly expanded their capabilities and applications in microbial metabolic engineering (Fig. 3). Emerging biosensor technologies, such as synthetic RNA-based biosensors and CRISPR-based sensing systems, offer higher sensitivity, specificity, and the ability to respond to a wider range of metabolites and environmental signals.<sup>30</sup> Integrating these biosensors with synthetic biology tools, allowing for the creation of more sophisticated feedback loops and control systems. For example, Jiang *et al.* developed an autonomous cascaded artificial dynamic (AutoCAD) regulation circuit based on the PadR and FdeR biosensor systems to maintain pathway balance, resulting in a 16.5-fold increase in naringenin titer. In fed-batch fermentation, this system achieved a naringenin titer of 277.2 mg L<sup>-1</sup>.<sup>31</sup> Biosensors can be coupled with genetic circuits to trigger the expression of specific genes in response to detected metabolites, providing a means for autonomous regu-







**Fig. 3** Versatile applications of TF-based biosensors. (a) In real time monitoring the products or intermediates. (b) Dynamic pathway regulation system for improved production. Biosensors were utilized to activate the synthetic pathway and repress the TCA cycle, to direct the carbon flux to synthesis. (c) Transcriptional biosensors as screening methods to allow enzymes or strains characterization and evolution.

lation of metabolic pathways. This integration of biosensors with synthetic biology enables the construction of self-regulating microbial systems that can adapt to changing conditions, optimize resource utilization, and enhance overall productivity. These innovations are pushing the boundaries of microbial metabolic engineering, making it possible to create more robust and efficient microbial cell factories for sustainable biomanufacturing.

## Biosensor-enabled optimization of lignocellulosic conversion

### Real-time monitoring of metabolic intermediates

To improve the lignocellulosic conversion, it first requires the efficient depolymerization of lignocellulose into bioavailable substrates. Then achieve more efficiently break down complex sugars derived from cellulose and hemicellulose or to direct metabolic intermediates to desired end products. And it's also critical to increase the overall yield and efficiency of the bio-conversion process and overcome challenges such as metabolic bottlenecks and by-product formation.<sup>55</sup> The ligninolytic activity of bacteria can release unmodified low-molecular-weight aromatics from lignin-rich waste streams. Several bacterial enzymes are capable of degrading lignocellulosic biomass and converting it into monomers. However, due to the heterogeneous and highly crosslinked structure of lignin, an efficient enzymatic process for this conversion is not yet available. Therefore, advancing the development and discovery of new enzymes is a critical step toward realizing an integrated lignocellulosic biorefinery.<sup>56</sup>

As summarized in Table 1, numerous biosensors that respond to sugars or key intermediates have been identified

and applied to monitor product or substrate concentrations. For instance, the XylR–PxylF system responds to xylose by using GFP as a reporter to monitor xylose concentration, with GFP intensity indicating the amount of xylose present. Tang *et al.* employed a range of biosensors containing a mutant XylR, which expanded the detection range nearly 10-fold compared to the control, enabling the detection of varying xylose concentrations (Table 2).<sup>33</sup> Also, biosensors can be used to detect compounds that are difficult to monitor using conventional methods. For example, CouR is a MarR family regulator, that negatively regulates the transcription of genes involved in the catabolism of *p*-coumarate in bacteria. *p*-coumaroyl-CoA cannot be detected using standard analytical methods, Liu *et al.* developed a novel biosensor, CouR, in *Saccharomyces cerevisiae* that responds to *p*-coumaroyl-CoA. Although it is challenging to quantify the sensor's concentration threshold and operating range, Liu successfully devised a dynamic regulatory circuit that enables real-time adjustment of *p*-coumaroyl-CoA production.<sup>57</sup> The correlation between fluorescence output and enzyme or pathway efficiency enables the monitoring of substrate utilization and final product production, facilitating optimization. These biosensors play a crucial role in enhancing substrate-to-product bio-conversion in lignocellulosic biomass processing by enabling real-time tracking of essential metabolic intermediates. This capability enables researchers to identify bottlenecks within the metabolic network and screen and optimize key enzymes.

### Biosensors in dynamic regulation

Biosensors can respond to a broad array of metabolites across diverse living microorganisms to maintain balanced cellular metabolism, extensive exploration of biosensor discovery and optimization techniques has led to the identification of an increasing number of metabolites as signaling molecules,



**Table 1** Summary of notable examples of biosensors applied for lignocellulose valorization

| Biosensors | Sensor type                          | Sensing molecular       | Reporter                                                                                                              | Host                                                          | Purpose                                       | Ref. |
|------------|--------------------------------------|-------------------------|-----------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------|-----------------------------------------------|------|
| XylR       | TF-based, repressor                  | Xylose                  | <i>yEGFP</i>                                                                                                          | <i>S. cerevisiae</i>                                          | Dynamic regulation of gene expression         | 32   |
| XylR       | TF-based, repressor                  | Xylose                  | <i>β-Galactosidase gene</i>                                                                                           | <i>Escherichia coli</i>                                       | Monitoring production                         | 33   |
| araF       | FERT nano sensor                     | L-Arabinose             | <i>eYFP</i>                                                                                                           | <i>Escherichia coli</i>                                       | Monitoring production                         | 34   |
| AraC       | TF-based, repressor                  | Arabinose               | <i>GFP</i>                                                                                                            | <i>Escherichia coli</i>                                       | Change the inducer scope                      | 35   |
| FLIPmal    | FERT                                 | Maltose                 | <i>eYFP</i>                                                                                                           | <i>Escherichia coli</i>                                       | Quantify production                           | 34   |
| RhaS       | TF based, activator                  | L-Rhamnose, L-mannose   | <i>sfgfp</i>                                                                                                          | <i>Escherichia coli</i>                                       | Change the inducer scope and sensitivity      | 36   |
| CelR       | TF-based, repressor                  | Cellulase               | <i>GFP</i>                                                                                                            | <i>Escherichia coli</i>                                       | Monitoring gene expression                    | 37   |
| MglB       | FERT                                 | Glucose                 | <i>GFP</i>                                                                                                            | <i>Escherichia coli</i>                                       | Analyse the designed FERT biosensor structure | 38   |
| YbeJ       | FERT                                 | Glutamate               | <i>Fluorescence</i>                                                                                                   | <i>Escherichia coli</i>                                       | Screening mutants                             | 39   |
| PcaU       | TF-based, repressor and an activator | Protocatechuic acid     | <i>GFP</i>                                                                                                            | <i>Escherichia coli</i>                                       | Screening enzyme activity                     | 40   |
| VanR       | TF-based, repressor                  | Vanillic acid           | <i>YFP</i>                                                                                                            | <i>Escherichia coli</i>                                       | Optimize biosensor dynamic range              | 41   |
| ADH7       | Inducible promoter                   | Vanillin                | <i>3-O-Methylgallate-O-demethylase (LigM), vanillin dehydrogenase (LigV) and protocatechuate decarboxylase (AroY)</i> | <i>Escherichia coli</i>                                       | Dynamic regulation of gene expression         | 42   |
| MuYqhC     | TF-based, repressor                  | Vanillin                | RFP                                                                                                                   | <i>B. subtilis</i>                                            | Screening enzyme activity                     | 43   |
| PadR       | TF-based, repressor                  | <i>p</i> -Coumaric acid | <i>YFP</i>                                                                                                            | <i>Escherichia coli</i> and <i>Corynebacterium glutamicum</i> | Screening and selection for optimal chassis   | 44   |
| FerC       | TF-based, repressor                  | Ferulic acid            | <i>eGFP</i>                                                                                                           | <i>Escherichia coli</i>                                       | Screening biosensor substrate                 | 45   |
| BenR       | TF-based, activator                  | Benzoic acid            | <i>gfp</i>                                                                                                            | <i>Escherichia coli</i>                                       | Screening novel enzyme                        | 46   |
| NahR       | TF-based, activator                  | 2-Hydroxybenzoic acid   | <i>lacZα and tetA</i>                                                                                                 | <i>Escherichia coli</i>                                       | Screening and selection active strains        | 47   |
| BldR       | TF-based, activator                  | Benzaldehyde            | <i>gfp</i>                                                                                                            | <i>Escherichia coli</i>                                       | Optimize biosensor specify and sensitivity    | 48   |
| EmrR       | TF-based, repressor                  | Phenol                  | <i>gfp</i>                                                                                                            | <i>Escherichia coli</i>                                       | Screening target genes                        | 49   |
| LvaR       | TF-based, repressor                  | Levulinic acid          | <i>sfgfp</i>                                                                                                          | <i>P. putida KT2440</i>                                       | Screening optimal chassis                     | 50   |
| ArgP       | TF-based, repressor                  | L-Arginine              | <i>gfp</i>                                                                                                            | <i>Escherichia coli</i>                                       | Screening enzyme mutant with better activity  | 51   |
| BenM       | TF-based, repressor                  | Adipic acid             | <i>sfgfp</i>                                                                                                          | <i>Escherichia coli</i>                                       | Screening optimal production strains          | 52   |
| FadR       | TF-based, repressor                  | Acyl-CoA                | <i>gfp</i>                                                                                                            | <i>Saccharomyces cerevisiae</i>                               | Screening gene targets                        | 53   |
| FapR       | TF-based, repressor                  | Malonyl-CoA             | RFP                                                                                                                   | <i>Escherichia coli</i>                                       | Dynamic regulation of metabolic flux          | 54   |

FERT (ferulic acid-responsive transcriptional regulator), TF (ranscription Factor), COMT (caffeic acid O-methyltransferase). eYFP: enhanced yellow fluorescent protein; Sfgfp: Superfolder green fluorescent protein; YFP: enhanced yellow fluorescent protein; rfp, mCherry.

which can be integrated into biosensor applications within dynamic regulatory circuits.<sup>63</sup> These biosensors are essential for monitoring and controlling metabolic flux in engineered microbial systems, adjusting pathways in real time based on environmental and intracellular cues.

Carbon flux optimization is essential for ensuring that the carbon atoms are efficiently channeled into desired metabolic products rather than being diverted into by-products or lost through inefficient pathways. By detecting key metabolites involved in central carbon metabolism, biosensors can inform

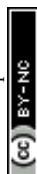


**Table 2** Typical applications of biosensors in lignocellulose valorization

| Applications               | Products                       | Biosensors                              | Mechanisms                                                                                                                                                                                                                                                  | Effectors                               | Achievements                                                                                                                                                                                                     | Ref. |
|----------------------------|--------------------------------|-----------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| Monitoring                 | Xylose                         | XylR                                    | In the absence of xylose, XylR does not bind to the operator xyO, repressing <i>reporter gene</i> expression. When xylose is present, XylR binds xylose, enabling its binding to xyO and activating transcription of <i>reporter</i> .                      | Xylose                                  | Screening the XylR mutants, the detecting range was increased by nearly 10-fold                                                                                                                                  | 33   |
|                            | Salicylic acid                 | MarR                                    | MarR protein binds on PmarO to inhibit promoter expression and SA binds with MarR protein to release the repression.                                                                                                                                        | Salicylic acid                          | Two promoter variants I12AII4T and I12AII14T that exhibited improved responsive strengths and shifted dynamic ranges were obtained                                                                               | 58   |
|                            | Levulinic acid                 | LvaR                                    | The LvaR regulator senses LA as a cognate ligand                                                                                                                                                                                                            | Levulinic acid                          | Screening optimal chassis, like <i>P. putida</i> KT2440, the maximal fluorescence increase was 12.3-fold                                                                                                         | 50   |
| Screening enzymes or genes | Lignin transformation products | EmrR                                    | EmrR is necessary and sufficient for the compound-dependent activation of the <i>emrRAB</i> operon.                                                                                                                                                         | Phenol                                  | Identified genes encoding six functional classes mediating lignin transformation phenotypes                                                                                                                      | 49   |
|                            | Vanillin                       | MuYqhC                                  | In the presence of an aldehyde, the transcriptional regulator YqhC activates the promoter of the <i>yqhD</i> gene, which drives the expression of a reporter gene ( <i>RFP</i> ), resulting in red fluorescence.                                            | Vanillin                                | Identified a COMT variant, Mu176, that displayed a 7-fold increase in the conversion rate                                                                                                                        | 43   |
| Dynamic regulation         | Protocatechuic acid            | Transcriptional repressor PadR          | An auto-regulatory system was established, by coexpressing key rate-limiting enzymes, 4-hydroxybenzoate hydroxylase, vanillate-O-demethylase, and transporter HcnK under the biosensor element                                                              | <i>p</i> -Coumaric acid ( <i>p</i> -CA) | A titer of 12.7 g L <sup>-1</sup> of protocatechuic acid                                                                                                                                                         | 59   |
|                            | Vanillic acid                  | Transcriptional repressor PP3359        | Two-layer genetic controller that interconnects two independent genetic sensors to decouple growth and production                                                                                                                                           | Feruloyl-CoA                            | Reduced metabolic stress by two-fold, while also increasing the growth rate and productivity by two-fold and five-fold, produced vanillic acid at titers up to 880 mg/L                                          | 60   |
|                            | Itaconic acid                  | Nitrogen starvation-detecting biosensor | Limiting the expression of the apparently toxic CadA protein to the production phase <i>via</i> dynamic regulation                                                                                                                                          | Nitrogen starvation                     | Maximum yield of 56% (mol mol <sup>-1</sup> ) and titer of 1.3 g L <sup>-1</sup> from <i>p</i> -coumarate, and 1.4 g L <sup>-1</sup> titer from monomeric aromatic compounds produced from alkali-treated lignin | 61   |
|                            | Catechol                       | Vanillin-inducible promoter ADH7        | This system is composed of a catechol biosynthesis pathway coexpressed with an active aromatic transporter CouP under induction by a vanillin self-inducible promoter, ADH7, to effectively convert the lignin-derived aromatics into value-added chemicals | Vanillin                                | Improved the catechol yields about 30% and 40% under promoter pTtrc and ADH7, respectively.                                                                                                                      | 42   |
|                            | Polyhydroxybutyrate            | PcaQ                                    | Control the functional genes expression in response to heterologous lignin-derived aromatics                                                                                                                                                                | Various lignin-derived monomers         | Polyhydroxybutyrate titer of 2.38 g L <sup>-1</sup> from the alkaline pretreatment liquor                                                                                                                        | 62   |

real-time adjustments to metabolic pathways, such as upregulating or downregulating specific enzymes to maintain balanced flux. This precision improves the overall efficiency of

microbial conversion processes, ensuring that more of the lignocellulosic substrate is converted into valuable products while minimizing waste.



To alleviate resource competition between cell growth and product synthesis, a dynamic regulation strategy was implemented by decoupling the two processes. Lo *et al.* has developed two versions of the controller, each equipped with glucose nutrient sensors but differing in their substrate sensing modules.<sup>60</sup> One controller specifically targets hydroxycinnamic acid, while the other targets oleic acid. The substrate-sensing module was placed under the direct control of the nutrient-sensing module, enabling decoupling of growth and metabolite production in the two-layer genetic circuit. To be specifically, they used the lignin-responsive transcriptional repressor PP3359, which inhibits the *ech* promoter and is deactivated by hydroxycinnamic CoA. The *fcs* gene was placed under the glucose-responsive *csiD* promoter, while *ech* and *vdh* were controlled by the *ech* promoter. PP3359 was expressed constitutively. This two-layer genetic circuit enabled prioritized biomass accumulation, followed by the induction of *fcs* expression to convert lignin-derived aromatics into thioester intermediates, thereby relieving repression of *ech* and *vdh*. The engineered circuits exhibited a 2-fold increase in growth rate and produced vanillic acid at titers up to 880 mg L<sup>-1</sup>.<sup>60</sup>

In the process of lignocellulosic conversion, engineered microbes often experience metabolic stress due to the demands placed on their metabolic machinery. This metabolic burden can lead to reduced growth rates, lower production efficiency, and instability in engineered strains. Biosensors offer a solution by allowing for the identification and mitigation of metabolic stress in real time. For example, biosensors that detect stress-related metabolites or intracellular signals can trigger adaptive responses in microbial systems, such as the downregulation of stress-inducing pathways or the activation of stress-relief mechanisms. Lignin-derived vanillin has been utilized as an inducer to develop an autoregulatory system for lignin valorization to catechol. The vanillin-inducible promoter *ADH7* was employed to dynamically regulate both the catechol biosynthetic and aromatic transport modules. Wu *et al.* constructed autoregulatory system, efficiently transports vanillin across the cell membrane and converts it to catechol, resulting in a yield improvement of approximately 30% and 40% under the control of the pT<sub>rc</sub> and *ADH7* promoters, respectively.<sup>42</sup> This approach addresses challenges related to the toxicity of lignin-derived aromatics and the high cost of exogenous inducers. Also, the biosensor responsive to lignin-derived *p*-coumaric acid was developed to intelligently sense lignin substrates and dynamically regulate the lignin metabolism network. In this system, *p*-coumaric acid binds to the PadR protein, releasing it from the *PpadC* promoter and activating the protocatechuic acid biosynthesis pathway. This dynamic regulation achieved a protocatechuic acid titer of 12.7 g L<sup>-1</sup>.<sup>59</sup>

A pivotal discovery is the regulatory element in *Ralstonia eutropha* H16. The regulatory protein PcaQ and its activated promoter *Ppca* were used to construct a self-induction system responsive to various lignin-derived monomers, enabling dynamic control of rate-limiting enzyme expression. Protein engineering of PcaQ, guided by hotspot prediction and mole-

cular docking, yielded a high-sensitivity mutant, PcaQ-R145K. The engineered strain, equipped with multifunctional modules, achieved a record polyhydroxybutyrate titer of 2.38 g L<sup>-1</sup> from the alkaline pretreatment liquor of *Pinus massoniana*.<sup>62</sup>

Additionally, Restricting the expression of toxic pathway enzymes to the product synthesis phase can effectively balance cell growth and bioproduction. During nitrogen limitation, the PHA pathway competes with the citric acid (TCA) cycle for acetyl-CoA *via* fatty acid biosynthesis. Producing itaconic acid during growth is challenging due to its inhibitory effects on enzymes in the glyoxylate shunt and citramalate cycle. A two-stage process that decouples growth from product synthesis can overcome issues such as product toxicity and slow catalyst growth. These strategies often leverage natural responses to nutrient or environmental stresses (*e.g.*, nitrogen, sulfur, phosphate limitation; oxygen or temperature shifts) that halt growth but preserve metabolic activity. Transcriptomic analysis identified the nitrogen starvation-responsive promoter *PurTA*, which was combined with T7 RNA polymerase and T7 lysozyme to construct a nitrogen-limitation biosensor. Dynamic control of the cytotoxic enzyme CadA (enzyme lysine decarboxylase 1) using this system significantly enhanced cell growth and offered a promising strategy for lignin-to-itaconic acid conversion.<sup>61</sup>

The development of aromatic-sensitive intelligent regulatory systems offers a powerful strategy for time-sequential regulation of multi-substrate transformations, a key requirement for efficient lignin valorization. By leveraging the responsiveness of engineered biosensors and transcriptional regulators to lignin-derived monomers, these systems enable precise, real-time control over metabolic flux. The continued refinement of these systems through advances in synthetic biology, protein engineering, and systems metabolic modeling will be crucial for optimizing pathway performance and scalability. Coupling such regulatory frameworks with robust microbial chassis and sustainable feedstock processing can pave the way toward economically viable and environmentally friendly lignin biorefineries.

### High-throughput screening and strain improvement

In addition to enabling dynamic regulation, biosensors also support high-throughput screening and strain optimization.<sup>64</sup> By linking biosensor outputs to key metabolites or target products, researchers can rapidly identify strains with improved metabolic performance or higher product yields. This automated screening approach greatly accelerates the discovery of promising enzymes, saving both time and labor.<sup>65</sup> Additionally, biosensors enable the rapid evaluation of thousands of genetic variants, facilitating the identification of novel metabolic configurations that conventional methods might overlook. For instance, the biosynthesis of vanillin is constrained by the conversion of protocatechuate to vanillate, a reaction catalyzed by catechol *O*-methyltransferase. Kunjapur *et al.* optimized the VanR-VanO system. The best rationally constructed sensor achieved 14-fold dynamic range. They





employed the evolved biosensor for rapid bioprospecting of natural catechol *O*-methyltransferases, leading to the identification of three previously uncharacterized active *O*-methyltransferases.<sup>41</sup> Dong *et al.* successfully applied a MuYqhC-based vanillin biosensor to identify a COMT variant, Mu176. This variant exhibited a 7-fold increase in conversion rate compared to the wild-type COMT. When large gene libraries are generated *via* mutagenesis or rational design, biosensors enable rapid screening of these libraries to identify efficient microbial strains. Siedler *et al.* applied padR to quickly sort droplets containing yeast cells that produced significant amounts of extracellular *p*-coumaric acid by utilizing the fluorescent signal from an *E. coli* biosensor.<sup>44</sup>

In strain improvement programs, biosensors not only aid in the initial screening process but also enable automated selection of high-performing strains throughout the development pipeline. Linking sensing and cellular adaptation specifically through the regulation of antibiotic resistance genes can enhance the evolution of biosensors, allowing for the enrichment of mutant libraries with improved phenotypes and productivity *via* adaptive laboratory evolution (ALE). This method has proven effective in increasing enzyme activity and metabolic productivity under selective conditions, boosting the production of metabolites such as tyrosine, L-valine, and muconic acid.<sup>52,66</sup> Overall, directed evolution using genetically encoded biosensors has facilitated the rapid and efficient engineering of proteins, metabolic pathways, and global metabolic networks.<sup>67,68</sup>

### Artificial intelligence and machine learning in biosensor development

Recently, the integration of artificial intelligence (AI) and machine learning (ML) has opened new frontiers in biosensor development, enabling smarter, faster, and more precise sensing platforms.<sup>69,70</sup> They are applied across various stages of biosensor development, from the initial design of recognition elements to advanced data analysis and real-time decision-making. These technologies facilitate the handling of large and complex biological datasets, allowing for real-time data analysis, predictive modelling, and adaptive system optimization. For example, Ding *et al.* trained a convolutional neural network (CNN) on large datasets linking ribosome binding sites (RBS) with transcription factor binding (TFB) dynamic ranges, developing a classification model (CLM-RDR) to enable intelligent regulation of TFB dynamic range.<sup>71</sup> And Zhou *et al.* generated a gradient promoter dataset using DNA barcoding to build a TFB library and characterized response curves *via* FACS-seq. Using an XGBoost model, they accurately predicted genotype-to-phenotype relationships and validated high-performing sequences, ultimately developing a malonyl-CoA biosensor with a dynamic range.<sup>72</sup>

Also, advancements in artificial intelligence (AI) have empowered machine learning and deep learning algorithms to effectively identify patterns in biological data and accurately predict the performance of bio-elements, offering a promising solution to overcome key technical barriers in regulating lignin

biological metabolism. It can predict optimal synthetic pathways and regulatory elements by analysing genomic, transcriptomic, and metabolic data. This reduces the trial-and-error typically associated with biosensor tuning and accelerates the design-build-test cycle. Moreover, AI-driven pattern recognition enhances signal interpretation in various biosensing modalities, including optical, fluorometric, and electrochemical sensors. Looking ahead, the field of AI-assisted design and activity prediction of bio-elements will be shaped by advances in deep reinforcement learning, unsupervised learning, and neural network architectures. Integrating AI with disciplines like systems biology and bioinformatics will deepen our understanding of complex biological systems and enhance the precision of bio-element design.<sup>70</sup> Continued interdisciplinary collaboration will be key to translating these tools from proof-of-concept to industrial implementation.

## Conclusion and outlook

The future economic viability of lignocellulosic biorefineries depends heavily on effective lignin valorization, as lignin serves as a valuable feedstock to produce a wide range of high value bioproducts. However, biological lignin valorization has not yet reached industrial or commercial scale. Recently, several reviews provided a comprehensive overview of lignin valorization, emphasizing multiscale metabolic regulation, covering key aspects such as critical enzymes involved in lignin biotransformation, metabolic pathway networks, genome-to-phenotype relationships, and predictive learning strategies.<sup>15,73</sup> In this review, we mainly focused on Biosensor-enabled metabolic engineering for lignocellulosic conversion. The biosensor-based technologies enable real-time detection, dynamic regulation, and the identification of potential enzyme catalysts, as well as efficient strain screening for targeted evolution. These capabilities could greatly accelerate the engineering of proteins, metabolic pathways, and global metabolic networks, which are crucial for facilitating lignocellulosic conversion. However, several technical and economic challenges must be addressed before full commercialization is feasible. A primary concern is the long-term stability and sensitivity of biosensors in industrial environments. Developing robust biosensors is critical to ensure their effectiveness in large-scale operations.

Additionally, further research is needed to explore biocatalytic enzymes and biotransformation pathways, enhance substrate fermentability and biotransformation efficiency, design high-performance microbial strains, and optimize fermentation conditions for the efficient production of a wide range of chemicals. Establishing biosensors that meet specific criteria, such as specificity, dynamic range, and detection range is essential for practical applications. The design of ideal biosensors remains a significant challenge, yet artificial intelligence techniques, particularly deep learning and machine learning, are beginning to be integrated into biosensor design.



These advances allow for the development of sophisticated biosensors with greater accuracy and efficiency.

When combined with machine learning algorithms that can analyze the large datasets generated by biosensors, these tools enable the screening and enrichment of positive mutations in proteins, metabolic pathways, and genome-wide networks from extensive libraries. Such innovations will not only increase the efficiency and resilience of biosensor-enabled biorefineries, but they will also transform the way lignocellulosic biomass converted into biofuels and biochemicals, paving the way for more sustainable and efficient industrial processes. As researchers work to overcome challenges in scalability and robustness, biosensor-driven systems will play a vital role in advancing next-generation biorefineries, contributing to a cleaner and more sustainable bioeconomy.

## Author contributions

Conceptualization, Y. Y. and Q. G.; writing – original draft preparation, Q. G.; visualization, Q. G., J. Z. and X. G; writing – review and editing, Q. G. and Y. Y.; All authors have read and agreed to the published version of the manuscript.

## Conflicts of interest

The authors declare no conflict of interest.

## Data availability

No primary research results, software, or code have been included, and no new data were generated or analyzed as part of this review.

## Acknowledgements

This work was supported by the National Institute of General Medical Sciences of the National Institutes of Health under award number R35GM128620. We also acknowledge the support from the College of Engineering, The University of Georgia, Athens, Georgia, United States.

## References

- 1 Z. Chen, L. Chen, K. S. Khoo, V. K. Gupta, M. Sharma, P. L. Show, *et al.*, Exploitation of lignocellulosic-based biomass biorefinery: A critical review of renewable biore-source, sustainability and economic views, *Biotechnol. Adv.*, 2023, **69**, 108265.
- 2 M. Galbe and O. Wallberg, Pretreatment for biorefineries: a review of common methods for efficient utilisation of lignocellulosic materials, *Biotechnol. Biofuels*, 2019, **12**, 294.
- 3 X. Li and Y. Zheng, Biotransformation of lignin: Mechanisms, applications and future work, *Biotechnol. Prog.*, 2020, **36**(1), e2922.
- 4 G. Liu and Y. Qu, Engineering of filamentous fungi for efficient conversion of lignocellulose: Tools, recent advances and prospects, *Biotechnol. Adv.*, 2019, **37**(4), 519–529.
- 5 A. Devi, S. Bajar, H. Kour, R. Kothari, D. Pant and A. Singh, Lignocellulosic Biomass Valorization for Bioethanol Production: a Circular Bioeconomy Approach, *BioEnergy Res.*, 2022, **15**(4), 1820–1841.
- 6 A. Joshi, K. K. Verma, V. D. Rajput, T. Minkina and J. Arora, Recent advances in metabolic engineering of microorganisms for advancing lignocellulose-derived biofuels, *Bioengineered*, 2022, **13**(4), 8135–8163.
- 7 A. K. Chandel, V. K. Garlapati, A. K. Singh, F. A. F. Antunes and S. S. da Silva, The path forward for lignocellulose biorefineries: Bottlenecks, solutions, and perspective on commercialization, *Bioresour. Technol.*, 2018, **264**, 370–381.
- 8 N. Xu, S. Liu, F. Xin, J. Zhou, H. Jia, J. Xu, *et al.*, Biomethane Production From Lignocellulose: Biomass Recalcitrance and Its Impacts on Anaerobic Digestion, *Front. Bioeng. Biotechnol.*, 2019, **7**, 191.
- 9 S. Sethupathy, G. M. Morales, Y. Li, Y. Wang, J. Jiang, J. Sun, *et al.*, Harnessing microbial wealth for lignocellulose biomass valorization through secretomics: a review, *Biotechnol. Biofuels*, 2021, **14**(1), 154.
- 10 R. Reshmy, P. Athiyaman Balakumaran, K. Divakar, E. Philip, A. Madhavan, A. Pugazhendhi, *et al.*, Microbial valorization of lignin: Prospects and challenges, *Bioresour. Technol.*, 2022, **344**(Pt A), 126240.
- 11 T. Han, A. Nazarbekov, X. Zou and S. Y. Lee, Recent advances in systems metabolic engineering, *Curr. Opin. Biotechnol.*, 2023, **84**, 103004.
- 12 T. Jiang, C. Li, Y. Teng, R. Zhang and Y. Yan, Recent advances in improving metabolic robustness of microbial cell factories, *Curr. Opin. Biotechnol.*, 2020, **66**, 69–77.
- 13 Y. Teng, J. Zhang, T. Jiang, Y. Zou, X. Gong and Y. Yan, Biosensor-enabled pathway optimization in metabolic engineering, *Curr. Opin. Biotechnol.*, 2022, **75**, 102696.
- 14 W. Yu, X. Xu, K. Jin, Y. Liu, J. Li, G. Du, *et al.*, Genetically encoded biosensors for microbial synthetic biology: From conceptual frameworks to practical applications, *Biotechnol. Adv.*, 2023, **62**, 108077.
- 15 R.-Y. Liu, B.-Z. Li, Y.-J. Yuan and Z.-H. Liu, Multiscale metabolic engineering in biological lignin valorization, *Innovation*, 2025, 100993.
- 16 L. T. Nguyen, D.-P. Phan, A. Sarwar, M. H. Tran, O. K. Lee and E. Y. Lee, Valorization of industrial lignin to value-added chemicals by chemical depolymerization and biological conversion, *Ind. Crops Prod.*, 2021, **161**, 113219.
- 17 S. Chung, Biodegradable polymers: from synthesis methods to applications of lignin-graft-polyester, *Green Chem.*, 2024, **26**, 10774–10803.
- 18 S. Sethupathy, G. M. Morales, L. Gao, H. Wang, B. Yang, J. Jiang, *et al.*, Lignin valorization: Status, challenges and opportunities, *Bioresour. Technol.*, 2022, **347**, 126696.



- 19 H. Wang, X. Peng, H. Li, A. Giannis and C. He, Recent Biotechnology Advances in Bio-Conversion of Lignin to Lipids by Bacterial Cultures, *Front. Chem.*, 2022, **10**, 894593.
- 20 H. Wang, Y. Pu, A. Ragauskas and B. Yang, From lignin to valuable products-strategies, challenges, and prospects, *Bioresour. Technol.*, 2019, **271**, 449–461.
- 21 J. Dharmaraja, S. Shobana, S. Arvindnarayan, R. R. Francis, R. B. Jeyakumar, R. G. Saratale, *et al.*, Lignocellulosic biomass conversion via greener pretreatment methods towards biorefinery applications, *Bioresour. Technol.*, 2023, **369**, 128328.
- 22 F. da Silva Fernandes, E. S. de Souza, L. M. Carneiro, J. P. Alves Silva, J. V. B. de Souza and J. da Silva Batista, Current Ethanol Production Requirements for the Yeast *Saccharomyces cerevisiae*, *Int. J. Microbiol.*, 2022, **2022**, 7878830.
- 23 M. M. Mitchler, J. M. Garcia, N. E. Montero and G. J. Williams, Transcription factor-based biosensors: a molecular-guided approach for natural product engineering, *Curr. Opin. Biotechnol.*, 2021, **69**, 172–181.
- 24 J. K. Michener, K. Thodey, J. C. Liang and C. D. Smolke, Applications of genetically-encoded biosensors for the construction and control of biosynthetic pathways, *Metab. Eng.*, 2012, **14**(3), 212–222.
- 25 C. Deng, Y. Wu, X. Lv, J. Li, Y. Liu, G. Du, *et al.*, Refactoring transcription factors for metabolic engineering, *Biotechnol. Adv.*, 2022, **57**, 107935.
- 26 J. Zhang, X. Gong, Q. Gan and Y. Yan, Application of Metabolite-Responsive Biosensors for Plant Natural Products Biosynthesis, *Biosensors*, 2023, **13**(6), 633.
- 27 A. B. Banares, K. N. G. Valdehuesa, K. R. M. Ramos, G. M. Nisola, W. K. Lee and W. J. Chung, A pH-responsive genetic sensor for the dynamic regulation of D-xylonic acid accumulation in *Escherichia coli*, *Appl. Microbiol. Biotechnol.*, 2020, **104**(5), 2097–2108.
- 28 Y. Fang, J. Wang, W. Ma, J. Yang, H. Zhang, L. Zhao, *et al.*, Rebalancing microbial carbon distribution for L-threonine maximization using a thermal switch system, *Metab. Eng.*, 2020, **61**, 33–46.
- 29 J. Tellechea-Luzardo, M. T. Stiebritz and P. Carbonell, Transcription factor-based biosensors for screening and dynamic regulation, *Front. Bioeng. Biotechnol.*, 2023, **11**, 1118702.
- 30 J. Wang, C. Li, T. Jiang and Y. Yan, Biosensor-assisted titratable CRISPRi high-throughput (BATCH) screening for over-production phenotypes, *Metab. Eng.*, 2023, **75**, 58–67.
- 31 T. Jiang, C. Li, Y. Zou, J. Zhang, Q. Gan and Y. Yan, Establishing an Autonomous Cascaded Artificial Dynamic (AutoCAD) regulation system for improved pathway performance, *Metab. Eng.*, 2022, **74**, 1–10.
- 32 W. S. Teo and M. W. Chang, Bacterial XylRs and synthetic promoters function as genetically encoded xylose biosensors in *Saccharomyces cerevisiae*, *Biotechnol. J.*, 2015, **10**(2), 315–322.
- 33 R. Q. Tang, J. M. Wagner, H. S. Alper, X. Q. Zhao and F. W. Bai, Design, Evolution, and Characterization of a Xylose Biosensor in *Escherichia coli* Using the XylR/xylo System with an Expanded Operating Range, *ACS Synth. Biol.*, 2020, **9**(10), 2714–2722.
- 34 T. Kaper, I. Lager, L. L. Looger, D. Chermak and W. B. Frommer, Fluorescence resonance energy transfer sensors for quantitative monitoring of pentose and disaccharide accumulation in bacteria, *Biotechnol. Biofuels*, 2008, **1**(1), 11.
- 35 S. Y. Tang, H. Fazelinia and P. C. Cirino, AraC regulatory protein mutants with altered effector specificity, *J. Am. Chem. Soc.*, 2008, **130**(15), 5267–5271.
- 36 C. L. Kelly, Z. Liu, A. Yoshihara, S. F. Jenkinson, M. R. Wormald, J. Otero, *et al.*, Synthetic Chemical Inducers and Genetic Decoupling Enable Orthogonal Control of the rhaBAD Promoter, *ACS Synth. Biol.*, 2016, **5**(10), 1136–1145.
- 37 K. K. Kwon, S. J. Yeom, D. H. Lee, K. J. Jeong and S. G. Lee, Development of a novel cellulase biosensor that detects crystalline cellulose hydrolysis using a transcriptional regulator, *Biochem. Biophys. Res. Commun.*, 2018, **495**(1), 1328–1334.
- 38 I. Reinartz, M. Sarter, J. Otten, H. Hofig, M. Pohl, A. Schug, *et al.*, Structural Analysis of a Genetically Encoded FRET Biosensor by SAXS and MD Simulations, *Sensors*, 2021, **21**(12), 4144.
- 39 R. M. de Lorimier, J. J. Smith, M. A. Dwyer, L. L. Looger, K. M. Sali, C. D. Paavola, *et al.*, Construction of a fluorescent biosensor family, *Protein Sci.*, 2002, **11**(11), 2655–2675.
- 40 R. K. Jha, T. L. Kern, D. T. Fox and C. E. M. Strauss, Engineering an *Acinetobacter* regulon for biosensing and high-throughput enzyme screening in *E. coli* via flow cytometry, *Nucleic Acids Res.*, 2014, **42**(12), 8150–8160.
- 41 A. M. Kunjapur and K. L. J. Prather, Development of a Vanillate Biosensor for the Vanillin Biosynthesis Pathway in *E. coli*, *ACS Synth. Biol.*, 2019, **8**(9), 1958–1967.
- 42 W. Wu, F. Liu and S. Singh, Toward engineering *E. coli* with an autoregulatory system for lignin valorization, *Proc. Natl. Acad. Sci. U. S. A.*, 2018, **115**(12), 2970–2975.
- 43 P. Dong, Y. Fan, Y. X. Huo, L. Sun and S. Guo, Pathway-Adapted Biosensor for High-Throughput Screening of O-Methyltransferase and its Application in Vanillin Synthesis, *ACS Synth. Biol.*, 2024, **13**(9), 2873–2886.
- 44 S. Siedler, N. K. Khatri, A. Zsohar, I. Kjaerbolting, M. Vogt, P. Hammar, *et al.*, Development of a Bacterial Biosensor for Rapid Screening of Yeast *p*-Coumaric Acid Production, *ACS Synth. Biol.*, 2017, **6**(10), 1860–1869.
- 45 L. F. Machado and N. Dixon, Development and substrate specificity screening of an in vivo biosensor for the detection of biomass derived aromatic chemical building blocks, *Chem. Commun.*, 2016, **52**(76), 11402–11405.
- 46 T. Uchiyama and K. Miyazaki, Product-induced gene expression, a product-responsive reporter assay used to screen metagenomic libraries for enzyme-encoding genes, *Appl. Environ. Microbiol.*, 2010, **76**(21), 7029–7035.
- 47 S. van Sint Fiet, J. B. van Beilen and B. Witholt, Selection of biocatalysts for chemical synthesis, *Proc. Natl. Acad. Sci. U. S. A.*, 2006, **103**(6), 1693–1698.



- 48 G. Fiorentino, R. Ronca and S. Bartolucci, A novel *E. coli* biosensor for detecting aromatic aldehydes based on a responsive inducible archaeal promoter fused to the green fluorescent protein, *Appl. Microbiol. Biotechnol.*, 2009, **82**(1), 67–77.
- 49 C. R. Strachan, R. Singh, D. VanInsberghe, K. Ievdokymenko, K. Budwill, W. W. Mohn, *et al.*, Metagenomic scaffolds enable combinatorial lignin transformation, *Proc. Natl. Acad. Sci. U. S. A.*, 2014, **111**(28), 10143–10148.
- 50 T. H. Kim, S. G. Woo, S. K. Kim, B. H. Yoo, J. Shin, E. Rha, *et al.*, A Genetically Encoded Biosensor for the Detection of Levulinic Acid, *J. Microbiol. Biotechnol.*, 2023, **33**(4), 552–558.
- 51 S. Jiang, R. Wang, D. Wang, C. Zhao, Q. Ma, H. Wu, *et al.*, Metabolic reprogramming and biosensor-assisted mutagenesis screening for high-level production of L-arginine in *Escherichia coli*, *Metab. Eng.*, 2023, **76**, 146–157.
- 52 R. Zhi, N. Cheng, G. Li and Y. Deng, Biosensor-based high-throughput screening enabled efficient adipic acid production, *Appl. Microbiol. Biotechnol.*, 2023, **107**(17), 5427–5438.
- 53 Y. Dabirian, P. G. Teixeira, J. Nielsen, V. Siewers and F. David, FadR-Based Biosensor-Assisted Screening for Genes Enhancing Fatty Acyl-CoA Pools in *Saccharomyces cerevisiae*, *ACS Synth. Biol.*, 2019, **8**(8), 1788–1800.
- 54 A. O. Johnson, M. Gonzalez-Villanueva, L. Wong, A. Steinbuchel, K. L. Tee, P. Xu, *et al.*, Design and application of genetically-encoded malonyl-CoA biosensors for metabolic engineering of microbial cell factories, *Metab. Eng.*, 2017, **44**, 253–264.
- 55 S. Y. Choi, W. J. Kim, S. J. Yu, S. J. Park, S. G. Im and S. Y. Lee, Engineering the xylose-catabolizing Dahms pathway for production of poly(D-lactate-co-glycolate) and poly(D-lactate-co-glycolate-co-D-2-hydroxybutyrate) in *Escherichia coli*, *Microb. Biotechnol.*, 2017, **10**(6), 1353–1364.
- 56 J. Gu, Q. Qiu, Y. Yu, X. Sun, K. Tian, M. Chang, *et al.*, Bacterial transformation of lignin: key enzymes and high-value products, *Biotechnol. Biofuels Bioprod.*, 2024, **17**(1), 2.
- 57 D. Liu, M. S. Sica, J. Mao, L. F. Chao and V. Siewers, A *p*-Coumaroyl-CoA Biosensor for Dynamic Regulation of Naringenin Biosynthesis in *Saccharomyces cerevisiae*, *ACS Synth. Biol.*, 2022, **11**(10), 3228–3238.
- 58 Y. Zou, C. Li, R. Zhang, T. Jiang, N. Liu, J. Wang, *et al.*, Exploring the Tunability and Dynamic Properties of MarR-PmarO Sensor System in *Escherichia coli*, *ACS Synth. Biol.*, 2021, **10**(8), 2076–2086.
- 59 J. Li, C. Yue, W. Wei, Y. Shang, P. Zhang and B. C. Ye, Construction of a *p*-coumaric and ferulic acid auto-regulatory system in *Pseudomonas putida* KT2440 for protocatechuate production from lignin-derived aromatics, *Bioresour. Technol.*, 2022, **344**(Pt B), 126221.
- 60 T. M. Lo, S. H. Chng, W. S. Teo, H. S. Cho and M. W. Chang, A Two-Layer Gene Circuit for Decoupling Cell Growth from Metabolite Production, *Cell Syst.*, 2016, **3**(2), 133–143.
- 61 J. R. Elmore, G. N. Dexter, D. Salvachua, J. Martinez-Baird, E. A. Hatmaker, J. D. Huenemann, *et al.*, Production of itaconic acid from alkali pretreated lignin by dynamic two stage bioconversion, *Nat. Commun.*, 2021, **12**(1), 2261.
- 62 Y. Zhao, L. Xue, Z. Huang, Z. Lei, S. Xie, Z. Cai, *et al.*, Lignin valorization to bioplastics with an aromatic hub metabolite-based autoregulation system, *Nat. Commun.*, 2024, **15**(1), 9288.
- 63 T. Jiang, C. Li, Y. Teng, J. Zhang, D. A. Logan and Y. Yan, Dynamic Metabolic Control: From the Perspective of Regulation Logic, *Synth. Biol. Eng.*, 2023, **1**(2), 10012.
- 64 W. Zeng, L. Guo, S. Xu, J. Chen and J. Zhou, High-Throughput Screening Technology in Industrial Biotechnology, *Trends Biotechnol.*, 2020, **38**(8), 888–906.
- 65 H. G. Lim, S. Jang, S. Jang, S. W. Seo and G. Y. Jung, Design and optimization of genetically encoded biosensors for high-throughput screening of chemicals, *Curr. Opin. Biotechnol.*, 2018, **54**, 18–25.
- 66 H. H. Chou and J. D. Keasling, Programming adaptive control to evolve increased metabolite production, *Nat. Commun.*, 2013, **4**, 2595.
- 67 Y. Mao, C. Huang, X. Zhou, R. Han, Y. Deng and S. Zhou, Genetically Encoded Biosensor Engineering for Application in Directed Evolution, *J. Microbiol. Biotechnol.*, 2023, **33**(10), 1257–1267.
- 68 T. C. Williams, I. S. Pretorius and I. T. Paulsen, Synthetic Evolution of Metabolic Productivity Using Biosensors, *Trends Biotechnol.*, 2016, **34**(5), 371–381.
- 69 T. Akkas, M. Reshadsedghi, M. Sen, V. Kilic and N. Horzum, The Role of Artificial Intelligence in Advancing Biosensor Technology: Past, Present, and Future Perspectives, *Adv. Mater.*, 2025, e2504796.
- 70 N. Ding, Z. Yuan, Z. Ma, Y. Wu and L. Yin, AI-Assisted Rational Design and Activity Prediction of Biological Elements for Optimizing Transcription-Factor-Based Biosensors, *Molecules*, 2024, **29**(15), 3512.
- 71 N. Ding, Z. Yuan, X. Zhang, J. Chen, S. Zhou and Y. Deng, Programmable cross-ribosome-binding sites to fine-tune the dynamic range of transcription factor-based biosensor, *Nucleic Acids Res.*, 2020, **48**(18), 10602–10613.
- 72 Y. Zhou, Y. Yuan, Y. Wu, L. Li, A. Jameel, X. H. Xing, *et al.*, Encoding Genetic Circuits with DNA Barcodes Paves the Way for Machine Learning-Assisted Metabolite Biosensor Response Curve Profiling in Yeast, *ACS Synth. Biol.*, 2022, **11**(2), 977–989.
- 73 N. Fu, R.-Y. Liu, Y. Zhou, B.-Z. Li, Y.-J. Yuan and Z.-H. Liu, Technological advances in ligninolytic enzymes for the biological valorization of lignin, *Green Chem.*, 2025, **27**(16), 4016–4039.

