BIOTRANS
LA ROCHELLE 2023

N°135 / PC
TOPIC(s) : Enzyme discovery and engineering / Industrial biocatalysis

Exploring sequence space to improve transglycosylation efficiency in CGTase

AUTHORS
Gareth SURMAN / UNIVERSITY OF MANCHESTER, 131 PRINCESS STREET, MANCHESTER
Sabine FLITSCH / UNIVERSITY OF MANCHESTER, 131 PRINCESS STREET, MANCHESTER

PURPOSE OF THE ABSTRACT

Cyclodextrin glycosyltransferases (CGTases) are multifunctional enzymes, performing four related reactions that each involve stereoselective α-glucosyl transfer on to an alcohol acceptor [1]. It has been shown to catalyse the glycosylation of a variety of acceptors [2-4]. However, this multifunctionality creates a challenge when trying to create polyglycosylated products biocatalytically, as the products are hydrolysed down to those containing fewer glucose units. We have developed a high throughput assay system in order to assess the degree of glycosylation, and applied this to study both directed evolution and metagenomics of CGTase.

[1] B. A. Van Der Veen et al, Eur. J. Biochem., 2000, 267, 658–665
[2] W. M. J. Kloosterman et al, Macromol. Biosci., 2014, 14, 1268–1279
[3] X. Tao et al, Crit. Rev. Biotechnol., 2019, 39, 249–257
[4] D. Svensson et al, Biotechnol. Bioeng., 2009, 104, 854–861

FIGURES

FIGURE 1

FIGURE 2

KEYWORDS

Biocatalysis | Glycoscience | Ancestral Sequence Reconstruction | CGTase

BIBLIOGRAPHY

[1] B. A. Van Der Veen et al, Eur. J. Biochem., 2000, 267, 658-665

[2] W. M. J. Kloosterman et al, Macromol. Biosci., 2014, 14, 1268-1279

[3] X. Tao et al, Crit. Rev. Biotechnol., 2019, 39, 249-257

[4] D. Svensson et al, Biotechnol. Bioeng., 2009, 104, 854-861