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Special Issue

Molecular Modeling of Carbohydrates

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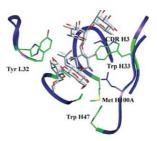
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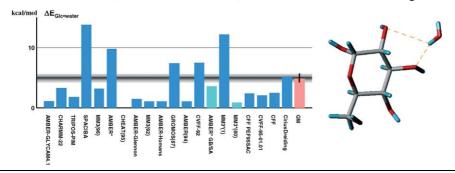
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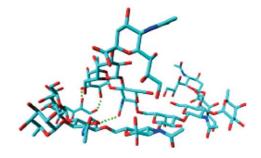
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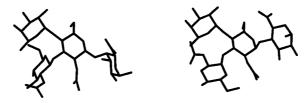
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Conformational analysis and dynamics of mannobiosides and mannotriosides using Monte Carlo/stochastic dynamics simulations

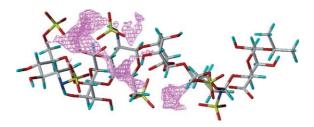
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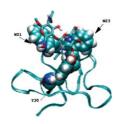
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Molecular dynamics simulations of glycosyltransferase LgtC

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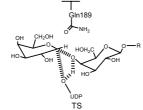




Molecular modeling insights into the catalytic mechanism of the retaining galactosyltransferase LgtC

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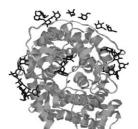
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The catalytic mechanism of the retaining glycosyltransferases LgtC was investigated using high level ab initio calculations. The preferred pathway is predicted to proceed by an unique $A_ND_NA_HD_H$ type of mechanism. The determined structure of the transition state, in which the hydrogen bond between the nucleophile and the leaving group oxygens facilitates the attack of the acceptor O-4' from the same side of the transferred galactose is exceptional and provides valuable information for designing stable analogues of TS as potent inhibitors of the bacterial LgtC.

Data mining the protein data bank: automatic detection and assignment of carbohydrate structures Thomas Lütteke.* Martin Frank and Claus-W. von der Lieth

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COVER

Well-defined glycoforms of glycoproteins can easily be obtained by oxidative coupling of synthetic thioaldoses with proteins that have a cysteine moiety in lieu of an asparagine residue carrying natural N-linked oligosaccharides. In vitro glycosylation offers several advantages such as quantitative conjugation, incorporation of oligosaccharides that display high bioactivities and the possibility of using convenient bacterial or yeast protein expression systems. The figure is related to Geert-Jan Boons' *Carbohydrate Research Award* paper, Carbohydr. Res., **2004**, *339*, 181–193.



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