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A rational approach to identification of wild type trans-sialidases for the production of human milk oligosaccharides

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In this study, sequence analysis and 3D alignment were used for the identification of a novel trans-sialidase, namely the trans-sialidase of Haemophilus parasuis. The H. parasuis trans-sialidase was one of four candidate enzymes selected from a database of 2909 protein sequences. It is the first time that a sequence analysis approach has been successful in identifying a trans-sialidase and additionally all remaining candidates (the sialidases of Pasteurella multosida, Actinomyces Oris and Manheimia Haemolytica) exhibited trans-activity, however they were ultimately not defined as trans-sialidases due to the comprehensive definition of a trans-sialidase. A trans-sialidase can be defined as a sialidase which, under a specific set of conditions, prefers the transfer of a sialic acid residue from a donor to an acceptor molecule over the hydrolysis of the donor. Trans-sialidases are sought after because they can be applied for the enzymatic production of human milk oligosaccharides (for addition to infant formula) from dairy side-stream products. So far, the only native trans-sialidase that has been found is the trans-sialidase of the human pathogen Trypanosomas cruzi. However, an additional trans-sialidase has been engineered through directed evolution of the sialidase of Trypanosomas rangeli. Rational inspection of the 3D structure of these known trans-sialidase was the basis for this study, and it is hoped that attributes of the newly identified H. parasuis trans-sialidase can be the basis of further trans-sialidase discovery.

Biography

Rune Thorbjørn Nordvang is in the final stages of his PhD at the Technical University of Denmark (DTU). In the BioEng group (at DTU) he has worked with all aspects of enzymatic production of human milk oligo-saccharides from dairy side stream products and has published 6 articles on the topic.

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