Glycoside hydrolases in bacteroides fragilis.

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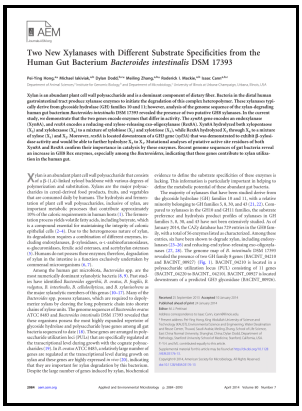
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Two New Xylanases with Different Substrate Specificities from the Human Gut Bacterium *Bacteroides intestinalis* DSM 17393

Description: -
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[PDF] Preferential Packing of Acidic Glycosidases and Proteases into Bacteroides Outer Membrane Vesicles

Amino Acids Analyses Quantitative determination of amino acids in cell-free supernatants from cultures and in cell-free extracts CFEs was carried out by ultra-HPLC UHPLC using the method described in. Corresponding IC50 values were 45, 37 and 32 nM, respectively, at an enzyme concentration of 2. Glycans are the major carbon sources available to the human colonic microbiota.

Purification of glycoside hydrolases from Bacteroides fragilis.

This model carboxylic acid-mediated activation of amido group bears some analogy to the mechanism employed by members of , , , , and. Conclusion The results presented provide an insight into the physiological and molecular mechanisms that allow B. The genes for the NAD P H-dependent glutamate dehydrogenase gdhB and the acetolactate synthase ilvB showed downregulation in the presence of both EPSs, whereas the gene coding for the major outer membrane protein OmpA ompA and the pyruvate phosphate dikinase ppdK displayed increased expression under the same conditions.

β

EPSs were isolated and purified from the cellular biomass of the producing strains harvested from agar-MRS plates supplemented with 0. Both, national and regional grants received cofounding from European Union FEDER funds.

Investigations of Bacteroides spp. towards next

A rapid method for isoelectric focusing in polyacrylamide gel.

Structural and functional analysis of a glycoside hydrolase family 97 enzyme from Bacteroides thetaiotaomicron

C, monomer structure of SusB with bound acarbose molecule shown as stick model in magenta at the active site pocket. In other microorganisms, OmpA functions as a porin that enables the passage of nutrients and different compounds into the cell ,. Notably, the carbohydrates present in the culture medium affected the profile of some amino acids differently.

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