Gal-3 and differences, but to shed light on the structural organization of the dimers N-neotetraose. The solved the x-ray crystal structures of rat Gal-1, human Gal-2, the CRD of human Gal-3 and the N-terminal CRD of rat domain or two CRDs linked in tandem. In addition to differences in San above the indole ring of Trp88. This indole ring is the prime hydro­
ily are composed of mal lectins characterized by tions have been proposed for these lectins, including roles in T cell
mortality receptors which are secreted by Vibrio cholerae
The Galectins are a large family of β-galactoside binding ani­
mucosal enzymes to facilitate catalysis, such as substrate distortion and su­
pticic F2, t1iantennary. Crystallographic studies of the enzymes, mutants and complexes are aimed at the analysis of the mechanisms of action and the basis for the substrate specificities of the enzymes. PNGase F is composed of two 8-stranded β-sand­wich domains that are positioned side-by-side. Loops that connect the β-strands form a cleft at the interface between the two do­
The enzymes re­
endoglucosidases are (α/β)-barrels. The structures of Endo F1 and H reveal distinct features associated with the rec­
Each of the glycosyl hydrolases with structural representatives for families of glycosyl hydrolases with structural representatives for
inhibitors plus substrates non-hydrolysable substrate analogues mechanism-based inhibitors and suicide substrates
Flavobacterium meningosepticum secretes four oligosaccha­
Endo F1, F2 and F3, as well as the related Endo H, cleave the (1→4)-glycosidic bond between the two N-acetylglucosamines of the chitobiose core. They differ strongly in their respective specificities for different oligosaccharide structures: F1 (and H), high-mannose; F2, biantennary; and, F3, triantennary. Crystallographic studies of the enzymes, mutants and complexes are aimed at the analysis of the mechanisms of action and the basis for the substrate specificities of the enzymes. PNGase F is composed of two 8-stranded β-sand­wich domains that are positioned side-by-side. Loops that connect the β-strands form a cleft at the interface between the two do­
Endo F1 and H reveal distinct features associated with the rec­
the branched high-mannose chain, the difference in tolerance for an α:(1-3)-fucose on the asparagine-proximal N­
endo-β-N-acetylgalactosaminidase (Endo) F1, F2 and F3, and the amidohydrolase, peptide-N-(N-acetyl-β-D-gluco­saminyl)asparagine amidase (PNGase) F. The enzymes re­move asparagine-linked oligosaccharides and are used as biochemi­cal tools for the analysis of glycoproteins. All four enzymes have unique substrate specificities. PNGase F removes the intact oligosaccharide chain and converts the asparagine to an aspartic acid. The minimum substrate for PNGase F consists of the asparagine residue with both the carboxyl and amino groups in peptide link­age and the chitobiose core of the oligosaccharide. Endo F1, F2 and F3, as well as the related Endo H, cleave the (1→4)-glycosidic bond between the two N-acetylglucosamines of the chitobiose core. These pathogens se­cretes four oligosaccha­