# ACTIVITY-BASED PROBES TARGETING MARINE FUCOIDAN HYDROLASES

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Marine glycans are vital biomolecules that play a pivotal role in the global carbon cycle, contributing to the fixation of approximately 50 gigatons of carbon by the oceans each year [1]. Glycans derived from marine organisms have gained significant attention due to their diverse biological activities and their potential applications across various industries. Among these, fucoidans – sulfated polysaccharides primarily composed of L-fucose residues – are of particular interest. Fucoidans display a high degree of structural heterogeneity, especially in their sulfation patterns, making it challenging to establish clear structure-function relationships [2]. This knowledge gap could potentially be narrowed by studying the enzymes that degrade these complex biopolymers, which may also serve as valuable tools for the consistent enzymatic extraction of well-defined fucoidan structures [3]. Fucoidans are typically broken down by marine microbes, yet their degradation pathways remain poorly understood and involve a wide array of enzymes classes, including sulfatases and glycosidases [4]. Among these are fucoidan hydrolases, or fucoidanases, which cleave the glycosidic linkages between sulfated fucose moieties [5]. Despite limited knowledge about these enzymes, studies suggest that they could operate *via* a retaining catalytic mechanism [6]. As this mechanism proceeds through a covalent enzyme-glycosyl intermediate, it presents the opportunity for covalent trapping of the active site residues using mechanism-based inhibitors and probes [7]. In this work, we designed, synthesized and applied new activity-based probes to selectively target fucoidan hydrolases from marine organisms.

**References:**

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