# CRAZY polysaccharides:
# sCReening of Actives enZYmes on a collection of polysaccharides

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Polysaccharides are very complex biomacromolecules and represent the most abundant biomass on land and in oceans. As such they mediate a plethora of biological functions, from energy storage, to structural molecules, or as the mediators of intra- and intercellular recognition within one organism or between organisms. Exploitation of this resource, from the production of original oligosaccharides (e.g. bioactives) toward fermentable monosaccharides (e.g. bioenergy), rely on the use of enzymes: the glycosides hydrolases (GH) and the polysaccharides lyases (PL).

GH and PL have been classified as a function of the reaction they catalyze (about 160 EC numbers) and by sequence homology (133 GH families and 23 PL families, CAZy classification: http://www.cazy.org). Despite the exponential deluge of sequence data resulting from genomic programs, the pace of discovery of new GH and PL enzymes remains constant and comparatively modest. The new sequence data essentially increase the number of enzymes classified in existing families, and do not contribute to the number of biochemically-characterized enzymes or of enzymes with a known 3-D structure.

In this context, we have designed and implemented a medium throughput screening platform for assessing GH and PL activities on a collection of polysaccharides substrates having known and unknown structures. Several examples of screening will be presented highlighting approaches leading to the discovery of new enzymes (*i.e.* new GH family or new modes of action).