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## Developing the bio-economy: Fast track discovery of new enzymes for effcient and value added biomass conversion

new fast track enzyme discovery technology platform has been developed. It dierentiates from existing approaches as it A is non-alignment based and facilitates prediction of function of the enzyme directly from the (genome) sequence. New enzymes and enzyme-based processes are being developed for producing biomass-based food ingredients, feed additives, health-promoting products, components for skincare and wound healing as well as fertilizer, bers and building blocks for chemicals. Enzyme discoveries of relevance for the following types of biomass feed stock have recently been made: biore nery, making value added products from green grass, clover, etc. Seaweed biomass, from species of brown algae, growing meters high in temperate/colder waters, have already now been documented to hold several components with potentials for being developed into new value chains. Feather is composed of the proteinaceous, highly recalcitrant keratin. It has been shown that a blend composed of three speciec types of fungal enzymes can be used for decomposing the keratin into peptides and amino acids. Interestingly, the keratin-degrading fungi in these studies showed four di erent LPMO genes, (Lytic Polysaccharide Monooxygenases) which may be directly involved in breaking down the keratin. Enzymes of relevance for improved processing of sh skin collagen are being studied in the project Collagen Hydrolysate funded as a Nordic Innovation program.

## **Biography**

Lene Lange is a Professor at the Center for Bioprocess Engineering, DTU Chemical Engineering, Denmark. She has held Research Director Positions in both industry and æ&æå^{iziblO`!!^}c|^Ek•@^k@[|å•kæáçi•[|^k][•ixi[]•ixi[]•kækKV@^kOæ}i•@kÞæxi[]æ|kOi[E^&[][{ ^kUæ}^Ebe^kD[[iiskKOi[E^&[][{ ^kUæ}][iiskKOi[E^&[][{ ^kUæ}][iiskKOi[E^k][][{ ^kUæ}][iiskKOi[E^k][][][iiskKOi[E^k][][iiskKOi[E^k]][iiskKOi[E^k][][iiskKOi[E^k]][iiskKOi[E^k]][iiskKOi[E^k][][iiskKOi[E^k]][iiskKOi[E^k]][iiskKOi[E^k][][iiskKOi[E^k]][iiskKOi[E^k]][iiskKOi[E^k]][iiskKOi[E^k][iiskKOi[E^k]][iiskKoo[E^k]][iiskKoo[E^k]][iiskKoo[E^k]][iiskKoo[E^k]][iiskKoo[E^k]][iiskKoo[E^k]][iiskKoo[E^k]][iiskKoo[E^k]][iiskKoo[E^k]][iiskKoo[E^k]][iiskKoo[E^k]][iiskKoo[E^k]][iiskKoo[E^k]][iiskKoo[E^k]][iiskKoo[E^k]][iiskKoo[E^k]][iiskKoo[E^k]][iiskKoo[E^k]][iiskKoo[E^k]][ii OUVÒÒNV@æijæyàthP^\h,^|a\*h[-h\^\*^æk@kæ!^hài\*&[ç^\^h[-h][ç^h\^}:^{^\*h[-hki{]|[ç^akài[{æ\*\*hk[};o~i\*]}hai[]^n,}^i?hi]:[&^\*\*-^th, iebh\*]^&i, iebh\*]^ çæ|^^k-![{kæ\*i[Éi}à~eliæ|k•iå^k-el^æ{•kæ}åk,æ•c^hji[ā~ko•kkå^ç^|[]{^}ol\_i-ko^hj^^,^k^}:^{^k}:^{^k}i] [£i]a~elie[i]{beuli}}[}.\*} {^^}chæ\*o\*ah\*o\*`~}.\*\* predicting function directly from sequence and using PPR analysis, combined with MS, phylogenetic analysis.

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