NTNU
Kunnskap for en bedre verden

Master's theses proposals

Department of Biotechnology and Food Science

Department of Biology

This document contains proposed projects relevant for students at MSc Biotechnology (2- and 5-year study), MSc Aquatic Food Production, the 2- and 5-year MSc Chemical Engineering and Biotechnology (MIKJ/MTKJ) and MSc Nanotechnology (MTNANO/sivilingeniørstudiet).

The different proposals might have different credits. This relates to the proposed theses being planned for different study programmes: the MSc Biotechnology (60 credits), MSc Aquatic Food Production (30 credits) or MSc Chemical Engineering and Biotechnology / Nanotechnology (30 credits). Some proposals may also be relevant as specialization project for the technology studies (15 credits).

Please contact supervisor directly if you have any questions regarding theses' proposals.

Academic year 2018/19

Date: 23.04.2018 v6.2

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Contents

Department of Biotechnology and Food Science

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Biveileder/-e: *Co-supervisor/-s:*	Gaston Courtade
Arbeidstittel på oppgaven/ *Preliminary title:*	**Development of chitin-based sorbents for protein purification**

Kort beskrivelse av oppgaven / *Short description of the project*:
The focus of this project will be to design and construct chitin-based materials for the extraction and purification of proteins from complex biological mixtures.

Bakgrunn og mål / *Background and Objectives:*
The production of proteins is a high-value industry with applications in all branches of biotechnology. A key step of the protein-production process is to achieve a high degree of purity of the protein products. Affinity chromatography is a powerful tool for the purification of specific proteins from a complex biological mixture, such as a fermenter. Chitin is a polysaccharide that is a good candidate for use in affinity chromatography because it selectively adsorbs proteins that bind chitin. In fact, chitin resins are already employed in affinity chromatography columns. However, the use of columns requires some degree of sample preparation and filtration. The aim of this project is to develop chitin-based materials that can be used for direct extraction of proteins from biological mixtures. Such materials would provide a rapid alternative method to extract and purify target proteins at different stages of a process without the need for sample preparation.

Eksperimentelt / *Experimental methods:*
- Development of methods for the production of chitin fibers.
- Characterization of chitin fibers (strength, swelling, protein adsorption).
- Design of a protocol for the use of chitin fibers in protein purification applications.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MTNANO
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng 60 credits / 30 credits

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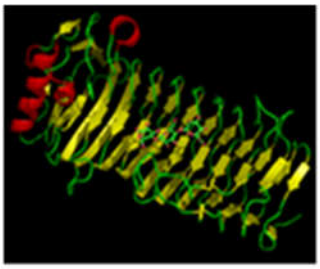
Biveileder/-e: *Co-supervisor/-s:*	Marit Sletmoen og/eller Anne Tøndervik (Sintef)
Arbeidstittel på oppgaven/ *Preliminary title:*	**Purification and characterization of design mannuronan-c-5 epimerases**

Kort beskrivelse av oppgaven / *Short description of the project*:
The focus of this project will be to study the interaction of alginate C-5 epimerases with substrate, and its product profile using biophysical techniques. The specific content of project may be adapted to the candidate's preferences.

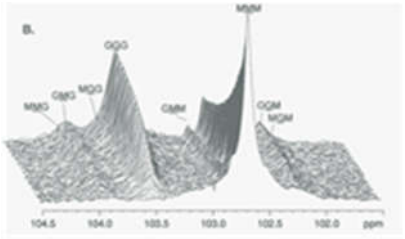
Bakgrunn og mål / *Background and Objectives:*

Azotobacter vinelandii is a soil bacteria, which are able to produce alginate, a polysaccharide. Alginate consists of mannuronic acid (M) and guluronic acid (G), and the properties of the polymer are, among other things, dependent on the distribution of these units. *A. vinelandii* synthesises alginate by first making polymannuronic acid (poly-M), of which some M-units are converted to G-units. This reaction is catalyzed by enzymes called epimerases, and *A. vinelandii* produce seven enzymes of this kind; AlgE1 to AlgE7. Poly-M can be epimerized in vitro and the various epimerases are shown to give different G-contents and different distributions of G-unites in the alginate that is produced



A-module of AlgE4

Certain alginates have turned out to be bioactive, and are therefore interesting with regards to medical applications. Researchers at NTNU/Sintef are trying to find new enzymes that can create alginates with tailored properties for these kinds of applications. This project will be about characterization of alginate epimerases. This involves protein production and purification of the enzymes. Characterization of the properties of the enzymes with regard to epimerization of poly-M. Gelling properties of the generated alginates and characterization.



Epimerase activity profile by NMR

Eksperimentelt / *Experimental methods:*

- Production and purification of the alginate epimerases.
- Characterization of the enzymes with regard to activity, substrate specificity and reaction pattern. Relevant methods for the characterization are Isothermal titration calorimetry (ITC), atomic force microscopy (AFM), Ion chromatography system (ICS), NMR and Time-resolved NMR.
- Characterization of epimerized alginates with regard to gelling properties, relevant for their biomedical applications.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MTNANO
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng 60 credits / 30 credits

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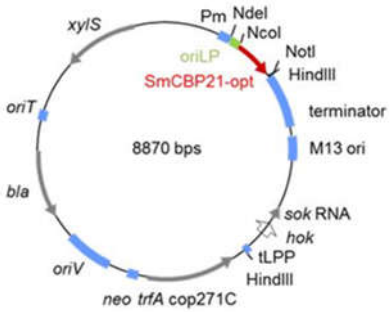
Biveileder/-e: *Co-supervisor/-s:*	Trygve Brautaset
Arbeidstittel på oppgaven/ *Preliminary title:*	**New heterologous protein expression system for isotope labeled proteins**

Kort beskrivelse av oppgaven / *Short description of the project*:
This project will focus on the further development of a new set of expression vectors for production of isotope labeled protein (for NMR applications) based on the *Pm*/XylS promoter system. The specific content of the project may be adapted to the candidate's preferences.

Bakgrunn og mål / *Background and Objectives:*
A common bottleneck in heterologous protein expression of isotope labelled protein in bacteria is the promoter system used. These promoter systems are mainly based on the carbohydrate metabolism of the cell, like the *Lac* and *ara—BAD* operons. This poses a problem when growing cells in a minimal medium with glucose as the sole carbon source, which results in poor regulation of the promoter system and low expression of the target protein.



Vector map of LPMO Expression cassette

A solution to the problem is to use a promoter system that is not influenced by the carbohydrate metabolism of the cell. The group of Prof. Svein Valla at our department has developed an expression system based on the *Pm*/XylS promoter system, which uses benzoate derivatives as inducers of the protein expression. Recently, we have published a work where *Pm*/XylS promoter system was used for the expression of an isotope labeled LPMO (lytic polysaccharide monooxygenase).

Aim of this project is to construct a new set of expression vectors for production of isotope labeled protein where expression level of the target protein is independent of media composition. The developed expression system will offer a large potential within structural biology and for protein expression in general.

Eksperimentelt / *Experimental methods:*
- *State-of-the-art* molecular genetics.
- Characterization of the of the expression system.
- Production and purification of the target protein.

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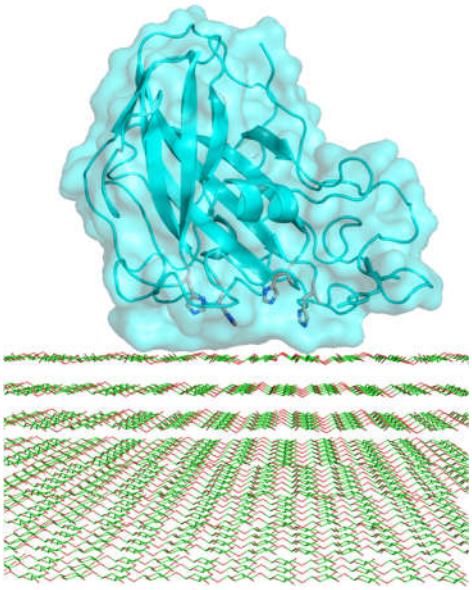
Arbeidstittel på oppgaven/ *Preliminary title:*	**Characterization of novel proteins for biorefinery applications**

Kort beskrivelse av oppgaven / *Short description of the project*:
The focus of this project will be to study new carbohydrate active enzymes by using biophysical techniques such as NMR spectroscopy. The specific content of project may be adapted to the candidate's preferences.

Bakgrunn og mål / *Background and Objectives:*
Biorefineries where biomass from marine and forestry resources are converted to monosaccharides are a cornerstone of bioeconomy. These monosaccharides can be used to produce bioethanol and value-added products. However, the inefficient hydrolysis of insoluble biomass (chitin and cellulose) is a bottleneck in the biorefining process. A way to overcome this obstacle is through a new family of enzymes - lytic polysaccharide monooxygenases (LPMOs) – that enhance the biomass degradation process by the oxidative cleavage of glycosidic bonds in chitin and cellulose. Since 2010, we have studied LPMOs in cooperation with NMBU, and we are interested in gaining a better understanding of the function and mode of action of LPMOs.



Eksperimentelt / *Experimental methods:*
- Recombinant protein production and purification.
- Acquisition of multidimensional NMR spectra and assignment of the protein backbone and side-chains.
- Protein structure determination.
- Dynamics studies with NMR spectroscopy and other techniques such as circular dichroism (CD).
- Measurements of interactions between LPMOs and other substrates/proteins.

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Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng 60 credits / 30 credits

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Biveileder/-e: *Co-supervisor/-s:*	André Voigt
Arbeidstittel på oppgaven/ *Preliminary title:*	**Comparative study of gene expression networks**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*

Network analysis has been central to uncovering important principles of interactome organization. Gene expression correlation networks consist of genes that showing strong similarities or dissimilarities in their expression patterns, making it possible to identify important gene clusters associated with a given phenotype or biological function.

The ability to understand consequences of genetic variation in an organism is a significant challenge in biology. The goal of this project is to use a recently developed network approach (Voigt, Nowick & Almaas) to study the variation of *gene co-expression patterns* in a recent high-quality gene-expression data set, such as GTEx (http://www.gtexportal.org/) for humans. For the interested candidate, there are possibilities to further develop the methodology.

Eksperimentelt / *Experimental methods:*
N/A

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Biveileder/-e: *Co-supervisor/-s:*	Christian Schulz, Martina Hall
Arbeidstittel på oppgaven/ *Preliminary title:*	**Identifying conserved regions in human metabolic proteins relevant for maintenance of protein function**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*

Understanding the consequences of DNA mutations, especially small mutations that are not discovered by the cell's repair mechanisms, is a significant challenge in biology. Especially in the metabolism of human cell's, small changes in a protein sequence may have a huge impact on the cell's efficiency and thereby a human's health.
This project aims to identify conserved areas within human metabolic proteins, which are crucial for maintaining protein functionality, and to relate the relevant amino acids to the DNA parts that could be used for studies using the HUNT database.
The candidate will assess relevant proteins and analyze them, following two project approaches that could be delineated as separate projects:

- **A)** Sequence comparison to identify conserved regions within a protein family, and across phylogenetically related species. The identified regions of relevance should be traced back to not only the genes but also to the amino acid (AA) bases of interest.
- **B)** Structural analysis of example proteins together with biochemical information will point to AAs that are crucial to maintain functionality (e.g. the binding site) or structure (and thereby functionality). These AAs should be related to the corresponding DNA bases.

The possibility to develop a pipeline for automatic comparison and analysis will be given and supported.

Eksperimentelt / *Experimental methods:*
The work will be performed at the computer.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MTNANO
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Biveileder/-e: *Co-supervisor/-s:*	Christian Schulz, Emil Karlsen
Arbeidstittel på oppgaven/ *Preliminary title:*	**Development of automated genome-scale metabolic reconstruction pipelines**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*

Flux Balance Analysis (FBA) is the most common method used to answer questions e.g. related to productivity of target substances or the systems level understanding of interactions within a cell. The used genome-scale metabolic models contain all by the genome encoded reactions for this strain; a raw draft may be generated fast but have to be manually curated and validated.

In our group, we have recently constructed AutoKEGGRec, a matlab function for generating a first draft reconstruction based on KEGG. Possible projects for the development of a fully functioning pipeline.

A) Develop matlab functions to aautomatically generate a fully function microbial community model. Microbial communities may consist of two to several hundred organisms, therefore automated curation is crucial.
B) Develop a matlab function for automatically generating a fully functioning "consolidated" genome-scale model, that consists of the combination of individual microbial models.

The development of these functions will be supported if necessary.

Eksperimentelt / *Experimental methods:*
The work will be performed at the computer.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Biveileder/-e: *Co-supervisor/-s:*	Olav Vadstein (olav.vadstein@ntnu.no)
Arbeidstittel på oppgaven/ *Preliminary title:*	**Microbial stabilization: a tool for combating pathogens in aquaculture systems?**

Background and Objectives:

Fish are sharing their living environment with high loads of bacteria. In nature, the fishes experience relatively stable microbial environments. In aquaculture systems, the reared animals are exposed to high and unstable loads of bacteria compared to the natural environments. For a number of reared marine species, we have previously demonstrated that stable microbial environments improve growth and survival. Stabilization of microbial communities in the rearing water can be obtained by so-called K-selection, i.e. keeping microbial loads close to the carrying capacity (the maximal microbial population size that the system can support). Recirculating aquaculture systems (RAS) are well suited for exerting microbial K-selection, because the water going in to the rearing tanks has a carrying capacity similar to that of the water inside the rearing tank. K-selected bacteria are typically specialists, characterized by low maximum growth rate, but with the ability to compete when the available resources are limited. In a system where the carrying capacity is dramatically increased in the rearing tank, e.g. by addition of fish feed in a flow-through system, rapid-growing, opportunistic bacteria will bloom. This would be an example of an r-selected system. R-selected bacteria have a high maximum growth rate, but are poor competitors when resources are limited. According to ecological theory, opportunistic rapid-growing bacteria would more easily bloom in an r-selected system with excess of resources, but would be outcompeted in a K-selected system. If stabilization of the water microbial community is found to prevent blooming of opportunistic bacteria, this could be a promising and sustainable strategy for preventing pathogenic invasion in aquaculture systems.

The aim of this project is to evaluate whether microbial stabilization is feasible a strategy to prevent blooming of pathogens in aquaculture systems

Experimental methods:

This master project will be part of a project involving a Fulbright research fellow, and the student will work closely together with this researcher. We will use lab-scale continuous bioreactors and aim at also build up a lab scale RAS for creating r- and K-selected microbial communities. Potential fish pathogens will be introduced to the systems under both K- and r-selected conditions, and the fate of these strains will be monitored by methods like qPCR and flow-cytometry combined with specific probing. For examining the dynamics of the microbial communities in the systems, methods based on analysis of sequence variation in the 16S rRNA gene will be used, like DNA sequencing of 16S rRNA amplicons and qPCR.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng

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Biveileder/-e: *Co-supervisor/-s:*	
Arbeidstittel på oppgaven/ *Preliminary title:*	**Network analysis as a tool for studying interactions in aquatic bacterial communities**

Bakgrunn og mål / *Background and Objectives:*

Aquatic microbial communities are highly dynamic. Environmental conditions, stochastic processes, and interactions (e.g. competition) between community members will influence the community composition. We have found that in aquaculture systems, stable microbial environments promote fish health. To be able to control aquatic microbial systems, we need knowledge about the factors structuring them. In biofilm communities, bacteria are known to interact with each other through many mechanisms, but for planktonic bacterial communities, little is known when it comes to communication and interactions. In this project, the aim is to investigate to what extent interactions between community members are taking place in planktonic bacterial communities. During the last decade, network approaches have been applied to a wide variety of biological challenges with great success. We will apply network analysis to large data sets generated by Illumina amplicon sequencing of bacterial communities, with the aim of identifying species co-occurrence relationships. To allow for comparisons between different types of microbial communities, the dataset will include also biofilm and/or fish microbiota samples.

Eksperimentelt / *Experimental methods:*

Depending on the interests of the student, the project may include experimental work, involving operating lab scale continuous bioreactors, sampling, DNA isolation, PCR, and Illumina amplicon sequencing. Alternatively, datasets already generated in the research group may be immediately used for network analyses. The student will use simple programming in python and an existing R-package for network analysis (WGCNA) to generate networks that reflect the interactions taking place in the bacterial communities.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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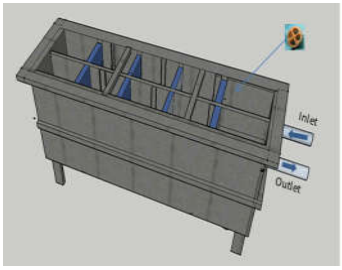
Biveileder/-e: *Co-supervisor/-s:*	Blanca M. Gonzalez Silva (blanca.g.silva@ntnu.no) Stein Wold Østerhus (stein.w.osterhus@ntnu.no)
Arbeidstittel på oppgaven/ *Preliminary title:*	**The microbial community associated with enhanced biological phosphorus removal (EBPR) from wastewater in continuous moving bed biofilm reactors (MBBR)**

Bakgrunn og mål / *Background and Objectives:*

Wastewater with high levels of organic matter (COD) Phosphorus (P) and Nitrogen (N) cause several problems, such as eutrophication, oxygen consumption and fish toxicity, when discharged to the aquatic environment. It is, therefore, necessary to remove these substances from wastewaters for reducing their potential negative impact. P removal is achieved by polyphosphate-accumulating organisms (PAOs) through enhanced biological phosphorus removal (EBPR) under alternating anaerobic-aerobic conditions. The aim of this project is to characterize microbial communities of an EBPR carried out in a pilot-scale Moving Bed Biofilm Reactor (MBBR) operated as a continuous biofilm process with circulating carrier media. Illumina sequencing of 16S rRNA amplicons and statistical analysis will be used for investigating the structure and dynamics of the bacterial communities.

Objectives:

- To provide a comprehensive insight into the key PAOs and determine their relative abundance.
- To identify the possible existence of nitrifying and denitrifying bacteria
- To identify the most dominant ordinary heterotrophic organisms.
- To link the performance of the EBPR with the microbial community structures.



Eksperimentelt / *Experimental methods:*

The student will take part in operating the MBBR reactors at the department of Water and wastewater systems engineering. Analyses of the microbial communities will be done by DNA extraction, PCR amplification of the 16S rRNA bacterial gene, analyses of the sequence diversity of the 16S rRNA amplikons. The student will also be involved in the data analyses.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng

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Biveileder/-e: *Co-supervisor/-s:*	Sigrid Hakvåg
Arbeidstittel på oppgaven/ *Preliminary title:*	**Study and development of genetic tools for the thermotolerant methylotrophic bacterium Bacillus methanolicus strain PB1**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*
Bacillus methanolicus is a thermotolerant bacterium that can efficiently utilize methanol as a sole carbon source. It has an optimum growth temperature of 50°C.
The methanol dehydrogenase gene, *mdh*, is crucial for methanol consumption in this bacterium.

Bacillus methanolicus is able to overproduce amino acids from methanol. Genetically engineered *B. methanolicus* strains overproducing different commercially interesting compounds such as L-lysine, L-glutamate, cadaverine and GABA, using methanol as raw material have been established[1, 2, 3, 4]

Genetic tools for modification of the strain MGA3 are developed, but remains to be tested in other wild type strains. Expanding the range of strains available for modifications will optimally also expand the range of products and production levels, and give further understanding of this bacterium. Of the wild type strains available in the lab, strain PB1 genetically differs the most from the model strain MGA3. The main focus of this project will be testing out, and possibly further develop, the different vectors and promoters used for MGA3 in PB1.

Alternative wild type strains will also be considered tested. At present, no transformation of strains other than MGA3 and PB1 has been performed, and protocols will need to be developed.

Eksperimentelt / *Experimental methods:*
- Cultivation
- Genetic modification
- Development of transformation protocols

References:

1. Brautaset T, Jakobsen ØMM, Degnes KF, Netzer R, Nærdal I, Krog A, Dillingham R, Flickinger MC, Ellingsen TE. (2010). *Bacillus methanolicus* pyruvate carboxylase and homoserine dehydrogenase I and II and their roles for L-lysine production from methanol at 50 degrees C. Appl. Microbiol. Biotechnol. 87,951-964
2. Schendel FJ, Dillingham R, Hanson RS, Sano K, Matsui K. (2000). Production of glutamate using wild type *Bacillus methanolicus*. US 6083728.
3. Irla M, Heggeset TMB,Nærdal I, Paul L, Haugen T, Le SB, Brautaset T, Wendisch VF.(2016) Genome-based genetic tool development for *Bacillus methanolicus*: Theta- and rolling circle-replicating plasmids for inducible gene expression and application to methanol-based cadaverine production. Front. Microbiol. 7:1481
4. Irla M, Nærdal I, Brautaset T, Wendisch VF. Methanol-based γ-aminobutyric acid (GABA) production by genetically engineered *Bacillus methanolicus* strains. (2016) Ind. Crops Prod

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	Can be adapted to 60 credits / 30 credits / 15 credits (specialization project)

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Arbeidstittel på oppgaven/ *Preliminary title:*	**Study of different promoters in the thermotolerant methylotrophic bacterium *Bacillus methanolicus***

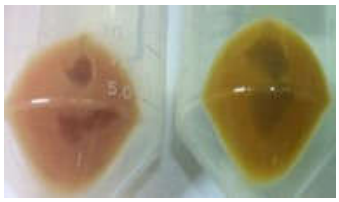
Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*

Bacillus methanolicus is a thermotolerant bacterium that can efficiently utilize methanol as a sole carbon source. It has an optimum growth temperature of 50°C.
The methanol dehydrogenase gene, *mdh*, is crucial for methanol consumption in this bacterium.

Introduction of the genes crtM and crtN from *Staphylococcus aureus* into *Bacillus methanolicus* MGA3 results in yellow pigmentation. The genes encode a dehydrosqualene synthase and dehydrosqualene desaturase, respectively, and expression of the genes results in the production of two C30 terpenoids, diaponeurosporene and diapolycopene providing yellow pigmentation. The resulting colour will allow the study of different promoters, including the mdh (methanol dehydrogenase) promoter. This will be the main focus of the project.

Alternative wild type strains will also be considered tested as potential hosts for carotenoid biosynthesis. At present, no transformation of strains other than MGA3 and PB1 has been performed, and protocols will need to be developed. Introducing the crtMN genes into these strains, and cultivating them on different C-sources, will yield more information on the physiology of the strains and on the regulation of the promoter(s).



WT crtMN

Eksperimentelt / *Experimental methods:*

- Cultivation
- Genetic modification
- Extraction and quantification of pigment
- Development of transformation protocols

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	Can be adapted to 60 credits / 30 credits / 15 credits (specialization project)

Production of therapeutic proteins in alternative bacterial species

Faglærer: Trygve Brautaset
Supervisor: Anne Krog (anne.krog@vectronbiosolutions.com), Tlf: 98404313,
Jostein Malmo (jostein.malmo@vectronbiosolutions.com), Tlf: 97152913

Background

Modern therapeutic proteins, such as insulin, are almost exclusively produced in *E. coli*. One of the challenges when producing recombinant proteins is solubility: a large fraction of the product is often found in an insoluble form, making it less useful for therapeutic applications.

The expression technology of Vectron Biosolutions was developed in *E. coli*, but can cover a broad range of bacterial species. By exploring the use of this technology in different bacterial species, the chances of finding a suitable production process for each protein is enhanced.

Project description

The goal of this project is to test and further develop the expression technology of Vectron Biosolutions for the production of proteins in alternative bacterial species.

Projects can be adjusted to fit different sp-profiles (15sp, 15+30sp or 60sp).

Tasks

Tasks depend on the final structure of the project, but will routinely include:

- Cloning of genes for therapeutic proteins into Vectron's vectors (PCR, gel electrophoresis, plasmid DNA isolation, plasmid purification, primer design).
- Transformation of *E. coli* with newly constructed vectors (make competent *E. coli* cells, transformation of *E. coli*)
- Using the expression of the reporter genes mCherry and beta-lactamase (growth experiments, enzyme activity assays).
- Expression of therapeutic proteins using the newly constructed vectors (bacterial growth experiments, protein isolation, SDS page, Western blot).
- Comparing the expression of the reporter genes and therapeutic proteins (bacterial growth experiments, protein isolation, SDS page, Western blot).
- Transferring the newly constructed vector into a new alternative host (transformation / conjugation / electroporation of alternative bacterial species).
- Comparing and evaluating the expression of soluble and insoluble protein fractions between *E. coli* and alternative hosts (bacterial growth experiments, protein isolation, SDS page, Western blot, protein (semi-)quantification).

About Vectron Biosolutions

Vectron Biosolutions is a small, dynamic company based at NTNU Gløshaugen. We provide state-of-the-art expression technology to both pharmaceutical and industrial companies worldwide. We welcome enthusiastic, independent students to further explore the possibilities our technology holds.

Reading

Brautaset, T., R. Lale, and S. Valla, *Positively regulated bacterial expression systems.* Microb Biotechnol, 2009. **2**(1): p. 15-30.

Veileder: *Supervisor:*	Professor Per Bruheim
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Webside / *webpage*:	http://www.ntnu.no/ansatte/per.bruheim
Biveileder/-e: *Co-supervisor/-s:*	Post doc Kanhaiya Kumar, PhD External collaborator/ supervisor: seniorforsker Alexander Wentzel, SINTEF Industri
Arbeidstittel på oppgaven/ *Preliminary title:*	**Metabolic profiling of antibiotic producing Streptomyces bacteria**

Bakgrunn og mål / *Background and Objectives:*

The MSc project is associated the NFR Digital Life/ Biotek2021 research project INBioPharm - Integrated Novel Natural Product Discovery and Production Platform for Accelerated Biopharmaceutical Innovation from Microbial Biodiversity.

This is a joint SINTEF and NTNU project with primary objective to provide a new, integrated platform for the more efficient discovery and production of novel bioactive compounds with high medical application potential from natural microbial biodiversity, promoting accelerated innovation in the biopharmaceutical market.

Background for the project is a large culture collection of Actionmycetes strains. They contain genetic and biosynthetic capabilities to synthesis new natural compounds of potential interest for therapeutic usage, e.g. antibacterial activities. This MSc project is closely associated with this research project and will focus on the usage and optimization of the bacterium *Streptomyces coelicolor* as host for heterologous expression of secondary metabolite clusters isolated from the Actinomycete culture collection.

Eksperimentelt / *Experimental methods:*

Bench-top bioreactor cultivations, including optimization and control of bioprocess conditions, of various antibiotic producing *Streptomyces* strains, sampling and sample processing for Metabolome and Fluxome (13C experimentation) analyses, mass spectrometric analysis (LC-MS, GC-MS, capIC-MS), enzymatic analysis and other biochemical assays of relevance to study onset and extent of antibiotic biosynthesis.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MBIOT5, MSBIOTECH, MTKJ, MIKJ,
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Hovedveileder: *Main supervisor:*	Professor Per Bruheim
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Webside / *webpage*:	http://www.ntnu.no/ansatte/per.bruheim
Biveileder/-e: *Co-supervisor/-s:*	Post doc Katsuya Fuchino, PhD
Arbeidstittel på oppgaven/ *Preliminary title:*	**Physiological studies of biofuel producing Zymomonas mobilis**

Bakgrunn og mål / *Background and Goal:*

This MSc project is associated the European Era-IB research project: "Z-Fuels: A novel bacterial system with integrated micro-bubble distillation for the production of acetaldehyde". The ultimate goal of Z-Fuels is to develop an integrated process in which low value waste (e.g. crude glycerol) is converted to a valuable biofuel and/or precursor chemical (acetaldehyde). The concept of Z-Fuels is to design, construct and operate a bacterial process, based on genetically engineered *Z. mobilis* with an integrated microbubble distillation system to convert complex sugary feedstocks and crude glycerol to acetaldehyde. Effective removal of acetaldehyde during the metabolic process will alleviate the inhibition and give higher yields. From the higher production quantities of acetaldehyde a more competitive and efficient route to butanol production can be obtained compared to current practise.

Eksperimentelt / *Experimental:*

Bioreactor cultivations (100 mL to 2 L operating volume), sampling and sample processing for Metabolome and Fluxome (13C experimentation) analyses, mass spectrometric analysis (LC-MS, GC-MS, capIC-MS), enzymatic analysis and other biochemical assays (especially for studies of respiratory chain)

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MBIOT5, MSBIOTECH, MTKJ, MIKJ
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Veileder: *Supervisor:*	Professor Per Bruheim
Kontaktinformasjon / epost *Contact information / email:*	Per.Bruheim@ntnu.no
Webside / *webpage*:	http://www.ntnu.no/ansatte/per.bruheim
Biveileder/-e: *Co-supervisor/-s:*	Marit H Stafsnes, PhD Zdenka Bartozova, PhD External collaborator/ supervisor: Inga Marie Aasen, SINTEF Industri
Arbeidstittel på oppgaven/ *Preliminary title:*	**Metabolic and lipidomic profiling of omega-3 fatty acid producing thraustochytrids**

Bakgrunn og mål / *Background and Objectives:*

The MSc project is associated the NFR Digital Life/ Biotek2021 research project "AurOmega - Microbial production of omega-3 fatty acids – a model-based approach"
This is a joint NTNU and SINTEF project to establish a knowledge platform on DHA synthesis and lipid accumulation in native DHA-producing thraustochytrids, and to develop these into high productivity omega-3 fatty acid producing cell factories. The overall aim of the project is to develop an economic competitive bioprocess for production of omega-3 fatty acids for the fish farm industry.

Background for the project is that the fish oil production, which is the current supply for omega-3 fatty acids in salmon farm feed, from wild fish catches cannot be further increased, continued growth of marine aquaculture will be completely dependent on development of new, sustainable sources of the essential omega-3 fatty acids, which are vital for salmon health and important for the status of salmon as a healthy food.

Thraustochytrids are unicellular, eukaryote, heterotrophic, obligate marine microorganisms, commonly found in seawater and sediments. They are able to accumulate high levels of lipids as triacylglycerols, with a high content of DHA. Total lipid contents of the cell mass above 80 % and DHA-contents above 80 % of total fatty acids have been reported. However, such extremes have never been obtained simultaneously Some strains producing high levels of carotenoids, squalene or exopolysaccharides have also been identified.

Eksperimentelt / *Experimental methods:*

Bench-top bioreactor cultivations including optimization and control of bioprocess conditions, sampling and sample processing for Metabolome and Fluxome (13C experimentation) analyses, mass spectrometric analysis (LC-MS, GC-MS, capIC-MS), enzymatic analysis and other biochemical assays of relevance to study the lipid accumulation mechanisms.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MBIOT5, MSBIOTECH, MTKJ, MIKJ,
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Hovedveileder: *Main supervisor:*	Professor Per Bruheim
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Webside / *webpage*:	http://www.ntnu.no/ansatte/per.bruheim
Biveileder/-e: *Co-supervisor/-s:*	PhD candidate Lisa Marie Røst, IBT Professor Marit Otterlei, Department of clinical and molecular medicine, NTNU
Arbeidstittel på oppgaven/ *Preliminary title:*	**Study of Carbon- and Energy Metabolism in Human Cancer Cells**

Bakgrunn og mål / *Background and Goal:*

While abnormal metabolism of cancer has been known for almost hundred years ("The Warburg Effect" – increased glucose consumption and lactate production), still much remain to be elucidated when it comes to why and how cancer acquires this change in metabolism. Several recent discoveries has elucidated the role many common oncogenes and tumor suppressors play in reprogramming of metabolic pathways during oncogenesis, and lately it has been revealed that rewiring of metabolism in cancer is not only a consequence of hyper-activation of signaling pathways that instruct cells to grow, but that altered metabolism in itself can play a tumorigenic role. Thus, cancer metabolism is receiving renewed and increasing focus as therapeutic target.
The expected achievement of the project is to generate more knowledge about cancer metabolism with potential identification of new cancer therapy targets.

Eksperimentelt / *Experimental:*

Mass Spectrometry (MS) is the most important technology used to investigate the metabolite pool (Metabolomics) and metabolic fluxes (Fluxomics) – two central analytical techniques to the study of the Carbon- and Energy metabolism of any biological system. These methodologies will be central in this MSc project, applied in combination with assays to monitor cell viability and status of signal transduction pathways.

For this particular project, the study will focus on metabolic adaption to hypoxic conditions (low oxygen tension, biologically relevant as tumors often are poorly oxygenated) in combination with exposure to known cytostatics and a new anti-cancer peptide-drug developed in the lab of external supervisor Marit Otterlei (Otterlei is founder of the NTNU spin off company APIM Therapeutics which currently is testing out their first drug in Clinical trials Phase I). A dedicated hypoxia chamber will be used for this purpose..

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 60 credits

Veileder: *Supervisor:*	Professor Per Bruheim
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Webside / *webpage*:	http://www.ntnu.no/ansatte/per.bruheim
Biveileder/-e: *Co-supervisor/-s:*	PhD candidate Lilja Brekke Thorfinnsdottir Professor Marit Otterlei, Department of clinical and molecular medicine, NTNU
Arbeidstittel på oppgaven/ *Preliminary title:*	**Inhibition of Antimicrobial Resistance development through targeting translation synthesis"**

Bakgrunn og mål / *Background and Objectives:*

Infections by multi drug resistant (MDR) bacteria represent an enormous health and economic challenge, the burden of which is steadily increasing. Globally, at least 700 000 people die because of MDR infections each year. To handle this emerging crisis, new antibiotics with novel mechanisms of action and new treatment regimens are required. However, a serious challenge is the fast development of resistance to new antibiotics. It can be widely spread and established in the population already at the early stages of introduction of the antibiotic to the clinical marked. Thus, either should the new antibiotics have a mechanism of action that makes development of resistance extremely challenging for the bacteria, or alternatively, antibiotics (both new and presently used clinically) should be used together with other agents that inhibit the bacteria's ability to develop resistance. A central mechanism in developing resistance is the translesion synthesis (TLS) that plays a critical part of the bacterial stress/ SOS response: error-free DNA polymerases are replaced with error-prone DNA polymerases which results in increased mutagenesis frequencies. Another recently realized fact is that sub-populations of bacterial cultures have properties to develop tolerance as a first stage of defence while preparing for developing of resistance. Actually, the antibiotic tolerance facilitates the evolution of resistance. Tolerance is closely connected with persistence and is associated with decreased growth rates and metabolic dormancy.

The biological model system in this MSc-project is based on a set of synthetic peptides with proven antibacterial, anti-mutagenic and anti-biofilm activities (developed by the Otterlei group). Their data suggests that these peptides interact with the bacterial β-clamp and shows that TLS in bacteria is inhibited at doses below its MIC (MIC is defined as the dose that is needed for 90% reduction in bacterial growth). Because development of MDR is largely dependent on TLS, the APIM-peptides have the potential to lower the mutation rates and, therefore, frequency of MDR development.

Eksperimentelt / *Experimental methods:*

The main aim of the project will be to expand the mechanistic understanding of resistance development. Secondary aim is to test if different peptides can inhibit this development via inhibition of TLS or other stress related mechanisms.

We have developed a set of mass spectrometry based quantitative metabolite profiling method that will be central for this project. These methods make is possible to monitor the primary carbon and energy metabolism and also the red-ox status and changes in cyclic nucleotide pools (important signal molecules during stress / SOS response). The analytical approach will be paired with our advanced cultivation technology and making it possible to study bacterial cultures at various growth rates (low to high dilution rates in continuous cultivations) and with continuous read outs of metabolic status.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MBIOT5, MSBIOTECH,
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng/ 60 credits

Hovedveileder: *Main supervisor:*	Bjørn E. Christensen
Kontaktinformasjon / epost *Contact information / email:*	bjorn.e.christensen@ntnu.no
Webside / *webpage*:	http://www.biotech.ntnu.no/nobipol/BEC_homepage.php
Biveileder/-e: *Co-supervisor/-s:*	Ingrid Vikøren Mo and Amalie Solberg
Arbeidstittel på oppgaven/ *Preliminary title:*	**Block polysaccharides**

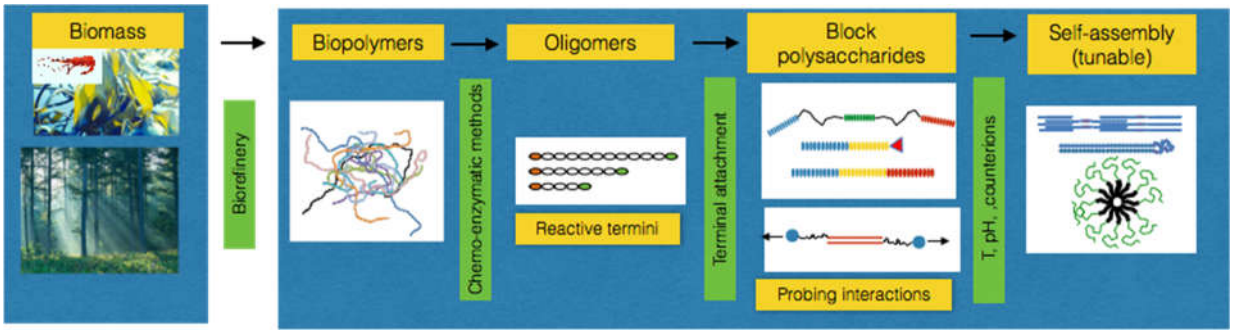

Figure 1. From biomass to block polysaccharides.

Background and Goal:

More effective exploitation of abundant polysaccharides in biomass, some of recalcitrant nature, is an area requiring new and innovative approaches. In response, we propose to develop and investigate a new class of **block polysaccharides**. It will be based on a strategy by first obtaining oligosaccharides from biomass, and subsequently target the chain termini for coupling to form linear block polymers (AB, ABC types). A key feature is that specific carbohydrate-carbohydrate interactions may induce self-assembly in an aqueous environment as opposed to synthetic block polymers, which are widely investigated due to their ability to self-assemble into a variety of nanostructures[1].

Experimental:

a) Obtain oligosaccharides (alginate, chitin, chitosan, dextran): xxxxxxxxxx
b) Activate at reducing end => xxxxxxxxxxx-L (L bifunctional linker)
c) Add another oligosaccharide to form xxxxxxxxxxx-L-yyyyyyyyyyyyy (diblock)
d) Verify structure (NMR, MS..)
e) Solubility and self-assembly

For MTKJ and MTNANO: Continued work as master project
For MBIOT5: Experimental work starts 2019 (take courses autumn 2018)

TBT4135 mandatory.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	15 ECTS project + 30 ECTS Master: MTKJ, MIKJ, MTNANO 60 ECTS: MBIOT5,
Omfang (studiepoeng): Credits (ECTS):	Flexible, dep. on study programme

Hovedveileder: *Main supervisor:*	Bjørn E. Christensen
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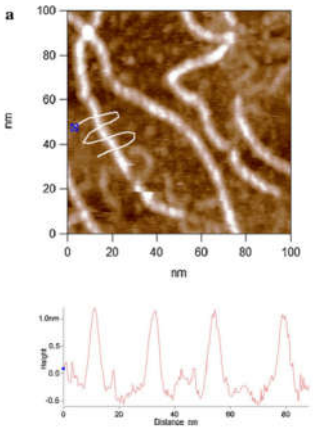
Webside / *webpage*:	http://www.biotech.ntnu.no/nobipol/BEC_homepage.php
Biveileder/-e: *Co-supervisor/-s:*	Dr. Marianne Øksnes Dalheim (Post doc. VISTA)
Arbeidstittel på oppgaven/ *Preliminary title:*	**EOR Biopolymers: Xanthan**

Background and Goal:



Xanthan is a bacterial polysaccharide produced by fermentation. It is, among others, commonly used as a food ingredient, but is also relevant for Enhanced Oil Recovery (EOR). We have support from VISTA (Statoil) to investigate xanthan for EOR.

Chemical substitution of double-stranded xanthan gives rise to modified properties, most importantly viscosity, thermal stability and biodegradability.

Experimental:

a) Purify double-stranded xanthan directly from fermentation broth
b) Prepare a range of Mw's by high shear (StarBurst Mini)
c) Determine pyruvate and acetate by NMR following cellulase degradation
d) Substitute by octylamine (carbodiiimide route), DS 0-0.5
e) Conformational properties by optical rotation and CD (new instrument at IBT)
f) Determine MWD for all samples by SEC-MALLS (+/- visc. detector)
g) Biodegradability in the disordered state

For MTKJ and MTNANO: Continued work as master project
For MBIOT5: Experimental work starts 2018 (take courses autumn 2017)

TBT4135 mandatory.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	15 ECTS project + 30 ECTS Master: MTKJ, MIKJ, MTNANO 60 ECTS: MBIOT5,
Omfang (studiepoeng): Credits (ECTS):	Flexible, dep. on study programme

Hovedveileder: *Main supervisor:*	Prof. Alexander Dikiy
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Webside / *webpage*:	http://folk.ntnu.no/dykyy/
Biveileder/-e: *Co-supervisor/-s:*	Dr. Elena Shumilina;
Arbeidstittel på oppgaven/ *Preliminary title:*	**Determination and analysis of novel bioactive compounds obtained from macro- and micro-algae**

Background and Objectives:
The aim of this project is to use NMR spectroscopy to determine industry relevant bioactive molecules from various algal extracts and to structurally characterise them.

Marine algae (contain a large amount of bioactive compounds (e.g. carotenoids, fucoidan, omega-3 and omega-6 fatty acids, pigments, amino acids, etc) that can be employed as pharmaceuticals, nutraceuticals, food additives, nutracosmeticals as well as for animal feed, fertiliser and biogas generation. The molecular content of different algae species differs greatly due to geography, time of the year and method of harvest and processing. However, little information is available on the most suitable harvesting time/geography and harvesting procedure to obtain the highest amount of bio-active compounds.

Experimental methods:
Within this project, several different extracts of algae will be studied using Nuclear Magnetic Resonance (NMR) in order to determine which bio-active compounds are present within them and measure their concentration. Certain bio-active compounds will be then further investigated and their structure determined using NMR.

No previous experience with the mentioned techniques is required.

The project results will be published in international scientific journal(s). We welcome students that have obtained relevant results to participate in the publication process as co-authors.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MSAQFOOD, MLREAL, MSBIO, MSMOLMED
Omfang (studiepoeng): Credits (ECTS):	60 credits

Hovedveileder: *Main supervisor:*	Prof. Alexander Dikiy
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Biveileder/-e: *Co-supervisor/-s:*	Dr. Elena Shumilina
Arbeidstittel på oppgaven/ *Preliminary title:*	**Determination of quality metabolites in different brands of cod fillets**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*
The aim of the work is to determine the quality and molecular changes due to storage of different brands of cod fillets utilising Nuclear Magnetic Resonance (NMR).

Fish is an important nutritive source for human consumption. The world fish food supply has grown dramatically in the last years, with an average growth rate of 3.2 percent per year in the period 1961–2009 (FAO, 2012). Atlantic cod (Gadus morhua) is a popular food product in Norway and worldwide.

Different companies sell cod of varying qualities. For the consumer it is important to know whether the price correlates with the quality of the product and how and for how long the fish should be stored, in order to keep all the metabolites that account for its health benefits.

Eksperimentelt / *Experimental methods:*
Within this project, the student will utilise a method developed in our laboratory to test A) the quality (amount of vitamins, amino acids, fatty acids, etc.) of cod purchased from different producers utilising NMR spectroscopy; B) characterise how these products change their metabolic profile over time and C) characterise how their metabolic profile changes depending on storage temperatures and time.

No previous experience with the mentioned techniques is required.

The project results will be published in international scientific journal(s). We welcome students that have obtained relevant results to participate in the publication process as co-authors.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MSAQFOOD, MLREAL, MSBIO, MSMOLMED
Omfang (studiepoeng): Credits (ECTS):	60 credits / 30 credits

Hovedveileder: *Main supervisor:*	Prof. Alexander Dikiy
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Webside / *webpage*:	http://folk.ntnu.no/dykyy/
Biveileder/-e: *Co-supervisor/-s:*	Dr. Elena Shumilina
Arbeidstittel på oppgaven/ *Preliminary title:*	**Development of a methodology to determine frauds in salmon products**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*
The aim of the work is to develop a method and protocol to determine salmon frauds utilising Nuclear Magnetic Resonance (NMR).

Fish is an important nutritive source for human consumption. The world fish food supply has grown dramatically in the last years, with an average growth rate of 3.2 percent per year in the period 1961–2009 (FAO, 2012). Atlantic salmon (Salmo salar) is a popular food product in Norway and worldwide due to its delicate taste and health benefits obtained from its metabolites (peptides, carbohydrates, vitamins, lipids).
However, as it happens with different fish, salmon products can be counterfeit to sell a lower quality product for a higher price. Several methods exist on how to determine frauds in fish, such as genetic verifications, isotope analysis, etc. However, most of them have several limitations.

Eksperimentelt / *Experimental methods:*
Within this project a method will be developed that will allow the detection of fraud products utilising NMR spectroscopy. Firstly, a model of salmon metabolites will be made by analysing both fresh and frozen samples of the fish. Subsequently, various frauds will be purposefully created to assess the validity of the developed methodology. The final stage of the project will be to create a protocol that might be used by authorities to detect counterfeits.

No previous experience with the mentioned techniques is required.

The project results will be published in international scientific journal(s). We welcome students that have obtained relevant results to participate in the publication process as co-authors.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MSAQFOOD, MLREAL, MSBIO, MSMOLMED
Omfang (studiepoeng): Credits (ECTS):	60 credits / 30 credits

Hovedveileder: *Main supervisor:*	Prof. Alexander Dikiy
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Webside / *webpage*:	http://folk.ntnu.no/dykyy/
Biveileder/-e: *Co-supervisor/-s:*	Dr. Elena Shumilina
Arbeidstittel på oppgaven/ *Preliminary title:*	**Determination of stress biomarkers in human saliva**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*
The aim of this project is to determine which molecules in human saliva correlate with stress and can be thus used as biomarkers.

Stress is a condition that affects both body and mind of people. High levels of stress trigger changes in the metabolism, hormonal levels and physiological reactions. Stress is currently mostly monitored by analysing the concentration of the hormone cortisol in blood. However, such method is invasive, costly, requires specialised personnel for collection and if carried out with not sterile equipment can result in contamination with diseases. Presently, methods that are non-invasive are gaining popularity, such as the analysis of cortisol in saliva samples. For such purpose an enzyme-linked immunosorbent assay (ELISA) is usually used. However, such method is relatively time consuming and as result gives the concentration of only one molecule in the sample.

Eksperimentelt / *Experimental methods:*
Within this project, it will be investigated whether other molecules can be found in saliva samples that change in quantity depending upon stress levels. In order to study a high number of molecules, Nuclear Magnetic Resonance (NMR) spectroscopy will be used. Saliva samples of stressed and not stressed people will be analysed both by NMR and by ELISA and the results will be compared.

The results of such research may help find an efficient and fast way to detect stress both in humans and animals.

No previous experience with the mentioned techniques is required.

The project results will be published in international scientific journal(s). We welcome students that have obtained relevant results to participate in the publication process as co-authors.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MSAQFOOD, MLREAL, MSBIO, MSMOLMED
Omfang (studiepoeng): Credits (ECTS):	60 credits

Supervisor:	Prof II Kurt Ingar Draget
Contact information / email:	Kurt.i.draget@ntnu.no
Co-supervisor/-s:	Dr. Catherine T. Nordgård
Preliminary title:	**«FoodProFuture» - Funksjonalitet til planteproteiener**

Bakgrunn og mål:
"Innovative and Sustainable Exploitation of Plant Proteins in Future Foods" – FoodProFuture – er et prosjekt med rundt 10 akademiske og 10 industrielle partnere. Hovedmålet med prosjektet er å øket bruk av planteprotein i norske matvarer. For at dette skal lykkes må funksjonaliteten av disse kartlegges. Ulike proteinfraksjoner fra norske avlinger vil bli kartlagt med tanke på viskositet, geling, emulsjonsstabilisering, vannbinding, etc. Prosjektet ledes fra UMB og NOFIMA på Ås

NTNU er inne i prosjektets WP 4 ("Quality of raw and processed plant materials and pilot products") hvor proteinfraksjonenes funksjonalitet opp mot mulige framtidige produkter står sentralt.

Aktuelle eksperimentelle metoder:

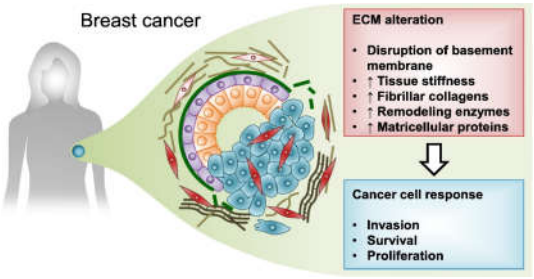
- Reologiske lavdeformasjonsmålinger (Kinexus reometer) under sol/gel transisjon
- Høydeformasjonsmålinger (SMS Texture Analyser).
- Emulsjoner og stabilitet av slike
- Kalorimetriske målinger for bestemmelse av denatureringstemperatur

Suitable for main profiles:	MBIOT5, MTKJ
Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng /

Hovedveileder: *Main supervisor:*	Prof. Kurt Draget
Kontaktinformasjon / epost *Contact information / email:*	Kurt.i.draget@ntnu.no
Webside / *webpage*:	www.
Biveileder/-e: *Co-supervisor/-s:*	Dr. Catherine Taylor Nordgård
Arbeidstittel på oppgaven/ *Preliminary title:*	**Oligosaccharide induced changes in extracellular matrix – network structure and micromechanical properties**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Goal:*



The extracellular matrix in breast cancer, Jacob Insua-Rodríguez, Thordur Oskarsson, ADDR 2016

The tumour microenvironment (extracellular matrix) is an active contributor to tumour growth and development. Our ongoing cancer research project has demonstrated that oligosaccharides can alter tumour extracellular matrix structures and reduce tumour growth *in vivo*. Collagen is a central component of the ECM and a current masters student has developed a method to simultaneously image the architecture of collagen matrices and track nanoparticle mobility within the matrix by multiple particle tracking (MPT). This project will build on that work by tracking the mobility of PEGylated nanoparticles in such matrices. Mobility data from these inert nanoparticles can be mathematically manipulated to give information about the micromechanical (microrheological) properties of the network. The goal of this project will be to determine if oligosaccharide induced alterations in collagen networks also lead to alterations in the microrheological properties of the networks. The microrheological characterization may be complemented with macrorheological characterization of the collagen networks.
The project student should be comfortable using simple Matlab scripts.

Eksperimentelt / *Experimental:*

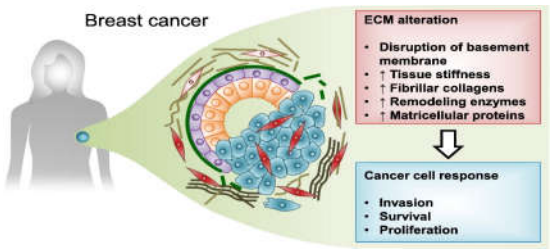
- Imaging of collagen gel matrix structure by (time resolved) confocal reflectance microscopy
- PEGylation of nanoparticles
- Multiple particle tracking microrheology
- (macrorheology of collagen gels)

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ, MBIOT5,
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng 60 credits / 30 credits /

Hovedveileder: *Main supervisor:*	Prof. Kurt Draget
Kontaktinformasjon / epost *Contact information / email:*	Kurt.i.draget@ntnu.no
Webside / *webpage*:	
Biveileder/-e: *Co-supervisor/-s:*	Dr. Catherine Taylor Nordgård
Arbeidstittel på oppgaven/ *Preliminary title:*	**Oligosaccharide induced changes in collagen pre and post gelling**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Goal:*



The extracellular matrix in breast cancer, Jacob Insua-Rodríguez, Thordur Oskarsson, ADDR 2016

The tumour microenvironment (extracellular matrix, ECM) is an active contributor to tumour growth and development. Our ongoing cancer research project has demonstrated that oligosaccharides can alter tumour extracellular matrix structures and reduce tumour growth *in vivo*. Collagen is a central component of the ECM and a current masters student has demonstrated that the addition of oligosaccharides to collagen before gelation results in alterations of the matrix architecture. This project will investigate whether exposure of collagen gels to oligosaccharides post gelation (as is most relevant to the *in vivo* situation) can also induce alterations in matrix architecture. This will be achieved by gelling collagen in advanced microscopy slides which allow a thin channel of the gel to be exposed to different, exchangeable aqueous environments on each side of the channel. The project may be expanded to include more complex ECM models such as Matrigel.
The project student should be comfortable using simple Matlab scripts.

Eksperimentelt / *Experimental:*

- Imaging of collagen gel matrix structure by (time resolved) confocal reflectance microscopy
- Analysis of matrix architecture
- (imaging of collagen in complex ECM gels)

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ, MBIOT5,
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng 60 credits / 30 credits /

Supervisor:	Prof II Kurt Ingar Draget
Contact information / email:	Kurt.i.draget@ntnu.no
Co-supervisor/-s:	Dr. Magnus N. Hattrem, Vitux AS
Preliminary title:	**Gelatin- og blandingsgeler**

Bakgrunn og mål:

Concordix er en ny og patentert leverigsform for legemidler og kosttilskudd utviklet ved institutt for bioteknologi og kommersialisert av Vitux. Teknologien tilbyr en unik, tyggbar gelepute hvor ulike aktive ingredienser kan inkorporeres, deriblant Omega-3, vitaminer og mineraler. Vitux har flere store internasjonale selskaper som kunder som videre selger produktene i blant annet apoteker og butikker. All forskning og utvikling skjer ved NTNU i Trondheim eller ved hovedkontoret i Oslo. Teknologien er basert på at aktive ingredienser inkorporeres i en olje-ivann emulsjon som er stabilisert av gelatin. I tillegg er det tilsatt søtningsstoffer og aromaer til formuleringen for å gi et velsmakende produkt. Selskapet har vokst mye de siste årene og har flere kunder i markeder utenfor Europa. Dette gir nye utfordringer, blant annet med hensyn til bruk av gelatin og varmere klima som kan påvirke produktstabiliteten. Et satsningsområde er å videreutvikle leveringsformen ved å benytte alternative vegetabilske biopolymerer som geleringsmiddel. Dette skyldes blant annet religiøse hensyn, men også en økende etterspørsel for vegetabilske alternativer. En polysakkaridbasert prototype har blitt utviklet som har vist lovende egenskaper. Det er ønskelig å karakterisere de funksjonelle egenskapene til dette leveringssystemet og evt. Å optimalisere disse. Reologisk karakterisering, in vitro lipolysestudier, dråpestørrelsesanalyser er aktuelle metoder. En utfordring med gelatingeler er at det lett degraderes ved høyere temperaturer og lav pH. Her vil polysakkarider kunne ha forbedrete egenskaper og gjøre produkter bedre egnet til tropiske strøk. En relevant problemstilling vil være å se på hvordan egenskapene til gelatin og polysakkaridgeler skiller seg fra hverandre, blant annet med hensyn på varmestabilitet, synerese, oppløsningstid i magen og frigjøring av de aktive ingrediensene. Det kan videre være relevant å se på muligheter for å bedre stabiliteten til gelatin geler ved å kombinere gelatin med andre biopolymere. Dette innebærer å se på faseegenskaper (blandbarhet, assositiv og segregativ faseseperasjon), reologiske egenskaper og in-vitro oppløsningsstudier. Varmestabilitet er en annen relevant problemstilling. Høy temperatur påvirker produktet negativt, gjennom raskere kjemiske reaksjoner og nedbrytning av gelatin/aktive ingredienser. Høyere temperaturer vil også kunne føre til at produktet hefter til pakningsfolien. Dette er ønskelig å bedre forstå denne prosessen. For å kvantifisere disse egenskapene kan ulike målemetoder bli benyttet som heft-målinger, kontaktvinkelmålinger og andre metoder for å kvantifisere interaksjoner i grenseflater.

Aktuelle eksperimentelle metoder:

- Kartlegging av faseoppførsel (eks. mikroskopi, CNS-analyse av ulike faser
- Reologiske lavdeformasjonsmålinger (Kinexus reometer)
- Høydeformasjonsmålinger (SMS Texture Analyser).
- Frigjøring av modellkomponenter i kunstig magevæske

Suitable for main profiles:	MBIOT5, MTKJ
Credits (ECTS):	60 credits / 30 credits

Supervisor:	Kurt I. Draget
Contact information / email:	
Co-supervisor/-s:	
Preliminary title:	**Gelatin gels and mixtures; optimizing physical properties**

Background and Objectives:
Gelatin has unique properties in that it melts at physiological temperatures. This implies that any bioactive formulated into a gelatin gel will be released in the stomach upon ingestion.

Under certain circumstances, however, this property will cause problems. This becomes evident when such products are launched in tropical and sub-tropical areas where the ambient temperature exceeds the melting temperature of gelatin.

This master project will focus on blends of mammalian gelatins and other biopolymers to evaluate if the overall melting temperature can be manipulated. This approach implies mapping of phase behavior (miscibility, associative and segregative phase behavior), rheological behavior and release of model compound(s) from lead candidates.

Experimental methods:
Some of the methods that may be used:

- Mapping of phase behavior (e.g. microscopy, CNS analysis of different phases)
- Small strain oscillating rheology (Kinexus general purpose rheometer)
- Large strain deformation (SMS Texture Analyser).
- Release of model compounds in artificial gastric juice

Suitable for main profiles:	MBIOT5, MTKJ
Credits (ECTS):	60 credits / 30 credits

Supervisor:	Kurt I. Draget
Contact information / email:	morten.j.dille@ntnu.no
Co-supervisor/-s:	Morten J. Dille
Preliminary title:	**Using emulsions to improve oral delivery of bioactive compounds**

Background and Objectives:
It is known that loading fat soluble compounds into emulsions in advance of oral ingestion may increase the uptake efficiency and bioavailability of the fat soluble ingredients. One example is in regards to fish oil (omega-3) where previous work at the department showed a significant increase in the uptake of orally taken omega-3 oils when the oils were pre-emulsified.

Part of the explanation of the observed effects may be due to a process called lipolysis in the small intestine, where fats and oils are broken down into fatty acids. The fatty acids then form micelles along with other surface active compounds present such as bile salts. These micelles are then absorbed by the intestinal wall followed by further processing and eventually transportation of micellar components to either the liver or the systemic blood circulation. Smaller oil droplets have a larger surface area relative to volume, which offers more area for the lipolysis enzymes (lipases) to work, leading to a potentially faster and more efficient lipolysis. Other parameters, such as oil type or emulsifier used may also affect the rate of lipolysis to significant degrees.

Any fat soluble compounds, such as vitamins or pharmaceuticals dissolved in the emulsion oil droplets may be taken up into the gradually forming micelles as lipolysis breaks down the emulsion. As the micelles are taken up by the cells in the intestinal wall, the bioactive compounds follow along. Thus, faster and more efficient lipolysis may lead to higher and more efficient uptake of ingredients loaded into the emulsion. However, the entire process from oral ingestion to transportation into the blood is highly complex, and many emulsion parameters may affect the various steps in unpredictable ways.

The objective of this project is to prepare emulsions with different parameters and compositions and examine their properties and behaviour in both in vitro and in vivo systems, with an overall goal of improved oral delivery of nutra- or pharmaceuticals. The student will have a lot of input in regards to which parameters will be tested and which experiments will be performed.

Experimental methods:
Some of the methods that may be used:

- High pressure homogenizer for emulsion preparation
- Laser diffraction/dynamic light scattering and microscopy for emulsion characterization
- In vitro gastric and intestinal transit/digestion models for testing e.g. emulsion stability and lipolysis/digestion efficiency of emulsions with different characteristics
- Pre-clinical trials (on rodents) of various emulsion systems

To be able to join in performing in vivo rodent experiments, having previous experience and certifications (FELASA C or similar) related to animal experiments, ideally on rodents, is necessary.

Suitable for main profiles:	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Credits (ECTS):	60 credits / 30 credits

Hovedveileder: *Main supervisor:*	Helga Ertesvåg
Kontaktinformasjon / epost *Contact information / email:*	helga.ertesvag@ntnu.no
Webside / *webpage*:	http://www.ntnu.no/ansatte/helga.ertesvag
Biveileder/-e: *Co-supervisor/-s:*	
Arbeidstittel på oppgaven/ *Preliminary title:*	**Polysaccharide production in *Azotobacter vinelandii* cysts**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Goal:*

Azotobacter vinelandii is a gram-negative bacterium that will enter a resting stage called cyst upon encountering adverse growth conditions. I have performed a transcriptome study and identified two gene clusters probably involved in producing polysaccharides that are expressed during encystment. No one knows which polysaccharides the clusters are involved in producing.

As a first attempt at unraveling what these genes are doing, I would like to inactivate one gene in each of these gene clusters and analyze the effect on encystment. Avin05390 and Avin30120 are the best candidates for genes to target. For a 15 stp project, making the constructs in *Escherichia coli* and transferring the plasmids to *A. vinelandii* will be a realistic aim, it will then be possible to continue the characterization, and perform other experiments defined by the student in a 30 stp project.

Eksperimentelt / *Experimental:*

1. Construct the recombination vectors (The standard techniques: Cloning, PCR, sequencing)
2. Transfer the vectors to *A. vinelandii.* (Conjugation, Homologous recombination)
3. Select and validate mutants.
4. Show if and how the mutation affects encystment
5. Use bioinformatic tools to present a hypothesis as to which polysaccharides the clusters are producing.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Hovedveileder: *Main supervisor:*	Helga Ertesvåg
Kontaktinformasjon / epost *Contact information / email:*	helga.ertesvag@ntnu.no
Webside / *webpage*:	http://www.ntnu.no/ansatte/helga.ertesvag
Biveileder/-e: *Co-supervisor/-s:*	
Arbeidstittel på oppgaven/ *Preliminary title:*	**Develop a CRISP-Cas9 mutagenesis system for *Azotobacter vinelandii***

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Goal:*

Azotobacter vinelandii is a gram-negative bacterium of some industrial interest. We are able to perform homologous recombination in the species. However, the procedure is hampered by the bacterium having many copies of its chromosome. The CRISPR-Cas9 system (Cas9 and guide RNA) has been found to function as a mutagenesis tool in several bacterial species. Unlike other techniques, this system is able to mutagenize several chromosomes at the same time and with high efficiency. So we would like to see if it works in *A. vinelandii.*

Two variants of the cas9 protein will be used. In order to be able to calculate mutation frequencies, an *A. vinelandii* strain containing a gene that can be detected by blue-white plate screening will be made. Interruptions of this gene can easily be spotted and quantified.

During the work standard methods for cloning and plasmid transfer will be used (including PCR, restriction cloning, sequencing, transformation and conjugation) as well as growth and analysis of mutant strains. The project can be scaled to the different credit levels, the full project needs at least 15+30 ECTS.

Eksperimentelt / *Experimental:*

1. Test a few promoters to find a good inducible promoter for *cas9* using reporter genes
2. Create an *A. vinelandii* test strain to allow for easy screening of mutants.
3. Construct the vector encoding Cas9 and guide RNA (The standard techniques: Cloning, PCR, sequencing)
4. Transfer the vector to *A. vinelandii* and check for mutagenesis. Quantify frequencies and see if the new method is an improvement when compared to the established method.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Hovedveileder: *Main supervisor:*	Helga Ertesvåg
Kontaktinformasjon / epost *Contact information / email:*	helga.ertesvag@ntnu.no
Webside / *webpage*:	http://www.ntnu.no/ansatte/helga.ertesvag
Biveileder/-e: *Co-supervisor/-s:*	
Arbeidstittel på oppgaven/ *Preliminary title:*	**G-block containing alginate produced by *Pseudomonas fluorescens***

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Goal:*

Alginate is a polysaccharide composed of mannuronic acid (M) and guluronic acid (G) that is widely used in industry and medicine. It is manufactured from brown algae, but is also produced by some bacteria, including *Pseudomonas fluorescens. P. fluorescens* is an efficient alginate producer, however, it is not able to make alginate containing consecutive G-residues. *Azotobacter vinelandii* is another alginate-producing bacterium. It secreted mannuronan C-5-epimerases that are create alginate with a high G-content. A similar enzyme has been found in *Pseudomonas syringae*. The aim of this project will be to try to express secreted mannuronan C-5-epimerases in *P. fluorescens* thereby obtaining a strain that produces a more valuable product. The new strain would have to express both the enzyme and a functional secretion system for the enzyme.

Eksperimentelt / *Experimental:*

1. Express selected mannuronan C-5 epimerases in *P. fluorescens*. In parallel, clone the secretion system (The standard techniques: Cloning, PCR, sequencing)
2. Transfer the vectors containing epimerase genes to *P. fluorescens.* (Conjugation)
3. Measure internal epimerase activity. (Enzyme work)
4. Transfer the vectors with the secretion system to *P. fluorescens* strain expressing the epimerase and measure extracellular enzyme activity.
5. Isolate alginate and use NMR to demonstrate production of alginate containing consecutive G-residues.

Within a 15 stp project point 1-3 may be achieved, Plasmids expressing some of the epimerase genes have already been constructed.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5,
Omfang (studiepoeng): Credits (ECTS):	30 sp studiepoeng / 15 studiepoeng 30 credits / 15 credits (specialization project)

Veileder: *Supervisor:*	Helga Ertesvåg
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Webside / *webpage*:	http://www.ntnu.no/ansatte/helga.ertesvag
Biveileder/-e: *Co-supervisor/-s:*	To be decided based on the needs of the specific project
Arbeidstittel på oppgaven/ *Preliminary title:*	**Biobased materials for more sustainable mineral extraction processes.**

Bakgrunn og mål / *Background and Objectives:*

The Master project is associated the NFR research project "Nanomorphology effects on the bioactivity and chemical activity of metal oxides, sulphides, and silicates" which starts in August 2018. The project is a cooperation between Dept. of Geoscience and Petroleum, IVT and the Depts. of Material Technology and of Biotechnology and Food Science at NV.

The mineral processing industry is currently facing the task of extracting minerals in an increasingly resource constrained ore and low-grade ore bodies in a sustainable manner. This necessitates knowledge on how very small particles behave during ore processing, in particular during froth flotation process. In this interdisciplinary project, nanotechnology and biotechnology are utilized to address this important challenge.

Bacteria and biopolymers produced by bacteria (proteins, polysaccharides, surfactants) may be used to increase the yield or may possibly replace some of the current toxic chemicals. This could increase the yield and decrease the amount of toxic waste from the mining industries. One part of the NFR project addresses this by growing and characterizing some interesting bacteria and their products, and by creating mutants with altered properties. The interaction of these cells and products with nanoparticles, made in another part of the project, will then be analyzed and used to describe improved processes.

In the time-period 2018-2019 the biotechnological part of the project will focus on the growth of the different bacteria, on mutant construction and on characterizing the resulting bacteria and products. Several master students may well work on different bacteria or different techniques within the project. The specific project will be tailored to the background and interests of the student.

Eksperimentelt / *Experimental methods:*

The techniques utilized will vary with the actual topic and with the length of the project. Mutant construction (genome editing) implies standard techniques like PCR, DNA sequencing, DNA transfer. Alternatively, characterization of the products produced by a bacterial species or mutant at different growth conditions could be the main focus.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MBIOT5, MSBIOTECH, MTKJ, MIKJ, MTNANO
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Veileder: *Supervisor:*	Helga Ertesvåg
Kontaktinformasjon / epost *Contact information / email:*	helga.ertesvag@ntnu.no
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Biveileder/-e: *Co-supervisor/-s:*	To be decided based on the needs of the specific project
Arbeidstittel på oppgaven/ *Preliminary title:*	**Genetic modification of omega-3 fatty acid producing thraustochytrids**

Bakgrunn og mål / *Background and Objectives:*

The Master project is associated the NFR Digital Life/ Biotek2021 research project "AurOmega - Microbial production of omega-3 fatty acids – a model-based approach"
This is a joint NTNU and SINTEF project to establish a knowledge platform on DHA synthesis and lipid accumulation in native DHA-producing thraustochytrids, and to develop these into high productivity omega-3 fatty acid producing cell factories.

Fish oil production from wild fish catches, which is the current supply for omega-3 fatty acids in salmon farm feed, cannot be further increased, and continued growth of marine aquaculture will be completely dependent on development of new, sustainable sources of the essential omega-3 fatty acids, which are vital for salmon health and important for the status of salmon as a healthy food.

Thraustochytrids are unicellular, eukaryote, heterotrophic, obligate marine microorganisms, commonly found in seawater and sediments. They are able to accumulate high levels of lipids as triacylglycerols, with a high content of DHA. . Total lipid contents of the cell mass above 80 % and DHA-contents above 80 % of total fatty acids have been reported. However, such extremes have never been obtained simultaneously. Some strains producing high levels of carotenoids, squalene or exopolysaccharides have also been identified.

In connection with the AurOmega project it is possible to define molecular biology projects tailored to the wishes of the student and the length of the master project. These will be performed in collaboration with researchers working on the project. One possible topic could be optimized vectors and methods, for instance to evaluate different promoters or to find new selectable markers. Through the project, we are obtaining hypothesis about genes that would be important for DHA biosynthesis. To generate mutants in such interesting genes and analyze the effect on fatty acid accumulation is another option for master projects. A third option could be to express genes in other hosts in order to verify that they encode the suspected enzyme activity.

Eksperimentelt / *Experimental methods:*

The techniques utilized will vary with the actual topic for and length of the project. All will contain standard techniques (Cloning, PCR, DNA sequencing). Other possible experiments might be: construction and characterization of the new strains, enzyme assays, measurement of reporter gene products, etc – all depending on the specific project.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MBIOT5, MSBIOTECH, MTKJ, MIKJ,
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Title

Nanowire-mediated electron transport in Bacteria

Contact

PhotoSynLab (*http://photosynlab.org)*
Assoc Prof Martin Hohmann-Marriott & Dr Rahmi Lale

Goal

Identify pathways that allow bacteria to donate electrons to external electron acceptors, such as iron oxide, manganese oxide or electrodes.

Introduction

There is strong evidence that bacterial pili have a function in donating electrons to iron oxides. However, this electron disposal has so far only been interpreted as to enable respiration of soil bacteria in anaerobic conditions. In contrast, we have collected data that indicates that pili are crucial for iron acquisition in bacteria. We hypothesise that pili are meditating electron donation to iron oxides, thereby converting insoluble ferric iron (Fe3+) into soluble ferrous iron (Fe2+), which can readily been taken up by bacteria. In addition to addressing the role of pili in iron acquisition, our proposal may also provide crucial understanding required to limit iron uptake by infectious bacteria and construction truly renewable photovoltaic devices.

Techniques

The student will use bioinformatics and access databases. To genetically manipulate bacteria the student will perform molecular biological approaches (e.g. PCR-amplification, plasmid construction and transformation.) Sterile culturing techniques will be used to grow bacterial cells and to select transformants. Analytical techniques (imaging and statistical techniques for the determination of growth parameters, HPLC & mass spectrometry for pigment analysis as well as potentimetric techniques) may be used to characterize the performance of the generated strains.

Literature

Reguera G., McCarthy K.D., Mehta T., Nicoll J.S., Tuominen M.T., Lovley D.R. (2005) Extracellular electron transfer via microbial nanowires. Nature, 435: 1098-1101.

Gorby Y.A., Yanina S., McLean J.S., Rosso K.M., Moyles D., Dohnalkova A., Beveridge T.J., et al. (2006) Electrically conductive bacterial nanowires produced by Shewanella oneidensis strain MR-1 and other microorganisms. Proc Natl Acad Sci USA 103: 11358-11363.

Lamb JJ, Hill RE, Eaton-Rye JJ, ***Hohmann-Marriott MF*** *(2014) Functional Role of PilA in iron acquisition in the cyanobacterium* **Synechocystis** *sp. PCC 6803. PLoS ONE 9(8):e105761****Title***

Title

Synthetic Biology - Development and implementation

Contact

PhotoSynLab (*http://photosynlab.org)*
Assoc Prof Martin Hohmann-Marriott & Dr Rahmi Lale

Project descriptions

We employ synthetic biology [1] to develop biology-based solutions for a sustainable future. We have projects on developing new biological chassis (including cyanobacteria and algae) and synthetic biology approaches. These approaches include the design of standardized biological modules [2] and implementation using high-throughput phenotyping and robotics.

Techniques

The student will genetically manipulate microorganisms. This work will involve molecular biology (e.g. PCR-amplification, plasmid construction and transformation). Sterile culturing techniques will be used to grow the selected model organism (*E. coli*, *Synechococcus, Nannochloropsis, Chlamydomonas, Sacchromyces)*. Suitable analytical techniques will be used to verify the developed synthetic biology approaches.

Literature

[1] Cameron DE, Bashor CJ, Collins JJ (2014) A brief history of synthetic biology. Nat Rev Microbiol 12: 381–390

[2] Ho-Shing O, Lau KH, Vernon W, Eckdahl TT, Campbell AM (2012) Assembly of standardized DNA parts using BioBrick ends in *E. coli*. Methods Mol Biol. 852: 61-76.

Title

Microfluidics application in microbiology

Contact

PhotoSynLab (*http://photosynlab.org*)
Adjunct Assoc. Prof. Rahmi Lale & Dr Swapnil Bhujbal

Goal

The utilization of droplet microfluidics and micro contact printing for single cell analysis and screening with applications in single cell functional metagenomics.

Introduction

Conventional cell-based assays measure the average response from a population of cells, assuming that an average response is representative of a typical cell within a population. However, this simplification and assumption of average behavior can result in a misleading interpretation. Single cell analysis using droplet microfluidics has become an important and emerging field in biological and biomedical research to understand the insights of heterogeneity between large populations at high resolution. Droplet microfluidics combined with micro contact provides a platform for characterization high number of single cells over prolonged periods of time[1]. We will explore above techniques to enrich metagenomic libraries in targeted populations to maximize functional expression and screening throughput, while reducing screening time and costs.

Techniques

The student will use interdisciplinary approach and state of art techniques like microfluidics (alginate based encapsulation), soft lithography, microcontact printing, confocal microscopy and image analysis.

Literature

1. Håti, A. G. *et al.* Microarrays for the study of compartmentalized microorganisms in alginate microbeads and (W/O/W) double emulsions. *RSC Adv.* **6,** 114830–114842 (2016)

2. Weibel, D. B., Diluzio, W. R. & Whitesides, G. M. Microfabrication meets microbiology. *Nat. Rev. Microbiol.* **5,** 209–18 (2007).

3. Zhu, Z. & Yang, C. J. Hydrogel Droplet Microfluidics for High-Throughput Single Molecule/Cell Analysis. *Acc. Chem. Res.* **50,** 22–31 (2017).

Hovedveileder: *Main supervisor:*	Associate professor Jørgen Lerfall
Kontaktinformasjon / epost *Contact information / email:*	jorgen.lerfall@ntnu.no
Webside / *webpage*:	https://innsida.ntnu.no/user/lerfall/ansatt/min-profil
Biveileder/-e: *Co-supervisor/-s:*	Anita N. Jakobsen
Arbeidstittel på oppgaven/ *Preliminary title:*	**A "trendy" cold smoked Atlantic salmon**

Short description of the project:

Background and Goal:

Cold smoked Atlantic salmon (CSS) is a lightly preserved product with water activity (A_w) between 0.93-0.98, so the effect of reduced bacterial growth is minor. The shelf life of a tradition CSS product ranges between 4-7 weeks. Substantial variations occur in smoking parameters between different smokehouses, and often each smokehouse has their own in-house receipt. This is reflected by the high variation in quality of CSS products available on the market. Furthermore, different smoking parameters is known to affect the product quality. CSS is often characterized by specific chemical properties, often based on the French standard NF V45-065; *i.e.* lipid <18% (w/w), water content <74%, a NaCl concentration of between 2.5 and 3.5% (w/w), and smoke treatment corresponding to 0.6 mg of phenol per 100 g of product.

In the last decade there has been a shift towards a more lightly processed CSS, which is produced with lower concentrations of NaCl (1.5-2.0%, w/w) and often in combination with liquid smoke instead of traditional smoke, produced by wooden chips. This trend pushes the limit of quality, shelf life and food safety of such products. CSS is considered a delicacy commonly consumed as a 'ready-to-eat' (RTE) product without any heat treatment. The absence of thermal treatment makes parameters such as salting and smoking utmost important in order to minimize the risk of foodborne hazards and spoilage.

The aim of the project is therefore to study quality, shelf life and food safety challenges related a "trendy" lightly processed CSS product produced with low concentration of NaCl (<2%) and smoked with liquid smoke. As a reference traditional produced CSS will be used.

Experimental:

The project will include processing of CSS and analyses related to chemio-physical quality, shelf life (bacterial growth) and spoilage parameters. To test the products according to food safety, a challenge study with a relevant pathogen such as *listeria innocua* can be included.

Relevant parameters and methodology can be: Colour (imaging), water activity, water holding capacity, texture, content of phenols (HPLC, spectrophotometry), small organic acids (HPLC), metabolites (HPLC, NMR), NaCl, and enzymatic activity, bacterial growth (APC, LAB, etc.) and more.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MBIOT5, MSBIOTECH or MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 credits / 30 credits

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Biveileder/-e: *Co-supervisor/-s:*	
Arbeidstittel på oppgaven/ *Preliminary title:*	**Physiological and chemical mechanisms related to liquid loss from muscle foods**

Kort beskrivelse av oppgaven / *Short description of the project*:

Background and Goal:

The fish and meat industry experiences a relatively large loss of liquids from muscle as a consequence of raw material characteristics, primary- and secondary processing and storage. This liquid loss leads to reduced quality of the product, and thereby lower profitability for the producer. Several factors are known to affect the loss of liquids including; pre-slaughter stress, temperature, pH, autolysis, bacterial growth, enzyme activity, protein denaturation etc..

The aim of the project will be to study mechanisms related to liquid loss of muscle foods. The main focus will be related to enzymatic activities and metabolites as affected by the choice of processing and packaging technology applied.

Experimental:

Different processing and packaging protocols will be tested on different raw materials (meat and fish) to quantify the liquid loss during storage. The project will thereafter search for a broad range of parameters (including enzyme activities, metabolites, protein denaturation and more) to explain specific mechanisms related to each investigated product.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MBIOT5, MSBIOTECH or MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 credits / 30 credits

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Biveileder/-e: *Co-supervisor/-s:*	Trygve Brautaset
Arbeidstittel på oppgaven/ *Preliminary title:*	**Metabolic engineering of *B. methanolicus* for production of 2,3-butanediol.**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*

The use of methanol as a carbon source in the biotechnological processes has recently become an issue of great interest due to its relatively low price, abundance, purity, and the fact that it is a non-food raw material. *Bacillus methanolicus* is a Gram-positive thermotolerant methylotroph considered to be a suitable candidate for methanol-based production of amino acids and their derivatives.

In this project, *B. methanolicus* will be engineered for production of 2,3-butanediol (2,3-BD). 2,3-BD is has versatile applications, it can be used as a liquid fuel, fuel additive, or antifreeze agent. Moreover, it can serve as a precursor of bulk chemicals such as 1,3-butadiene, methyl ethyl ketone, polyesters and gammabutyrolactone. The project will consist of the search through the genome for the genes potentially involved in the native 2,3-BDO biosynthesis pathways, characterization of the wild type strains with regard to native 2,3-BDO production and resistance to this compound, and creation of 2,3-BDO producing strains.

Eksperimentelt / *Experimental methods:*

The project will include

- basic molecular biology work (e.g. plasmid construction, transformation into *E. coli* and *B. methanolicus*),
- analysis of wild type strains for their applicability for production of 2,3-BD (e.g. tolerance to 2,3-BDO),
- construction of producing strains and characterization
- if time permits, methanol-based fed-batch fermentations of producing strains.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 credits / 30 credits / 15 credits

Veileder: *Supervisor:*	Marta Irla
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Biveileder/-e: *Co-supervisor/-s:*	Trygve Brautaset
Arbeidstittel på oppgaven/ *Preliminary title:*	**Development of gene deletion tools for *B. methanolicus* for generation of sporulation deficient and biologically contained platform strains**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*
The use of methanol as a carbon source in the biotechnological processes has recently become an issue of great interest due to its relatively low price, abundance, purity, and the fact that it is a non-food raw material. *Bacillus methanolicus* is a Gram-positive thermotolerant methylotroph considered to be a suitable candidate for methanol-based production of amino acids and their derivatives.
In this project, the gene deletion system based on the application of thermosensitive plasmid and counter selection markers will be developed. The newly established system will be applied for deletion of genes involved in sporulation, cell autolysis and protection from UV-light. This way a safe, biologically contained strain for future industrial applications will be developed and if possible, directly applied for methanol-based production of γ-aminobutyric acid (precursor of bioplastics).

Eksperimentelt / *Experimental methods:*
The project will include

- basic molecular biology work (e.g. plasmid construction, transformation into *E. coli* and *B. methanolicus*),
- analysis of plasmids with regards to their themosensitivity and putative counter selection markers,
- strain characterization (ability to sporulate, UV-sensitivity),
- construction of GABA producing strains and characterization (HPLC),
- if time permits, methanol-based fed-batch fermentations of GABA producing strains,
- if time permits, establishment of new method in our lab: Ordered Gene Assembly in *Bacillus subtilis* (OGAB), developed in 2003 by Tsuge et al.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 credits / 30 credits / 15 credits

Veileder: *Supervisor:*	Marta Irla
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Biveileder/-e: *Co-supervisor/-s:*	Trygve Brautaset
Arbeidstittel på oppgaven/ *Preliminary title:*	**Use of regulatory circuits for controlled gene expression in *B. methanolicus***

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*
The use of methanol as a carbon source in the biotechnological processes has recently become an issue of great interest due to its relatively low price, abundance, purity, and the fact that it is a non-food raw material. *Bacillus methanolicus* is a Gram-positive thermotolerant methylotroph considered to be a suitable candidate for methanol-based production of amino acids and their derivatives.
In this project, the novel system for controlled gene expression will be developed. The system is based on the function of lysine riboswitches which regulate expression of genes involved in the lysine metabolism. First, lysine riboswitches derived from *B. methanolicus* and *B. subtilis* will be tested for regulation of plasmid-based expression of reporter gene *sfGfp.* In next steps, the lysine riboswitch will be used for controlled expression of genes involved in lysine metabolism.

Eksperimentelt / *Experimental methods:*
The project will include

- basic molecular biology work (e.g. plasmid construction, transformation into *E. coli* and *B. methanolicus*),
- analysis of sfGFP fluorescence of created by the means of flow cytometry,
- construction of producing strains and characterization (HPLC),
- if time permits, methanol-based fed-batch fermentations producing strains.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 credits / 30 credits / 15 credits

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Biveileder/-e: *Co-supervisor/-s:*	Hanne Tobiassen, Salmar
Arbeidstittel på oppgaven/ *Preliminary title:*	**Genetiske – og fenotypiske analyser av *E.coli*-stammer fra miljø-, produkt- og prosessprøver fra et lakseslakteri**

Kort beskrivelse av oppgaven / *Short description of the project*:
Bakgrunn og mål / *Background and Goal:*

Lakseindustrien er en av de største næringer i regionen. Mye av laksen omsettes og forbrukes i lettprosessert tilstand. Det er viktig at produktet er fri for patogener. Hvor kommer eventuell kontaminering fra, miljøet, fisken eller prosessen? Dette kan studeres gjennom analyser og karakteriseringer av isolerte stammer. Salmar har igjennom sesongen (2017-2018) isolert *E.coli* stammer fra forskjellige kontamineringskilder. Hva er kilden til kontaminering av deres produktet?

Eksperimentelt / *Experimental:*

1. Innsamling av stammer fra bedrift, innledende studier
2. Stammene identifiseres med BIOLOG Gen III systemet (IBT, NTNU)
3. Tilleggs-karakterisering med genetiske metoder, eks. PCR av spesifikke gener og sekvensering av 16S.

Resultatene danner grunnlag for en eventuell helgenom-sekvensering av utvalgte stammer fra bedriften.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	
Omfang (studiepoeng): Credits (ECTS):	45 sp 45 credits

Hovedveileder: *Main supervisor:*	Turid Rustad
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Biveileder/-e: *Co-supervisor/-s:*	Estefania Noriega, NOFIMA Stavanger estefania.noriega@nofima.no
Arbeidstittel på oppgaven/ *Preliminary title:*	**Plasma Activated Water for Food Decontamination**

The use of non-thermal atmospheric-pressure gas **plasma** (APP) for microbial decontamination of food products and shelf-life extension has gained increasing interest over the past decade (Fig1). Plasma, which is considered the 4th state of the matter, consists of an ionised gas dissociated by an energy input (e.g. electrical discharge). Plasma generated in air produces a wealth of Reactive Oxygen and Nitrogen Species, intense electric fields and UV radiation, which interact synergistically to damage cell membranes/wall and intracellular components (e.g. DNA/RNA). A recent approach for the delivery of plasma generated species to biological targets is to "activate" water/liquids through exposure to plasma discharges. Plasma species directed towards a volume of water give rise to numerous antimicrobial chemical species causing the acidification of the liquid (Fig2). Thus, **plasma activated water** (PAW) is an eco-friendly and cost-effective alternative (just air, water and electricity) to chlorine-based sanitisers employed for food disinfection. PAW can be produced rapidly and stored for several hours (under chilled conditions) and provides a number of advantages over direct APP treatment, e.g. ease of application, defined dose, storability, offsite generation.

Objectives

The Master thesis will investigate the potential of PAW to enhance the microbiological safety and shelf-life of food products relevant for the Norwegian bioeconomy. Specific objectives include:

- Antimicrobial efficacy of PAW on selected food product categories as a function of process variables, and storage time and temperature of the activated water.
- Stability of PAW-treated products towards storage time and temperature.

Specific activities

State-of-the-art (literature) review on the potential of PAW for food decontamination.
Characterisation of the PAW composition (antimicrobial species) as a function of:
Process variables: plasma power, exposure time, water source and pH, stirring.
Storage time and temperature of the activated water.
Characterisation of the PAW efficacy for the control of relevant microbial agents (e.g. *Listeria monocytogenes*) in selected food products (e.g. seaweeds, fruits/vegetables, cereal grains), as a function of process variables and PAW's storage time/temperature.
Microbiological and quality assessments (e.g. colour, texture, pH, water activity, etc.) of PAW-treated products towards storage time and temperature.

References

- Scholtz et al. Nonthermal plasma-A tool for decontamination and disinfection. Biotechnol Adv. (2015), 33 (6 Pt 2).
- Mir et al. Understanding the Role of Plasma Technology in Food Industry. Food Bioprocess Technol. (2016), 9(5): 734-750

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Arbeidstittel på oppgaven/ *Preliminary title:*	**Role of innovative processing technologies in the valorisation of rest raw materials**

The production of water-soluble **protein hydrolysates** for human consumption represents a value- added solution for the re-utilisation of rest raw materials from the food industry. Hydrolysis of food proteins can be achieved by chemical (use of acid or alkali) or enzymatic processes, the latter based on the proteolytic breakdown (via exogenous proteases) of the proteins to smaller peptides and free aminoacids. It is regarded as a mild and efficient process resulting in high product yield without prejudicing the nutritional quality of the final product. **Advanced volumetric heating and innovative (non-thermal) technologies** (Fig1), such as high pressure processing (HPP), microwave heating (MW) and sonication (US), can enhance the extraction of intracellular compounds via physical mechanisms (i.e. pressure, electromagnetic field, cavitation) and improve the enzymatic hydrolysis of rest raw materials (degree of hydrolysis, recovery yield, hydrolysis time, amount of enzyme, peptide profile) by facilitating the access to cleavage sites (specific peptide sequences) through changes in the protein structure (e.g. protein unfolding). Thus, the resulting hydrolysates exhibit improved functionality and properties (e.g. digestibility, antioxidant capacity, allergenicity, sensory attributes, protein recovery, microbiological safety, solubility, emulsifying/foaming/water-holding capacity, oil/fat absorption).

Objective

The Master thesis will investigate the potential of innovative technologies to enhance the enzymatic hydrolysis of rest raw materials and sensory, bioactive & functional properties of protein hydrolysates.

Specific activities

- State-of-the-art (literature) review on enzymatic hydrolysis assisted by innovative processing.
- Effect of innovative technologies (HPP, MW and US) implemented as either a pre-treatment or a simultaneous treatment, on the enzymatic hydrolysis (degree of hydrolysis, recovery yield, peptide profile) of rest raw materials (e.g. chicken bones, tendons, feathers; fish heads, skin) by using 2 different enzymes (hydrolysates with different molecular size distribution):
- HPP: Pressure range, temperature and exposure time
- MW: Power range, temperature and exposure time
- US: Power range, temperature and exposure time
- Characterisation of hydrolysates: composition (e.g. protein, lipid, carbohydrate content), physico-chemical and sensory properties, structural changes (e.g. protein unfolding via differential scanning calorimetry), bioactivity (e.g. antioxidant activity).

References

- Alemán et al. Enzymatic hydrolysis of fish gelatin under HP treatment. Int J Food Sci Technol. (2011), 46:1129-1136.
- Nguyen et al. Impact of microwave−assisted enzymatic hydrolysis on functional and antioxidant properties of rainbow trout *Oncorhynchus mykiss* by−products. Fish Sci. (2017), 83:317-331.

Passer for: *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Arbeidstittel på oppgaven/ *Preliminary title:*	**Proteiningredienser fra restråstoff**

Hovedmålet med oppgaven vil være å undersøke sammenhengen mellom råstoff, prosessbetingelser og fraksjonering har på egenskapene til fiskeproteinhydrolysater.

Bakgrunn og mål:
Enzymatisk hydrolyse er en prosesseringsteknikk som kan benyttes for å produsere høyverdige ingredienser fra restråstoff. Prosessen er basert på bruk av kommersielle enzymer (proteaser) som bryter peptidbindinger, forenkler degraderingen av råstoffet og fører til utskillelse av oljen. Resultatet er tre fraksjoner; proteinhydrolysat (vannløselig protein), olje og grakse (uløselig proteiner, fosfolipider og bein). Råstoffsammensetning, enzymtype og prosessbetingelsene vil påvirke egenskapene til sluttproduktene, noe som gjør det nødvendig å utvikle prosesser skreddersydd for det restråstoffet det er tenkt brukt på. SINTEF Fiskeri og havbruk har gjennom flere prosjekter utviklet teknologier for utnyttelse av restråstoff fra fisk og kylling. Et resultat av dette er ulike ingredienser som kan ha funksjonelle egenskaper ved prosessering av mat, gi økt næringsverdi og påvirke sensoriske og teknologiske egenskaper i ferdig produkt.

Eksperimentelt*:*
Prosjektarbeidet vil bli knyttet opp mot aktiviteter som SINTEF Fiskeri og havbruk har i prosjekter på dette området. Det vil være behov for forsøk og analysering av både ingredienser og ferdig produkt.
Aktiviteter som kan inngå i dette prosjektet:

- Karakterisering av kjemisk sammensetning i ingrediensene
- Pilotforsøk hvor modellprodukter testes ut
- Fysio-kjemiske, sensoriske og teknologiske analyser.
- Analyse av bioaktive og funksjonelle egenskaper

Det er plass for flere studenter innen denne problemstillingen

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Hovedveileder: *Main supervisor:*	Turid Rustad
Kontaktinformasjon / epost *Contact information / email:*	turid.rustad@ntnu.no
Webside / *webpage*:	www.ntnu.no
Biveileder/-e: *Co-supervisor/-s:*	Oppgaven gjøres i samarbeid med Kystmiljø (SES) medveileder Tina Olaussen
Arbeidstittel på oppgaven/ *Preliminary title:*	**Effect of storage and transportation temperature on quality of fish rest raw materials**

Bakgrunn og mål / *Background and Goal:*

Rest- and by-products from slaughtering and processing of fish contain valuable protein and lipid as well as vitamins and minerals. Today, most of these by-products goes to low value fish silage for use as animal feed. Slaughtering and processing of farmed fish generate fresh, high quality rest- and by-products. These raw materials therefore has great potential to be used for products to more demanding, but also better paying markets such as ingredients, e.g. protein hydrolysates. In some cases the by-products are transported from the slaughtering plant to the byproduct processing plant. By-products are highly perishable and contain active enzymes that lead to degradation of lipids and proteins. One of the most fundamental challenges are decomposition of rest raw material and formation of undesirable compounds like biogenic amines (BAs) such as histamine, tyramine, putrescine, cadaverine and phenylethylamine in poorly stored raw materials or later during processing.

It is therefore a need for preservation of the by-products. One possibility is chilling, another could be to sort the byproducts into fractions of different stability.

The aim of the work is to study the effect of different storage and chilling conditions on the stability of fish rest raw materials.

Eksperimentelt / *Experimental:*

*Experimental part will cover de*fining raw material composition, storage as well as processing parameters for production of safe and high quality products to be used in functional applications as high value ingredients.

This will involve:

- Determination of chemical composition of raw material
- Characterization of degradation products (including biogenic amines) by traditional and rapid analytical techniques like NMR
- Determination of degradation as a function of time and temperature.
- Study the effect of sorting the by-products into different fractions.
- Study degradation of the by-products in different atmospheres, such as nitrogen.
- Determination of the viscosity as a function of time and temperature.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ/MBIOT5/MSBIOTECH/FTMAT/
Omfang (studiepoeng): Credits (ECTS):	15/30/45/60 studiepoeng / credits /

Veileder: *Supervisor:*	Turid Rustad
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Webside / *webpage*:	
Biveileder/-e: *Co-supervisor/-s:*	Pierrick Stevant, Møreforskning/NTNU
Arbeidstittel på oppgaven/ *Preliminary title:*	**Flavor compounds in seaweed**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*

Seaweeds have been used for centuries in Asian cuisine for their nutritional properties and rich and unique flavors. In Western countries, macroalgae have not been a significant food source throughout the past centuries and uses as food have been limited to coastal communities along the Atlantic littoral (e.g. Iceland, Ireland, Wales, Brittany, Galicia). Seaweeds are characterized by high levels of minerals and dietary fibers, along with proteins of high quality and a number of potent antioxidants, making them an attractive raw material for product development in food applications. In addition to the nutritional benefits, edible seaweed species, including common species along the coast of Europe (e.g. *Saccharina latissima*, *Alaria esculenta*, *Porphyra* spp.), are increasingly recognized as versatile and delicious whole foods (Chapman et al. 2015; Mouritsen 2016), promoted by health food trends and the use of locally available natural ingredients.

Since the description of "umami", derived from Japanese "umai" (delicious) and "mi" (essence or taste) by the Japanese chemist Ikeda in 1908, who related this flavor sensation to monosodium glutamate (MSG) found in large quantities in *konbu* (*Saccharina japonica*), some studies attempted to describe the sensory characteristics of edible seaweeds in relation to their content in flavor substances i.e. free amino-acids, volatile compounds (Le Pape et al. 2002) free sugars and salts. There is a large body of scientific literature about the nutritional composition of various seaweed species and their health benefits, but few studies on the effects of processing and storage conditions on the organoleptic properties of edible seaweeds. Preliminary results obtained at NTNU revealed a general increase in the free amino acid content of *S. latissima* stored under certain conditions with an effect on the sensory perception of the product (Stévant and Rustad, unpublished results).

Eksperimentelt / *Experimental methods:*

This thesis will investigate the effects of processing and storage conditions on the flavor compounds and sensory perception of edible seaweed species available along the Norwegian coast. The data collection may include qualitive chemical analyses of seaweed products (e.g. free amino-acids, degree of protein hydrolysis, volatile compounds) and quantitative descriptive methods (e.g. simplified sensory description).

References

Chapman AS, Stévant P & Emblem Larssen W (2015) Food or fad? Challenges and opportunities for including seaweeds in a Nordic diet. Bot Mar. 58(6).

Le Pape MA, Grua-Priol J & Demaimay M (2002) Effect of Two Storage Conditions on the Odor of an Edible Seaweed, *Palmaria palmata*, and Optimization of an Extraction Procedure Preserving its Odor Characteristics. Journal of Food Science. 67(8), 3135-3139.

Mouritsen OG (2016) Those tasty weeds. Journal of Applied Phycology, 1-6.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Biveileder/-e: *Co-supervisor/-s:*	Ulf Erikson, SINTEF
Arbeidstittel på oppgaven/ *Preliminary title:*	**Bestemmelse av kvalitetsendringer i fisk ved bruk av ny metodikk**

Bakgrunn og mål / *Background and Objectives:*

Det er et økende salg av frossen tint fisk. Denne selges også som fersk. Det er derfor behov for målemetoder som kan skille mellom fersk og frossen tint fisk. Noen målemetoder finnes – men disse er tidkrevende og lite presise. For å kunne forbedre og utvikle nye og bedre prosesseringsmetoder for bla fisk er det behov for gode målemetoder for å bestemme endringer i råstoffet som funksjon av prosessbetingelser. Dette vil for eksempel være å bestemme når proteindenatureringen begynner – bla ved varmebehandling – hvis vi ønsker mildere varmebehandling – hva skjer med proteinene (og tekstur med mer). Det er også mulig å studere effekt av ulike tinemetoder osv.

Eksperimentelt / *Experimental methods:*

Oppgaven vil gå ut på å bruke måle endringer i proteiner ved hjelp av endringer i overflatespenning ved hjelp av et nytt utviklet instrument og koble dette til målinger med konvensjonelle metoder.

Det vil bli gjort målinger på fersk fisk som er behandlet på ulik måte, fersk, lagret og frossen tint. Prøvene vil bli analysert ved hjelp av overflatespenningsmetoden og ved metoder slik som endringer i proteinløselighet, vannbindingsevne, tekstur og evt endringer i enzymaktivitet.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ
Omfang (studiepoeng): Credits (ECTS):	15 studiepoeng

Hovedveileder: *Main supervisor:*	Turid Rustad
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Webside / *webpage*:	
Biveileder/-e: *Co-supervisor/-s:*	Revilija Mozuraityte, SINTEF Fisheries and Aquaculture, Janna Cropotova, NTNU
Arbeidstittel på oppgaven/ *Preliminary title:*	**Processing to retain quality and stability of healthy nutrients in model mackerel products**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Goal:*

The aim of this work is to optimize the processing steps of sous vide products from mackerel. Mackerel fillets will be subjected to sous vide (light heat) treatment) using different process parameters. The focus will be on the quality and stability of healthy nutrient such as omega – 3 fatty acids and proteins.

Consumption of fatty fish such as mackerel provides numerous important nutrients linked both to their lipids, proteins and water soluble components. The lipids in mackerel are rich in long chain n-3 polyunsaturated fatty acids (LC n-3 PUFA) with well documented beneficial effects e.g. on cardiovascular diseases. However, the LC n-3 PUFA are highly susceptible to oxidation resulting in rapid quality loss such as reduced sensory quality (undesirable taste and flavour) of the product. Increased intake of fatty fish like mackerel is beneficial for population health. However, to achieve this there is a need to develop tasty products where the health beneficial components are preserved for instance by using milder preservation conditions. **This work will screen the changes in lipids and proteins during processing of mackerel during sous vide mackerel treatments.** The ability of natural antioxidants like herbs to increase the oxidative stability of the model products will be studied. This master project is connected to the JPI HDL project ProHealth.

Eksperimentelt / *Experimental:*

The methods involved in the study will be mainly: compositional analysis (lipid, water, protein content) and quality analysis (amount of peroxides, conjugated dienes, thiobarbituric reactive substances and free fatty acids, protein denaturation and oxidation).

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ,
Omfang (studiepoeng): Credits (ECTS):	15/30 sp studiepoeng

Hovedveileder: *Main supervisor:*	Turid Rustad
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Biveileder/-e: *Co-supervisor/-s:*	Jørgen Lerfall, IMAT
Arbeidstittel på oppgaven/ *Preliminary title:*	**Storage quality of ready-to-eat Atlantic salmon treated with soluble gas stabilization (SGS)-technology and gentle heating**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*

For å øke inntak av sjømat er det behov for utvikling av attraktive, stabile og velsmakende produkter. Det vil si produkter som er lettvinte å bruke og har god holdbarhet. For å utvikle slike produkter er det nødvendig med mer kunnskap både om råstoffene som skal inngå og hvordan disse påvirkes av prosess og lagring samt om hvordan prosessering og ingredienser påvirker holdbarhet. Oppgaven går ut på å optimalisere kombinasjonen av SGS- og varmebehandling av Atlantisk laks for å sikre god kjemisk og mikrobiell holdbarhet av laks. Ulike SGS betingelser (tid, temperatur, emballasje), varmebehandling (type, temperatur + tid kombinasjon) vil bli studert. Spesielt for varmebehandling vil man se på hvordan kvaliteten av laksen påvirkes ved lett varmebehandling samt hvilke varmebehandlingsmetoder som kan benyttes. I tillegg vil man måle hvor mye varmebehandlingen påvirker innløsningen av CO_2.

Eksperimentelt / *Experimental methods:*

SGS-teknologi vil bli testet i kombinasjon med forskjellige varmebehandlinger. Hvor mye CO_2-som blir løst opp vil bli bestemt. For å følge kvalitetsendringer vil mikrobiell, kjemisk og/eller fysikalsk kvalitet ved forskjellige behandlinger (enkeltvis og i kombinasjon) bli bestemt.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Hovedveileder: *Main supervisor:*	Turid Rustad
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Biveileder/-e: *Co-supervisor/-s:*	Rasa Slizyte og Kirsti Greiff
Arbeidstittel på oppgaven/ *Preliminary title:*	**Funksjonelle ingredienser i mat**

Hovedmålet med oppgaven vil være å undersøke hvilke effekter tilsetning av ulike ingredienser har på fysio-kjemiske, sensoriske og teknologiske egenskaper i mat.

Bakgrunn og mål:
Enzymatisk hydrolyse er en prosesseringsteknikk som kan benyttes for å produsere høyverdige ingredienser fra restråstoff. Prosessen er basert på bruk av kommersielle enzymer (proteaser) som bryter peptidbindinger, forenkler degraderingen av råstoffet og fører til utskillelse av oljen. Resultatet er tre fraksjoner; proteinhydrolysat (vannløselig protein), olje og grakse (uløselig proteiner, fosfolipider og bein). Råstoffsammensetning, enzymtype og prosessbetingelsene vil påvirke egenskapene til sluttproduktene, noe som gjør det nødvendig å utvikle prosesser skreddersydd for det restråstoffet det er tenkt brukt på. SINTEF Fiskeri og havbruk har gjennom flere prosjekter utviklet teknologier for utnyttelse av restråstoff fra fisk og kylling. Et resultat av dette er ulike ingredienser som kan ha funksjonelle egenskaper ved prosessering av mat, gi økt næringsverdi og påvirke sensoriske og teknologiske egenskaper i ferdig produkt.

Eksperimentelt*:*
Prosjektarbeidet vil bli knyttet opp mot aktiviteter som SINTEF Fiskeri og havbruk har i prosjekter på dette området. Det vil være behov for forsøk og analysering av både ingredienser og ferdig produkt.
Aktiviteter som kan inngå i dette prosjektet:

- Karakterisering av kjemisk sammensetning i ingrediensene
- Pilotforsøk hvor modellprodukter testes ut
- Fysio-kjemiske, sensoriske og teknologiske analyser.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Biveileder/-e: *Co-supervisor/-s:*	Alex Dikiy, Rasa Slizyte/Revilija Mozuraityte (SINTEF)
Arbeidstittel på oppgaven/ *Preliminary title:*	**Technological solutions for production of safe and high quality proteins from salmon rest raw materials**

Bakgrunn og mål / *Background and Objectives:*

Rest- and by-products from slaughtering and processing of farmed salmon contain valuable protein and lipid as well as vitamins and minerals. Today, most of these by-products goes to low value fish silage for use as animal feed. The slaughtering and processing of the farmed fish generate fresh, high quality rest- and by-products that may be separated into different fractions. These raw materials therefore has great potential to be used for products to more demanding, but also better paying markets such as ingredients, e.g. protein hydrolysates, for use in functional stage specific diets for poultry, pet food including nutritional supplements for human consumption. This requires hygienic handling of the by-products to ensure food safety as well as methods to generate storage-stable products.

One of the most fundamental challenges are decomposition of rest raw material and formation of undesirable compounds like biogenic amines (BAs) such as histamine, tyramine, putrescine, cadaverine and phenylethylamine in poorly stored raw materials or later during processing. The overall project idea is to develop **technological toolbox to control safety, quality and stability of proteins from salmon rest raw materials for dietary functional application**. The technological toolbox will include the solutions to prevent formation of undesirable components (BA), microbiological control and establishing product stability through the processing chain.

Eksperimentelt / *Experimental methods:*

*Experimental part will cover de*fining raw material composition, storage as well as processing parameters for production of safe and high quality products to be used in functional applications as high value ingredients.

This will involve:

- Determination of chemical composition of raw material
- Characterization of degradation products (including biogenic amines) by traditional and rapid analytical techniques like NMR
- Identification where during different technological steps, undesirable components are formed.
- Identification the stability of the protein concentrate as a function of dry matter, pH, degree of hydrolysis and storage temperature.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Biveileder/-e: *Co-supervisor/-s:*	Grete Hansen Aas Kristin Bjørdal
Arbeidstittel på oppgaven/ *Preliminary title:*	**Marine protein ingredients in functional food**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Goal:*
Fish rest raw material is mainly used for production of feed. Processing into products/ingredients for human consumption will increase profitability. The local industry at Møre has started the production of protein meal from rest raw material both from herring and white fish. Human consumption of the valuable fish proteins are depending on finding a good way to administer this. How these powders may be suited to increase protein content in different foods is not well described. They may be added to different processed seafood or administered in liquids for nutrient drinks/sports nutrition. Different protein ingredients are available for testing.

The aim of this study is to test different ways to administer these fish powders, and to test how this addition will affect the functional properties as well as the sensory properties of the products. This study can also be extended to include marine lipids.

Eksperimentelt / *Experimental:*
The task will be to find a suitable model product and test inclusion of different levels of protein. The functional properties (water holding, texture ..) and quality measured by sensory attributes will then be tested.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Biveileder/-e: *Co-supervisor/-s:*	name/-s
Arbeidstittel på oppgaven/ *Preliminary title:*	**Extraction and properties of salmon gelatine**

Bakgrunn og mål / *Background and Objectives:*
Several million tonnes of marine rest raw materials (MRRM) are generated in Europe each year. Some countries have traditionally utilised significant parts of the MRRM as silage, which is often processed into fish and animal feed or well, as a biofuel feedstock for anaerobic digesters. Only a small fraction of MRRM is used for human consumption or other value-added applications. In other countries, due to the lack of specialised infrastructure, MRRM are wasted or sent directly for animal feed without any attempt to extract the valuable components.
Fish skin and other MRRM (like backbones, viscera) are rich in collagen, and a good source for gelatine extraction. Extraction of fish gelatine usually involve acid or alkaline pre-treatment of gelatine rich raw material prior to gelatine extraction .Due to a lower content of the amino acids proline and hydroxyproline, gelatines from cold-water fish species are known to have lower gel strength, as well as lower gelling and melting temperatures, compared to gelatine from mammals and warm-water fish species. Fish gelatine is used in cosmetic, food and pharmaceutical applications, and in contrast to bovine gelatine, it is not associated with the risk of Bovine Spongiform Encephalopathy, and unlike porcine gelatine, it is Halal compliant. However, the suboptimal physical properties have limited the commercial interest in cold-water fish gelatine.
Optimisation of extraction from different start material like fish RRM and co-fractions after other technological processing (like thermal extraction and enzymatic hydrolysis), technological steps like different extraction parameters (extraction temperature and time, pH, fractionation of extracted) as well as separation of different gelatine fractions and chemical or enzymatic modifications will be applied to improve the properties of fish gelatine.

Eksperimentelt / *Experimental methods:*
Gelatine will be isolated from sorted and unprocessed fractions of fish RRM (skin, backbones) and from the insoluble fractions obtained after fractionation/hydrolysis of fish viscera into oil, stick water/hydrolysate and sediments. Several extraction parameters (like extraction temperature and time, pH, fractionation of extracted gelatine) for improving gelatine extraction technologies with the focus on yield, bioactive and textural properties will be tested. Molecular weight distribution, amino acid composition as well as viscosity, film forming capacity and gel strength, bioactive properties like ACE inhibition, antioxidativy will be analysed on extracted gelatines.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Webside / *webpage*:	www.ntnu.no
Biveileder/-e: *Co-supervisor/-s:*	nameKristine Kvangarsnes
Arbeidstittel på oppgaven/ *Preliminary title:*	**Characterization of rest raw material from organic Atlantic salmon**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Goal:*
NTNU Ålesund rules a full scale production of organic Atlantic Salmon. The diet is specialized and contain higher amount of marine ingredients during this production. The rest raw material may have special properties due to this.

The aim of this study is to characterize the rest raw material of organic salmon to exploit possible properties and evaluate utilization both as a consumption products and as an ingredient. Organic salmon oil or organic salmon meal – evaluate market and possibilities

Eksperimentelt / *Experimental:*
Chemical analysis of different fractions of raw material of organic salmon. Fatty acid profiles. Amino acid analysis. Comparison with conventional produced salmon. Coordinated experiments with our phd.student.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Webside / *webpage*:	www.
Biveileder/-e: *Co-supervisor/-s:*	Revilija Mozuraityte (Revilija.Mozuraityte@sintef.no), Ana Karina Carvajal (ana.k.carvajal@sintef.no)
Arbeidstittel på oppgaven/ *Preliminary title:*	**Processing of mackerel oil for quality and stability**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*

2014 Norwegian and foreign vessels landed ca 280 000 and 150 000 metric tonnes of mackerel, respectively. At present only 2-4 % of the mackerel is filleted by the domestic processing industry, but there are several initiatives to increase this share, to increase the profitability of the mackerel industry. An increasing filleting share – will results in increased volume of available rest raw materials from mackerel. Mackerel rest raw materials are very rich in long-chain omega-3 polyunsaturated fatty acids (LC-PUFA) such as EPA and DHA. Therefore, Norwegian fish oil processing industry is interested to use rest raw material from mackerel to produce mackerel oil for supplement market. Unfortunately, long-chain omega-3 PUFAs are especially labile with respect to oxidation. Without enhanced protection marine lipids oxidize virtually instantly which causes formation of undesirable rancid flavours and odours. Moreover, the color of the oil can change as the result of lipid-protein oxidation also. Therefore, the stabilisation and optimal processing technologies are necessary for mackerel oils.
Therefore, **the aim of this study to find important processing steps for extraction and processing of mackerel oil for good quality and stability.**

Eksperimentelt / *Experimental methods:*
The student will study the extraction of oil from mackerel rest raw material and possibilities to stabilise it by adding antioxidants early in the process. The color development and effect of processing parameters will be studied. Short path distillation will be used to study the distillation of the mackerel oils to improve the quality. The analysis that student will perform will be: fatty acid composition using GC-FID, lipid quality – peroxide value, anisidine value, lipid protein interaction – measurement of Schiff bases (at NTNU) and others according the needs.
The work will take place at SINTEF SeaLab, but some analysis will be also performed at NTNU.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Hovedveileder: *Main supervisor:*	Marit Sletmoen
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Biveileder/-e: *Co-supervisor/-s:*	
Arbeidstittel på oppgaven/ *Preliminary title:*	**Molecular mechanisms underlying bacterial adhesion**

Background and Goal:
The control of bacterial adhesion is of interest in different application fields including but not limited to: food industry, transport, human and animal health, oil production, antifouling materials etc. The adhesion to mucosal surfaces are particularly relevant in order to understand and improve human health. The exact molecular mechanisms underlying the adhesion are for many systems unknown. In this project, we plan to identify the molecular factors involved in microbial adhesion to mucosal surfaces using single molecule techniques including atomic force microscopy (AFM) and optical tweezers (OT).

Experimental:
The main experimental approach will be the direct determination of bacteria – surface interactions using AFM. The study will include quantification of the interaction abilities of various bacterial strains immobilized onto AFM tips, when allowed to interact with mucin-coated or other relevant surfaces. These investigations will be combined with microscopic inspection of the mucosal surfaces. A particular focus will be given to elucidating the role of glycan structures for bacterial adhesion.

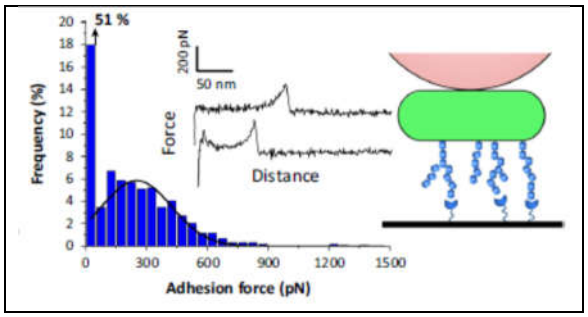


Illustration of single cell force spectroscopy assay. The illustration is taken from a review paper (Dufrêne, Trends in Microbiology June 2015, Vol. 23, No. 6) and illustrates the approach used in the study "Single-cell force spectroscopy of probiotic bacteria" (Beaussart, A. *et al*. (2013) Biophys. J. 104, 1886–1892) were carbohydrate interactions of probiotic bacteria were quantified using AFM.

The topic can be adjusted to fit with the expected workload for 60, 30 or 15 credits.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MTNANO
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

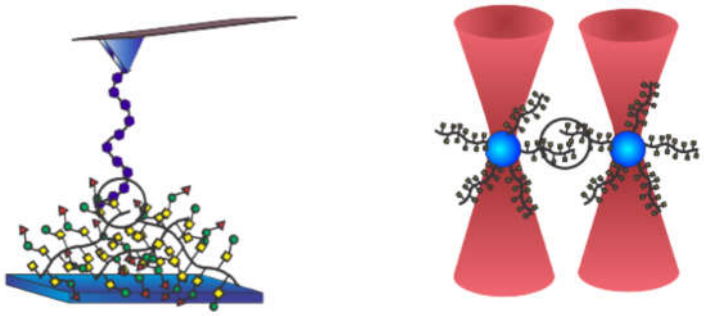
Hovedveileder: *Main supervisor:*	Marit Sletmoen
Kontaktinformasjon / epost *Contact information / email:*	marit.sletmoen@ntnu.no
Webside / *webpage*:	https://www.ntnu.edu/ibt/research/biopol
Biveileder/-e: *Co-supervisor/-s:*	
Arbeidstittel på oppgaven/ *Preliminary title:*	**Carbohydrate antigens in human health and disease**

Background and Goal:

The recognition of glycans by carbohydrate-binding proteins (lectins) is an important regulatory mechanism in healthy and diseased immune physiology. We are investigating the effect of the aberrant glycosylation occurring in the majority of human cancers. We are currently investigating how certain carbohydrate based tumor-associated antigens interact with specific lectins present on antigen presenting cells. These interactions are believed to have consequences for the further progression of the cancer.

Experimental:

The main experimental approach will be the direct determination of glycan interactions using the sensitive force probes atomic force microscopy (AFM) and/or optical tweezers (OT). These techniques allow determining intermolecular interaction forces with picoNewton resolution. They are therefore powerful tools to provide new information concerning specific biological interactions.



Biomacromolecules to be investigated are immobilized onto flat surfaces or onto the tip of AFM cantilevers for investigations using AFM (left) or onto the surface of polystyrene beads for investigation using optical tweezers (right).

The topic can be adjusted to fit with the expected workload for 60, 30 or 15 credits.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MTNANO
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Hovedveileder: *Main supervisor:*	Marit Sletmoen
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Biveileder/-e: *Co-supervisor/-s:*	
Arbeidstittel på oppgaven/ *Preliminary title:*	**Bacterial adhesion to glycosylated surfaces**

Background and Goal:
Glycans comprise the outer face of cells, and cellular interactions within and between species therefore often involve glycan binding and recognition. Many of these glycans exist as part of mucin molecules. Throughout evolution, opportunistic pathogens have developed the ability to target glycan structures on host cells to facilitate infection. Glycans therefore present attractive drug targets for infectious disease prevention and treatment.

Experimental:
We propose to develop glycan microarrays and to use these as tools to study glycan interactions as well as bacterial attachment to glycosylated molecules. The microarrays will present patches of mucins displaying glycans of a predefined structure, surrounded by mucins displaying glycans of a different structure (Figure 1). The PDMS stamps needed to deposit mucins in micron-sized patches will be prepared using lithographic techniques present in NTNU Nanolab. In a first series of experiments we will investigate the ability of glycan self-interaction to assure stable immobilization of micronsized particles onto glycan presenting surfaces (Figure 1). Of particular interest will be functionalization with mucins carrying truncated glycans as found on cancerous tissue. The amount and position of the bound polystyrene beads will be determined by light microscopy. Furthermore, we hypothesize that the potential of a bacterium to colonize a mucosal surface depends on its ability to bind to specific glycans carried by mucins exposed on the surface. Studies of bacterial adhesion to glycan presenting surface spots will be performed as explained in figure 1 C.

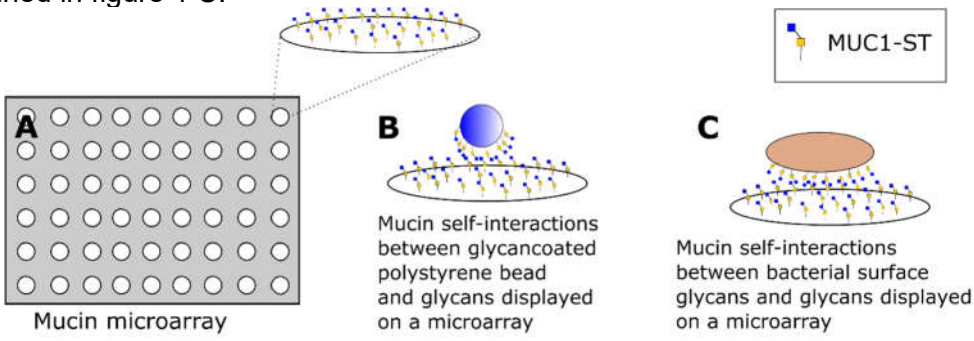

Figure 1: A: We propose to prepare glycan microarrays consisting of patches functionalized with a mucin displaying the glycan sialyl-Tn (STn). B: MUC1-STn functionalized polystyrene beads (diameter 1 – 3 micrometers) will be used to investigate the ability of STn glycans to mediate adhesion of micronsized particles to STn-presenting surfaces. The amount and position of the bound polystyrene beads will be determined by light microscopy. C: The glycan arrays will be used to asses and compare the adhesion abilities of chosen bacteria to mucins with well-characterized glycosylation patterns.

The topic can be adjusted to fit with the expected workload for 60 or 30 credits.

Suitable for main profiles:	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MTNANO
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Hovedveileder: Main supervisor:	Marit Sletmoen
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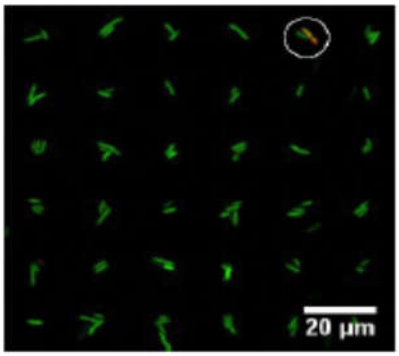
Biveileder/-e: Co-supervisor/-s:	
Arbeidstittel på oppgaven/ Preliminary title:	**Preparation and study of cellular microarrays**

Background and Goal:

We have developed bacterial microarrays that can form the basis for efficient studies of heterogeneity within populations of bacteria (Arnfinnsdottir et al, The design of simple bacterial microarrays. Development towards immobilizing single living bacteria on predefined micro-sized spots on patterned surfaces. *PlosOne*, **10** (2015), 6, Article Number e0128162). Such microarrays could be prepared for also other microorganisms. The display in microarrays in regular arrays is relevant for efficient studies of the effect of changing external parameters on their behaviour.



Bacterial microarrays observed using fluorescence microscopy.

We are interested in studying the effect of antibiotics as well as other forms of antimicrobial agents on the behavior of bacteria and yeast cells. The investigation of the mode of action of these antimicrobial agents could benefit from the preparation of ordered arrays. Microscopic inspection of the arrays over time will provide insight into the influence of the added compounds on the cells.

Experimental:

The work will include some or all of the following tasks:

- Preparation of PDMS stamps needed for deposition of chemicals in an ordered pattern on glass surfaces. The stamps will be prepared using lithographic tools available in NTNU Nanolab.
- Identification of optimal surface functionalization for immobilization of the relevant bacterium or yeast cells.
- Studies of bacterial or yeast microarrays using light microscopy.

The topic can be adjusted to fit with the expected workload for 60 or 30 credits.

Suitable for main profiles:	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MTNANO
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Biveileder/-e: *Co-supervisor/-s:*	Finn Aachmann
Arbeidstittel på oppgaven/ *Preliminary title:*	**Alginate matrices for tissue engineering**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*

Alginate is a attractive biopolymer for use as scaffold (matrix) in tissue engineering. Although alginate entrapment is a very gentle technique for immobilizing living cells, many cells need specific interaction with the matrix for their proliferation and viability. Such anchoring depending behaviour is common for most mammalian cells and the alginate network itself is non-interacting. Peptides known from the extracellular matrix (ECM) to interact with integrins in the cell membrane can be linked to alginate and induce attachment of cells to the alginate. Interactions between ECM and integrins have been shown to determine cell morphology, viability and differentiation, and is thus highly relevant study objects in tissue engineering. Of particular interest is the covalent linkage of peptides that can be used to crosslink the alginate and that cells by secreted enzymes can degrade and by this modify their microenvironment. **The aim of the project is to design novel alginate matrices covalent cross-linked with peptides that can be degraded by proteases and with cell adhesion properties.**

Eksperimentelt / *Experimental methods:*

Different peptides will be covalently link to alginate using a novel method developed at IBT, NTNU. NMR spectroscopy, light scattering (SEC-MALS) and viscosity measurements, will be relevant method for product characterisation (e.g. degree of coupling and crosslinking). Hydrogel properties, such as gel elasticity and stability will be studied. Studies of cell interactions with the developed materials on 2D gels and in 3D gels using confocal microscopy may be a part of the project depending on the student interests and the progress of the project.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Hovedveileder: *Main supervisor:*	Berit L. Strand
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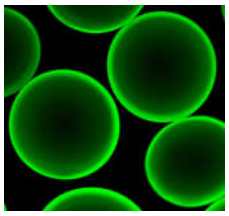
Webside / *webpage*:	http://www.ntnu.edu/biotech/research/biopol
Biveileder/-e: *Co-supervisor/-s:*	Abba E. Coron
Arbeidstittel på oppgaven/ *Preliminary title:*	**Strategies for stabilising alginate beads of intermediate G content**

Project description:

Alginate microbeads have through many years of research shown great potential as an immunoisolation system for the entrapment of insulin-producing cells. The preferential use of alginate gels in cell immobilisation is primarily due to the gentle environment they provide for the entrapped material. Alginate is a binary heteropolymer containing 1,4-linked β-**D**-mannuronic acid (M) and α-**L**-guluronic acid (G) residues, known for its gel forming properties in the presence of divalent cations. The use of alginate gels for cell encapsulation provides many challenges related to its application, which includes destabilisation of the gel network in terms of swelling and gel dissolution, as well as increased pore size, at physiological conditions (Mørch et al., 2006). Traditionally, a polycation layer has been applied to stabilise the alginate gel beads. However, the conventional polycation layer (poly-L- lysine) has been found to be highly immune stimulating, associated with cellular overgrowth on the surface of the alginate capsule (Strand et al., 2001), in addition to activating the complement system (Rokstad et al., 2011). The functional properties of alginate are essentially governed by the content of M and G. In a recent *in vivo* study performed by Tam et al. (2011), alginate isolated from *Laminaria hyperborea* leaf with an intermediate G content was found to be biocompatible. However, the alginate displayed a low degree of stability in terms of swelling and bead fragmentation upon transplantation.

The aim of the current project, with the possibility of a continuation to a master's project, is to explore different strategies for stabilising alginate beads made from *L. hyperborea* leaf alginate, which has already shown to be a promising candidate for cell transplantation in terms of biocompatibility. These strategies include the incorporation of short and extremely long G-blocks into the gelling system, in combination with varying the type and concentration of gelling ions used. The size stability of the alginate beads will be studied at physiological conditions (saline experiments). In addition, the diffusional properties of the added G-blocks will be assessed through fluorescence-labelling of the alginates, followed by confocal-laser-scanning microscopy (CLSM) analysis.



Fluorescence-labelled *L. hyperborea* leaf alginate beads, visualised by CLSM.

References

Mørch, Y. A., Donati, I., Strand, B. L. & Skjåk-Bræk, G. 2006. *Biomacromolecules,* 7**,** 1471-80.

Rokstad, A. M., Brekke, O.-L., Steinkjer, B., Ryan, L., Kollárikóva, G., Strand, B. L., Skjåk-Bræk, G., Lacík, I., Espevik, T. & Mollnes, T. E. 2011. *Acta Biomaterialia,* 7**,** 2566-2578.

Strand, B. L., Ryan, L., In't Veld, P., Kulseng, B., Rokstad, A. M., Skjåk-Bræk, G. & Espevik, T. 2001. *Cell Transplantation,* 10**,** 263-275.

Tam, S. K., Dusseault, J., Bilodeau, S., Langlois, G., Halle, J. P. & Yahia, L. 2011. *J Biomed Mater Res A,* 98**,** 40-52.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	30 sp studiepoeng / 15 studiepoeng 30 credits / 15 credits (specialization project)

Hovedveileder: *Main supervisor:*	Olav Vadstein
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Biveileder/-e: *Co-supervisor/-s:*	Sigurd Einum (IBI) / Ingrid Bakke (IBT)
Arbeidstittel på oppgaven/ *Preliminary title:*	**The effects of microbiota on fitness variation within and among Daphnia genotypes**

Background and Objectives:

For many organisms it has been shown that the microbiota contributes to the health and disease of the host. In cultures of many animals, both invertebrates and vertebrates, considerable culture-to-culture variation has been observed in the performance/fitness of the organism. It has been suggested that parts of this variation can be caused by differences in the microbiota of the culture. Variation among replicate cultures containing the same genotype of the cultured species can be caused by founding effects and drift, and is therefore of a random type. In contrast, systematic variation among cultures containing different genotypes that have been previously exposed to a common environment would suggest that different genotypes impose different selective pressures on the microbiota community. In the case where different genotypes have different fitness, the question is to what extent these differences are explained by their associated microbiota?

In our Daphnia lab we are currently running population dynamics experiments where we observe considerable random variation in population growth and carrying capacity among replicates within clones, as well as systematic variation among clones. The role of microbiota in this variation remains unknown, but the biology of Daphnia makes it an attractable model system to study such effects. The goal of this project is to:

1. Test for differences in the microbiota in water and associated with animals between and within (among replicates) clones of Daphnia.
2. Test if it is possible to reduce culture-to-culture and temporal variation in fitness of Daphnia by experimental manipulation of microbiota of the culture within clones (i.e. reduce random source of variation)
3. Test if variation in fitness among clones can be partly caused by their associated microbiota.

Experimental methods:

Experiments will be conducted at Dept. Biology and molecular work Dept. Biotechnology.
The student will run parallel replicates of two genetically unique clones of *Daphnia* with verified differences in fitness and estimate population growth rate and carrying capacity of each replicate. The study will test 1) for systematic differences in microbiota composition between the two clones, 2) whether across-culture (within clone) transfer of microbiota reduces random culture-to-culture variation in fitness. If microbiota composition differs between the two clones, containers containing individual *Daphnia* juveniles of the two clones will be inoculated with microbiota from cultures of the two clones in a 2x2 fashion, and juvenile growth, age at reproduction and offspring production will be recorded to test how microbiota composition contributes to differences in these life history traits among clones.

Methods include cultivation studies and characterization of the microbial community based PCR-based amplification of the 16S-rRNA gene.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MBIOT5, MSBIOTECH og MACODEV
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng 60 credits

Department of Biology

Hovedveileder: Main supervisor:	Henrik Jensen, Associate Professor, Centre for Biodiversity Dynamics, Department of Biology (https://www.ntnu.edu/biology/jensen-lab)
Biveileder(e): Co supervisor	Arild Husby, Thor Harald Ringsby, Bernt-Erik Sæther, and/or Jonathan Wright may be co-supervisor(s)
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Spatio-temporal dynamics of genes for ecologically important traits in house sparrows**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Knowing the genetic architecture of ecologically important traits is fundamental to our understanding of many ecological and evolutionary processes in natural populations. I can offer a number of exciting MSc-projects which focus on identifying the genetic architecture of such traits, and the causes and consequences of the traits' genetic architectures. The MSc-projects will use state-of-the-art genomic and eco-evolutionary data from a unique long-term study of a house sparrow (*Passer domesticus*) model system. Ecologically important traits are traits related to fitness (survival and reproduction) and they will therefore be important for both ecological and evolutionary dynamics in natural populations. Examples of such types of traits are morphological traits behavioural traits, physiological traits, parasite load, and life-history traits. A trait's genetic architecture consists of information on which genes affect the trait, locations of these genes in the genome, and how the genes affect the phenotype. Eco-evolutionary data have been collected on an individual based level from natural and experimental insular house sparrow populations in northern Norway since 1993. More than 27,000 individuals are included in our data base. The genomic data consists of a reference house sparrow genome, SNP-genotype data on 6500 SNPs for ca. 2300 individuals and 185,000 SNPs for ca. 4000 individuals, and information on polymorphisms within ca. 140 candidate genes for various ecologically important traits. The eco-evolutionary and genomic data will be used in statistical analyses to determine genetic architecture by mapping genes for various ecologically important traits using QTL-mapping (linkage mapping/GWAS) and/or study effects of candidate genes directly. Further statistical analyses will then be carried out to examine causes and consequences for spatio-temporal eco-evolutionary dynamics in the model system. Students choosing one of these MSc-projects will have the opportunity to get experience from fieldwork, molecular genetic laboratory work and cutting edge statistical analyses of eco-evolutionary and genomic data.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Ecology, Behaviour, Evolution and Biosystematics, Natural Resources Management, Biotechnology

Hovedveileder: Main supervisor:	Henrik Jensen, Associate Professor, Centre for Biodiversity Dynamics, Department of Biology (https://www.ntnu.edu/biology/jensen-lab)
Biveileder(e): Co supervisor	Postdoc Alina Niskanen
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**The genetic basis for inbreeding depression in house sparrows**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Anthropogenic changes of the environment, such as habitat destruction, are the major causes of high rates of population declines and extinctions. As population sizes decline they become vulnerable to inbreeding, which is expected to decrease individual fitness (called inbreeding depression) and population growth rates. As a consequence, inbreeding depression is one of the most important genetic processes affecting the persistence of small and threatened populations. Despite its importance, the genetic mechanisms underlying inbreeding depression are not well known. For example, it is unclear whether inbreeding depression is mainly caused by small genome-wide effects or single genes with large effects. We can offer MSc-projects that will focus on I) investigating the genome-wide architecture of inbreeding depression, identify specific loci important for inbreeding depression, and identify the functional genetic variation within these loci, and II) examining the interaction between environmental conditions and inbreeding depression. To achieve these goals, the projects will use state-of-the-art genomic tools, long-term individual-based data on fitness and environmental records from a unique study system of pedigreed wild house sparrow (*Passer domesticus*) populations. Data on approximately 4,000 adult house sparrows from 11 Norwegian experimental and non-experimental island populations will be used. The birds have been genotyped for 185,000 genome-wide single nucleotide polymorphisms. Students choosing one of these MSc-projects will have the opportunity to get experience from fieldwork, molecular genetic laboratory work and cutting edge statistical analyses of eco-evolutionary and genomic data.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Ecology, Behaviour, Evolution and Biosystematics, Natural Resources Management, Biotechnology

Hovedveileder: Main supervisor:	Henrik Jensen, Associate Professor, Centre for Biodiversity Dynamics, Department of Biology (https://www.ntnu.edu/biology/jensen-lab)
Biveileder(e): Co supervisor	Thor Harald Ringsby, Bernt-Erik Sæther, and/or PhD-stipendiat Dilan Saatoglu may be co-supervisor(s)
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**The genetics of dispersal in house sparrows**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Dispersal (migration) of individuals between populations may affect both ecological and evolutionary dynamics and is consequently a very important process in natural populations. For example, immigration will increase population size, reduce inbreeding and introduce genetic variation. Furthermore, dispersal reduces genetic differentiation between populations. Accurate knowledge about the number of immigrants and where they dispersed from is crucial to understand both causes and consequences of dispersal. I can offer exciting MSc-projects where the goal is to combine ecological data with genetic analyses to identify the number and origin of immigrants to natural island-populations of house sparrows (*Passer domesticus*) at the Helgeland coast in northern Norway. This information will then be used to identify population and landscape characteristics that explain variation in dispersal in space and time, and to examine the consequences of dispersal for both ecological, population genetic and evolutionary processes. Eco-evolutionary data on e.g. dispersal has been collected on an individual based level from 18 natural house sparrow populations in an island metapopulation at Helgeland since 1993. In total more than 17,500 individuals are included in this data base. The genetic data consists of genotypes on 14 microsatellites for >12000 individuals, SNP-genotype data on 6500 variable SNPs distributed across the genome for ca. 1100 individuals, and SNP-genotype data on 185,000 SNPs for ca. 3300 individuals. Students choosing one of these MSc-projects will have the opportunity to get experience from fieldwork, molecular genetic laboratory work and cutting edge statistical analyses of eco-evolutionary and genomic data.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Ecology, Behaviour, Evolution and Biosystematics, Natural Resources Management, Biotechnology

Hovedveileder: Main supervisor:	Henrik Jensen, Associate Professor, Centre for Biodiversity Dynamics, Department of Biology (https://www.ntnu.edu/biology/jensen-lab)
Biveileder(e): Co supervisor	Thor Harald Ringsby and postdoc Thomas Kvalnes
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Heritability and fitness effects of egg colour in house sparrows**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Egg colour and egg colour pattern has been shown to affect fitness in a number of bird species. This may be because colour and pattern influence the level of camouflage against predation or because colour and pattern may affect the probability of egg parasitism, either intra-specificially (e.g. by cockoo) or intra-specificially («egg dumping»). The goal of the MSc-project is to estimate the heritability (additive genetic variance) of egg colour and egg pattern, as well as genetic correlations between these traits and other fitness-related traits in house sparrows (*Passer domesticus*). Such estimates are very rare because few data sets exist where such analyses are possible. The project will then examine the effect of egg colour and pattern on individual fitness (measured by survival and reproductive output). Data on egg colour and egg pattern has been collected in up to five insular house sparrow populations at Helgeland between 2003 and 2009. Digital photographs that can be used to determine egg colour and egg pattern have been taken of more than 400 clutches. Clutches were assigned to individual females by genetic parentage analyses. Large and genetically determined pedigrees (containing almost 10,000 individuals) will be used with the data on egg colour and pattern to estimate quantitative genetic parameters using “animal models”. Students choosing this MSc-project will have the opportunity to get experience from fieldwork, molecular genetic laboratory work, quantitative genetic analyses, and statistical analyses of eco-evolutionary data.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Ecology, Behaviour, Evolution and Biosystematics, Natural Resources Management, Biotechnology

Hovedveileder: Main supervisor:	Henrik Jensen, Associate Professor, Centre for Biodiversity Dynamics, Department of Biology (https://www.ntnu.edu/biology/jensen-lab)
Biveileder(e): Co supervisor	Bernt-Erik Sæther, Thor Harald Ringsby, Henrik Pärn, and/or PhD-student Sindre Sommerli may be co-supervisor(s)
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Population genetics of water voles**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	To understand populations' ability to evolve in response to environmental change and persist in the face of habitat fragmentation and spatio-temporal fluctuations in demography due to e.g. anthropogenic effects, it is important to understand the causes and consequences of temporal changes in genetic variation within and between populations. In 2015 we started a large-scale field study on water voles (*Arvicola amphibius*) on islands at the coast of Helgeland. Our aim is that this will be a model system we can use to examine questions related to population dynamics and population genetics processes in such a fragmented system, which has large spatio-temporal fluctuations in population size. I can offer exciting MSc-projects with focus on important population genetics processes in water voles; inbreeding, genetic drift, genetic bottlenecks, founder events, and genetic population structure. Methods for genotyping individual voles on 13 microsatellites are already established. In addition, we will in collaboration with a research group at the University of Aberdeen develop high-throughput genomic resources for water voles that we aim to use in the proposed MSc-projects. Students choosing these MSc-projects will gain skills in carrying out high-quality fieldwork on the beautiful Helgeland coast, experience with molecular genetic laboratory work, and good knowledge about statistical analyses of population genetic data.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Ecology, Behaviour, Evolution and Biosystematics, Natural Resources Management, Biotechnology

Hovedveileder: Main supervisor:	Åse Krøkje
Biveileder(e): Co supervisor	
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Induction of genotoxic endpoints and biotransformation enzymes in liver cells (cell line) exposed to defined mixtures of chemical compounds.**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Cells from rat or fish liver (cell line) will be exposed for mixtures of pollutants, in environmentally relevant concentrations, *in vitro*. Compounds in mixtures will often interact, and result in a higher (synergistic) or a lower (antagonistic) effect compared with that of a single-component exposure. To improve hazard identification and environmental risk evaluation, it is important to study how pollutants behave in mixtures. The aim of these projects is to develop and test out methods to evaluate complex mixtures with regard to interaction effects, which can occur between single compounds in a mixture. Pollutants, which occur in the terrestrial or aquatic environment, will be used in environmentally relevant concentrations. A statistical method for experimental design will be used to achieve a cost- and time effective performance of mixture studies, most probably factorial design. Eventual interactions will be studied by use of genotoxic endpoints (f ex DNA-adducts, DNA-strand breaks, micronucleus or chromosomal aberrations) or induction of biotransformation enzymes (CYP1A1 and conjugation enzymes). Multivariate regression models, such as projection to latent structures (PLS), can be used to evaluate possible interactions in mixtures. 1-2 master projects
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Environmental Toxicology and Chemistry

Hovedveileder: Main supervisor:	Jens Rohloff
Biveileder(e): Co supervisor	Richard Strimbeck
Arbeidstittel på oppgaven (max 20 word): Preliminary title:	**Ecological Urban Production of Vegetables**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	The master project(s) is/are integrated as part of a regional research project aiming at the utilisation of compost derived from manure and food waste for the ecological production of vegetables. Major active partners involve Skjetlein vgs (*Naturbrukslinje*) and the company Global Green Energy (GGE). Sub-goals include (a) Development and optimisation of compost products (mixtures) to be used as growth substrate (b) Increase knowledge about innovative soil substrate(s) by the use of a compost bioreactor (c) Improve recruitment to education and research within urban farming and ecological food production Possible master projects: 1. Investigation of effects of compost products in vegetable production (e.g. tomato, salad, herbs) on crop growth, yield and quality. Focus areas: plant physiology, phytochemistry, food chemistry 2. Investigation of effects of manure/food waste ratio and bioreactor conditions on composting process and composition with regard to soil substrate quality and commercial value. Focus areas: microbiology, biochemistry, agriculture
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Biology, Biotechnology, LUR

Hovedveileder: Main supervisor:	Thorsten Hamann
Biveileder(e): Co supervisor	Timo Engelsdorf
Arbeidstittel på oppgaven (max 20 word): Preliminary title:	**Functional analysis of candidate genes mediating plant cell wall integrity maintenance**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	The plant cell wall is the first line of defense of all plants against stress. It is a highly dynamic structure, which also provides different materials relevant for society. Plant cell wall signaling processes are essential during defense and are also intricately involved in maintaining functional integrity of the cell wall during growth and response to biotic stress. Recently the host lab has performed extensive transcriptomics and phospho-proteomics experiments to identify genes maintaining plant cell wall integrity during development and defense in *Arabidopsis thaliana*. The aim of the project is to functionally characterize several of these candidate genes in order to dissect the molecular mechanism underlying plant cell wall integrity maintenance. The project will initially involve sterile tissue culture work to generate biological material, qRT-PCR-based confirmation of transcriptomics results, LC-MS-based measurements of phytohormones in gene knockout plants, cloning of reporter-protein fusion and promoter reporter constructs, which will be followed by generation of transgenic plants to perform cellbiological and expression studies using advanced microscopy (confocal microscopy in combination with image analysis). Generating the data on gene function is the prerequisite to achieve the long-term of this project, which is to use the genes identified in Arabidopsis as leads to improve performance of food crops and facilitate bioenergy production from ligno-cellulosic biomass.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Biologi, bioteknologi

Hovedveileder: Main supervisor:	Thorsten Hamann
Biveileder(e): Co supervisor	Timo Engelsdorf
Arbeidstittel på oppgaven (max 20 word): Preliminary title:	**Development of novel analytical tools to analyze plant cell wall signaling**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Plant cell wall signaling processes are essential during interaction between the plant and the environment as well as during development. They are also intricately involved in maintaining functional integrity of the cell wall during growth and response to biotic stress. Currently there are no suitable tools available to study early, fast cell biological processes during cell wall integrity maintenance. The host lab has performed recently extensive transcriptomics experiments and identified genes, which are responding to cell wall integrity impairment. The aim of the project is to use the candidate genes as starting place to develop novel markers. The project will initially involve tissue culture work to generate biological material, qRT-PCR-based confirmation of transcriptomics results and cloning of reporter-protein fusion constructs, which will be followed by generation of transgenic plants to perform cellbiological studies of the reporter fusion constructs using advanced microscopy (confocal microscopy in combination with image analysis).
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Biologi, bioteknologi

Hovedveileder: Main supervisor:	Martin Kuiper - kuiper@ntnu.no – 73550348 – DU1-111 IBI
Biveileder(e): Co supervisor	Astrid Lagreid, IKM-DMF; Denis Thieffry, ENS/Paris; other co-supervisors (IBI, IBT) will take part, depending on the topic of the master proposal.
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Implementation of Boolean models for cell perturbation analysis and drug development**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	The use of network and model based approaches to describe, explain and understand biological processes is an essential approach in Systems Biology. Tools that enable this approach range from Cytoscape (network based) to CellDesigner (pathway-based) to full-fledged mathematical modeling platforms. One of the more basic modeling paradigms is based on Boolean logics, where interactions between model components (proteins, genes) only need to be described in terms of activation and inhibition, and the regulatory rules are described using AND, OR, and NOT logics. We are developing user-friendly, semi-automated software tools (see Flobak et al 2015), in the new initiative DrugLogics (www.DrugLogics-NTNU.org), part of the NTNU Digital Life theme. DrugLogics aims to develop Boolean model based approaches to help develop Personalized Medicine approaches to treat cancer. This initiative offers possibilities for a variety of Master projects: - The assembly of a 'causal statement' knowledge base that integrates information from resources like Reactome and SIGNOR that can be used to build Boolean models - The building of Boolean models to simulate the effect of experimental perturbations on the behavior of specific cells (plant, animal, microorganism) - The simulation of these Boolean models to predict the effects of mutations or other perturbations and the subsequent experimental validation - and many more …
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Biology / Biotechnology
Reference:	Flobak Å et al. Discovery of drug synergies in gastric cancer cells predicted by logical modelling. PloS Comp. Biol. 2015 DOI: 10.1371/journal.pcbi.1004426. www.druglogics-ntnu.org www.colosys.org https://www.ntnu.edu/crossover-research https://www.ntnu.edu/health/druglogics www.reactome.org, http://signor.uniroma2.it/

Hovedveileder: Main supervisor:	Professor Berit Johansen
Biveileder(e): Co supervisor	Dr. Astrid Feuerherm, Dr Thuy Nguyen, Dr. Linn-Karina Selvik
Arbeidstittel på oppgaven (max 20 word): Preliminary tittel:	**Lipid signaling mechanisms in inflammation.**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Obesity is a major risk factor for lifestyle diseases. Lifestyle is affecting severity of chronic diseases, including cardiovascular diseases and rheumatism. Common symptom between obesity, lifestyle and chronic disease is inflammation (1,2). Investigations regarding molecular mechanisms of inflammation will give insights on how different aspects of lifestyle, hormonal responses, e.g. insulin, will affect disease progression and severity (3,4). Hormones under study include cytokines, insulin, chemokines, eicosanoids and adipokines. Model systems: Synoviocytes, cellular model for rheumatoid arthritis; Monocytes, cellular model for white blood cells. **Possible master theses:** 1) Characterization of insulin signaling in synoviocytes 2) Characterization of adipokin signaling in synoviocytes 3) Characterization of microRNA as a regulatory mechanism of synoviocyte biology 4) Characterisation of TLR2/4-induced responses, and possible involvement of cPLA2 in an osteoclast cell model 5) Metabolomics detection human samples (collaboration with Dr Jens Rohloff) 6) Systems biology of human intervention samples (collaboration with Prof. Martin Kuiper.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	MBIOT5, MBI-celle/molekylærbiologi, MSc Biotechnology (2yr)

1. WHO, *Global status report on noncommunicable diseases 2010. Description of the global burden of NCDs, their risk factors and determinants.*, WHO, Editor. 2011. p. 1-176.

2. Kelly, T., et al., *Global burden of obesity in 2005 and projections to 2030.* International Journal of Obesity, 2008. **32**(9): p. 1431-1437.

3. Ouchi, N., et al., *Adipokines in inflammation and metabolic disease.* Nat Rev Immunol. **11**(2): p. 85-97.

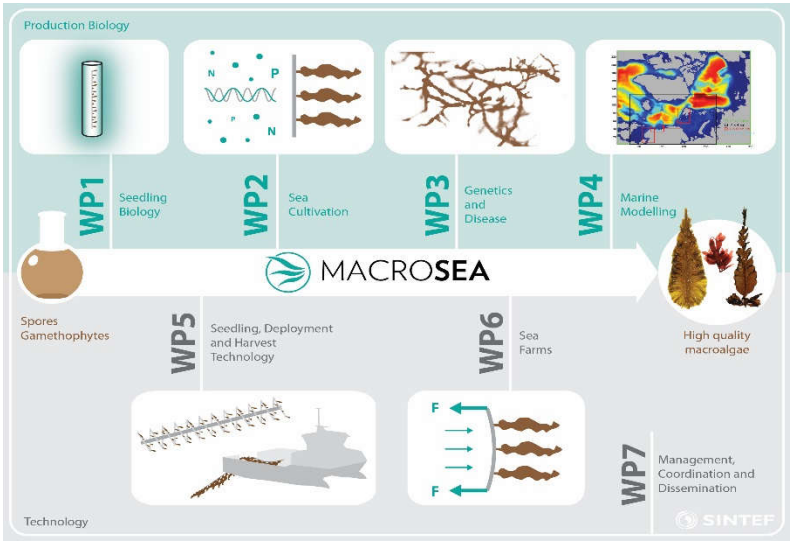
4. Gregor, M.F. and G.S. Hotamisligil, *Inflammatory mechanisms in obesity.* Annu Rev Immunol, 2011. **29**: p. 415-45.

Hovedveileder: Main supervisor:	Augustine Arukwe
Biveileder(e): Co supervisor	
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Identification of key cellular targets of toxicants as potential *xenosensor* biomolecules in fish**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Our group is part of a big NFR funded biotechnology "Digital life" project entitled "dCod 1.0: decoding systems toxicology of Atlantic cod (*Gadus morhua*) – environmental genomics for ecosystem quality monitoring and risk assessment" in collaboration with several national (UiB, UiO, NMBU) and international partners The project will pursue a research line in environmental omics that identifies key cellular targets of toxicants as potential *xenosensor* biomolecules. An illustrating example is the use of transcription factors such as the peroxisome proliferator-activated receptors (PPARs), aryl hydrocarbon receptor (AhR) and estrogen receptor (ER) in multiple assays for toxicants and endocrine disruptors in fish systems. We are looking for 4-5 master students to work together with a PhD fellow in delivering our part of the project. We will develop and structure out a candidate-specific *in vivo* or *in vitro* research plan that fits with the overall aims of dCod. Otherwise, the overall objective of our research is to develop diagnostic gene, enzyme and protein response tools in the study of the molecular and physiological mechanisms of the effects of xenoestrogens and xenobiotic, and their interactions in wildlife species. In our laboratory, these studies are performed in both *in vitro* and *in vivo* systems.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Environmental Toxicology and Chemistry; cell and molecular biology

Main supervisor:	Tor Jørgen Almaas
Co supervisor	
Preliminary title:	**Electrophysiological characterization of receptor neurons on insects: taste receptors (feet, flagellum, mouth-parts), receptors for temperature, humidity and touch (antenna, feet), olfactory receptors (flagellum).** (One student – one sensory modality)
Short description of the project:	By electrophysiological techniques the neurophysiological properties of sensory neurons will be described: sensitivity, specificity and temporal response pattern. Electrochemically sharpened tungsten electrodes or glass capillary electrodes are being positioned by micromanipulators in the extracelluar space close to the receptor cell in order to record actionpotentials as respons to the relevant stimulus. Special designed stimulation equipment are applied for the stimulation procedures. Please contact the supervisor for more information about the lab and how to design the individual project.
Suitable for (main profiles):	Physiology, ecology, cell biology
Hovedveileder: Main supervisor:	Rolf Erik Olsen
Biveileder(e): Co supervisor	Bjørg Egelandsdal, Erik Slinde, NMBU

Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Krebs cycle in fish performance and quality**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	The Krebs cycle is running in cell mitochondria and is the main provider of NADH for the synthesis of ATP which is the energy all living organisms need for growth and survival. Limitations in intermediates in the cycle will limit available energy for the animal. In a growing animal increasing the Krebs cycle output can increase energy availability and therefore growth performance over time. In pigs being slaughtered, boosting the Krebs cycle has been shown to increase product quality. The cause is unknown, but it is probably linked to a faster depletion of tissue oxygen and thereby lower lipid peroxidation. It is currently unknown if these mechanisms are valid in fish. But salmon in particular is a fatty species with high potential for rancidity. **The project will include feeding studies, quality assessment and cell tissue cultures.**
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Nutrient chemistry, chemistry, aquaculture, cell biology

Main supervisors:	Kjell Inge Reitan, Geir Johnsen, Atle Bones, Yngvar Olsen (one)
Co supervisors:	Jorunn Skjermo, Silje Forbord, Aleksander Handå (one or two)
Preliminary title:	**MACROSEA - A knowledge platform for industrial macroalgae cultivation in Norway (2016-2019)**
Short description of the project:	You will take part in the enthusiastic MACROSEA project team at SINTEF and NTNU and contribute to successful and predictable production of high quality biomass making significant steps towards industrial macroalgae cultivation in Norway.



The primary objective is to establish an interdisciplinary knowledge platform on fundamental production biology and technology for macroalgae cultivation over a wide range of climatic, ecological and physical conditions. Secondary objectives are: **(i)** to increase the principal knowledge on biological performance and environmental requirements for optimized chemical composition and biomass production, and **(ii)** to obtain technological specifications and develop generic model and simulation tools for farm systems and biomass production. The brown kelps *Saccharina latissima* and *Alaria esculenta* (large volumes, low value), and the red alga *Palmaria palmata* (small volumes, high value) will be studied as promising species for industrial cultivation in Norway.

Topics for 5-7 master thesis in MACROSEA:

- Develop cultivation and quality parameters
- Develop quality indicators (genetic markers)
- Characterize importance of light
- Characterize N metabolism and photosynthetic capabilities
- Characterize NH4 uptake (IMTA)
- Measure quality parameters for seedlings with different latitudinal origin (Western, Mid and Northern Norway)
- Perform a regional study of growth and quality together in Western, Mid and Northern Norway

Contact: Project leader Aleksander Handå.
Aleksander.handa@sintef.no - mob. 91577232

Suitable for:	Marine Biology, Aquaculture, Photobiology,Cell biology,Genetics

Main supervisor:	Professor Kjell Inge Reitan (NTNU) Kjell.i.reitan@ntnu.no
Co supervisors	Seniorforsker Aleksander Handå (SINTEF) Forsker Kari Attramadal (SINTEF)
Preliminary title (max 20 word):	**Cultivation of Polychaeta for waste treatment, improved resource utilisation and production of raw material for feed in aquaculture**: **Thesis I:** Growth and reproduction of polychaetes under intensive culture conditions **Thesis II:** Metabolism and nutritional value of polychaetes under intensive culture conditions
Short description of the project (max 300 word):	**Motivation:** The Norwegian salmon production is estimated to increase from 1.2 to 3 million tons, with a use of 3.6 million tons feed per year in 2030. To realize this growth, there are at least two major challenges that must be solved; *environmental impact and feed supply.* There is accordingly a need to develop strategies to a) decrease waste effluents and bio-deposit impacts from aquaculture and b) replace feed ingredients with proteins and lipids from new resources outside the human food chain. Polychaetes of the *Nereis* family seem promising for both. **Polychaeta** are filter- and detritus feeding marine worms that have several industrial applications. Polychaete biomass is rich in marine fatty acids and a valuable raw material for feed. In addition, the polychaetes grow fast at optimal conditions. The ability to convert organic waste to high quality biomass is useful in a range of issues related to aquaculture. E.g. polychaete cultivation combines waste treatment with improved resource utilisation and production of raw materials that are in high demand. **Master thesis** This will be the first studies of intensive polychaete production as a method to treat fish farm wastes in Norway. The main focus will be on production biology of polychaetes under intensive culture conditions to increase our understanding of: • Growth and reproduction (Thesis I) • Metabolism and biochemical composition (Thesis I and II) • Nutrient budgets (C,N,P) (Thesis II) • The potential of polychaetes to recycle wastes from aquaculture (Thesis I and II) ***Research team:*** *You will be part of a new enthusiastic research team on polychaetes. The team consists of researchers and engineers at NTNU Biology and SINTEF Fisheries and Aquaculture. You will contribute to the establishment of a knowledge platform for decision support to stakeholders considering using polychaete cultures to recycle waste effluents from various types of aquaculture systems.*

Suitable for (main profiles):	Biology/aquaculture
Hovedveileder: Main supervisor:	Professor Kjell Inge Reitan, NTNU Kjell.i.reitan@ntnu.no
Biveileder(e): Co supervisor	Research Scientist Matilde S. Chauton, SINTEF Research Scientist Kari J. K. Attramadal, SINTEF
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Nitrogen-rich waste water from fish farming as a resource in cultivation of microalgae**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	The outlet water from the fish farming tanks contains a lot of nitrogen, in some cases at levels that are relevant as growth fertilizer for successful cultivation of microalgae. This nitrogen concentration of the outlet water may give a microalgae biomass of 10^6 -10^7 cells/ml (depending on the algae species). Most of the nitrogen originate from the excretion of the fish and microbial degradation of fish feed. The nitrogen in the water is available as ammonia, nitrite and nitrate. Ammonia (NH_3) is toxic to fish, and must therefore be removed from the fish tank systems, and is a waste product in the fish farming units. The microalgae need nitrogen, mainly in the form of nitrate, nitrite or ammonium (NH_4^+). The reuse of the N-rich water from the fish tanks is interesting as a resource in the microalgae production, but we need to have more knowledge about the amount of N that are in water system and what forms it exists in. In this task, we will pick up the water with a fish breeder, and analyze and analyze the main nutrient nitrogen compounds as well as phosphorous, and use the water in cultivation trials with 2-3 different algae. The algaewill be selected among candidates with interesting chemical profile and uses for biomass production. Timescale: Spring 2016-Autumn 2017
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Biology, Biotechnology, Marine Coastal Development

Hovedveileder: Main supervisor:	Prof. Kjell Inge Reitan
Biveileder(e): Co supervisor	Forskere Andreas Hagemann og Matilde S. Chauton, SINTEF
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Rhodomonas sp. og N-omsetning: Optimalisering av dyrkingsmedium i produksjonssammenheng**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Mikroalgen Rhodomonas sp. er interessant som fôr i produksjon av hoppekreps, bl.a fordi den har en god fettsyreprofil og balansert proteininnhold. Rhodomonas og andre svelgflagellater har dessuten spesielle pigmenter, fykobiliner, som er rike på N. Den kjemiske profilen varierer imidlertid med dyrkingsbetingelser og varighet på produksjonsperioden, og dette er en utfordring for å etablere stabil produksjon av algebiomasse med forutsigbar kjemisk profil. Et annet viktig element i storskalaproduksjon av mikroalger er kostnadene ved tilførsel av makronæringsstoffer (N, P el silikat) eller mikronæringsstoffer (spormetaller, vitaminer) og det er veldig relevant å vite mer om hvordan man kan utnytte disse komponentene bedre i dyrkingen. I denne oppgaven vil det derfor være fokus på å dyrke Rhodomonas under ulike vekstbetingelser med fokus på N-omsetningen og biomasseutbytte. Det vil også bli lagt vekt på å se hvor effektivt komponentene i næringsmediet utnyttes, for å foreta en optimalisering av næringsmedium for produksjon av Rhodomonas sp. Denne oppgaven vil knyttes til arbeidet som foregår hos C-feed, et nyetablert firma som produserer og selger copepode-egg.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	

Hovedveileder: Main supervisor:	Prof. Kjell Inge Reitan
Biveileder(e): Co supervisor	Forskere Matilde S. Chauton og Kari J. K. Attramadal, SINTEF
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Bruk av nitrogenrikt vann fra fiskeoppdrett til produksjon av mikroalger**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Vann fra fiskeoppdrettskar inneholder mye nitrogen, i noen tilfeller så mye at det er på nivå med det som tilsettes i standard algedyrkingsmedium og nok til å produsere 10^6-10^7 celler/ml (avhengig av hvilken alge). Mye av nitrogenet stammer fra ekskresjon og urea-produksjon hos fisken og foreligger som ammoniakk, nitritt og nitrat i vannet. Ammoniakk (NH3) er giftig for fisken og man må derfor fjerne det. Mikroalger trenger N, hovedsakelig i form av nitritt eller ammonium (NH4+). Gjenbruk av N-rikt vann fra fiskeanlegg er interessant i mikroalgeproduksjon, men vi må ha mer kunnskap om hvor mye N som er i omløp i vannet og hvilke former det foreligger i. I denne oppgaven vil vi hente vann hos en fiskeoppdretter og analysere og analysere hovednæringsstoffene N og P, og så bruke det i dyrkingsforsøk med 2-3 forskjellige alger. Algene velges ut fra sin kjemiske profil og anvendelsesområder for biomassen.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	

Hovedveileder: Main supervisor:	Ann- Kristin Tveten
Biveileder(e): Co supervisor	Helene Fjørtoft, Anne Stene
Arbeidstittel på oppgaven (max 20 word): Preliminary title:	**Sea lice (L. salmonis) microbiota and their role in dispersal of pathogens**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	The coastal region of north west Norway have high densities of farmed fish, in addition to several different stocks of wild salmonid species. Increased production have the potential risk of increasing the number and dispersal of pathogenic like virus, parasites and bacteria. Interactions of pathogens between farmed and wild salmonids have been identified. Sea lice is a major problem in both wild and farmed salmonids in areas of high aquaculture activity. Sea lice can potentially delay the national goals of increased growth in the fish farming industry. The microbiota may vary geographically and may play a role in dispersal of the multiple pathogens. Known diseases caused by pathogens are; viruses: ILA, IPN, PD, VHS, HSMB, CMS, bacteria; vibriose, BKD, Furunkulose, and Yersiniose- and parasites; Paramoeba perurans (AGD) and Parvicapsul. In this project we would like to: • Map the microflora of sea lice to determine the sea lice role as a vector for the pathogen. • Establish methods for detection of a selection of the pathogens and determine their prevalence in sea lice. • If possible, study geographical variations We would like to focus on the interactions between farmed and wild salmon fish. We would like to focus on the intersection between the environment, the salmonid fish and pathogen in defined areas. The fish will be grouped in farmed salmon, rainbow trout, escaped farmed salmon (time in the sea after the escapes are determined by external confirmation), wild salmon. Collection of wild salmonid fish are in cooperation with the Institute of marine research and NINA and the local fishermen with wedge-net license. The project is a part of the PhD for Helene Fjørtoft, and financed through RFF and Miljøskapings fondet
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Marine biology - biotechnology - molecular biology - microbiology

Hovedveileder: Main supervisor:	Prof. Kjell Inge Reitan
Biveileder(e): Co supervisor	Forskere Matilde S. Chauton, SINTEF
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Upscaling microalgae biomass production and post-harvesting processing to extract high-value compounds**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	We are looking for new resources to meet the demands for protein and essential lipids in the near future. Microalgae are a promising resource for applications such as feed production or extraction of high-value compounds such as lipids. Upscaled biomass production is a focus area, and we must solve challenges both upstream in the production end and downstream on the harvest and processing end. This work will focus on the production of microalgae biomass in a pilot system, a 250 L photobioreactor, and harvesting e.g. by centrifugation. After harvesting the biomass must be stabilized e.g. by lyophilization before it is ready for processing. Here the focus will be on obtaining protein-rich bulk material and high-value lipids such as EPA/DHA, and analysis of the fractions.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	

Hovedveileder: Main supervisor:	Prof. Kjell Inge Reitan
Biveileder(e): Co supervisor	Forsker Matilde S. Chauton, SINTEF
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Høyverdi-komponenter fra marine mikroalger: Protein-og lipidinnhold utvalgte mikroalger under varierende dyrkingsbetingelser.**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Mikroalger er en fremtidig kilde til proteiner og fett, inkludert høyverdi-komponenter EPA/DHA som brukes i helsekost og fôr. Mikroalger har et gunstig proteininnhold, og mange har også et høyt innhold av essensielle fettsyrer. Innholdet varierer imidlertid fra art til art, og med dyrkingsbetingelser. Vi trenger mer kunnskap om proteininnhold og hvilke alger som inneholder mest EPA/DHA, og under hvilke betingelser man får størst utbytte av disse komponentene. Oppgaven består i å dyrke 3-4 ulike mikroalger under forskjellige betingelser og analysere biomasseutbytte, protein- og lipidinnhold og aminosyre/fettsyreprofiler. Relevante dyrkingsbetingelser kan være variasjoner i lyskvalitet (LED vs konvensjonelt lys), temperatur og variasjoner i næringstilgang som f.eks nitrogenbegrensning.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	