Kjeldsen group - Massespektrometri af proteiner: Fra grundforskning til proteomics

Forskningsleder Frank Kjeldsen

Gruppens kerneforskningsområder

Forskningen i Kjeldsen Gruppen omhandler proteinkarakterisering ved hjælp af massespektrometri. Nedenstående ses fire fokusområder:

1) Kemisk stabilisering af labile post-translationelle modifikationer. I dette område undersøger vi specielt designede metalkomplekses effekt på kemiske bindinger i labile modifikation fundet på proteiner. Målet er at udvikle metoder som kan forbedre denne analyse.

2) Fotokemisk katalyse af proteiner. I dette område undersøge vi om en række fotoaktive metalioner kan anvendes til at skabe modifikationer i proteiner som har farmaceutisk relevans.

3) Analyse og fortolkning af ikke trivielle ioner i massespektrometri. Kraftig automatisering af fortolkning af massespektre har præget feltet det seneste årti. Det er på trods af at kun ca.50% af fragment-ioner i massespektre fra peptider/proteiner kan tilordnes. Det betyder tab af analytisk information. Gruppen arbejder ihærdigt på udvikling af algoritmer til at opnå bedre fortolkning.

4) Metal nanopartikler bliver anvendt i stor udstrækning i dag til produktion og emballage. Eksponering er uundgåelig og gruppen studerer med cellekulturer disse forhold ved at anvende kvantitativ massespektrometri og andre analytiske metoder.

Er du interesseret i at skrive projekt i gruppen, så kontakt:
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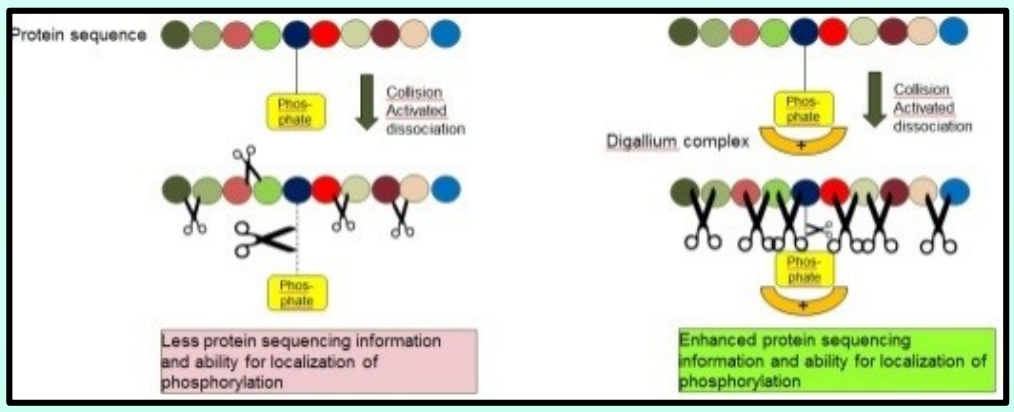
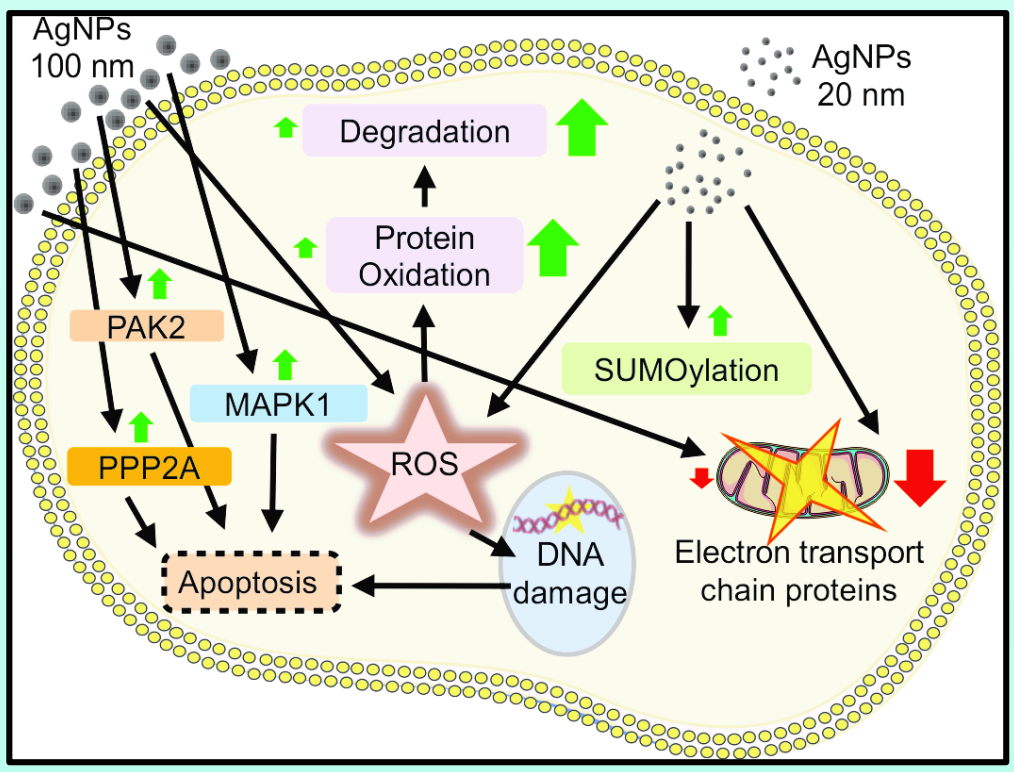
Tlf: 65502439





Projekter	Beskrivelse
Dimetal Phosphate Ester Stabilization (DIMPES).	Application of novel chemistries in proteomics is an exciting field that certainly has the potential to solve many current challenges. While sequencing of non-modified peptide ions with mass spectrometry is becoming routine, phosphopeptide analysis remains a challenge. The reason is the significant instability of the phosphate ester bond, which result in facile phosphate ester group detachment. A novel invention allow for increased phosphate ester bond stabilization in peptide ions achieved by conjugation of the phosphate motif with a gallium complex. We investigate its full analytical potential to expand our knowledge of the phosphoproteome of cells.
Characterizing nanoparticle protein corona using tandem mass spectrometry	The project is about characterization of proteins attached to nanoparticles. To this use the student will apply advanced mass spectrometric techniques. The dynamics of proteins attached to metal nanoparticles is essential for the understanding of how metal nanoparticles enter the living cell. The project could also include working with cell cultures exposed to nanoparticles. The student´s work will be part of and in conjunction with similar activities of other group members.
Investigation of a fundament novel route to form C-terminally amidate peptidens	An important characteristic of more than 50% of all biologically active peptides in humans is that they are C-terminally amidated (-CO-NH2). In this project you will investigate a fundament novel route to form C-terminally amidate peptides. This method is based on a strong and specific binding of the uranyl ion (UO_2^{2+}) to phosphates in proteins and peptides, which when followed by UV irradiation induces cleavage specifically and efficiently at the position of the phosphorylated site. Notably, the uranyl photo cleavage of peptides and proteins predominantly results in C-terminal amidated cleavage products.