

*The Chemistry Department is pleased to present*



# *Albert J. R. Heck*

Utrecht University  
Netherlands Proteomics Center

*“Complementary mass spectrometry–based methods for probing protein assemblies”*

## **ANALYTICAL MELOCHE SEMINAR**

Mass Spectrometry based proteomics has played a pivotal role in revealing the plethora of protein interactions that take place inside a cell, wherein proteins form protein assemblies and/or signalling networks. Especially using affinity purification of a tagged proteins followed by mass spectrometric analysis of its binding partners a wealth of data has been gathered revealing the all-embracing protein networks present in cells. Following the charting of all these interactions, a next step will be to now gather more in-depth structural and functional information on these individual protein assemblies. This may come from in-depth high-resolution structural models, as well as detailed information on how they function and dynamically evolve during cellular perturbations. Mass spectrometry may also contribute to this next level of protein interaction analysis although it does require partly different and novel approaches. To contribute to this emerging new area in proteomics, our group is developing new methods using native mass spectrometry and cross-linking mass spectrometry with the aim to bridge the gap between interaction proteomics and structural biology. These new innovations and applications of them in interaction proteomics will be central in this presentation.

**Monday  
April 17**

**3:30 pm  
1315  
Chemistry**