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Thursday, March 21, Invited lecture

L5

STRUCTURAL BIOLOGY AT THE DIFFRACTION LIMITED SYNCHROTRON SOURCE MAX IV

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The MAX IV Laboratory is a new synchrotron in Lund, Sweden which operates two storage rings and a short-pulse facility. The MAX IV 3 GeV storage ring is the first synchrotron ring with a multi-bend achromat design providing higher photon beam brilliance and coherence.

A number of beamlines interesting for Structural Biologists is in operation or under development at this facility. Amongst these beamlines are the protein crystallography beamline BioMAX and MicroMAX, the small angle scattering beamline CoSAXS and the X-ray absorption spectroscopy beamline Balder. There are also opportunities for using imaging techniques such as m-XRF and soft-Xray STXM. The beamlines will be presented with a slight emphasis on the protein diffraction beamlines.

Friday, March 22, Session II

L6

COMPARATIVE STRUCTURAL ANALYSIS OF LECTIN FAMILY FROM *PHOTORHABDUS SPP*

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Photorhabdus is a genus of gram-negative bioluminescent bacteria living in a symbiosis with *Heterorhabditis* nematodes forming a highly entomopathogenic complex. Such a complex is used in agriculture as a nature-based insecticide. However, some members of this genus are human pathogens as well. Understanding the mechanisms that determine interaction between *Photorhabdus* and its symbionts/hosts could be highly beneficial not only in biotechnologies but also in clinical reasearch and drug development.

Cell-cell interactions are frequently mediated by sugar-binding proteins – lectins. Based on the genome analysis, there has been identified potential lectins in number of *Photorhabdus* species. Recently, we examind two of them in further details, namely PLL from *P. laumondii* (formerly *P. luminescens*) [1] and PHL from *P. asymbiotica* [2, 3]. Both lectins share the basic structural features, e.g. -barrel fold with seven blades or presence of multiple binding sites per monomer. However, despite rather high sequence similarity, some non-marginal differences were detected: oligomeric state, binding site preferences and organization. This lead us to investigate this lectin family in further details.

We analyzed several homologues of proteins PLL and PHL from *Photorhabdus spp.* We managed to prepare some of them in recombinant form and perform basic analysis, as well as solve structure of these proteins in free form and in complexes with naturally occuring saccharide lig-