

[Print this Page for Your Records](#)[Close Window](#)**Session Title:** Membrane Physical Chemistry II**Presentation Number:** 1121-Pos**Abstract Title:** A new approach for studying chain order and phase coexistence in model membranes using grazing incidence x-ray scattering**Location:** Halls A/B/C/D**Topic:** 3A Membrane Physical Chemistry**Author Block:** **Thalia T. Mills**¹, Stephanie Tristram-Nagle², Frederick A. Heberle¹, Nelson F. Morales¹, Jing Wu¹, Jiang Zhao¹, Norbert Kucerka³, Detlef M. Smilgies⁴, John F. Nagle², Gerald W. Feigenson¹.
¹Cornell University, Ithaca, NY, USA, ²Carnegie Mellon University, Pittsburgh, PA, USA, ³Chalk River Laboratories, Chalk River, ON, Canada, ⁴Cornell High Energy Synchrotron Source, Ithaca, NY, USA.**Page Number in Print** 237a**Abstract Issue:**

We have used grazing incidence wide-angle x-ray scattering (GIWAXS) on oriented lipid multilayers to measure chain order and to examine liquid-liquid coexistence in the system DOPC/DPPC/cholesterol, a model for the outer leaflet of the cell plasma membrane. The addition of cholesterol to either DOPC or DPPC greatly changes the GIWAXS pattern, which can be attributed to a change in ordering of the acyl chains. By using Maier-Saupe theory to describe the chain orientational distribution, we can fit our x-ray data to extract the average chain molecular order parameter, S_{mol} . While this type of analysis has been well-used for liquid crystals, to our knowledge, it has not been applied to x-ray data for model membranes. For these mixtures, the values of S_{mol} determined by GIWAXS are consistent with earlier NMR data. In addition to examining the effect of cholesterol on DOPC and DPPC chain order, we have measured GIWAXS for ternary mixtures where fluorescence microscopy indicates the coexistence of liquid-disordered (Ld) and liquid-ordered (Lo) phases. In order to fit to the GIWAXS data for these mixtures, we require two values of S_{mol} , one for the Ld phase and one for the Lo phase. This approach provides a new method for examining chain order and phase coexistence in model membranes without the need to add a perturbing probe.

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