

Gaetano T. Montelione
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Gaetano Montelione is an expert and innovator in the fields of structural biology and protein NMR. Montelione is currently endowed chair in structural bioinformatics and professor of chemistry at the Rensselaer Polytechnic Institute. He was born in Bronx, New York, and graduated from Half Hollow Hills High School, Dix Hills NY, and from Cornell University, Ithaca NY, B.S. *summa cum laude*. Montelione carried out Ph.D. studies jointly with Profs. Harold Scheraga at Cornell University and Kurt Wüthrich at the ETH, Zurich, and postdoctoral studies with Prof. G. Wagner at Univ of Michigan. He was appointed as Assistant Professor at Rutgers, The State University of New Jersey in 1989, and eventually promoted to Distinguished Professor of Molecular Biology and Biochemistry. In 2010 he was appointed as the inaugural Jerome and Lorraine Aresty Endowed Chair. For many years Montelione served as Director of the NIH Northeast Structural Genomics Consortium (NESG) (2000 – 2016) at Rutgers University, which developed a successful high-throughput pipeline for protein sample and 3D structure production. More than 1,300 structures were determined by the NESG team, lead by Montelione, using crystallography and NMR. Most of these were the first structures determined from large protein families, providing the basis for modeling of hundreds of thousands of homologous proteins. With Prof. G. Wagner, Montelione carried out pioneering work on triple-resonance NMR pulse sequence development. Montelione has made key contributions in computational NMR methods development, including the development of software for automated analysis of protein resonance assignments, automated analysis of 3D structures, and for protein NMR model quality assessment. The group's biomedical focus areas include structure-function studies of proteins and complexes involved in cancer biology and influenza virus infection. Work with R. Krug on the influenza A non-structural protein 1 (NS1) has provided the basis for creation of attenuated virus vaccines. The lab's current methods-development focus involves combining evolutionary sequence co-variance restraints from bioinformatics together with sparse NMR data to determine the 3D structures of challenging proteins, including membrane proteins associated with cancer biology. As an advisor to the world-wide Protein Data Bank, Montelione leads efforts to standardize methods for protein NMR model validation. Montelione is also a member of several academic and commercial structural biology advisory groups, co-chair of the international wwPDB Task Force on NMR Structure Validation, member of the Organizing Committee for the Critical Assessment of Protein Structure Prediction (CASP), and Foreign Expert Advisor in Protein Engineering to the Key Laboratory of Biotechnology at Jiangnan University, Wuxi, China.