Molecular mechanisms of ribonucleoproteins formed by long non-coding RNAs and chromatin remodeling enzymes

M. Colombo, T. Uroda, I. Garcia Ferrer, A. Ponce Salvatierra, O. Pessey, F. Chandler, I. Chillon, M. Marcia
EMBL Grenoble, 71 Avenue des Martyrs, 38042 Grenoble Cedex 09, **mmarcia@embl.fr**

Ribonucleoproteins formed by long non-coding RNAs (lncRNAs) regulate key stages of gene expression and are implicated in severe diseases, like cancer and neural disorders. Yet, lncRNAs are the least characterized RNA class in terms of structure and function. Principles of lncRNA-protein recognition are also poorly characterized, partly because lncRNA-binding proteins, like *Polycomb* group chromatin remodelers (PcGs), do not possess canonical RNA-binding domains. Obtaining structural insights into lncRNA-protein complexes is needed to elucidate their molecular mechanism, but the massive size of lncRNAs and the complexity of their protein interaction network makes it challenging to determine their 3D structure.

Recent advances in cryo-electron microscopy revolutionized the types of targets that can now be structurally studied at high resolution. Synergistically with *in vitro* biophysical studies (i.e. crosslinking, mass spectrometry, and chemogenetic mapping), *in vivo* functional approaches and bioinformatic analyses, cryo-electron microscopy will thus serve as a leading technique in our lab to obtain unprecedented molecular insights into lncRNA-protein complexes.