



A/Professor Hans Elmlund & A/Professor Dominika Elmlund

Biomedicine Discovery Fellows

Lab Heads, Structure and Dynamics of
Macromolecules by Cryo-EM Laboratory



Monash Biomedicine Discovery Institute
Cancer Program

OTHER PROGRAM AFFILIATIONS



Development and Stem Cells



Infection and Immunity

EMAIL hans.elmlund@monash.edu, dominika.elmlund@monash.edu

TELEPHONE +61 3 9905 0002

WEB simplecryoem.com

Our lab uses cryogenic electron microscopy (cryo-EM) to elucidate the structure and dynamics of large macromolecules involved in processes of fundamental biological and medical importance. In addition, we develop new computational methods for solving the most challenging problems in cryo-EM image processing and integrative structural biology. Biological topics include cancer biology, transcription regulation & mRNA export. Cryo-EM images will be acquired at the newly established Clive & Vera Ramaciotti Centre for Structural Cryo-EM, housing the world-class FEI Titan KRIOS instrument.

Research Projects

1. Cryo-EM of the housekeeping transcription initiation complex
2. Molecular basis of protein import into the mitochondrion using cryo-EM (Collaboration with Professor Trevor Lithgow)
3. New Computational Methods for Cryo-EM Image Processing & Integrative Structural Biology



Titan Krios electron microscope and a model of a transcription pre-initiation complex.

Selected significant publications:

1. **Elmlund D, Elmlund H.** 2015. Cryogenic electron microscopy and single-particle analysis. *Annu Rev Biochem.* 84:499-517.
2. Park J*, **Elmlund H***, Ercius P* et al. 2015. 3D structure of individual nanocrystals in solution by electron microscopy. *Science.* 349 (6245): 290-5. ***equal contribution**
3. Murakami K*, **Elmlund H***, et al. 2013. Architecture of an RNA polymerase II transcription pre-initiation complex. *Science.* 342(6159):1238724. ***equal contribution**
4. **Elmlund H, Elmlund D,** Bengio S. 2013. PRIME: probabilistic initial 3D model generation for single-particle cryo-electron microscopy. *Structure.* 21(8): 1299-306.
5. **Elmlund D, Elmlund H.** 2012. SIMPLE: Software for ab initio reconstruction of heterogeneous single-particles. *J Struct Biol.* 180(3):420-7.
6. **Elmlund D,** Davis R, **Elmlund H.** 2010. Ab initio structure determination from electron microscopic images of single molecules coexisting in different functional states. *Structure.* 18(3):354-65.
7. **Elmlund D, Elmlund H.** 2009. High-resolution single-particle orientation refinement based on spectrally self-adapting common lines. *J Struct Biol.* 167(1):83-94.