

Marlene Oeffinger is a mid-career investigator and Associate Research Professor at the IRCM in Montreal, where her RNP Biochemistry group is investigating the dynamics of RNA maturation pathways using proteomic and biochemical approaches. As post-doctoral fellow in Mike Rout's lab at Rockefeller University, she was trained in mass spectrometry by Brian Chait and, during that time, developed a more efficient single-step affinity purification mass spectrometry approach that allows the detection of transient interaction on dynamic macromolecular complexes. She has since continued to develop and apply MS approaches, including a targeted crosslinking-MS approach that allows to capture the dynamic changes of vicinal interactomes of bait proteins. She is strongly involved in making proteomic approaches more accessible, to develop proteomic strategies for her collaborators, and apply mass spectrometry to a broader variety of species, such as the red algae *Cyanidioschyzon merolae*, and, most recently, the Archaea *Haloferax volcanii* in a collaborative endeavour to characterize its pre-ribosomal proteome. During her time as independent investigator she has received a CIHR New Investigator Award, and FRQ-S Chercheur Boursiers Junior 1 and 2 Awards.



Publications

1. Scott DD, Trahan C, Zindy PJ, Delubac M, Aguilar LC, Van Nostrand EL, Adivarahan S, Wei KE, Yeo GW, Zenklusen D and **Oeffinger M**. Nol12 is a multifunctional RNA binding protein at the nexus of RNA and DNA metabolism. *Nucl. Acids Res.* **2017**. Dec 1;45(21):12509-12528.
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3. Trahan C and **Oeffinger M**. A simple targeted crosslinking-mass spectrometry approach to determine spatial organization and near-neighbors within macromolecular complexes. *Nucl. Acids Res.* **2016** Feb; 44(3): 1354-69.
4. **Oeffinger M**. Two Steps Forward – One Step Back: Advances in Affinity Purification Mass spectrometry of Macromolecular Complexes. *Proteomics.* **2012** May;12(10):1591-608.
5. **Oeffinger M**, Wei KE, Rogers R, DeGrasse JA, Chait BT, Aitchison JD and Rout MP. Comprehensive analysis of diverse ribonucleoprotein complexes. *Nature Methods.* **2007** Nov; 4(11): 951-6.

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