Dear Faculty, Postdocs, Students, and Friends:

You are cordially invited to attend a special seminar presented by the Institute for Integrative Genome Biology

UC RIVERSIDE | UNIVERSITY OF CALIFORNIA Institute for Integrative Genome Biology

Dr. Joanna Kufel

Institute of Genetics and Biotechnology

University of Warsaw

TITLE: "How non-canonical translation expands yeast mitochondrial proteome"

DATE: Friday, March 18, 2022
TIME: 12:00 pm PST

MEETING ID: 924 2795 4599 PASSCODE: 777538

Host: Dr. Xuemei Chen

Abstract: One way of boosting the regulatory potential and complexity of the cellular proteome is by means of alternative processes, including noncanonical translation. In particular, utilization of non-standard initiation start sites results in the expression extended/truncated proteoforms. The resulting alternative proteome often confers unique properties. In particular, initiation of translation at upstream in-frame cognate non-AUG codons leads to the synthesis of N-terminally extended isoforms, some of which gain a mitochondrial targeting signal (MTS) and are localized to mitochondria. These proteins often have a potential dual localization, with the major form residing in the nucleus or the cytoplasm and the alternative isoform targeted to mitochondria, and represent a so-called "dark mitoproteome". Mitochondrial targeting of some of these proteins may require upstream MTSs to facilitate co-translational protein transport to mitochondria by promoting localized translation on the mitochondrial membrane. Several of newly identified mitochondria-localized proteins are associated with RNA-related processes, namely transcription, RNA processing and decay, and ribosome biogenesis or function. In most cases, it is not clear how these additional mitochondrial factors contribute to the activity of this organelle.