A mature oocyte contains the full complement of maternal proteins and mRNAs required for fertilization and subsequent early embryonic development. Numerous studies have pointed to conservation of molecular functions by multitude of transcripts in evolutionary remote oocytes of mouse, bovids, *Xenopus laevis* and *Ciona intestinalis*. However, insufficient information is available on the conservation at the proteome level, even though proteome profiling data is found for a few model and non-model organisms. Proteomic profiling offers a novel insight into different aspects of oocyte function, due to the occurrence of translational silent mRNAs that are activated only after fertilization.

Here, we expand our knowledge on primordial attributes of oogenesis by comparing the proteomes of mature ovulated oocytes of the Cnidaria basal eumetazoan, the starlet sea anemone *Nematostella vectensis*, with published data of mammalian mouse mature oocytes. We identified 1,837 proteins in *N. vectensis* oocytes, including many known oocyte- and germ-cell-specific markers and proteins associated with RNPs. Our findings suggest highly conserved enriched functional pathways between *N. vectensis* and the mouse, including the translation machinery, metabolic pathways, and oocyte specific proteins. Vitellogenin, a major component of egg yolk proteins, which is not found in mammalian oocytes, constitutes 67% of *N. vectensis* oocytes and is putatively synthesized within the oocyte, and transported from adjacent cells. This study provides the first catalog of cnidarian oocyte proteins, revealing highly conserved ancient organization of life processes. It affords an insight into a basal oocyte template of eumetazoa that remained conserved for over 500 million years of evolution.