Knowledge of all the types of molecules that are produced in cells as they establish different tissues and organs is key to understanding normal development and design efficient therapeutics. Even today, after the sequencing of entire genomes, there is limited information on how molecules downstream, such as proteins and metabolites, contribute to cell processes. The limitation has been a lack of sufficiently sensitive mass spectrometry technologies that can measure these biomolecules with scalability in space and time and compatibility for live development, a prerequisite for functional biology. In this presentation, we will discuss technological developments from our laboratory to transform mass spectrometry proteomics and metabolomics to single cells. We used these technologies to determine the proteomic and metabolomic profile of identified cells in live Xenopus laevis frog embryos and neurons in mouse brain tissues. Molecular measurements with separation using capillary electrophoresis and detection by (trapped ion mobility) time-of-flight or orbitrap mass spectrometry revealed quantitative molecular differences between cells of different phenotypes. Through follow-up functional experiments, we discovered molecules capable of altering normal cell fate decisions in the chordate embryo. The technology was scalable to smaller cells, including electrophysiologically identified neurons in the mouse brain. Quantification of ~300–800 different proteins revealed reproducible proteomic differences between dopaminergic, serotonergic, and parvalbumin interneurons. Microprobe capillary electrophoresis mass spectrometry expands the molecular toolbox of cell biology and neuroscience.