X-ray Fluorescence Microscopy (XFM) is a powerful method for imaging trace element concentration, distribution, and speciation in biological cells and tissues at the nanoscale. However, one limitation of XFM for imaging biological systems is detecting the trace-element distribution in the context of subcellular organelles and individual proteins. For visible light microscopy, the most ubiquitous method for imaging individual proteins within the context of a living cell is the use of intrinsically fluorescent proteins, such as GFP and YFP, that are co-expressed as a fusion tag along with the protein of interest. However, visualization of these tags is limited by the wavelengths of visible light except by applying specialized super resolution approaches. Here, we are developing lanthanide-binding tags (LBTs), which are GFP-like analogs of minimal size for XFM. LBTs are short peptide sequences comprised of 15-20 naturally occurring amino acids that bind trivalent lanthanide ions with a nano-molar affinity. Due to their relatively small size, LBTs are easily integrated into the target protein sequence and have little or no effect on the structure or function of the resulting fusion protein. For this study, LBTs were co-expressed with either an outer membrane protein (OmpA) or a cytosolic protein (ubiquitin) in *Escherichia coli*. The cells were exposed to either Eu$^{3+}$ or Er$^{3+}$ and were imaged using XFM. Europium and Erbium were chosen because their L$_3$ emission edge, $L_{\alpha1}$ = 5848 eV for europium and $L_{\alpha1}$ = 6948 eV for erbium, has the least overlap with other exogenous elements in the cell. XFM results show a uniform Eu distribution within cells containing the ubiquitin-LBT, and a surface-localized Eu distribution in cells containing the OmpA-LBT. Further work is ongoing to quantify the LBT concentrations and binding specificity within the cells. The initial results are promising and show that the LBTs can enable better than 10 nm resolution imaging of individual proteins in cells and tissues while simultaneously obtaining trace-element distribution and speciation throughout the cell.