Pathologists histopathological evaluation is the gold standard for cancer diagnostics, but there are situations in which histology does not allow for a definitive and accurate diagnosis. Due to the limitation of the Hematoxylin and Eosin stain, additional staining by immunofluorescence or immunohistochemistry has often been explored and allowed advances in cancer classification, treatment, and associated companion diagnostics. While recent advances in multiplexed imaging technologies would significantly improve understanding of cancer, they have distinct disadvantages that prevent their integration into routine clinical histopathology workflows, mainly due to costly, labor-intensive and time-consuming tasks for image data acquisition as well as lack of quantitative image analytics. To facilitate compatibility with clinical histopathology, we have developed a novel deep learning method to efficiently infer the distribution of specific protein abundance from tissue and cell morphologies in histopathological images. First, the proposed models could potentially provide appropriate augmented digital interpretation based on H&E by efficiently substituting for multiplexed methods so pathologists can easily detect the cancerous cells in a less time-consuming manner and improve their efficiency and accuracy. Second, we could use this framework as development of improved and standardized method for validating antibody specificity and selectivity.