



# Novel bioinformatic identification of differentially expressed tissue-specific and cancer-related proteins from the Human Protein Atlas for biomarker discovery

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**ABSTRACT.** Identification of cancer-associated and tissue-specific proteins is important for research on carcinogenesis mechanisms and biomarker discovery. Here we performed a new strategy to identify candidate cancer proteins by mining immunohistochemistry protein profiles. Proteins with quantitative values from 14 normal tissues and their corresponding cancer tissues were compared and analyzed using bioinformatics. The final results included identification of tissue-specific proteins and differentially expressed proteins in different cancer types that are primarily involved in energy metabolism and cell invasion. From the tissue-specific proteins, secreted and membrane proteins were further screened and functionally clustered. These primarily belonged to the gene families of endogenous ligands, cluster of differentiation molecules, and solute carriers, and were mainly involved in the processes of cell motility, hormone metabolism, adhesion, and transport. Further studies are warranted to validate the candidates identified herein and substantiate the suggested enriched functions. The results

from this study might provide a reliable resource to study underlying carcinogenesis mechanisms and discover potential cancer targets for the development of therapeutic targets and of early diagnosis and disease response markers.

**Key words:** Cancer; Bioinformatics; Immunohistochemistry; Biomarkers