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Expression of novel cancer biomarkers in ovarian cancer tissues and cells

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APs are involved in the continuous assembly and disassembly of tubulin into microtubules and are critical for function of all cells. Cancer cells cannot proliferate, transport intracellular molecules or change their shape without formation and remodeling of microtubules that make up the mitotic spindle. Microtubules/MAPs have become targets for cancer chemotherapy; however, since tubulin/microtubules are ubiquitous, taxol-like drugs that target MAPs, have become candidates for tailored targeting. As is known, taxol-like drugs have many side effects and a poor therapeutic index. Thus, unique MAPs are a better choice as anti-cancer targets. We have discovered a novel MAP1A-like protein in OVCA and other cancers that may be useful in this regard. Our original studies arose from the observation that estrogen mustard (EM) binds to MAP1A. In studying this relationship in OVCA, we found that the precipitated MAP protein has a molecular size of 80kDa (hence the name p80) instead of 350kDa that has been reported for the wild type MAP1A. Tissue Specificity includes: MAP1A is expressed only in the brain. p80 is present in many cancers thus far studied (cervical, uterine, breast, endometrial, and leukemia), but not in glioblastoma. This adds possible value as a tumor marker to p80's interest as a unique target for cancer chemotherapy.

Biography

Ahmed Fadiel is a Molecular Biologist with extensive experience in Bioinformatics, Clinical Informatics, Genomics, and Proteomics. He has completed two Master degrees (MS, Cytogenetics; MS, Clinical Informatics) and a PhD in Molecular Genetics. He has years of research and teaching experience wherein he elucidates complex biological phenomena such as cancer initiation, progression and Fetal Growth Restriction. In addition, he explores protein folding and ligand-receptor interactions. He has also received extensive training in data analysis, mining, and processing and has gone on to develop numerous databases and whole genome analysis tools as well as participated in the development of several national and international research programs. He is a member of various societies and organization's has won an assortment of national & international awards, sat on various editorial & organizing boards and been the invited speaker at numerous conferences.

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