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according to the nonparametric Wilcoxon–Mann–Whitney test (p < 0.05) with Benjamini and Hochberg adjustment for p-values. Over one third of these compounds were identified only in the malignant ascites. The major significant differences between the malignant and control ascites were observed for fatty acids and their derivatives, which are known to be among the key components of intercellular signaling.

In summary this study extended our knowledge of the protein and metabolomic composition of the ovarian cancer ascites and revealed its specific features which were associated with the function of the ascitic fluid as a medium of interaction between the malignant cells and their environment. 

**Keywords:** Ovarian cancer ascites, Proteomics, Metabolomics.

**TUE-201**

**Quantitative expression analysis of the apoptotic gene BCL2L12 in breast cancer: association with clinical and molecular prognostic parameters**

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**Introduction:** Apoptosis is a highly orchestrated, genetically regulated form of cell death, the impairment of which is crucial in breast cancer (BC) development and progression. BCL2L12, a member of the BCL2 family of apoptosis-related genes, has been studied in various malignancies, revealing its potential role as a tumor biomarker. It has been recently found that BCL2L12 is subjected to alternative splicing, resulting in the generation of 13 alternatively spliced variants. The aim of this study was the quantification of BCL2L12 splice variants 1 and 2 (v.1 and v.2) expression at the mRNA level and the assessment of their biomarker potential in BC.

**Methods:** Total RNA was extracted from 40 pairs of BC and normal tissues. Thereafter, RNA was reverse transcribed into first-strand cDNA, which in turn was used as template in a SYBR Green based Real-Time PCR assay. Relative quantification analysis was conducted using the comparative Ct (2^ΔΔCt) method, and the associations of BCL2L12 variants expression with various clinicopathological parameters, were evaluated by statistical analysis.

**Results:** BCL2L12 v.1 mRNA levels were found to be significantly (p = 0.003) higher in malignant compared to their matched non-cancerous breast tissues. Moreover, BCL2L12 v.1 demonstrated increased expression in premenopausal women (p = 0.026) as well as in those with early TNM stage tumors (p = 0.039). Interestingly, significant BCL2L12 v.1 upregulation (p = 0.044) was observed in triple negative BC. Regarding BCL2L12 v.2, a negative correlation with patients’ age was found (tmin = −0.376; p = 0.017), whereas increased BCL2L12 v.2 expression levels were associated with advanced tumor grade (p = 0.022) and ER-negativity (p = 0.01).

**Conclusion:** Our preliminary results indicate a possible involvement of BCL2L12 v.1 and v.2 in BC progression and suggest their potential as biomarker in this malignancy.

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**Keywords:** Apoptosis, Breast Cancer.

**TUE-203**

**Redox role of STAT3 in cellular survival during oxidative stress**

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Signal Transducer and Activator of Transcription 3 (STAT3) is a transcription factor that is essential for embryogenesis and is involved in the development and maintenance of several tissues,