
Abstract:
We compared the protein expression pattern of triple-negative breast carcinomas (HER2-, ER-, PR-) versus those being positive for HER2 and negative for the hormone receptors (HER2+, ER-, PR-) by 2-D DIGE and mass spectrometry. We obtained differential expression patterns for several glycolytic enzymes (as for example MDH2, PGK1, TKT, Aldolase1), cytokeratins (CK7, 8, 9, 14, 17, 19), further structure proteins (vimentin, fibronectin, L-plastin), for NME1-NME2, lactoferrin, and members of the Annexin family. Western blot analysis and immunohistochemistry were conducted to verify the results. The identified marker proteins may advance a more detailed characterization of triple-negative breast cancers and may contribute to the development of better treatment strategies.