

Using network and functional enrichment clustering analysis to find therapeutic targets for breast cancer: the role of Cyclin-dependent kinase 2

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With population aging rapidly in developed and developing countries, covering medical needs for breast cancer diagnosis and treatments is a priority in Latin America [1].

Statistical methods for gene expression clustering, protein-protein interactions [2], functional enrichment decisions and topological network analysis [3] allowed we inferred, from *MCF-7* breast cancer cell line estrogen deprivation results [4] and the several well-known breast cancer biomarkers, a group of estrogen-responding genes with good significance and impact. These genes are those most significantly responding to estrogen changes with high connectivity degree and good representativity of functional enrichment.

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