

Review of: "Proteomic network analysis of bronchoalveolar lavage fluid in ex-smokers to discover implicated protein targets and novel drug treatments for chronic obstructive pulmonary disease"

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In this study, the authors reanalyzed a previously published proteomic dataset. Using a less stringent criteria, the authors identified 233 differentially expressed proteins in bronchoalveolar lavage fluid from ex-smokers with moderate COPD compared with healthy controls. NIH's Database for Annotation, Visualization and Integrated Discovery (DAVID) and Ingenuity's Ingenuity Pathway Analysis (IPA) were used for network analysis to identify potential crucial hub proteins. The authors then employed an in-house bioanalytic docking (BANDOCK) protocol in Computational Analysis of Novel Drug Opportunities (CANDO) platform to identify FDA approved drugs that could be repurposed to treat COPD, based on their putative interaction with the differentially expressed proteins. Although the methodology used in this study is novel and interesting, the validity of this approach is difficult to evaluate without candidate drug studies in animals or humans.