

Poster 21 Proteomic analyses of human-derived macrophages predict human data for anti-inflammatory drugs

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Inflammatory Bowel Disease (IBD) encompasses chronic inflammatory disorders such as Crohn's disease and ulcerative colitis, characterized by an aberrant immune response. This study investigates the proteomic profiles of human monocyte-derived macrophages (MDMs) under inflammatory conditions and evaluates the effects of anti-inflammatory drugs, including mesalazine, prednisolone, and 6-mercaptopurine. Using proteomic techniques, we analyzed the protein expression patterns in both cell lysates and supernatants following lipopolysaccharide (LPS) stimulation and drug treatment. Our findings reveal distinct differences in protein expression between intracellular and extracellular environments, highlighting the role of macrophages in immune modulation. The study identified key inflammatory biomarkers and elucidated the molecular mechanisms of drug action, demonstrating that changes in the macrophage proteome correspond to physiological conditions in humans. This research underscores the potential of macrophage proteomics as a predictive model for human data, paving the way for personalized therapeutic strategies in IBD treatment.