Background: Murine colon proteome studies have been a subject of interest for many scientists in the last decade, because of its importance in physiological absorptive mechanism and for better elucidating colon disorders. However, most researches focused on malignant colon disorders (colorectal carcinoma) rather than its normal state. We had constructed a comprehensive murine colon catalogue as a guide reference for current and ongoing colon research.

Methods: In-gel trypsin digested mice colon protein extract was extensively analyzed using ESI-IT-TOF-Ms/Ms (Hitachi NanoFrontier LD., Tokyo, Japan). Colon proteome outputs were then ranked according to its relative abundance using NSAF, PAF and emPAI. To profile GO annotation, enrichment, and depletion analysis were performed by BiNGO and ClueGo plug-ins of Cytoscape. For secondary structure prediction of membrane and globular proteins, Gravy index were also calculated to predict globular and membrane proteins. A complete colon proteome catalogue was finally constructed and deposited in a public repository.

Result: Generated mice colon proteome catalogue contained 1226 high confidence protein with at least 2 peptides above homology and identity threshold of MASCOT scoring. Around 80,000 high quality Ms/Ms spectra were captured. Results showed that around 69% of proteins with pI ranged from 4–5 while the rest were extremely acidic or basic proteins (3–12). These candidates fall in different Mw ranged from 4 to 600 KDa. Cellular localization showed that 81.2% of these proteins were globular while 18.1 were membranous. Parsed protein dataset into subcellular localization using BiNGO revealed 64% protein localized in mitochondria, cytoskeleton and endoplasmic reticulum. On the other hand, 17% were in the nucleus and same in plasma membrane. Only 2% were extracellular. Functional GO network speculation showed involvement of 1199 identifier in 10 essential metabolic pathways.

Keywords: Murine, colon, proteome, pathways