Comparison of Different High-Abundant Proteins Removal Method in Protemoe Analysis of Human Serum Samples Using 2D-PAGE

Hyun-Jung Kim, Eun-Hee Jo, Shin-Ae Yu, Do-Youn Lee,
Mi-Ryung Kim and Chan-Wha Kim
School of Life Sciences and Biotechnology, Korea University, Seoul 136-701, Korea.
TEL: +82-2-3290-3439, FAX: +82-2-3290-3957, E-mail: cwkim@korea.ac.kr

Serum or plasma proteins may often serve as indicators of disease and a rich sorce for biomarker discovery. Many of the rapidly evolving technologies of proteome analysis are used to find additional clinically informative protein markers.[1] However the large dynamic range of proteins in serum or plasma makes the analysis very difficult because high-abundant proteins trend to mask those of lower abundance.[2] In this study, we have removed the high abundant proteins from human serum samples using multiple immunoaffinity resins and three depletion kits. The investigation was based on SDS-PAGE, quantification of total protein and 2-DE analysis of the serum samples before and after the depletion step. As a result, the Multiple Affinity Removal Column removed a total of six high-abundant proteins (albumin, IgG, antitrypsin, IgA, transferring, and haptoglobin) specially based on reproducibility and binding specificity, and it will offer the most hopeful depletion effect.

References

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