

## Author's Accepted Manuscript

A human proteomic dataset from untreated and depleted/enriched serum samples

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PII: S2352-3409(18)30693-0S0039-9140(18)30326-6  
DOI: <https://doi.org/10.1016/j.dib.2018.06.042>  
Reference: DIB2737

To appear in: *Data in Brief*

Received date: 28 March 2018  
Accepted date: 18 June 2018

Cite this article as: Salvatore Pisanu, Grazia Biosa, Laura Carcangiu, Sergio Uzzau and Daniela Pagnozzi, A human proteomic dataset from untreated and depleted/enriched serum samples, *Data in Brief*, <https://doi.org/10.1016/j.dib.2018.06.042>

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**Data Article****Title:**

A human proteomic dataset from untreated and depleted/enriched serum samples

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**Abstract**

We present a proteomic dataset generated from a human serum sample and the enriched/depleted fractions obtained by seven commercial products. This report is related to the research article entitled “Comparative evaluation of seven commercial products for human serum enrichment/depletion by shotgun proteomics” [1]. All samples were analyzed by LC-MS/MS, label free quantitation using the spectral counting approach, and Gene Ontology (GO) annotation. Protein relative abundances and functions were reported.

**Specifications Table**

|                            |  |
|----------------------------|--|
| Subject area               | Biology  |
| More specific subject area | Proteomics   |
| Type of data               | A. Tables with all identified proteins, and peptides.<br>B. Protein relative abundance (NSAF), and Gene Ontology annotation. |
| How data was acquired      | Q Exactive mass spectrometer interfaced with an UltiMate 3000 RSLCnanoLC system (Thermo Fisher Scientific)                   |
| Data format                | xlsx file (Excel tables)   |

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