Data in Brief 12 (2017) 584–588

Contents lists available at ScienceDirect

Data in Brief

journal homepage: www.elsevier.com/locate/dib

Data Article

Dataset of protein species from human liver

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ARTICLE INFO

Article history:
Received 17 February 2017
Received in revised form
25 April 2017
Accepted 27 April 2017
Available online 4 May 2017

ABSTRACT

This article contains data related to the research article entitled "Zipf's law in proteomics" (Naryzhny et al., 2017) [1]. The protein composition in the human liver or hepatocarcinoma (HepG2) cells extracts was estimated using a filter-aided sample preparation (FASP) protocol. The protein species/proteoform composition in the human liver was determined by two-dimensional electrophoresis (2-DE) followed by Electrospray Ionization Liquid Chromatography-Tandem Mass Spectrometry (ESI LC-MS/MS). In the case of two-dimensional electrophoresis (2-DE), the gel was stained with Coomassie Brilliant Blue R350, and image analysis was performed with ImageMaster 2D Platinum software (GE Healthcare). The 96 sections in the 2D gel were selected and cut for subsequent ESI LC-MS/MS and protein identification. If the same protein was detected in different sections, it was considered to exist as different protein species/proteoforms. A list of human liver proteoforms detected in this way is presented.

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http://dx.doi.org/10.1016/j.dib.2017.04.051
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Specifications Table

Subject area	Biology
More specific subject area	Proteomics
Type of data	Tables, Figure
How data was acquired	2-DE, Mass spectrometry ESI LC-MS/MS
Data format	analyzed
Experimental factors	Tissue grinding in liquid nitrogen. Protein extraction by Rabillound buffer
Experimental features	2D electrophoresis (1st dimension: pH 3–11 gradient; 2nd dimension: 12% PAGE). Cutting the gel to 96 sections. Trypsin digestion of proteins. ESI LC-MS/MS analysis of the peptides.
Data source location	The data was collected at Institute of Biomedical Chemistry, Moscow, Russia
Data accessibility	The data is with this article. It is also deposited in the Mendeley Data http://dx.doi.org/10.17632/k2rwm88v6b. http://dx.doi.org/10.17632/2997h4fcfz.1

Value of the data

- The data allow the estimation of the distribution of proteins and protein species/proteoforms in human liver cells according to their abundance.
- It is possible to easily extract information about sets of proteoforms that are encoded by the same genes and the abundance of these protein species/proteoforms as well.
- The data could be a starting point for quantitative research of protein species/proteoforms

1. Data

The extracts of human liver or HepG2 cells were treated with trypsin using the FASP protocol. The peptides produced were analyzed by ESI LC-MS/MS. The lists of proteins detected are presented in Supplementary Table 1. The extracts of human liver tissue (300 μg of protein) were also run by 2-DE (Fig. 1). The gel produced was stained with Coomassie Brilliant Blue R350. Image analysis was performed by ImageMaster 2D Platinum software (GE Healthcare, Pittsburgh, PA, USA). Next, 96 sections were selected, given pI/Mw coordinates, and cut for subsequent ESI LC-MS/MS analysis (Fig. 1). A list of all proteins detected by Mascot (only without hemoglobin) in the human liver extracts is presented in Supplementary Table 2. Hemoglobin was removed as a major contaminant of blood plasma proteins. If the same protein was identified in different sections, it was considered to exist as different proteoforms. According to this rule, a total of 14667 proteoforms were identified.

2. Experimental design, materials and methods

2.1. Cells

Human cells (hepatocellular carcinoma (HepG2) were cultured in medium (DMEM/F12 or RPMI-1640 supplemented with 10% fetal bovine serum (FBS) and 100 U/ml penicillin) under standard conditions (5% CO_2, 37 °C) [2–4]. To prepare samples for protein extraction, the cells were detached with 0.25% Trypsin-EDTA solution, washed 3 times with PBS, and treated with Rabillound lysis buffer (7 M urea, 2 M thiourea, 4% CHAPS, 1% DTT, 2% ampholytes, pH 3–10, protease inhibitor mixture) [2,5]. Liver tissue samples were provided within the framework of collaboration on the Chromosome-Centric

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