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Data Article

Changes over lactation in breast milk serum proteins involved in the maturation of immune and digestive system of the infant

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ABSTRACT

Here we provide data from shot-gun proteomics, using filtered-aided sample preparation (FASP), dimethyl labeling and LC–MS/MS, to quantify the changes in the repertoire of human milk proteins over lactation. Milk serum proteins were analyzed at week 1, 2, 3 4, 8, 16, and 24 in milk from four individual mothers. A total of 247 proteins were identified, of which 200 proteins were quantified. The data supplied in this article supports the accompanying publication (Zhang et al., 2006) [1]. The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium (Vizcaíno et al., 2016) [2] via the PRIDE partner repository with the dataset identifier PXD003465.

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Specifications Table

Subject area	Biology
More specific subject area	Lactation stage induced changes in the human milk proteome
Type of data	Raw LC/MSMS datafiles. Spreadsheets containing raw output from MaxQuant as well as filtered and annotated output.
How data was acquired	Filtered-aided sample preparation (FASP), dimethyl labeling followed by LC–MS/MS (Thermo Orbitrap-XL).
Data format	.RAW files (Thermo proprietary) and Excel files for data analysis output.
Experimental factors	Milk serum from week 1 until week 24 in lactation
Experimental features	Individual human milk serum samples were separated by ultracentrifugation, digested with trypsin (using FASP), labeled with dimethyl labeling, and analyzed by LC–MS/MS. The dimethyl ratios were determined for each peptide and normalized peptide ratios per protein were used for further data analysis.
Data source location	Samples were collected from women who gave birth at the obstetric department in VU University medical center (VUmc) in Amsterdam.
Data accessibility	The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium [2] via the PRIDE partner repository with the dataset identifier PXD003465. An Excel document with data output is linked directly to this article.

Value of the data

- This data shows qualitative and quantitative variability of the human milk proteome, both between mothers and over lactation.
- A large number of proteins were identified, and a substantial proportion of those with altered abundance as lactation advances have functions associated with immunity and digestion.
- These data lead to a better understanding of the importance of human milk serum proteins in health and development of infants, which can be used as reference in improving infant formula.

1. Data

The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium [2] via the PRIDE partner repository with the dataset identifier PXD003465. Data analysis output from MaxQuant is made available as Excel document, both as raw output as well as filtered and annotated output.

The raw MaxQuant output contains all the distinct proteins that were identified and quantified along with the number of peptides detected, and the dimethyl labeling ratios. The filtered and annotated output contains filtered proteins based on the identification criteria (At least two peptides per protein) and biological functions, determined by querying the GO database and Uniprot database. This filtered and annotated dataset is the basis of the accompanying publication “Changes over lactation in breast milk serum proteins involved in the maturation of immune and digestive system of the infant” [1].