



## Data Article

# Ischemia-Challenged human umbilical vascular endothelial cells: Proteomics data



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## ABSTRACT

[Human umbilical vascular endothelial cells (HUVECs) underwent ischemia, ischemia/reperfusion and normal control (sham) treatment and marked as group I, IR and NC, respectively, were detected by quantitative proteomics and bioinformatics analyses. Proteins in Beclin-1/LC3-II-dependent canonical macroautophagy pathway were verified in details. The significantly up-regulated proteins encoded by autophagy-related genes (ATGs) included ATG2A, ATG3, ATG4B, ATG5, ATG7, ATG9A, ATG12, ATG16 and ATG101. The significantly enhanced lysosomal proteins comprised Cathepsin B, Cathepsin D, lysosome-associated membrane protein 1 (LAMP1) and LAMP2. However, the differentially expressed proteins excluded Beclin-1, microtubule-associated protein light chain 3 (LC3)-I and LC3-II. Western blot analyses verified that the protein expressions of Beclin-1, LC3-I and LC3-II were neither upregulated nor downregulated in ischemia-challenged HUVECs.]

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## Specifications Table

Subject	Health and medical sciences
Specific subject area	The relationship between autophagy and treatment of various pathophysiological settings
Type of data	Table
How data were acquired	Mass spectrometry
Data format	Raw
Parameters for data collection	Human umbilical vascular endothelial cells (HUVECs) under lethal ischemia and/or reperfusion treatment were considered for data collection
Description of data collection	HUVECs received ischemia (I) treatment for three hours and/or reperfusion (IR) treatment for 24 h were analyzed. The ischemia condition was applied to cells at log phase and 60%–80% confluency, where cells were cultured in ischemia buffer (118 mM NaCl, 24 mM NaHCO <sub>3</sub> , 20 mM sodium lactate, 16 mM KCl, 2.5 mM CaCl <sub>2</sub> , 1 mM NaH <sub>2</sub> PO <sub>4</sub> , 0.5 mM sodium EDTA, pH 6.8) without glucose and fetal bovine serum in a hypoxia incubator (N <sub>2</sub> :O <sub>2</sub> :CO <sub>2</sub> = 94%:1%:5%) at 37 °C for designated time periods. HUVECs after ischemia treatment were incubated in Dulbecco's modified Eagle's medium supplemented with 1 g/L glucose, 10% fetal bovine serum, 100 units of penicillin and 100 µg of streptomycin in a regular incubator (5% CO <sub>2</sub> , 37 °C) for 24 h to mimic reperfusion conditions. Differentially expressed proteins in HUVECs in the I, IR and NC groups were assessed by proteomics and bioinformatics analyses through a PTM-BIO (PTM-Biolabs Co. Ltd., Hangzhou, China) protocol.
Data source location	Institution: PTM-Biolabs Co. Ltd., City/Town/Region: Hangzhou, Country: China
Data accessibility	Primary data sources: Human umbilical vascular endothelial cells Repository name: [Mendeley Data] Data identification number: <a href="https://doi.org/10.17632/hjym79tgn6.1">https://doi.org/10.17632/hjym79tgn6.1</a> Direct URL to data: <a href="https://data.mendeley.com/datasets/hjym79tgn6/1">https://data.mendeley.com/datasets/hjym79tgn6/1</a>
Related research article	Y. Ma, C. Li, Y. He et al., Beclin-1/LC3-II dependent macroautophagy was uninfluenced in ischemia-challenged vascular endothelial cells, <i>Genes &amp; Diseases</i> , <a href="https://doi.org/10.1016/j.gendis.2021.02.010">https://doi.org/10.1016/j.gendis.2021.02.010</a> [1]

## Value of the Data

- The inability of endothelial cells to perform their physiological function (a setting termed endothelial cells dysfunction) or pathological blood vessel formation (a process known as pathological angiogenesis) are common features of various diseases, affecting millions of people worldwide.
- Patients suffer from flap necrosis, limb necrosis, heart failure, stroke, diabetes or even cancer, and researchers in these fields as well as in soft tissue engineering can benefit from these data.
- The data of ischemia-challenged vascular endothelial cells can be used/reused for further insights of experiments on manipulation of autophagy in highly proliferative vascular endothelial cells.

## 1. Data Description

Table 1 shows the overview of differentially expressed proteins in three comparable groups, namely comparable group I/NC, IR/NC and IR/I. Comparable group I/NC and IR/NC showed the same upregulated and downregulated trends.

Table 2 shows the specific data of differentially expressed proteins in comparable group I/NC. The significantly upregulated autophagic proteins included ATG2A, ATG3, ATG4B, ATG5, ATG7, ATG9A, ATG12, ATG16 and ATG101. However, the differentially expressed proteins excluded Beclin-1, LC3-I and LC3-II. The significantly enhanced lysosomal proteins were cathepsin B, cathepsin D, LAMP1 and LAMP2.

Table 3 shows the specific data of differentially expressed proteins in comparable group IR/NC. The significantly upregulated autophagic proteins included ATG2A, ATG3, ATG4B, ATG5, ATG7, ATG9A, ATG12, ATG16 and ATG101 but excluded Beclin-1, LC3-I and LC3-II. The significantly enhanced lysosomal proteins were cathepsin B, cathepsin D, LAMP1 and LAMP2.

Table 4 shows the specific data of differentially expressed proteins in comparable group IR/I. The significantly upregulated autophagic and lysosomal proteins included ATG2A but excluded any proteins as mentioned above.

## 2. Experimental Design, Materials and Methods

### Quantitative proteomics study

To determine the autophagic status of HUVECs under the ischemia condition, ischemic HUVECs were assessed through proteomics analysis by using a PTM-BIO (PTM-Biolabs Co. Ltd., Hangzhou, China) protocol. Briefly, HUVECs in the I, IR and NC groups received ischemia, ischemia/reperfusion and sham treatment, respectively, were collected and processed in accordance with the manufacturer's protocol for the 9-plex tandem mass tag Kit (Thermo Fisher Scientific, MA, USA). The peptides were subjected to mass spectrometry in a Q Exactive Plus Hybrid Quadrupole-Orbitrap (Thermo Fisher Scientific) followed by liquid chromatography–tandem mass spectrometry (LC-MS/MS) in a Q Exactive™ Plus (Thermo Fisher Scientific) coupled online to the HPLC system. Tandem mass spectra were searched against the SwissProt Human database. The mass tolerance for precursor ions was set at 20 ppm in the first search and 5 ppm in the main search, and the mass tolerance for fragment ions was set at 0.02 Da. For the protein quantification method, the LC-MS/MS data were processed using the Mascot search engine (v2.3.0). The false discovery rate was adjusted to <1% and the peptide ion score was set at  $\geq 20$ .

## 3. Bioinformatics analysis

To interpret the proteins that were isolated, fractioned and purified in the proteomics analysis, gene ontology proteome annotation was performed by using the UniProt-GOA database (<http://www.ebi.ac.uk/GOA/>). The Kyoto Encyclopedia of Genes and Genomes (KEGG) database was employed to identify enriched pathways by the two-tailed Fisher's exact test that compared the enrichment of differentially expressed proteins against all identified proteins. In the functional enrichment-based clustering analysis, the quantified proteins in this study were initially divided into three quantitative categories according to the following quantification ratios: Q1 ( $0 < I/NC \text{ ratio} < 1/1.5$ ), Q2 ( $1/1.5 < I/NC \text{ ratio} < 1.5$ ) and Q3 ( $I/NC \text{ ratio} > 1.5$ ). A corrected p-value  $< 0.05$  was considered significant. Next, quantitative category-based clustering was performed with a p-value  $< 0.05$ . The filtered p-value matrix was transformed using the function  $x = -\log_{10}(\text{p-value})$ . Finally, the x-values were z-transformed for each category. The resulting z-scores were clustered by one-way hierarchical clustering (Euclidean distance, average linkage clustering) in Genesis. Clustering membership was visualized by a heat map using the "heatmap.2" function in the "gplots" R-package (Lucent Technologies Inc., Murray Hill, NJ, USA).

## Ethics Statement

All experiments comply with the ARRIVE guidelines and were carried out in accordance with the National Institutes of Health guide for the care and use of Laboratory animals. This

study was approved by the Chongqing Medical University Medical Center Institutional Animal Care and Use Committee (IRB: (2020)044).

### **CRedit Author Statement**

**Yaping Ma:** Methodology, Investigation, Software and Visualization; **Chaofan Li:** Methodology, Investigation, Software and Visualization; **Yan He:** Writing, Original draft preparation and Revising; **Tiwei Fu:** Software and Validation; **Li Song:** **Qingsong Ye:** Writing, Original draft preparation and Revising; **Fugui Zhang:** Conceptualization, Supervision, Writing, Reviewing and Editing.

### **Declaration of Competing Interest**

*The authors declare that they have no known competing financial interests or personal relationships which have or could be perceived to have influenced the work reported in this article.*

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### **Supplementary Materials**

Supplementary material associated with this article can be found in the online version at doi:[10.1016/j.dib.2021.107121](https://doi.org/10.1016/j.dib.2021.107121).

### **Reference**

- [1] Y. Ma, C. Li, Y. He, T. Fu, L. Song, Q. Ye, F. Zhang, Beclin-1/LC3-II dependent macroautophagy was uninfluenced in ischemia-challenged vascular endothelial cells, *Genes. Dis.* (2021) In Press, doi:[10.1016/j.gendis.2021.107121](https://doi.org/10.1016/j.gendis.2021.107121).