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Data Article

Data detailing the platelet acetyl-lysine proteome

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ABSTRACT

Here we detail proteomics data that describe the acetyl-lysine proteome of blood platelets (Aslan et al., 2015 [1]). An affinity purification – mass spectrometry (AP-MS) approach was used to identify proteins modified by Nε-lysine acetylation in quiescent, washed human platelets. The data provide insights into potential regulatory mechanisms of platelet function mediated by protein lysine acetylation. Additionally, as platelets are anucleate and lack histone proteins, they offer a unique and valuable system to study the regulation of cytosolic proteins by lysine acetylation. The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium (Vizcaino et al., 2014 [2]) via with PRIDE partner repository with the dataset identifier PXD002332.

Specifications table

Subject area	Biology
More specific subject area	Proteomic analysis
Type of data	MS data

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How data was acquired	Data acquired on a Thermo Orbitrap Fusion Tribrid Mass Spectrometer configured with an EasySpray NanoSource
Data format	.raw (raw mass spectrometry data files)
Experimental factors	Washed human platelet lysates digested with trypsin.
Experimental features	Acetyl-lysine peptides from platelet lysate digests were enriched using Cell Signaling PTMScan Acetyl-Lysine Motif Kit.
Data source location	Proteomics Shared Resource, Oregon Health & Science University, Medical Research Building Room 521, 3181 SW Sam Jackson Park Road, Portland, OR 97239 USA
Data accessibility	Deposited to the ProteomeXchange with identifier PXD002332. http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD002332

Value of the data

- This data provides the first description of the platelet acetyl-lysine proteome.
- Platelets – the cellular mediators of hemostasis and thrombosis – are anucleate and lack histones, yet they are molecularly equipped to regulate and execute adhesion, cytoskeletal remodeling, metabolic, secretion, apoptotic and other processes common to cellular function and physiology. Accordingly, platelets serve as an ideal cellular model to study roles of lysine acetylation in cell biology apart from roles in transcriptional regulation.
- The data suggest roles for lysine acetylation in the regulation of actin cytoskeletal dynamics, mitochondrial metabolic processes and other cellular activities in platelets.
- Given the developing roles of lysine acetylation in the regulation of diverse cellular activities, this data is important for understanding the molecular basis of platelet function.
- As aspirin – a prevalent antiplatelet drug – acts as a generalized acetylation agent that is capable of modifying lysine residues by Nε-acetylation, the data offers insights into potential secondary targets of aspirin that may impact cellular function.

1. Data, experimental design, materials and methods

1.1. Data

The data in the PRIDE Archive provide the first description of the acetyl-lysine proteome of platelets – the cellular mediators of hemostasis and thrombosis [3].

1.2. Preparation of washed human platelets

Purified platelets were isolated from 100 ml human venous blood drawn from healthy volunteers by venipuncture into sodium citrate in accordance with an IRB-approved protocol at Oregon Health & Science University as previously described [1,4]. Briefly, citrated blood was centrifuged at 200*g* (20 min) to obtain platelet rich plasma (PRP). PRP was centrifuged at 1000*g* (10 min) in the presence of prostacyclin (0.1 μg/ml). PRP-isolated platelets were resuspended in modified HEPES/Tyrode buffer (129 mM NaCl, 0.34 mM Na_2HPO_4, 2.9 mM KCl, 12 mM $NaHCO_3$, 20 mM HEPES, 5 mM glucose, 1 mM $MgCl_2$; pH 7.3) and washed one time with centrifugation at 1000*g* for 10 min in modified HEPES/Tyrode buffer. Purified platelets ($>$ 97.5% purity as determined by flow cytometry) were collected into in modified HEPES/Tyrode buffer for proteomics analyses described below.