## Accepted Manuscript

Lysine acetylation and cancer: A proteomics perspective

Jeovanis Gil, Alberto Ramírez-Torres, Sergio Encarnación-Guevara

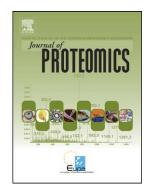
PII: S1874-3919(16)30440-7

DOI: doi: 10.1016/j.jprot.2016.10.003

Reference: JPROT 2689

To appear in: Journal of Proteomics

Received date: 13 June 2016 Revised date: 7 October 2016 Accepted date: 9 October 2016



Please cite this article as: Gil Jeovanis, Ramírez-Torres Alberto, Encarnación-Guevara Sergio, Lysine acetylation and cancer: A proteomics perspective, *Journal of Proteomics* (2016), doi: 10.1016/j.jprot.2016.10.003

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

**ACCEPTED MANUSCRIPT** 

**Title:** Lysine acetylation and cancer: a proteomics perspective.

**Authors:** Jeovanis Gil<sup>1\*</sup>, Alberto Ramírez-Torres<sup>1</sup>, Sergio Encarnación-Guevara<sup>1\*</sup>.

**Author address:** <sup>1</sup>Programa de Genómica Funcional de Procariontes, Centro de Ciencias Genómicas-UNAM. Av. Universidad s/n, Col. Chamilpa, Cuernavaca, Morelos. CP 62210. México.

## **Corresponding Authors**

Jeovanis Gil email: jeovanis@ccg.unam.mx

Tel.: +52 777 3291600

Sergio Encarnación-Guevara email: encarnac@ccg.unam.mx

Tel.: +52 777 3291899

Running title: Acetyl-proteomics and cancer.

Keywords: Lysine Acetylation, Lysine Acetyltransferases, Lysine Deacetylases,

Bromodomains, Cancer, Proteomics, Stoichiometry.

Summary: Lysine acetylation is a reversible modification controlled by two groups of enzymes: lysine acetyltransferases (KATs) and lysine deacetylases (KDACs). Acetylated lysine residues are recognized by bromodomains, a family of evolutionarily conserved domains. The use of high-resolution mass spectrometry-based proteomics, in combination with the enrichment of acetylated peptides through immunoprecipitation with anti-acetyl-lysine antibodies, has expanded the number of acetylated proteins from histones and a few nuclear proteins to more than 2,000 human proteins. Because acetylation targets almost all cellular processes, this modification has been associated with cancer. Several KATs, KDACs and bromodomain-

## Download English Version:

## https://daneshyari.com/en/article/7634063

Download Persian Version:

https://daneshyari.com/article/7634063

<u>Daneshyari.com</u>