EPIGENETIC REGULATION OF CHROMATIN STRUCTURE
ALICIA ROQUE

PROFILE

RESEARCH

RESEARCH INTERESTS

Our research is focused on histone H1 and its role in the epigenetic regulation of chromatin higher-order structure and dynamics. In humans, there are seven H1 somatic subtypes or variants. H1 subtypes are present in different proportions, depending on the cell type and stage of development. While H1 subtypes can compensate for the H1 depletion of one or two subtypes, numerous studies suggest that they are functionally distinct. H1 subtype composition is also altered in pathological states, especially in cancer, highlighting the importance of H1 for cellular homeostasis. Therefore, we are interested in studying the regulation of the expression of H1 subtypes in health and disease. Our findings may provide further evidence of the functional differentiation of H1 subtypes, the compensatory effects upon H1 perturbation, and the role of H1 in carcinogenesis.

STRATEGIC OBJECTIVES

The main target of our work is to understand how the H1 subtype composition is regulated at transcriptional and post-transcriptional levels, combining genomic and proteomic approaches. We also aim to study of H1 alterations in cancer and their role in this disease.

For additional details, please visit our website https://sites.google.com/view/esfureH1 or follow us on twitter **@histone H1**

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MAIN RESEARCH LINES

Transcriptional regulation of the H1.0 and H1x gene promoters and their role in the compensation of H1 variants upon perturbation.

Role of the epitranscriptome in the regulation of H1 somatic subtypes.

Regulation of the mRNA and protein levels of H1 somatic subtypes in cancer cell lines.

Alterations of H1 subtypes in cancer: Levels of mRNA, proteins, and PTMs.

LAB FEATURED PUBLICATIONS

1. Ponte I, Andrés M, Jordan A, Roque A. Towards understanding the regulation of histone H1 somatic subtypes with OMICs. J Mol Biol. 2021;433(2):166734. doi: 10.1016/j.jmb.2020.166734.

2. Andrés M, García-Gomis D, Ponte I, Suau P, Roque A. Histone H1 Post-Translational Modifications: Update and Future Perspectives. Int J Mol Sci. 2020; 21:5941. doi: 10.3390/ijms21165941.

3. Chaves-Arquero B, Pantoja-Uceda D, Roque A, Ponte I, Suau P, Jiménez MA. A CON-based NMR assignment strategy for pro-rich intrinsically disordered proteins with low signal dispersion: the C-terminal domain of histone H1.0 as a case study. J Biomol NMR. 2018;72(3-4):139-148. doi: 10.1007/s10858-018-0213-2.

4. Ponte I, Romero D, Yero D, Suau P, Roque A. Complex evolutionary histone of the mammalian histone H1.1-H1.5 gene family. Molecular Biology and Evolution. 2017;34:545-558. doi: 10.1093/molbev/msw241.

5. Roque A, Ponte I, Suau P. Post-translational modifications of the intrinsically disordered terminal domains of histone H1: effects on secondary structure and chromatin dynamics. Chromosoma. 2017;126:83-91. doi: 10.1007/s00412-016-0591-8.

6. Roque A, Ponte I, Suau P. Interplay between histone H1 structure and function. Biochim Biophys Acta. 2016; 1859: 444-454. doi: 10.1016/j.bbagrm.2015.09.009.

7. Castaño J, Morera C, Sesé B, Boue S, Bonet-Costa C, Martí M, Roque A, Jordan A, Barrero MJ. SETD7 Regulates the Differentiation of Human Embryonic Stem Cells. Plos One 2016; 11: 1-21. doi: 10.1371/journal.pone.0149502.

8. Roque A, Sortino R, Ventura S, Ponte I, Suau P. Histone H1 Favors Folding and Parallel Fibrillar Aggregation of the 1-42 Amyloid-β Peptide. Langmuir. 2015;31(24):6782-90. doi: 10.1021/la504089g.

9. Lopez R, Sarg B, Lindner H, Bartolomé S, Ponte I, Suau P, Roque A. Linker histone partial phosphorylation: effects on secondary structure and chromatin condensation. Nucleic Acids Res. 2015;43(9):4463-76. doi: 10.1093/nar/gkv304.

10. Sarg B, Lopez R, Lindner H, Ponte I, Suau P, Roque A. Identification of novel post-translational modifications in linker histones from chicken erythrocytes. J Proteomics. 2015;113:162-77. doi: 10.1016/j.jprot.2014.10.004.