CURRICULUM VITAE RESUMIDO

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Puestos académicos: Catedrático de Medicina

Puestos asistenciales: Jefe de Sección de Medicina Interna

FORMACIÓN: Doctor en Medicina

Especialista en Medicina Interna

LÍNEAS DE INVESTIGACIÓN

- Fisiopatología, genética y epigenética de enfermedades esqueléticas
- Epidemiología clínica

PUBLICACIONES RECIENTES DESTACADAS

- López-Delgado L, et al. Abnormal bone turnover in individuals with low serum alkaline phosphatase. Osteoporos Int. 2018 doi: 10.1007/s00198-018-4571-0. [Epub ahead of print]
- Del Real A, Riancho-Zarrabeitia L, López-Delgado L, Riancho JA. Epigenetics of Skeletal Diseases. Curr Osteoporos Rep. 2018;16(3):246-255.
- Delgado-Calle J, et al.MMP14 is a novel target of PTH signaling in osteocytes that controls resorption by regulating soluble RANKL production. FASEB J. 2018;32(5):2878-2890.
- Alonso N, et al.Identification of a novel locus on chromosome 2q13, which predisposes to clinical vertebral fractures independently of bone density. Ann Rheum Dis. 2018;77(3):378-385
- García-Ibarbia C ,et al Non-synonymous WNT16 polymorphisms alleles are associated with different osteoarthritis phenotypes. Rheumatol Int. 2017; 37(10):1667-1672.
- Robinson-Cohen C, et al. Genetic Variants Associated with Circulating Parathyroid Hormone. J Am Soc Nephrol. 2017;28(5):1553-1565.
- Del Real A, et al. Differential analysis of genome-wide methylation and gene expression in mesenchymal stem cells of patients with fractures and osteoarthritis. Epigenetics. 2017;12:113-122.
- García-Hoyos M, et al. Diverging results of areal and volumetric bone mineral density in Down syndrome. Osteoporos Int. 2017;28:965-972.
- Brennan-Olsen SL et al. DNA methylation and the social gradient of osteoporotic fracture: A conceptual model. Bone. 2016;84:204-12

- Zheng HF et al. Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. Nature. 2015;526:112-7.
- Riancho-Zarrabeitia L et al. Clinical, biochemical and genetic spectrum of low alkaline phosphatase levels in adults. Eur J Intern Med. 2016
- Garmilla-Ezquerra P et al. Analysis of the bone microRNome in osteoporotic fractures. Calcif Tissue Int. 2015; 96:30-7.
- Fernández AF et al. H3K4me1 marks DNA regions hypomethylated during aging in human stem and differentiated cells. Genome Res. 2015;25:27-40.
- Gokhman D et al. Reconstructing the DNA methylation maps of the Neandertal and the Denisovan. Science. 2014;344:523-7
- Rodriguez-Fontenla C et al. Assessment of osteoarthritis candidate genes in a meta-analysis of nine genome-wide association studies. Arthritis Rheumatol. 2014; 66:940-9.
- Evangelou E et al . A meta-analysis of genome-wide association studies identifies novel variants associated with osteoarthritis of the hip. Ann Rheum Dis. 2014;73:2130-6
- García-Ibarbia C et al . Missense polymorphisms of the WNT16 gene are associated with bone mass, hip geometry and fractures. Osteoporos Int. 2013;24:2449-54.
- Delgado-Calle J et al. Genome-wide profiling of bone reveals differentially methylated regions in osteoporosis and osteoarthritis. Arthritis Rheum. 2013;65:197-205
- Estrada K et al. Genome-wide meta-analysis identifies 56 bone mineral density loci and reveals 14 loci associated with risk of fracture. Nat Genet. 2012;44:491-501.
- Riancho JA et al Pharmacogenomics of osteoporosis: a pathway approach. Pharmacogenomics. 2012; 13:815-29.
- Delgado-Calle J et al. Role of DNA methylation in the regulation of the RANKL-OPG system in human bone. Epigenetics. 2012;7:83-91.
- Delgado-Calle J et al. , DNA methylation contributes to the regulation of sclerostin expression in human osteocytes. J Bone Miner Res. 2012;27:926-37.

PROYECTOS RECIENTES CON FINANCIACIÓN COMPETITIVA (Investigador principal)

- Amgen-SEIOMM: “Análisis de la expresión y metilación de los genes RANKL y OPG en fragmentos óseos y osteoblastos humanos”. (2009-10).
- ISCIII-FIS: “Implicación de mecanismos epigenéticos en enfermedades esqueléticas prevalentes” (2010-12, PI 09/0539).
- FEIOMM: “Interacción entre osterix, runx2 y esclerostina: mecanismos moleculares y repercusión sobre la masa ósea” (2014-15).
- ISCIII-FIS: "Metilación de ADN: factor patogénico y biomarcador en los trastornos de la formación ósea" (PI12/00615, 2013-16).
- ISCIII-FIS: “Estudio de las células troncales mesenquimales en la osteoporosis: Papel de los RNAs largos no codificantes (lncRNAs) y potencial regenerativo” (PI16/00915;2017-19).