- Brief Report: Inhibition of miR-145 Enhances Reprogramming of Human Dermal Fibroblasts to Induced Pluripotent Stem Cells. Barta T, Peskova L, Collin J, Montaner D, Neganova I, et al. Stem cells (Dayton, Ohio). 2016; 34(1):246-51.
- Family-based genome-wide association study in Patagonia confirms the association of the DMD locus and cleft lip and palate. Fonseca RF, de Carvalho FM, Poletta FA, Montaner D, Dopazo J, et al. European journal of oral sciences. 2015;
- 3. Babelomics 5.0: functional interpretation for new generations of genomic data. Alonso R, Salavert F, Garcia-Garcia F, Carbonell-Caballero J, Bleda M, et al. Nucleic acids research. 2015; 43(W1):W117-21.
- 4. Therapeutic targets for olive pollen allergy defined by gene markers modulated by Ole e 1-derived peptides. Calzada D, Aguerri M, Baos S, **Montaner D**, Mata M, et al. Molecular immunology. 2015; 64(2):252-61.
- 5. A new overgrowth syndrome is due to mutations in RNF125. Tenorio J, Mansilla A, Valencia M, Martínez-Glez V, Romanelli V, et al. Human mutation. 2014; 35(12):1436-41.
- 6. Understanding disease mechanisms with models of signaling pathway activities. Sebastian-Leon P, Vidal E, Minguez P, Conesa A, Tarazona S, et al. BMC systems biology. 2014; 8:121.
- 7. A novel locus for a hereditary recurrent neuropathy on chromosome 21q21. Calpena E, Martínez-Rubio D, Arpa J, García-Peñas JJ, Montaner D, et al. Neuromuscular disorders: NMD. 2014; 24(8):660-5.
- 8. Quantitative modeling of clinical, cellular, and extracellular matrix variables suggest prognostic indicators in cancer: a model in neuroblastoma. Tadeo I, Piqueras M, Montaner D, Villamón E, Berbegall AP, et al. Pediatric research. 2014; 75(2):302-14.
- 9. Pathway network inference from gene expression data. Ponzoni I, Nueda M, Tarazona S, Götz S, **Montaner D**, et al. BMC systems biology. 2014; 8 Suppl 2:S7.
- 10. Differential gene-expression analysis defines a molecular pattern related to olive pollen allergy. Aguerri M, Calzada D, Montaner D, Mata M, Florido F, et al. Journal of biological regulators and homeostatic agents. 2013; 27(2):337-50.
- 11. Defining the genomic signature of totipotency and pluripotency during early human development. Galan A, Diaz-Gimeno P, Poo ME, Valbuena D, Sanchez E, et al. PloS one. 2013; 8(4):e62135.
- 12. Four new loci associations discovered by pathway-based and network analyses of the genome-wide variability profile of Hirschsprung's disease. Fernández RM, Bleda M, Núñez-Torres R, Medina I, Luzón-Toro B, et al. Orphanet journal of rare diseases. 2012; 7:103.
- 13. The protease MT1-MMP drives a combinatorial proteolytic program in activated endothelial cells. Koziol A, Gonzalo P, Mota A, Pollán Á, Lorenzo C, et al. FASEB journal: official publication of the Federation of American Societies for Experimental Biology. 2012; 26(11):4481-94.
- 14. Extensive translatome remodeling during ER stress response in mammalian

- cells. Ventoso I, Kochetov A, **Montaner D**, Dopazo J, Santoyo J. PloS one. 2012; 7(5):e35915.
- 15. Large-scale transcriptional profiling and functional assays reveal important roles for Rho-GTPase signalling and SCL during haematopoietic differentiation of human embryonic stem cells. Yung S, Ledran M, Moreno-Gimeno I, Conesa A, Montaner D, et al. Human molecular genetics. 2011; 20(24):4932-46.
- Differential lipid partitioning between adipocytes and tissue macrophages modulates macrophage lipotoxicity and M2/M1 polarization in obese mice.
  Prieur X, Mok CY, Velagapudi VR, Núñez V, Fuentes L, et al. Diabetes. 2011; 60(3):797-809.
- 17. Functional genomics of 5- to 8-cell stage human embryos by blastomere single-cell cDNA analysis. Galán A, Montaner D, Póo ME, Valbuena D, Ruiz V, et al. PloS one. 2010; 5(10):e13615.
- The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. Shi L, Campbell G, Jones WD, Campagne F, Wen Z, et al. Nature biotechnology. 2010; 28(8):827-38. NIHMSID: NIHMS235927
- 19. Babelomics: an integrative platform for the analysis of transcriptomics, proteomics and genomic data with advanced functional profiling. Medina I, Carbonell J, Pulido L, Madeira SC, Goetz S, et al. Nucleic acids research. 2010; 38(Web Server issue):W210-3.
- 20. Multidimensional gene set analysis of genomic data. Montaner D, Dopazo J. PloS one. 2010; 5(4):e10348.
- 21. Hypoxia promotes efficient differentiation of human embryonic stem cells to functional endothelium. Prado-Lopez S, Conesa A, Armiñán A, Martínez-Losa M, Escobedo-Lucea C, et al. Stem cells (Dayton, Ohio). 2010; 28(3):407-18.
- 22. Initial genomics of the human nucleolus. Németh A, Conesa A, Santoyo-Lopez J, Medina I, **Montaner D**, et al. PLoS genetics. 2010; 6(3):e1000889.
- FM19G11, a new hypoxia-inducible factor (HIF) modulator, affects stem cell differentiation status. Moreno-Manzano V, Rodríguez-Jiménez FJ, Aceña-Bonilla JL, Fustero-Lardíes S, Erceg S, et al. The Journal of biological chemistry. 2010; 285(2):1333-42.
- 24. DNA methylation epigenotypes in breast cancer molecular subtypes. Bediaga NG, Acha-Sagredo A, Guerra I, Viguri A, Albaina C, et al. Breast cancer research: BCR. 2010; 12(5):R77.
- 25. Parallel changes in gene expression in peripheral blood mononuclear cells and the brain after maternal separation in the mouse. van Heerden JH, Conesa A, Stein DJ, Montaner D, Russell V, et al. BMC research notes. 2009; 2:195.
- 26. SNOW, a web-based tool for the statistical analysis of protein-protein interaction networks. Minguez P, Götz S, Montaner D, Al-Shahrour F, Dopazo J. Nucleic acids research. 2009; 37(Web Server issue):W109-14.
- 27. Gene set-based analysis of polymorphisms: finding pathways or biological

- processes associated to traits in genome-wide association studies. Medina I, **Montaner D**, Bonifaci N, Pujana MA, Carbonell J, et al. Nucleic acids research. 2009: 37(Web Server issue):W340-4.
- 28. Gene set internal coherence in the context of functional profiling. Montaner D, Minguez P, Al-Shahrour F, Dopazo J. BMC genomics. 2009; 10:197.
- 29. Cryptochrome-1 expression: a new prognostic marker in B-cell chronic lymphocytic leukemia. Lewintre EJ, Martín CR, Ballesteros CG, Montaner D, Rivera RF, et al. Haematologica. 2009; 94(2):280-4.
- 30. Analysis of chronic lymphotic leukemia transcriptomic profile: differences between molecular subgroups. Jantus Lewintre E, Reinoso Martín C, **Montaner D**, Marín M, José Terol M, et al. Leukemia & lymphoma. 2009; 50(1):68-79.
- 31. Direct functional assessment of the composite phenotype through multivariate projection strategies. Conesa A, Bro R, García-García F, Prats JM, Götz S, et al. Genomics. 2008; 92(6):373-83.
- 32. GEPAS, a web-based tool for microarray data analysis and interpretation. Tárraga J, Medina I, Carbonell J, Huerta-Cepas J, Minguez P, et al. Nucleic acids research. 2008; 36(Web Server issue):W308-14.
- 33. Babelomics: advanced functional profiling of transcriptomics, proteomics and genomics experiments. Al-Shahrour F, Carbonell J, Minguez P, Goetz S, Conesa A, et al. Nucleic acids research. 2008; 36(Web Server issue):W341-6.
- 34. Molecular profiling related to poor prognosis in thyroid carcinoma. Combining gene expression data and biological information. Montero-Conde C, Martín-Campos JM, Lerma E, Gimenez G, Martínez-Guitarte JL, et al. Oncogene. 2008; 27(11):1554-61.
- 35. CLEAR-test: combining inference for differential expression and variability in microarray data analysis. Valls J, Grau M, Solé X, Hernández P, Montaner D, et al. Journal of biomedical informatics. 2008; 41(1):33-45.
- 36. Functional profiling of microarray experiments using text-mining derived bioentities. Minguez P, Al-Shahrour F, **Montaner D**, Dopazo J. Bioinformatics (Oxford, England). 2007; 23(22):3098-9.
- 37. ISACGH: a web-based environment for the analysis of Array CGH and gene expression which includes functional profiling. Conde L, Montaner D, Burguet-Castell J, Tárraga J, Medina I, et al. Nucleic acids research. 2007; 35(Web Server issue):W81-5.
- 38. FatiGO +: a functional profiling tool for genomic data. Integration of functional annotation, regulatory motifs and interaction data with microarray experiments. Al-Shahrour F, Minguez P, Tárraga J, Medina I, Alloza E, et al. Nucleic acids research. 2007; 35(Web Server issue):W91-6.
- 39. Evidence for systems-level molecular mechanisms of tumorigenesis. Hernández P, Huerta-Cepas J, **Montaner D**, Al-Shahrour F, Valls J, et al. BMC genomics. 2007; 8:185.
- 40. Functional profiling and gene expression analysis of chromosomal copy number alterations. Conde L, Montaner D, Burguet-Castell J, Tárraga

- J, Al-Shahrour F, et al. Bioinformation. 2007; 1(10):432-5.
- 41. From genes to functional classes in the study of biological systems. Al-Shahrour F, Arbiza L, Dopazo H, Huerta-Cepas J, Mínguez P, et al. BMC bioinformatics. 2007; 8:114.
- 42. Prophet, a web-based tool for class prediction using microarray data. Medina I, Montaner D, Tárraga J, Dopazo J. Bioinformatics (Oxford, England). 2007; 23(3):390-1.
- 43. The detection, treatment and control of high blood pressure in older British adults: cross-sectional findings from the British Women's Heart and Health Study and the British Regional Heart Study. Patel R, Lawlor DA, Whincup P, Montaner D, Papacosta O, et al. Journal of human hypertension. 2006; 20(10):733-41.
- 44. BABELOMICS: a systems biology perspective in the functional annotation of genome-scale experiments. Al-Shahrour F, Minguez P, Tárraga J, Montaner D, Alloza E, et al. Nucleic acids research. 2006; 34(Web Server issue):W472-6.
- 45. Next station in microarray data analysis: GEPAS. Montaner D, Tárraga J, Huerta-Cepas J, Burguet J, Vaquerizas JM, et al. Nucleic acids research. 2006; 34(Web Server issue):W486-91.
- 46. Self-reported smoking cessation interventions were not associated with quitting in older women. Schroeder K, Lawlor DA, Montaner D, Ebrahim S. Journal of clinical epidemiology. 2006; 59(6):622-8.
- 47. Selective pressures at a codon-level predict deleterious mutations in human disease genes. Arbiza L, Duchi S, **Montaner D**, Burguet J, Pantoja-Uceda D, et al. Journal of molecular biology. 2006; 358(5):1390-404.
- 48. How acceptable are innovative health-care technologies? A survey of public beliefs and attitudes in England and Wales. Calnan M, Montaner D, Horne R. Social science & medicine (1982). 2005; 60(9):1937-48.
- 49. Coronary heart disease prevention in clinical practice: are patients with diabetes special? Evidence from two studies of older men and women. Emberson JR, Whincup PH, Lawlor DA, Montaner D, Ebrahim S. Heart (British Cardiac Society). 2005; 91(4):451-5.
- 50. Clustering of risk factors and social class in childhood and adulthood in British women's heart and health study: cross sectional analysis. Ebrahim S, Montaner D, Lawlor DA. BMJ (Clinical research ed.). 2004; 328(7444):861.