Comisión Interministerial de Ciencia y Tecnología

Curriculum vitae

Nombre: Miguel Pérez Enciso

Fecha: Winter 2024

Apellidos: Pérez Enciso Nombre: Miguel
DNI: 50057022Y Fecha de nacimiento : 25 Mayo 1963 Sexo: V

Situación profesional actual

Organismo: Centre de Recerca en Agrigenòmica
Facultad, Escuela o Instituto:
Depto./Secc./Unidad: Statistical and Population Genomics
Dirección postal: Campus Bellaterra, 08193

Teléfono (indicar prefijo, número y extensión): 935636600 – ext 3346
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Especialización (Códigos UNESCO):
Categoria profesional: Contrato labora ICREA indefinido Fecha de inicio: 2003-09-01
Situación administrativa
x Plantilla ☐ Contratado ☐ Interino ☐ Becario
☐ Otras situaciones especificar:

Dedicación A tiempo completo x
A tiempo parcial ☐

Líneas de investigación

Breve descripción, por medio de palabras claves, de la especialización y líneas de investigación actuales.

I have a long experience in Quantitative and Statistical Genetics. Although my primary research area has focused on animals, I have a strong interest in plants, including two year research experience in one of the largest multinational companies in corn and soy breeding. I have developed an eclectic career with numerous contributions (>160 in total, 52 since 2014) to a wide array of topics, from optimizing selection response with a constraint in inbreeding to sophisticated Bayesian methods, QTL and microarray analyses, or machine learning applications in genomic prediction.

Currently, I am working primarily in the application of new machine learning methods, such as deep learning, to genomic prediction. I am also interested in the use of new data (e.g., images, videos) and of microbiome for genomic prediction. I edited a special issue in *J Anim Breed Genet* on metagenomics January 2020. A paper on the use of deep learning in the human biobank dataset was published in Genetics (https://www.genetics.org/content/210/3/809), highlighted in November's issue (120 citations since 2018, 50 altmetric score). I recently published a review in Genes on applications of deep learning to genomic prediction (https://www.mdpi.com/2073-4425/10/7/553), current altmetric score of 47 and ~20,000 downloads since July 2019 and ~100 citations. An associated github site is in https://github.com/miguelperezenciso/DLpipeline.

Since its appearance in ca. 2009, I have been actively working in next generation sequence (NGS) data analysis and its applications, in Agriculture. In that year, I organized the first conference in Europe fully dedicated to NGS (http://bioinformatics.cragenomica.es/numgenomics/ngs2009/index.html). I published the first RNAseq study in pigs (http://www.ncbi.nlm.nih.gov/pubmed/22067327, highly accessed) and the first Iberian pig sequence, I contributed to pig genome publication (Nature 2012). I published a letter in Nature Genetics (March 2015), which was cover in the journal, together with other related papers. I participated in the consortium that sequenced the pig genome (Nature 2012, ~ 1,200 citations).

ICREA: https://www.icrea.cat/Web/ScientificStaff/Miguel-Perez-Enciso-255
GOOGLE: https://scholar.google.es/citations?user=Lpl_-dcAAAAJ&hl=es
ORCYD: http://orcid.org/0000-0003-3524-995X
github: https://github.com/miguelperezenciso
Grupo: https://www.cragenomica.es/research-groups/statistical-and-population-genomics

Formación Académica

Titulación Superior	Centro	Fecha
CC Biológicas	U Complutense Madrid	1986

Doctorado	Centro	Fecha
CC Biológicas	U Complutense Madrid	1990

Actividades anteriores de carácter científico profesional

Puesto	Institución	Fechas
Postdoc	University of Illinois (USA)	1990-91
Postdoc	University of Wisconsin (USA)	1991-92
Postdoc	INRA, Jouy-en-Josas (Francia)	1992-93
Investigador	IRTA, Lleida	1993-99
Funcionario CR1	INRA, Toulouse (Francia)	1999-2003
Investigador ICREA	UAB - Barcelona	2003 - 2022
Profesor asociado tiempo parcial	UAB - Barcelona	2005 - 2022
Investigador Genética Cuantitativa	Corteva Agriscience	2022 - 2024
Investigador ICREA	UAB - Barcelona	2024 -

Idiomas (R = regular, B = bien, C = correctamente)

Idioma	Habla	Lee	Escribe
Inglés	c	c	c
Francés	r	c	r

Participación en Proyectos de I+D financiados en Convocatorias públicas.

(nacionales y/o internacionales)

1. Toro, M.A., et al, "Aplicación de nuevas metodologías genéticas a la conservación y selección de poblaciones porcinas españolas".1989-1993, CIT-INIA, Madrid. INIA.
2. Pérez-Enciso, M. "Linear and non-linear models for animal genetic evaluation",1991-1992. National Center for Supercomputing Applications, University of Illinios, Urbana-Champaign. Proyecto financiado por el NCSA (EE.UU.).
3. Noguera, J. L. et al. Constitución, desarrollo y evaluación de una línea de cerdas hiperprolíficas (1990-1995) INIA
4. Estany, J., Noguera, J. L., Babot, D., Alfonso, L., Pérez-Enciso, M., Tibau, J., "Selección en poblaciones abiertas de porcino con especial referencia al desarrollo de líneas maternas". 1996 - 1998. CICYT 5214.
5. Pérez-Enciso M., Sánchez, A., Toro, M. A., Oliver, M. A., Moreno, F. P. et al. (1996 - 1999) "Detección de genes que afectan a la calidad de la carne en el cerdo Ibérico y Landrace mediante marcadores moleculares". CICYT AGF96-2510
6. Pérez Enciso, M. (coord. español) et al. (1996 - 1997) "Diseño de experimentos para la detección de genes de efecto cuantitativo en poblaciones animales". Acción integrada España/UK (Roslin Institute) HB95-70.
7. Blasco (coord. español) et al. 1996. "Análisis genético de las componentes del tamaño de camada en especies prolíficas" Acción integrada España / Francia (INRA), 70B.
8. Andersson et al. (coord. UdL-IRTA, M. Pérez-Enciso y J.L. Noguera) 1997 - 1999.Transferring QTL technology to pig breeding industry (PigQTech) - A demonstration project. Unión Europea, IV Programa Marco. BIO4-CT97-962243
9. M. Pérez Enciso (coord. español) et al. "Desarrollos metodológicos para la detección y utilización de genes de efecto cuantitativo (QTLS) en poblaciones animales " Acción integrada España / Francia (INRA), 1998-2000.
10. Barillet et al. "Using genetics to improve the quality and safety of sheep products", UE, QLK5-2000-00656.
11. M. Pérez Enciso et al. 2001-2002. Outils statistiques pour la quantification de la variabilité génétique par des marqueurs moléculaires. Bureau des ressources génétiques.
12. M. Pérez Enciso et al. (2004-2007). Huella de la selección, desequilibrio de ligamiento y mapeo ultrafino en la especie porcina, MEC (AGL2004-0103), 107k€.
13. A Sánchez et al. (2004-2008). Análisis genómico mediante microarrays de la arquitectura genética de fenotipos complejos en porcino. Acción estraégica en genómica (GEN2003-20658-C05), 205,000 €.
14. L. Silió et al. 2004-2007. Expresión genómica de QTL y genes candidatos para calidad de carne en diversas líneas de porcino. Acción estratégica del INIA (CPE03-010-03), 350,000 €.
15. M. Pérez-Enciso et al. (2008) Impacto de la domesticación y de la colonización de américa sobre la diversidad genética porcina (A/5267/06), AECI, 15k€.
16. M. Pérez-Enciso et al. (2008-2010), La huella de la domesticación y la selección sobre genes candidatos del metabolismo adiposo y del comportamiento en porcino (AGL2007-65563-C02-01/GAN) MICINN. 130 k€.
17. M. Pérez Enciso y L.S. Huang. Asociación entre genes candidatos y caracteres de interés económico en razas chinas y europeas de porcino. Acción complementaria internacional 2008-2009, MEC, PCI2006-A7-0523, 12000€
18. M. Pérez Enciso y H. Soto. Variabilidad genética en la población feral porcina de la isla del coco y criolla de Costa Rica. Acción complementaria internacional 2008-2009, MEC, PCI2006-A7-0529, 8000€

19. P. Puigdomenech et al. (2008-2012). Centre for Research in Agrigenomics (CRAG) Proyecto Consolider, 530,000 €.
20. A. Sánchez et al. (2009-2013), Grupo de Calidad Generalitat de Cataluña, 75,000€.
21. L. Andersson et al. (España, A. Sánchez et al) 2008-2011. Unravelling the molecular basis of common complex human disorders using the dog as a model system (LUPA), EC-FP7. 350k€ (UAB).
22. M. Bink et al. (2009-2013). Statistical challenges on the 1000€ genome sequences in plants (Cost action TD0801).
23. M. Pérez-Enciso et al. (2009). Next generation meeting organization, Genoma España, 6k€.
24. M. Pérez-Enciso et al. (2009). Next generation meeting organization, MICINN, 5k€
25. M. Ledur et al. (2010-2013) y 25 investigadores de Embrapa, universidades brasileñas, ministerio de agricultura brasileño, empresa privada Sadia SA y UAB.. Identificação de genes de interesse para a suinocultura por meio da genotipagem de SNPs em grande escala e comparação de metodologias de seleção em Programa de Melhoramento Genético Nacional. EMBRAPA Macroprograma 2, 1 Millón Reales.
26. Pérez-Enciso M et al. 2011-2013. Genómica porcina de nueva generación: Adaptación a climas extremos. AGL2010-14822 (181.500 €).
27. Pérez-Enciso M y Ramos-Onsins SE. 2014. Herramientas de nueva generación para la explotación de la diversidad genómica en especies domésticas. MINECO (190.000 €).
28. A. Sánchez et al. (2014-2018), Grupo de Calidad Generalitat de Cataluña, 40,000€. Renovado en 2018.
29. R01GM101219-04 (NIH). Statistical Tools for Whole-Genome Analysis & Prediction of Complex Traits and Diseases. G De Los Campos (Michigan State University, USA). $719,695 total asked, $42,000 to MPE.

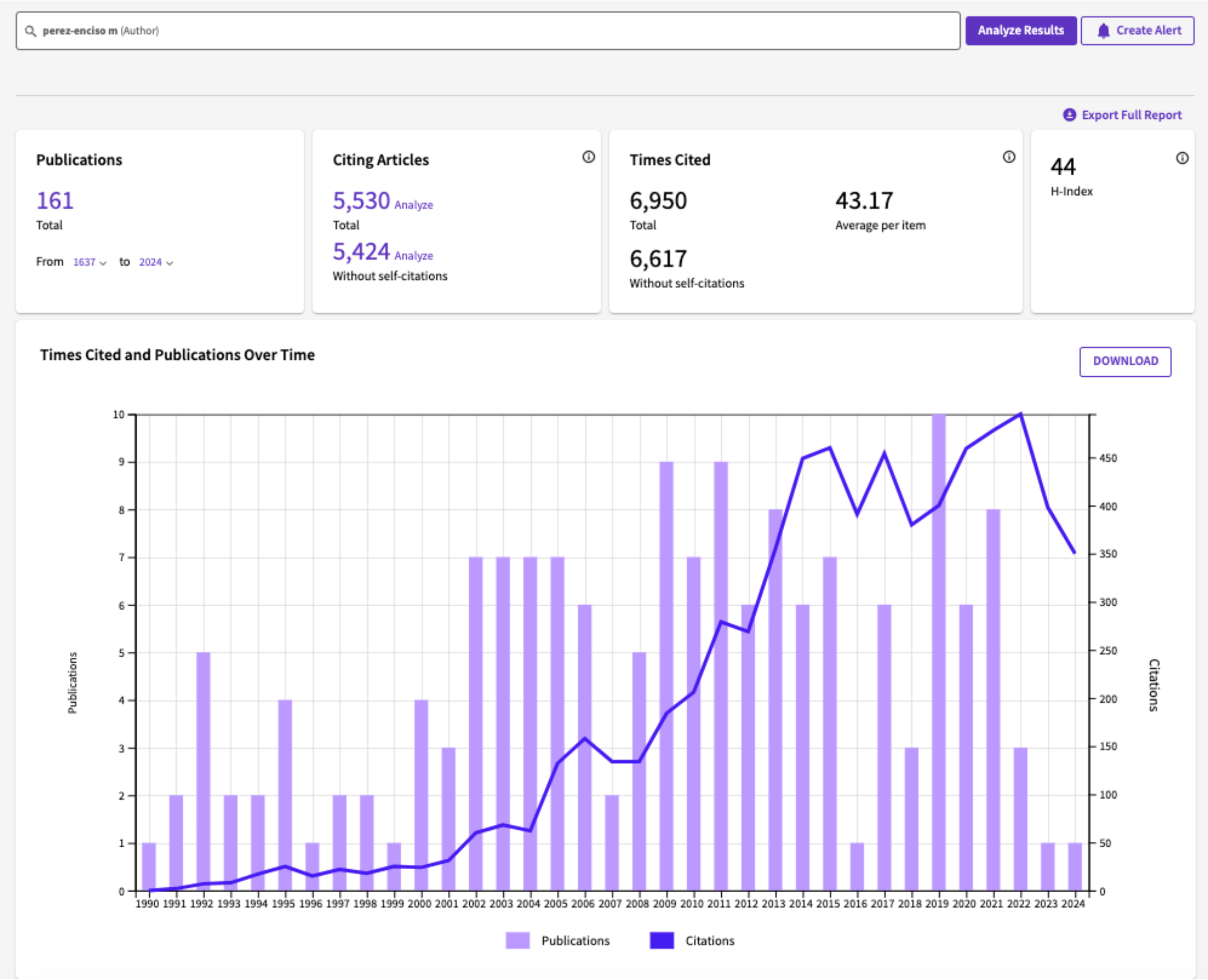
30. Ramos-Onsins SE y Perez-Enciso M. 2016. Utilización de secuencias completas para la mejora de especies domesticas. MINECO (AGL2016-78709-R, 135.000 €).

31. Pérez-Enciso M. 2020. La belleza de lo profundo: aplicaciones del deep learning a la prediccion genomica. MINECO PID2019-108829RB-I00. 130.000 € (approx)

Nota: Si necesita más casos, añádalos utilizando las funciones de copiar y pegar con el 2º caso.

Publicaciones o Documentos Científico-Técnicos (h-index = 39)

CITATIONS



perez-enciso m (Author)

Publications
161
Total
From 1637 to 2024

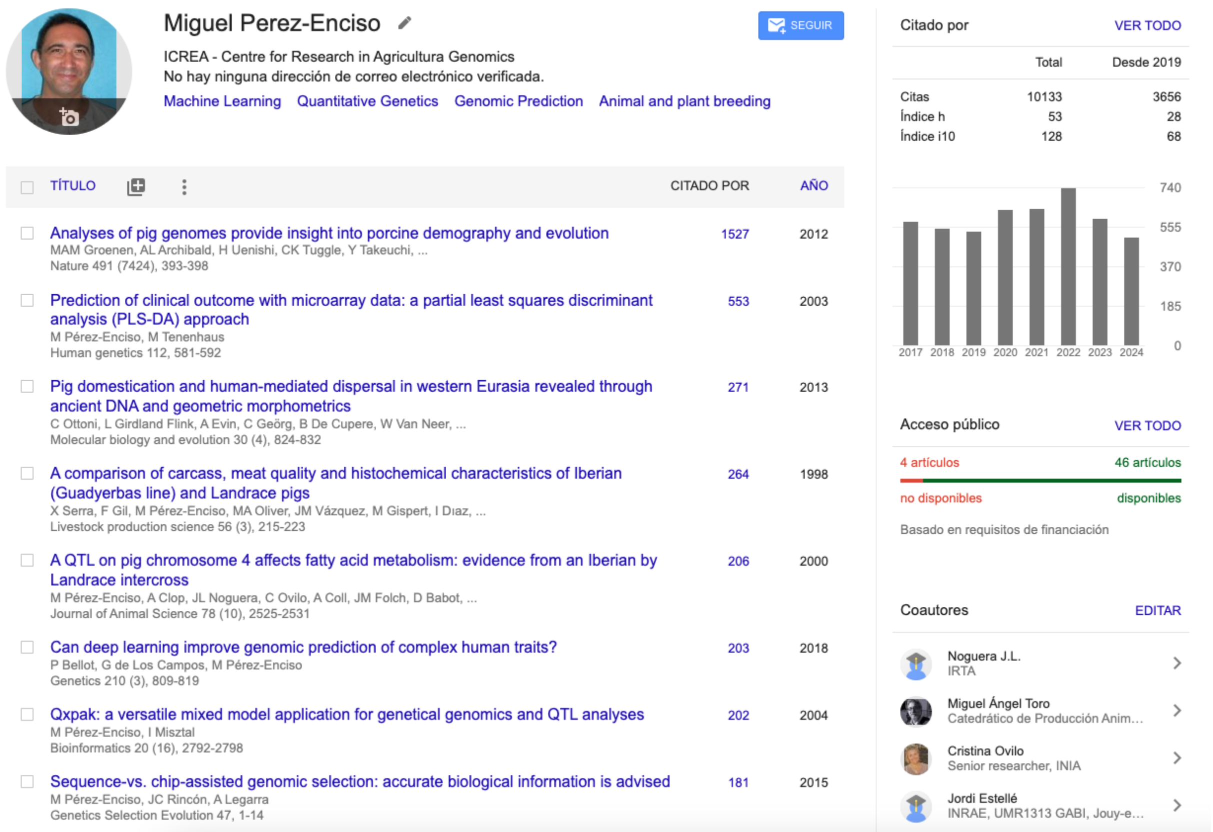
Citing Articles
5,530
Total
5,424
Without self-citations

Times Cited
6,950
Total
43.17
Average per item
6,617
Without self-citations

44
H-Index

Times Cited and Publications Over Time

Google scholar



Miguel Perez-Enciso

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Machine Learning Quantitative Genetics Genomic Prediction Animal and plant breeding

☐ TÍTULO	CITADO POR	AÑO
☐ Analyses of pig genomes provide insight into porcine demography and evolution MAM Groenen, AL Archibald, H Uenishi, CK Tuggle, Y Takeuchi, ... Nature 491 (7424), 393-398	1527	2012
☐ Prediction of clinical outcome with microarray data: a partial least squares discriminant analysis (PLS-DA) approach M Pérez-Enciso, M Tenenhaus Human genetics 112, 581-592	553	2003
☐ Pig domestication and human-mediated dispersal in western Eurasia revealed through ancient DNA and geometric morphometrics C Ottoni, L Girdland Flink, A Evin, C Geörg, B De Cupere, W Van Neer, ... Molecular biology and evolution 30 (4), 824-832	271	2013
☐ A comparison of carcass, meat quality and histochemical characteristics of Iberian (Guadyerbas line) and Landrace pigs X Serra, F Gil, M Pérez-Enciso, MA Oliver, JM Vázquez, M Gispert, I Dıaz, ... Livestock production science 56 (3), 215-223	264	1998
☐ A QTL on pig chromosome 4 affects fatty acid metabolism: evidence from an Iberian by Landrace intercross M Pérez-Enciso, A Clop, JL Noguera, C Ovilo, A Coll, JM Folch, D Babot, ... Journal of Animal Science 78 (10), 2525-2531	206	2000
☐ Can deep learning improve genomic prediction of complex human traits? P Bellot, G de Los Campos, M Pérez-Enciso Genetics 210 (3), 809-819	203	2018
☐ Qxpak: a versatile mixed model application for genetical genomics and QTL analyses M Pérez-Enciso, I Misztal Bioinformatics 20 (16), 2792-2798	202	2004
☐ Sequence-vs. chip-assisted genomic selection: accurate biological information is advised M Pérez-Enciso, JC Rincón, A Legarra Genetics Selection Evolution 47, 1-14	181	2015

Citado por

	Total	Desde 2019
Citas	10133	3656
Índice h	53	28
Índice i10	128	68

Acceso público

4 artículos no disponibles
46 artículos disponibles
Basado en requisitos de financiación

Coautores

Noguera J.L.
IRTA

Miguel Ángel Toro
Catedrático de Producción Anim…

Cristina Ovilo
Senior researcher, INIA

Jordi Estellé
INRAE, UMR1313 GABI, Jouy-e…

Full publication list

1 Toro, M.A., Pérez-Enciso, M., 1990. Optimization of selection response under restricted inbreeding, Genetics Selection Evolution 22:93-107.

2 Pérez-Enciso, M., Toro, M. A., 1991. A note on prediction of response to artificial selection with indices of unequal information. Livestock Production Science 29:335-340.

3 Toro, M.A., Silió, L., Pérez-Enciso, M., 1991. A note on the use of mate selection in closed MOET schemes, Animal Production 53:403-406.

4 Pérez-Enciso, M., Fernando, R.L., 1992. Genetic evaluation with uncertain parentage: a comparison of methods, Theoretical and Applied Genetics 84:173-179.

5 Pérez-Enciso, M., Toro, M.A., 1992. Classical and mixed model analysis of an index selection experiment for fecundity in Drosophila melanogaster. Journal of Animal Science 70:2673-2681.

6 Pérez-Enciso, M., Gianola, D., 1992. Estimates of genetic parameters for litter size in six strains of Iberian pigs. Livestock Production Science 32:283-293.

7 Misztal, I., Pérez-Enciso, M., 1993. Sparse matrix inversion in Restricted Maximum Likelihood estimation of variance components by Expectation-Maximization. Journal of Dairy Science 76:1479-1483.

8 Pérez-Enciso, M., Tempelman, R.J., Gianola, D., 1993. A comparison between linear and Poisson mixed models for litter size in Iberian pigs. Livestock Production Science 35:303-316.

9 Olesen, I., Pérez-Enciso, M., Gianola, D., Thomas, D.L., 1994. A comparison of normal and nonnormal mixed models for number of lambs born in Norwegian sheep. Journal of Animal Science72:1166-1173.

10 Pérez-Enciso, M., Foulley, J.L., Bodin, L., Poivey, J. P., 1994. Genetic implications of a bivariate threshold model for litter size components. Journal of Animal Science 72:2775-2786

11 Pérez-Enciso, M., Foulley, J.L., Bodin, L., Elsen, J.M., Poivey, J.P., 1995. Genetic improvement of litter size in sheep. A comparison of selection methods. Genetis Selection Evolution 27:43-61.

12 Pérez-Enciso, M., 1995. Use of the uncertain relationship matrix to compute effective population size. Journal of Animal Breeding and Genetics 112:327-332.

13 Pérez-Enciso, M., Bidanel, J.P., Baquedano, I., Noguera, J.L. 1996. A comparison of alternative genetic models for litter size in pigs. Animal Science 63: 255-264.

14 Matos, C.A.P., D.L. Thomas, D. Gianola, M. Pérez-Enciso, L.D. Young. 1997. Genetic analysis of discrete reproductive traits in sheep using linear and nonlinear models: II. Goodness of fit and predictive ability. Journal of Animal Science 75:88-94.

15 Pérez-Enciso, M., Bidanel, J.P. 1997. Selection for litter size components: A critical review. Genetics Selection Evolution 29:483-496.

16 Pérez-Enciso, M. 1998. Sequential Bulked Typing: A rapid approach for detecting QTLs. Theoretical and Applied Genetics 96:551-557.

17 Serra X., F. Gil, M. Pérez-Enciso, M.A. Oliver, J.M. Vázquez, M. Gispert, I. Díaz, F. Moreno, R. Latorre, J.L. Noguera. 1998. A comparison of carcass, meat quality and histochemical characteristics of Iberian and Landrace pigs. Livestock Production Science 56: 215-223.

18 Pérez-Enciso, M, MA Toro. 1999. Robust QTL effect estimation using the Minimum Distance method. Heredity 83: 347-353.

19. Ovilo, C, Pérez-Enciso M, Barragan, C, Clop A., Rodriguez C. Oliver M.A., Toro M.A., Noguera J.L. 2000. A QTL for intramuscular fat and backfat thickness is located on porcine chromosome 6. Mammalian Genome 11:344-346.

20. Pérez-Enciso M, L Varona. 2000. QTL mapping in F2 crosses between outbred populations. Genetics. 155:391-405.

21. Pérez-Enciso, M, A. Clop, J. L. Noguera, C. Óvilo, A. Coll, J. M. Folch, D. Babot, J. Estany, M. A. Oliver, I. Díaz, A. Sánchez. 2000. A QTL on pig chromosome 4 affects fatty acid metabolism: evidence from an Iberian by Landrace intercross. Journal of Animal Science 78:2525-2531.

22. Pérez-Enciso M, Varona L., Rothschild MF, 2000b. Computation of identity by descent probabilities conditional on DNA markers via a Monte Carlo Markov Chain Method. Genetics Selection Evolution, 32:467-482.

23. Varona L., L. A. García-Cortés, M. Pérez-Enciso, 2001. Bayes Factors for detection of Quantitative Trait Loci. Genetics Selection Evolution 33:133-152.

24. Ponz R., Moreno C., Allain D., Elsen J.M., Lantier F., Lantier I., Brunel J.C., Pérez-Enciso M. 2001. Assessment of genetic variation explained by markers for wool traits in sheep via a segment mapping approach. Mammalian Genome, 12:569-571.

25. Pérez-Enciso, M, Fernando R.L., Bidanel, J.P., Le Roy, P. 2001. QTL analysis in crosses between outbred lines with dominance and inbreeding. Genetics 159: 413-422.

26. Walling, G., Haley, C. S., Pérez-Enciso, M., Thompson, R., Visscher, P. 2002. On the mapping of QTL at marker and non-marker locations. Genetical Research, 79: 97-106.

27. Clop, A., A. Cercós, A. Tomàs, M. Pérez-Enciso, L. Varona, J.L. Noguera, A. Sànchez, M. Amills. 2002. Assignment of the 2,4-dienoyl-CoA reductase gene (DECR) to Porcine Chromosome 4. Animal Genetics. Animal Genetics 33:164-165.

28. Pérez-Enciso, M, Roussot, O. 2002. A method for computing identity by descent probabilities and quantitative trait loci mapping with dominant (AFLP) markers. Genetical Research, 79: 247-258.

29. Ovilo C, M. A. Oliver, J. L. Noguera, A. Clop, C. Barragán, L. Varona, M. C. Rodríguez, M. Toro, A. Sánchez, M. Pérez-Enciso, L. Silió. 2002. Test for positional candidate genes for body composition on pig chromosome 6. Genet Sel Evol 34: 465-479.

30. Ovilo, C., A. Clop, J.L. Noguera, M.A. Oliver, C. Barragán, C. Rodríguez, L. Silió, M.A. Toro, A. Coll, J.M. Folch, A. Sánchez, D. Babot, L. Varona, M. Pérez-Enciso. 2002b. QTL mapping for meat quality traits in an Iberian x Landrace F2 pig population. J. Anim. Sci., 80:2801-2808.

31. Pérez-Enciso, M., A. Clop, J. M. Folch, A. Sánchez, M. A. Oliver, C. Óvilo, C. Barragán, L. Varona, J. L. Noguera. 2002. Exploring alternative models for sex linked QTL in outbred populations: application to an Iberian x Landrace pig intercross. Genetics 161:1625-1632.

32. Varona, L., C. Ovilo, A. Clop, J. L. Noguera, M. Pérez-Enciso, A. Coll, J. M. Folch, C. Barragán, M. A. Toro, D. Babot, A. Sánchez. 2002. QTL mapping for growth and carcass traits in an Iberian by Landrace pig intercross: additive, dominant and epistatic effects. Genetical Research 80:145-154.

33. Gianola D., Pérez-Enciso M., Toro. M. A. 2003. Genomic assisted prediction of genetic value: Beyond the ridge. Genetics, 163: 347-365.

34. Pérez-Enciso, M. 2003 Fine mapping of complex trait genes combining pedigree and linkage disequilibrium information: A Bayesian unified framework. Genetics. 163: 1497-1510.

35. Pérez-Enciso M, Tenenhaus M. 2003. Prediction of clinical outcome with expression data: A partial least squares approach. Human Genetics, 112:581-592.
36. Pérez-Enciso, M., Toro, M. A., Tenenhaus M., Gianola, D. 2003. Combining expression and molecular marker information for gene mapping: a simulation study. Genetics. 164:1597-1606.
37. J. L. Noguera, L. Varona, L. Gómez-Raya , A. Sánchez, D. Babot, J. Estany, L. A. Messer, M. Rothschild, M. Pérez-Enciso, 2003. Estrogen Receptor Polymorphism in Landrace pigs and its association with litter size performance. Livestock Production Science. 82:53-59.
38. Clop, A., C. Ovilo, M. Perez-Enciso, A. Cercos, A. Tomas, A. Fernandez, A. Coll, J. M. Folch, C. Barragán, I. Díaz, M. A. Oliver, L. Varona, L. Silió, A. Sánchez, J.L Noguera. 2003 Detection of QTL affecting fatty acid composition in the pig. Mamm. Genom. 14:650-656.
39 Abdallah, J., Goffinet, B., Cierco-Ayrolles, C., Pérez-Enciso, M. 2003. Linkage disequilibrium fine mapping of quantitative trait loci: a simulation study. Genet. Sel. Evol. 35:513-532.
40. Pérez-Enciso, M. 2004. In silico study of transcriptome genetic variation in outbred species. Genetics 166: 547-554.
41. Abdallah, J., Mangin, B., Goffinet, B., Cierco-Ayrolles, C., Pérez-Enciso, M. 2004 A comparison between methods for linkage disequilibrium fine mapping of quantitative trait loci. Genetical Research, 83:41-47.
42. Pérez-Enciso, M., Misztal, I. 2004. Qxpak: A versatile mixed model application for genetical genomics and QTL analyses. Bioinformatics 20: 2792-2798.
43. Cosseddu GM, Perez-Enciso M, Fellous M, Vaiman D., 2004. Interspecific chromosome-wide transcription profiles reveal the existence of mammalian-specific and species-specific chromosome domains. J Mol Evol. 2004, 59:317-328.
44. Mercadé A, J Estellé, JL. Noguera, JM. Folch, L Varona, L Silió, A Sánchez, M Pérez-Enciso. 2005. On growth, fatness and form: A further look at porcine's chromosome 4 in an Iberian x Landrace cross. 2005. Mamm Genome16:374-382.
45. Esteso G., J. Estellé, M. Pérez-Enciso. 2005. Assignment of *RAD51C* gene to porcine chromosome 12 and identification of intronic variability. Anim Genet. 36:461-462..
46. Pérez-Enciso M, A. Mercadé, J. P. Bidanel, H. Geldermann, S. Cepica, H. Bartenschlager, L. Varona, D. Milan, and J. M. Folch. 2005. Large scale, multibreed multitrait analyses of QTL experiments: The case of porcine X chromosome. J Anim Sci 83:2289-2296
47. Estellé J., A. Mercadé, J.L. Noguera, M. Pérez-Enciso, C. Óvilo, A. Sánchez, J.M. Folch. 2005. Effect of the porcine IGF2-intron3-G3072A substitution in an outbred Large White population and in an Iberian by Landrace cross. J Anim Sci, 83:2723-2728
48. Pérez-Enciso E, P. Gómez García-Bernal, M Pérez-Enciso. 2005. ATLAS: a Java based tool for managing genotypes. 2005. J Hered, 96:623-625.
49. Jacobsson L., HB Park, P Wahlberg, R Fredriksson, M Pérez-Enciso, P. B. Siegel, L. Andersson. 2005. Many QTLs with minor additive effects are associated with a large difference in growth between two selection lines in chickens. Genet Res, 86:115-125
50. Mercadé, A., J. Estellé, M. Pérez-Enciso, L. Varona, L. Silió, J. L. Noguera, A. Sánchez, J. M. Folch. 2006. Characterization of the porcine *acyl-CoA synthetase long-chain 4* (*ACSL4*) gene and its association with growth and meat quality traits. Anim Genet. 37:219-224
51. Pérez-Enciso, M. 2006. Multiple Association Analysis via Simulated Annealing (MASSA). Bioinformatics 22: 573-580.
52. Tomás, A. J. Casellas, O. Ramírez, M. Pérez-Enciso, C. Rodríguez, J.L. Noguera and A. Sánchez. 2006. Polymorphism of the porcine dopamine β-hydroxylase (*DBH*) gene and its relation with reproduction and piglet survivability in an Iberian × Meishan F_2 intercross. Anim Genet, 37:279-282.
53. Mercadé, A., M. Pérez-Enciso, L. Varona, E. Alves, J. L. Noguera, A. Sánchez, J. M. Folch. 2006. Adipocyte fatty-acid binding protein is closely associated to the porcine *FAT1* locus on chromosome 4. J. Anim Sci, 83: 2723-2728
54. Ojeda, A., Rozas, J., Folch, JM, Pérez-Enciso, M. 2006. Unexpected high polymorphism at FABP4 gene unveils a complex history for pig populations. Genetics, 174:2119-2127
55. Estellé, J, M. Pérez-Enciso, A. Mercadé, L. Varona, E. Alves, A. Sánchez, and J. M. Folch. 2006. Characterization of the porcine *FABP5* gene and its association with the *FAT1* locus in an Iberian by Landrace cross. Animal Genetics, 37:589-591.
56. Pérez-Enciso M, Quevedo JR, Bahamonde A, 2007. Genetical genomics: use all data. BMC Genomics, 8:69.

57. Pérez-Enciso, M. 2007. Emerging tools for quantitative trait loci detection. Scand Section A 57:202-207 (invited review)
58. Ojeda A., L.-S. Huang J. Ren, A. Angiolillo, I.-C.Cho, H. Soto, C. Lemús-Flores, S.M. Makuza, J.M. Folch, M. Pérez-Enciso. 2008. Selection in the making: A Worldwide Survey of Haplotypic Diversity around a Causative Mutation in Porcine *IGF2.* Genetics. 178:1639-1652
59. Ferraz AL, Ojeda A, Lopez-Bejar M, Fernandes LT, Castello A, Folch JM, Perez-Enciso M: Transcriptome architecture across tissues in the pig. *BMC Genomics* 2008, 9:173.
60. Estelle J, Gil F, Vazquez JM, Latorre R, Ramirez G, Barragan MC, Folch JM, Noguera JL, Toro MA, Perez-Enciso M, 2008.: A QTL genome scan for porcine muscle fiber traits reveals overdominance and epistasis. *J Anim Sci* 86:3290-3299.
61. Ojeda A, Estellé J, Folch JM, Pérez-Enciso M (2008) Nucleotide variability and linkage disequilibrium pattern at porcine FABP5 gene. Anim Genet 39:468-473,
62. Pérez-Enciso M 2008 Population and quantitative genetics for a cause. *J Anim Breed Genet*, 125:217-218. (Invited editorial)
63. Salas, A., F. Subirada, M: Pérez-Enciso, F. Blanch, I. Jeusette, V. Romano, C. Torre. 2009. Plant polyphenol intake alters gene expression in canine leukocytes. J. Nutrigenetics and Nutrigenomics 2:43-52.
64. Estelle J., Mercade A., Perez-Enciso M., Pena R.N., Silio L., Sanchez A. & Folch J.M. 2009. Evaluation of FABP2 as candidate gene for a fatty acid composition QTL in porcine chromosome 8. *J Anim Breed Genet* 126, 52-8.
65. Chen C., Guo Y., Yang G., Yang Z., Zhang Z., Yang B., Yan X., Perez-Enciso M., Ma J., Duan Y., Brenig B. & Huang L. (2009) A genome wide detection of quantitative trait loci on pig maternal infanticide behavior in a large scale White Duroc x Erhualian resource population. *Behav Genet* 39, 213-219.
66. Pérez-Enciso M, ALJ Ferraz, A Ojeda, M López-Béjar. 2009. Impact of breed and sex on porcine endocrine transcriptome: A Bayesian biometrical analysis BMC Genomics, 10:89
67. Duthie C.A., G Simm, M. Pérez-Enciso, A. Doeschl-Wilson, E. Kalm, P.W. Knap, R. Roehe. 2009. Genomic scan for quantitative trait loci of chemical and physical body composition and deposition on pig chromosome X including the pseudoautosomal region of males. Genet Sel Evol, 41:27.
68. Ramirez O., Ojeda A., Tomas A., Gallardo D., Huang L.S., Folch J.M., Clop A., Sanchez A., Badaoui B., Hanotte O., Galman-Omitogun O., Makuza S.M., Soto H., Cadillo J., Kelly L., Cho I.C., Yeghoyan S., Perez-Enciso M. & Amills M. 2009. Integrating Y-Chromosome, Mitochondrial and Autosomal Data to Analyse the Origin of Pig Breeds. *Mol Biol Evol*. 26:2061-2072.
69. Fernandes L.T., Tomas A., Bensaid A., Perez-Enciso M., Sibila M., Sanchez A. & Segales J. (2009) Exploratory study on the transcriptional profile of pigs subclinically infected with porcine circovirus type 2. *Anim Biotechnol* 20, 96-109.
70. Estelle J., Fernandez A.I., Perez-Enciso M., Fernandez A., Rodriguez C., Sanchez A., Noguera J.L. & Folch J.M. (2009) A non-synonymous mutation in a conserved site of the MTTP gene is strongly associated with protein activity and fatty acid profile in pigs. *Anim Genet*. 40:813-820.
71. Ledur MC, Navarro N, Pérez-Enciso M. 2010. Large-scale SNP genotyping in crosses between outbred lines: how useful is it? *Heredity*. 105:173-182
72. M. Pérez-Enciso, L. Ferretti. 2010. Massive parallel sequencing in animal genetics: wherefroms and wheretos (invited review). Anim. Genet. 41:561-569.
73. A Reverter, N.J. Hudson, S.H. Nagaraj, M. Pérez-Enciso, B.P. Dalrymple 2010. Regulatory Impact Factors: Unraveling the transcriptional regulation of complex traits from expression data. Bioinformatics, 26:896-904.
74. Esteve A, Ojeda A, Huang LS, Folch JM, Perez-Enciso M, 2011. Nucleotide variability of the porcine SERPINA6 gene and the origin of a putative causal mutation associated with meat quality. *Anim Genet*. 42:235-241.
75. Ferretti L, Perez-Enciso M, Ramos-Onsins S, 2010. Optimal neutrality tests based on the frequency spectrum. *Genetics* 186: 353-365.
76. Luaces O, Quevedo JR, Perez-Enciso M, Diez J, Del Coz JJ, Bahamonde A, 2010. Explaining the genetic basis of complex quantitative traits through prediction models. *J Comput Biol* 17: 1711-1723.

77. Ojeda A, Ramos-Onsins SE, Marletta D, Huang LS, Folch JM, Perez-Enciso M, 2011. Evolutionary study of a potential selection target region in the pig. *Heredity* 106: 330-338.
78. Perez-Enciso M, 2010. Leipzig: the dawn of the genomes era. *J Anim Breed Genet* 127: 338.
79. Ramayo Y, Shemereteva IN, Perez-Enciso M. 2011. Mitochondrial DNA diversity in wild boar from the Primorsky Krai Region (East Russia). Anim Genet. 42:96-99.
80. Ramayo-Caldas Y, Castello A, Pena RN, Alves E, Mercade A, Souza CA *et al* 2010. Copy number variation in the porcine genome inferred from a 60 k SNP BeadChip. *BMC Genomics* 11: 593.
81. Esteve-Codina A, R. Kofler, H. Himmelbauer L. Ferretti, A.P. Vivancos, M.A.M. Groenen, J.M. Folch, M.C. Rodríguez, M. Pérez-Enciso. 2011. Partial short-read sequencing of a highly inbred Iberian pig and genomics inference thereof. Heredity, 107: 256-64.
82. Amaral AJ, Ferretti L, Megens H-J, Crooijmans RPMA, Nie H, Ramos-Onsins SE, Perez-Enciso M, Schook LB, Groenen MAM. 2011. Genome-wide footprints of pig domestication and selection revealed through massive parallel sequencing of pooled DNA. Plos One, 2011 Apr 4:e14782.
83. Perez-Enciso M, Misztal I, 2011. Qxpak.5: Old mixed model solutions for new genomics problems. *BMC Bioinformatics* 2011, 12:202.
84. Yang B, Bassols A, Saco Y, Perez-Enciso M, 2011. Association between plasma metabolites and gene expression profiles in five porcine endocrine tissues. Genet Sel Evol, 43:28.
85. Yang B, Navarro N, Noguera JL, Munoz M, Guo TF, Yang KX, Ma JW, Folch JM, Huang LS, Perez-Enciso M, 2011. Building phenotype networks to improve QTL detection: a comparative analysis of fatty acid and fat traits in pigs. J Anim Breed Genet, 128:329-343.
86. Esteve-Codina A, Kofler R, Palmieri N, Bussotti G, Notredame C, Perez-Enciso M, 2011. Exploring the gonad transcriptome of two extreme male pigs with RNA-seq. BMC Genomics, 12:552.
87. Quevedo JR, Bahamonde A, Perez-Enciso M, Luaces O, 2012. Disease Liability Prediction from Large Scale Genotyping Data Using Classifiers with a Reject Option. *IEEE/ACM Trans Comput Biol Bioinform* 2012.
88. Ramayo-Caldas Y, Mercade A, Castello A, Yang B, Rodriguez C, Alves E, Diaz I, Ibanez-Escriche N, Noguera JL, Perez-Enciso M, Fernandez, A. I. Folch, J. 2012. Genome-Wide Association Study for Intramuscular Fatty Acid Composition in an Iberian x Landrace Cross. *J Anim Sci*. 90(9):2883-93.
89. Montaldo H, Castillo-Juárez H, Campos-Montes G, Pérez-Enciso M. 2012. Effect of the data family structure, tank replication, and the statistical model, on the estimation of genetic parameters for body weight at 28 days of age in the Pacific white shrimp (Penaeus (Litopenaeus) vannamei Boone, 1931). Aquaculture Research, 1-9.
90. Burgos-Paz W, Souza CA, Castello A, Mercade A, Okumura N, Sheremet'eva IN, Huang LS, Cho IC, Paiva SR, Ramos-Onsins S, Pérez-Enciso M. 2012. Worldwide genetic relationships of pigs as inferred from X chromosome SNPs. *Anim Genet*. doi: 10.1111/j.1365-2052.2012.02374.x.
91. Raineri E, Ferretti L., Esteve-Codina A., Nevado B., Heath S., Pérez-Enciso M. 2012. SNP calling by sequencing pooled samples. BMC Bioinformatics. 2012 Sep 20;13:239.
92. Ramayo-Caldas Y, Mach N, Esteve-Codina A, Corominas J, Castelló A, Ballester M, Estellé J, Ibáñez-Escriche N, Fernández AI, Pérez-Enciso M, Folch JM. 2012. Liver transcriptome profile in pigs with extreme phenotypes of intramuscular fatty acid composition. BMC Genomics. 2012 Oct 11;13(1):547.
93. Simianer H, Pérez-Enciso M. 2012. International conference on quantitative genetics 4: big science for complex traits. J Anim Breed Genet. 129(5):343-4 (Invited editorial).
94. Groenen, M. A., A. L. Archibald, H. Uenishi, C. K. Tuggle, Y. Takeuchi, M. F. Rothschild, C. Rogel-Gaillard, C. Park, D. Milan, H. J. Megens, S. Li, D. M. Larkin, H. Kim, L. A. Frantz, M. Caccamo, H. Ahn, B. L. Aken, A. Anselmo, C. Anthon, L. Auvil, B. Badaoui, C. W. Beattie, C. Bendixen, D. Berman, F. Blecha, J. Blomberg, L. Bolund, M. Bosse, S. Botti, Z. Bujie, M. Bystrom, B. Capitanu, D. Carvalho-Silva, P. Chardon, C. Chen, R. Cheng, S. H. Choi, W. Chow, R. C. Clark, C. Clee, R. P. Crooijmans, H. D. Dawson, P. Dehais, F. De Sapio, B. Dibbits, N. Drou, Z. Q. Du, K. Eversole, J. Fadista, S. Fairley, T. Faraut, G. J. Faulkner, K. E. Fowler, M. Fredholm, E. Fritz, J. G. Gilbert, E. Giuffra, J. Gorodkin, D. K. Griffin, J. L. Harrow, A. Hayward, K. Howe, Z. L. Hu, S. J. Humphray, T. Hunt, H. Hornshoj, J. T. Jeon, P. Jern, M. Jones, J. Jurka, H. Kanamori, R. Kapetanovic, J. Kim, J. H. Kim, K. W. Kim, T. H. Kim, G.

Larson, K. Lee, K. T. Lee, R. Leggett, H. A. Lewin, Y. Li, W. Liu, J. E. Loveland, Y. Lu, J. K. Lunney, J. Ma, O. Madsen, K. Mann, L. Matthews, S. McLaren, T. Morozumi, M. P. Murtaugh, J. Narayan, D. T. Nguyen, P. Ni, S. J. Oh, S. Onteru, F. Panitz, E. W. Park, H. S. Park, G. Pascal, Y. Paudel, M. Perez-Enciso, R. Ramirez-Gonzalez, J. M. Reecy, S. Rodriguez-Zas, G. A. Rohrer, L. Rund, Y. Sang, K. Schachtschneider, J. G. Schraiber, J. Schwartz, L. Scobie, C. Scott, S. Searle, B. Servin, B. R. Southey, G. Sperber, P. Stadler, J. V. Sweedler, H. Tafer, B. Thomsen, R. Wali, J. Wang, S. White, X. Xu, M. Yerle, G. Zhang, J. Zhang, S. Zhao, J. Rogers, C. Churcher and L. B. Schook (2012). "Analyses of pig genomes provide insight into porcine demography and evolution." Nature 491:393-8.

95. Burgos-Paz, W., C. A. Souza, H. J. Megens, Y. Ramayo-Caldas, M. Melo, C. Lemus-Flores, E. Caal, H. W. Soto, R. Martinez, L. A. Alvarez, L. Aguirre, V. Iniguez, M. A. Revidatti, O. R. Martinez-Lopez, S. Llambi, A. Esteve-Codina, M. C. Rodriguez, R. P. Crooijmans, S. R. Paiva, L. B. Schook, M. A. Groenen and M. Perez-Enciso (2013). "Porcine colonization of the Americas: a 60k SNP story." Heredity (Edinb) 110:321-30.
96. Esteve-Codina, A., Y. Paudel, L. Ferretti, E. Raineri, H. J. Megens, L. Silio, M. C. Rodriguez, M. A. Groenen, S. E. Ramos-Onsins and M. Perez-Enciso (2013). Dissecting structural and nucleotide genome-wide variation in inbred Iberian pigs. BMC Genomics 14:148.
97. Ottoni, C., L. G. Flink, A. Evin, C. Georg, B. De Cupere, W. Van Neer, L. Bartosiewicz, A. Linderholm, R. Barnett, J. Peters, R. Decorte, M. Waelkens, N. Vanderheyden, F. X. Ricaut, C. Cakirlar, O. Cevik, A. R. Hoelzel, M. Mashkour, A. F. Karimlu, S. S. Seno, J. Daujat, F. Brock, R. Pinhasi, H. Hongo, M. Perez-Enciso, M. Rasmussen, L. Frantz, H. J. Megens, R. Crooijmans, M. Groenen, B. Arbuckle, N. Benecke, U. S. Vidarsdottir, J. Burger, T. Cucchi, K. Dobney and G. Larson (2013). "Pig domestication and human-mediated dispersal in western Eurasia revealed through ancient DNA and geometric morphometrics." Mol Biol Evol 30: 824-32.
98. Perez-Enciso, M. (2013). Future implications of full-scale genomics for animal breeding: personalized indices? J Anim Breed Genet 130: 2-3.
99. Ferretti, L, Ramos-Onsins, S.E., Pérez-Enciso, M. 2013. Population genomics from pool sequencing. Mol. Ecol. 22:5561-5576.
100. Herrero-Medrano JM, Megens HJ, Groenen MA, Ramis G, Bosse M, Pérez-Enciso M, Crooijmans RP. (2013) Conservation genomic analysis of domestic and wild pig populations from the Iberian Peninsula. BMC Genet. 14:106.
101. Pérez-Enciso, M. 2014. Genomic relationships computed from either next generation sequence or array SNP data. J. Anim. Breed. Genet. 131:85-96
102. Nevado, N., Ramos-Onsins, S.E., Pérez-Enciso, M. 2014. Re-sequencing studies of non-model organisms using closely-related reference genomes: optimal experimental designs and bioinformatics approaches for population genomics. Mol. Ecol. 23: 1764–1779.
103. Ramayo-Caldas Y, Ballester M, Fortes MR, Esteve-Codina A, Castelló A, Noguera JL, Fernández AI, Pérez-Enciso M, Reverter A, Folch JM. 2014. From SNP co-association to RNA co-expression: Novel insights into gene networks for intramuscular fatty acid composition in porcine. BMC Genomics 15:232.
104. Nevado B, Perez-Enciso M. 2015. Pipeliner: software to evaluate the performance of bioinformatics pipelines for next-generation resequencing. Mol Ecol Resour. 15:99-106. doi: 10.1111/1755-0998.12286.
105. Herrero-Medrano JM, Megens HJ, Groenen MA, Bosse M, Pérez-Enciso M, Crooijmans RP. 2014. Whole-genome sequence analysis reveals differences in population management and selection of European low-input pig breeds. BMC Genomics. 15:601. (highly accessed).
106. Cantet RJ, Christensen OF, Pérez-Enciso M, van der Werf JH. 2014. 10th WCGALP in beautiful Vancouver. J Anim Breed Genet. 13:409-12 (invited editorial).
107. Ramírez O, Burgos-Paz W, Casas E, Ballester M, Bianco E, Olalde I, Santpere G, Novella V, Gut M, Lalueza-Fox C, Saña M, Pérez-Enciso. 2015. Genome data from a sixteenth century pig illuminate modern breed relationships. Heredity 114:175-84.
108. da Silva EC, de Jager N, Burgos-Paz W, Reverter A, Perez-Enciso M, Roura E. 2014. Characterization of the porcine nutrient and taste receptor gene repertoire in domestic and wild populations across the globe. BMC Genomics. 15:1057.
109. AI Fernández, M Muñoz, E Alves, JM Folch, JL Noguera, M Perez-Enciso, MC Rodríguez, L Silió. 2014. Recombination of the porcine X chromosome: a high density linkage map. BMC Genetics 15:148.

110. Pérez-Enciso M, Burgos-Paz, Ramos-Onsins SE. 2015. On genetic differentiation between domestic pigs and Tibetan wild boars. Nat Genet. 47:190-192
111. E. Bianco, B. Nevado, S.E. Ramos-Onsins, M. Pérez-Enciso. 2015. A deep catalog of autosomal single nucleotide variation in the pig. PLoS One. 10(3):e0118867.
112. Bianco E, Soto HW, Vargas L, Pérez-Enciso M. 2015. The chimerical genome of Isla del Coco feral pigs (Costa Rica), an isolated population since 1793 but with remarkable levels of diversity. Mol Ecol. 24:2364-78. doi: 10.1111/mec.13182.
113. Pérez-Enciso M, JC Rincón’ A Legarra. 2015. Sequence- vs. chip-assisted genomic selection: Accurate biological information is advised Genet Sel Evol 47:43, doi: 10.1186/s12711-015-0117-5
114. Pérez-Enciso M, A Legarra. 2016. A combined coalescence gene-dropping tool for evaluating genomic selection in complex scenarios (ms2gs). J Anim Breed Genet. 133:85-91. doi: 10.1111/jbg.12200.
115. Pérez-Enciso M, De Los Campos, G, Hudson N, Kijas J, Reverter A. 2017. The 'heritability' of domestication and its functional partitioning in the pig. Heredity 118:160-168..
116. Pérez-Enciso M, Forneris N., De Los Campos G, Legarra A. 2017. Evaluating sequence-based genomic prediction with an efficient new simulator. Genetics 205:939-953.
117. Pérez-Enciso M. 2017. Animal Breeding learning from Machine Learning. J Anim Breed Genet. 134:85-86, Invited editorial.
118. Leno-Colorado J, Hudson N, Reverter A, Pérez-Enciso M. 2017.A Pathway-Centered Analysis of Pig Domestication and Breeding in Eurasia. G3 (Bethesda). doi: 10.1534/g3.117.042671.
119. Forneris NS, Vitezica ZG, Legarra A, Pérez-Enciso M. 2017. Influence of epistasis on response to genomic selection using complete sequence data. Genet Sel Evol. 2017 Aug 25;49(1):66. doi: 10.1186/s12711-017-0340-3.
120. Bin Yang, Leilei Cui, Miguel Perez-Enciso, Aleksei Traspov, Richard P. M. A. Crooijmans, Natalia Zinovieva, Lawrence B. Schook, Alan Archibald, Kesinee Gatphayak, Christophe Knorr, Alex Triantafyllidis, Panoraia Alexandri, Gono Semiadi, Olivier Hanotte, Deodália Dias, Peter Dovč, Pekka Uimari, Laura Iacolina, Massimo Scandura, Martien A. M. Groenen, Lusheng Huang and Hendrik-Jan Megens. Genome-wide SNP data unveils the globalization of domesticated pigs. Genetics Selection Evolution 2017 49:71 doi.org/10.1186/s12711-017-0345-y.
121. Marina Naval-Sanchez, Quan Nguyen, Sean McWilliam, Laercio Porto-Neto, Ross Tellam, Tony Vuocolo, Antonio Reverter, Miguel Perez-Enciso, Rudiger Brauning, Shannon Clarke, Alan McCulloch, Wahid Zamani, Saeid Naderi, HamidReza Rezaei, Francois Pompanon, Pierre Taberlet, Kim Worley, Richard Gibbs, Donna Muzny, Shalini Jhangiani, Noelle Cockett, Hans Daetwyler, and James Kijas, 2018. Sheep Genome Functional Annotation Reveals Proximal Regulatory Elements Contributed to the Evolution of Modern Breeds. Nat Comm. 9 859. doi:10.1038/s41467-017-02809-1.
122. Hudson NJ, Naval-Sánchez M, Porto-Neto L, Pérez-Enciso M, Reverter A. 2018. RAPID COMMUNICATION: A haplotype information theory method reveals genes of evolutionary interest in European vs. Asian pigs. J Anim Sci. 96:3064-3069. doi: 10.1093/jas/sky225.
123. Bellot P, De Los Campos G, Pérez-Enciso M. 2018. Can deep learning improve prediction of complex traits in humans? Genetics 210:809-819, doi: 10.1534/genetics.118.301298.
124. Zingaretti L, Monfort A, Pérez-Enciso M. 2019. pSBVB: A Versatile Simulation Tool To Evaluate Genomic Selection in Polyploid Species. G3 9:327-334. https://doi.org/10.1534/g3.118.200942.
125. Dufflocq P, Pérez-Enciso M, Llhorente JP, Yáñez JM. 2019. Accuracy of genomic predictions using different imputation error rates in aquaculture breeding programs: A simulation study. Aquaculture 53:225-230.
126. Ramon E, Belanche-Muñoz Ll, Pérez-Enciso M. 2019. HIV drug resistance prediction with weighted categorical kernel functions. BMC Bioinformatics. 20:410. https://doi.org/10.1186/s12859-019-2991-2
127. Cho, IC, Park, HB, Ahn JI, Han SH, Lee JB, Lim HT, Yoo CK, Jung EJ, Kim DH, Sun WS., Ramayo-Caldas Y, Kim SG, Kang YJ, Kim YK, Shin HS, Seong PN, Hwang IS, Park BY, Hwang S, Lee SS, Ryu YC, Lee JH, Ko MS, Lee K, Andersson G, Pérez-Enciso M, Lee JW (2019). A functional regulatory variant of MYH3 influences muscle fiber-type composition and intramuscular fat content in pigs. PLOS Genetics, 15(10), e1008279. https://doi.org/10.1371/journal.pgen.1008279

128. Pérez-Enciso M., Zingaretti L.M. 2019. A Guide on Deep Learning for Complex Trait Genomic Prediction. Genes 10: 553. https://doi.org/10.3390/genes10070553
129. Ramayo-Caldas Y, Zingaretti L, Popova M, Estellé J, Bernard A, Pons N, Bellot P, Mach N, Rau A, Roume H, Perez-Enciso M, Faverdin P, Edouard N, Ehrlich D, Morgavi DP, Renand G. 2020. Identification of rumen microbial biomarkers linked to methane emission in Holstein dairy cows. J Anim Breed Genet. 137:49-59 doi: 10.1111/jbg.12427.
130. Pérez-Enciso M., Ayala-Ramirez LC, Zingaretti L.M. 2020. SeqBreed: a python tool to evaluate genomic prediction in complex scenarios. Genetics Selection Evolution 52:7.
131. Nye J, Zingaretti L.M., Pérez-Enciso M. 2020. Estimating conformational traits in dairy cattle with DeepAPS: a two-step Deep learning Automated Phenotyping and Segmentation approach. Frontiers in Genetics 11:513.
132. Zingaretti LM, Gezan SA, Ferrão LFV, Osorio LF, Monfort A, Muñoz PR, Whitaker VM, Pérez-Enciso M. 2020**.** Exploring Deep Learning for Complex Trait Genomic Prediction in Polyploid Outcrossing Species. Front Plant Sci. 11:25. doi: 10.3389/fpls.2020.00025.
133. Ramírez-Ayala LC, Rocha D, Ramos-Onsins SE, Leno-Colorado J, Charles M, Bouchez O, Rodríguez-Valera Y, Pérez-Enciso M, Ramayo-Caldas Y. 2021. Whole-genome sequencing reveals insights into the adaptation of French Charolais cattle to Cuban tropical conditions.Genet Sel Evol. 53:3. doi: 10.1186/s12711-020-00597-9.
134. Ramon E, Belanche-Muñoz Ll, Molist F, Quintanilla R, Pérez-Enciso M, Ramayo-Caldas Y. 2021 KernInt: a kernel framework for integrating supervised and unsupervised analyses in spatio-temporal metagenomic datasets. Frontiers in Microbiology. 12:609048. https://doi.org/10.3389/fmicb.2021.609048
135. Pérez-Enciso M, Steibel JP. 2021. Phenomes: The current challenge in animal breeding. Genet Sel Evol. 53:22
136. Pérez-Enciso M. 2021. Breeding beyond genomics. J Anim Breed Genet. 138:275–276. Invited editorial. https://onlinelibrary.wiley.com/doi/epdf/10.1111/jbg.12547
137. Wu Z, Gong H, Zhang M, Tong X, Ai H, Xiao S, Pérez-Enciso M, Yang B, Huang L. 2021 A worldwide map of swine short tandem repeats and their associations with evolutionary and environmental adaptations. *Genet Sel Evol* 53:39 https://gsejournal.biomedcentral.com/articles/10.1186/s12711-021-00631-4
138. Zingaretti LM, Monfort A, Pérez-Enciso M. 2021. Automatic fruit morphology phenome and genetic analysis: An application in the octoploid strawberry. Plant Phenomics, https://spj.sciencemag.org/journals/plantphenomics/aip/9812910/
139. Pérez-Enciso M, Zingaretti LM, Ramayo-Caldas Y, de los Campos G. 2021. Opportunities and limits of combining microbiome and genome data for complex trait prediction. Genet Sel Evol. 53:61. https://gsejournal.biomedcentral.com/articles/10.1186/s12711-021-00658-7
140. Gianola D, Cantet RJ, Dekkers JCM, **Pérez-Enciso M. 2022,** Rohan Fernando: a road from Sri Lanka to Ames. Genet Sel Evol. 54:9. doi: 10.1186/s12711-022-00704-y.
141. Vourlaki IT, Castanera R, Ramos-Onsins SE, Casacuberta JM, **Pérez-Enciso M.** Transposable element polymorphisms improve prediction of complex agronomic traits in rice. Theor Appl Genet. 2022 Sep;135(9):3211-3222. doi: 10.1007/s00122-022-04180-2.
142. Calle-García J, Ramayo-Caldas Y, Zingaretti LM, Quintanilla R, Ballester M, **Pérez-Enciso M. 2023.** On the holobiont 'predictome' of immunocompetence in pigs. Genet Sel Evol. 55:29. doi: 10.1186/s12711-023-00803-4.
143. Vourlaki, IT; Ramos-Onsins, SE; Pérez-Enciso M; Castanera, R. 2024. Evaluation of deep learning for predicting rice traits using structural and single-nucleotide genomic variants, Plant Methods 20:121

Participación en contratos de I+D de especial relevancia con Empresas y/o Administraciones
(nacionales y/o internacionales)

Título del contrato/proyecto: Análisis de datos de microarrays

Tipo de contrato:
Empresa/Administración financiadora:Affinity pet care
Entidades participantes:UAB
Duración, desde: 2006 hasta: 2006
Investigador responsable: MPE
Número de investigadores participantes: 1
PRECIO TOTAL DEL PROYECTO: 3000

Organización congreso Next Generation Sequencing (ngs2009.uab.es), Illumina, UAB / UPF / BSC, 2009; M. Pérez-Enciso; 4 investigadores; 4000 €

Organización congreso Next Generation Sequencing (ngs2009.uab.es), Roche;, UAB / UPF / BSC, 2009; M. Pérez-Enciso; 4 investigadores; 4000 €

Organización congreso Next Generation Sequencing (ngs2009.uab.es), Applied; UAB / UPF / BSC, 2009; M. Pérez-Enciso; 4 investigadores; 4000 €

Organización congreso Next Generation Sequencing (ngs2009.uab.es), Keygene, UAB / UPF / BSC, 2009; M. Pérez-Enciso; 4 investigadores; 2000 €

Organización congreso Next Generation Sequencing (ngs2009.uab.es), Sistemas genómicos, UAB / UPF / BSC, 2009; M. Pérez-Enciso; 4 investigadores; 900 €

Nota: Si necesita más casos, añádalos utilizando las funciones de copiar y pegar con el 2º caso.

Patentes y Modelos de utilidad

Inventores (p.o. de firma):
Título:

N. de solicitud: País de prioridad: Fecha de prioridad:
Entidad titular:
Países a los que se ha extendido:
Empresa/s que la están explotando:

Inventores (p.o. de firma):
Título:

N. de solicitud: País de prioridad: Fecha de prioridad:
Entidad titular:
Países a los que se ha extendido:
Empresa/s que la están explotando:

Nota: Si necesita más casos, añádalos utilizando las funciones de copiar y pegar con el 2º caso.

Estancias en Centros extranjeros
(estancias continuadas superiores a un mes)

CLAVE: D = doctorado, P = postdoctoral, I = invitado, C = contratado, O = otras (especificar).

Centro:
Localidad: País Fecha: Duración (semanas):
Tema:
Clave:

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1. Department of Animal Sciences, University of Illinois, Urbana-Champaign (Illinois, EE.UU.), agosto 1990 - julio 1991. Funded by INIA (Spain).
2. Department of Meat and Animal Science, University of Wisconsin, Madison (Wisconsin, EE.UU.), agosto 1991 - agosto 1992. Funded by INIA (Spain)
3. Station de Génétique Quantitative et Appliquée, INRA, Jouy-en-Josas, Francia, octubre 1992 - octubre 1993. Funded by INRA.
4. Roslin Institute, Edimburgo, 1 - 31 mayo 1996; 1 - 15 diciembre 1996. Funded by ministerio de educación, España.
5. Iowa State University, 15 junio - 15 agosto 1999, funded by Iowa State University.
6. Department of Meat and Animal Science, University of Wisconsin, Madison (Wisconsin, EE.UU.), marzo 2002 - abril 2002. Funded by U. of Wisconsin.
7. Dept. of Statistics, Oxford, julio 2010 (un mes), funded by AGAUR (Spain).
8. Dept. of Animal Breeding and Genetics, Wageningen University, agosto-octubre 2013 (dos meses). Funded by Wageningen University.
9. Dept. of Statistics, University of Alabama Birmingham, agosto-septiembre 2014 (un mes). Funded by University of Alabama.
10. CSIRO Feb – April 2015, funded by McMaster fellowship (Australia)
11. Dept of Epidemiology and Statistics, University of Michigan, East Lansing (MI, USA), 13 Feb 2020 – 15 March 2020.

Nota: Si necesita más casos, añádalos utilizando las funciones de copiar y pegar con el 2º caso.

Contribuciones a Congresos

Last invited communications

M. Pérez-Enciso, 2006. QTL software and computational challenges in the post-qtl era. Conferencia invitada. World Congress on genetics Applied to livestock production, 2006, Belo Horizonte, Brasil. http://www.wcgalp.org/proceedings/2006

M. Pérez-Enciso, 2007, Emerging tools for QTL detection. Meeting in honor of Daniel Sorensen, Denmark

M. Pérez-Enciso, 2007, QTL software and beyond. QTL and MAS meeting, Toulouse, Invited conference.

M. Pérez-Enciso, 2008, Sex, chips, ... and microarrays. 3rd International Symposium on Animal Functional Genomics 7-9 june 2008, Edinburgh, invited conference.

M. Pérez-Enciso, 2008,. Chair and Session organizer of Animal Domestication Genomics. Annual Meeting of Society Molecular Biology Evolution, Barcelona. June

M. Pérez-Enciso, 2008, Strategies to identify complex trait loci. Invited conference at Chinese Annual Meeting for Animal Breeding, Jiangxi, 16-17 october

M. Pérez-Enciso, 2009, Next generation animal sequencing to meet tomorrow's needs. EAAP 60th meeting, FABRE session on Sustainability in Livestock production 24 August 2009, Barcelona

M Pérez-Enciso, 2009, Next generation sequencing for next generation genomics. Statistical Genetics of Livestock for the Post-Genomic Era, Madison, WI USA, 5 May 2009. https://www.animalgenome.org/community/angenmap/hmail/archive/2906.html

M. Pérez-Enciso, 2009. Statistical challenges of NGS in animal genetics, Animal Bioinformatics workshop sponsored by the EC-US Task force on Biotechnology Research, Cambridge, UK, 6-7 december 2009.

M. Pérez-Enciso, 2009, Genomics inference from ultrasequencing data. Symposium on developments in genome-wide evaluation and genomic selection, Wageningen University, 15 diciembre 2009, Holanda.

M. Groenen, Amaral A., Megens H.-J., Larson G., Archibald A.L., Muir W., Malhi R., Crooijmans R.P., Ferretti L., Ramos-Onsins S.E., Perez-Enciso M. & Schook L. (2010) The Porcine HapMap Project: Genome-Wide Assessment Of Nucleotide Diversity, Haplotype Diversity And Footprints Of Selection In The Pig In: *Plant & Anmal Genomes XVIII Conference*, S Diego.

HJ Megens, Zare Y., Amaral A., Crooijmans R.P., Ferretti L., Ramos-Onsins S.E., Perez-Enciso M. & Groenen M. (2010) Application Of Massive Parallel Sequencing For Inferring Genome-Wide Nucleotide Diversity And Signatures Of Selection In Chicken. In: *Plant & Anmal Genomes XVIII Conference*, S Diego.

M. Pérez-Enciso, 2010. Beyond Bioinformatics: The Impact of Next Generation Sequencing Technologies in Agrigenomics, 3rd Annual Agrigenomics World Conference, 8-9th july, Brussels. http://www.AgriGenomics.eu.

M. Pérez-Enciso, B. Yang, LS Huang. 2010. Advances in porcine meat quality genomics. INVITED Conference World Congress Applied Livestock Production; august Leipzig; http://www.wcgalp2010.org/.

M. Pérez-Enciso et al, 2010, El genoma del cerdo Ibérico: una visión global desvelada por las nuevas técnicas de secuenciación; conferencia invitada; VII congreso internacional del cerdo mediterráneo, octubre 2010, Córdoba; http://www.uco.es/congresos/cerdomediterraneo/.

M. Pérez-Enciso, 2012. The colonization of the Americas from a livestock (porcine) point of view: A 60k SNP story. Portugaliae Genetica: Iberian Peninsula: at the gate between the Mediterranean and the Atlantic worlds. Porto.

Nota: Si necesita más casos, añádalos utilizando las funciones de copiar y pegar con el 2º caso.

https://www.ipatimup.pt/Site/ActivityView.aspx?EventId=5&ActualActivityId=0&ActivityId=1584

M. Pérez-Enciso, 2012. Livestock population genomics with NGS data. Curso CRG, Barcelona.

M. Pérez-Enciso, 2014, The genomes of the porcine species. Workshop in Translational Genomics. Universitat de Vic, 7 March 2014.

J. Hickey et al. 2014. Sequencing Millions of Animals for Genomic Selection 2.0. World Congress Applied Livestock Production; August, Vancouver. http://www.wcgalp.org/proceedings/2014/sequencing-millions-animals-genomic-selection-20

M. Pérez-Enciso. 2015. Diachrony and Synchrony When Studying Pig Genomes. Plant and Animal Genome XXIII conference, San Diego, USA. Invited conference. https://pag.confex.com/pag/xxiii/webprogram/Paper14545.html

M. Pérez-Enciso. Sequencing bone and living fossil pig genomes. En: The Challenge of Inference from Genome to Phenome, 25-27th March 2015, Brisbane, Australia (conf. invitada).

M. Pérez-Enciso et al. 2015. Big is beautiful: Biology informed sequence exploitation. AAABG Australian meeting, Lorne, Australia. Invited conference. http://www.aaabg.org/aaabghome/proceedings21.php

M. Pérez-Enciso. 2016. Sequence based virtual breeding: A tool to evaluate GWAS and genomic selection in massive datasets. International Conference on Quantitative Genetics. Madison, Wisconsin, USA. Invited conference. https://www.icqg5.org/speakers

M. Pérez-Enciso. 2017. Use of sequence for genomic selection. Biotecnologias e Recursos Genéticos: projeção para o future. Santarem, Portugal. Invited conference.

M. Pérez-Enciso. 2018. Mejora genética y selección genómica en porcino. JORNADAS SOBRE "GENÓMICA PARA LA MEJORA DE LAS PRODUCCIONES Y LA GESTIÓN DE LA BIODIVERSIDAD", Facultad de Veterinaria, U Santiago de Compostela, Lugo. http://www.usc.es/campusterra/sites/default/files/Díptico_CAST_Mail_0.pdf

M. Pérez-Enciso. 2018. Genomic selection: Is it worth the sequence? III LACSC: Congreso Internacional en Estadística Computacional. Universidad de Costa Rica, San Pedro. Invited conference. . http://www.cimpa.ucr.ac.cr/simmac/es/programa.html

M. Pérez-Enciso. 2019. Phenotypic prediction workshop. U. Florida, Gainesville. http://ufgi.ufl.edu/seminars-events/phenotypic-prediction-workshop-2019/. Invited conference.

M. Pérez-Enciso. 2019. Sequence assisted genomic prediction: The uncomfortable truth. 8-11 july, ASAS meeting, Austin, TX, USA. Invited conference within symposium.

M. Pérez-Enciso. 2021. Aprendizaje automático y predicción genómica. Congreso Sociedad Española de Genética. 16 june.

M. Pérez-Enciso. 2021. Shallow and deep learning in breeding. Intelligence Artificielle et Génétique Animale - 29 juin. INRAE Seminar.

M. Pérez-Enciso. *Loving and hating deep learning.* Invited Talk, Eucarpia Biometrics meeting on Plant Breeding, Paris, 2022

M. Pérez-Enciso. "Beyond Genomic Prediction: Predicting Highly Multidimensional Objects". Invited talk Gordon Conference on Quantitative Genetics and Genomics, Ventura, CA, 2023

Tesis Doctorales dirigidas

Jordi Estellé (co director), 2008, Analysis of QTL and candidate genes for porcine meat and fat quality in an Iberian by Landrace swine cross. UAB, Cum laude, premio extraordinario de doctorado. Actualmente funcionario CR2 del INRA francés en París, Jouy en Josas.

Ana Ojeda (director), 2009. Nucleotide diversity, domestication and modern breeding in pigs, UAB, Cum laude, premio extraordinario de doctorado.

Yang Bin (director), 2011. Network modeling for quantitative traits in pigs. UAB, Cum laude. Apto cum laude. Actualmente investigador en JiangXi Agricultural University, China.

Anna Esteve-Codina (director), 2012. 'Characterization of the Iberian pig genome and transcriptome using high throughput technologies'. Actualmente investigadora en el Centro Nacional de Análisis Genómico (CNAG). Apto cum laude.

Yuliaxis Ramayo-Caldas (codirector), 2013. 'Dissecting the genetic basis of Pig intramscular fatty acid composition' Apto cum laude. Actualmente postdoc en el INRA, Jouy-en-Josas. Apto cum laude. Actualmente funcionario CR2 del INRA francés en París, Jouy en Josas.

William Burgos-Paz (director), 2014. Ancestry and diversity of American villaje pigs. 7 julio 2014. Apto cum laude. Posición actual: Corpoica, Colombia.

Erica Bianco (director, 2015). Using genome-wide polymorphisms to explore demography and feralization in the pig species. Apto cum laude. Current position: postdoc in David Comas' group, UPF, Barcelona.

Jordi Leno-Colorado (director, defendida el 5 julio 2019). Effect of domestication in the pig genome.

Lino Ramírez-Ayala (director, 2016-2020). EVALUACIONES GENÓMICAS DE LAS RAZAS DE GANADO VACUNO EN CLIMAS TROPICALES.

Elies Gurrera (director, 2017-2020). Estrategias de kernel para la predicción de fenotipos complejos

Laura Zingaretti (director, 2017-2020). Deep and shallow learning solutions for modern Agriculture.

Ioanna Vourlaki (codirector, 2023). Detecting signals of polygenic variability in domestication and in breeding.

Nota: Si necesita más casos, añádalos utilizando las funciones de copiar y pegar con el 2º caso.

Participación en comités y representaciones internacionales

Título del Comité:

Entidad de la que depende:
Tema:

Fecha:

Título del Comité:

Entidad de la que depende:
Tema:

Fecha:

Nota: Si necesita más casos, añádalos utilizando las funciones de copiar y pegar con el 2º caso.

Experiencia en organización de actividades de I+D

Organización de congresos, seminarios, jornadas, etc., científicos-tecnológicos

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Título:

Tipo de actividad: Ambito:

Fecha:

Conference on next generation sequencing: challenges and opportunities. 1-3 Octubre 2009. Casa Convalescència, Barcelona. http://ngs2009.uab.es Principal organizador. Cita de Kevin Davies, editor de Bio-IT world:

> *More than 150 delegates attended the 3-day conference. Speakers included Rick Wilson (The Genome Center at Washington University) on cancer genome sequencing; Carlos Bustamante (Cornell University) on principal component analysis of human populations; Gabor Marth (Boston College) on bioinformatics tools for next-gen data analysis; and Gil McVean (University of Oxford) on the 1000 Genomes Project.*
>
> *The meeting included many talks on applications beyond human genomes, including metagenomics and plant genomics. Discussing work on epigenetics, Stephan Beck (University of London) played a video simulation of nanopore sequencing as practiced by Oxford Nanopore Technologies, which has the benefit of being able to detect methylated cytosines, the so-called "fifth base." Beck noted that reports of a "sixth base" earlier this year make the field even more challenging.*
>
> *The conference was superbly organized by Miguel Perez-Enciso (UAB, Universitat Autonoma de Barcelona) and colleagues. A decision has yet to be made on whether the meeting will be held in 2010, despite the glaring need for more first-rate forums for the booming European next-gen sequencing community.*
> http://www.bio-itworld.com/BioIT_Article.aspx?id=94994&terms=barcelona

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Curso sobre 'Systems biology: holism approaches to to genetics and genomics in livestock species". Mayo 2009, Toni Reverter, CSIRO (Australia).

Curso taller de bioperl, a cargo de Bruno Contreras (CSIC, Zaragoza), 25-29 enero 2010, UAB (http://www.eead.csic.es/compbio/material/bioperl/).

Organizador 'STATseq TRAINING SCHOOL ON "Functional Annotation of Genome Sequences in Agricultural Species"', 24-26 April 2013, Helsinki.
http://www.nextgenerationsequencing.it/en/2013/01/statseq-training-school-on-functional-annotation-of-genome-sequences-in-agricultural-species/

Organizador 17 Reunión Nacional de Mejora Genética Animal, Centre de Recerca en Agrigenòmica, Barcelona, 5-6 junio 2014. http://rnmga17.cragenomica.es/

Nota: Si necesita más casos, añádalos utilizando las funciones de copiar y pegar con el 2º caso.

Experiencia de gestión de I+D

Gestión de programas, planes y acciones de I+D

Evaluador

- Agencia Nacional de Evaluación y Prospectiva, España.1999, 2002, 2003, 2004, 2010, 2011,2012, 2013,…
- Agencia Nacional de Promoción Científica y Tecnológica Argentina, 1999, 2003
- The Wellcome Trust (UK), 2001.
- Programa Ramón y Cajal, Area de Ganadería, 2002.
- Ministère de la Recherche, programa de genómica animal (Francia) 2004, 2005, 2006
- Czech Science Foundation, 2006
- Comisión para la promoción de personal investigador INRA (2007 – 2011).
- Centro Nacional de Genotipado, CEGEN, septiembre 2008
- Senacyt, Panamá, 2007, 2008, 2009, 2016
- Cegen (Plataforma de Genoma España) 2008
- Programa Marco Europeo FP7: 2011
- Netherlands Genomics Initiative: 2011
- FONCYT Argentina 2012.
- Freiburg Institute for Advanced Studies (FRIAS, www.frias.uni-freiburg.de) and the University of Freiburg fellowships (2013)
- 2014, 2017: Wageningen Institute of Animal Sciences (WIAS) evaluation of PhD proposal.
- 2014: Evaluador del programa de doctorado de calidad (DK) Interim Evaluation Doctoral Programme (DK 'Vollantrag zu Population Genetics'), de FWF – Austrian Science Fund.
- Revisor ocasional PNAS, Nature Genetics, Nature Communications, PLos Genetics, GigaScience, Molecular Ecology.
- Innumerables artículos en revistas
- Publons (desde 2018): https://publons.com/author/1438761/miguel-perez-enciso#profile
- 2015. Comisión para la elección de personal investigador CR en el INRA.
- 2016: Netherlands Organisation for Scientific Research (NWO-CW)
- 2016: Genoscope, France.
- 2018: Miembro del panel de reclutamiento de una plaza junior en Biología Computacional en el CRAG (2018).
- 2018. Comité de Evaluación de la Unidad GABI (Biología Integrativa) del INRA, Jouy-en-Josas
- 2019, Natural Sciences and Engineering Research Council of Canada.
- 2020, ERC Starting Grant panel, in the field 'Applied Life Sciences, Biotechnology and Molecular and Biosystems engineering'.
- 2022, LUKE, Finland, professorship evaluator

Otros

- Miembro de la Comisión de Investigación de la UAB 2005-2008.
- Editor de la sección de Genética de Animal (sucesora de Anim. Sci. y Annales de Zootechnie). 2005-2006.
- Member of the Editorial Board, J Anim Science sept. 2006 –2008.
- Member of the Editorial Board, Animal Biotechnology 2008
- Editor Asociado GSE 2005 – 2010
- Editor asociado BMC Bioinformatics 2010 –
- Editor Asociado Frontiers in Livestock Genomics: 2010 – 2012
- Editor asociado J. Anim. Breed. Genet. 2012 - 2021
- Miembro de la Junta Directiva de la Sociedad Española de Genética: 2011 – 2014

- Miembro de la Junta de Investigación del CRAG (2011-2014)
- Miembro de tribunales de tesis en España, Suecia, Dinamarca, Argentina, Australia, Francia, Holanda, Finlandia, China.

Otros méritos o aclaraciones que se desee hacer constar

(utilice únicamente el espacio equivalente a una página).

Página personal ICREA:

https://www.icrea.cat/Web/ScientificStaff/Miguel-Perez-Enciso-255

Página github:

https://github.com/miguelperezenciso

Página grupo:

https://bioinformatics.cragenomica.es/numgenomics/

Para impacto en prensa general, buscar 'secuencia cerdo Ibérico' , 'secuencia cerdo antiguo', por ejemplo. Para artículo de divulgación en El País: https://elpais.com/autor/miguel_perez_enciso/a