CURRICULUM VITAE - XAVIER DE LA CRUZ MONTSERRAT

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PERSONAL DATA

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Full name: Francisco Javier de la Cruz Montserrat
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Present situation: ICREA (Institució Catalana de Recerca i Estudis Avançats) Research Professor since november 2001.

The Clinical and Translational Bioinformatics Group [back to Contents page]

RESEARCH INTERESTS

During my career, I have focused on two main research areas: (i) the molecular-level study of biological processes, using models that incorporate different sources of information (e.g., biophysical, structural and biochemical principles, etc.); (ii) the design/development of the computational tools required for the biomedical application of our research. This duality is reflected in my publication profile.

Presently, my main research aims at understanding the molecular basis of hereditary disease, integrating two complementary aspects: the molecular impact of causative variants and how genetic background regulates the propagation of this impact. At a technical level, to reach our objective, in my group we combine the results of the most advanced genomic experiments (single-cell, Hi-C, etc.) using state-of-the-art machine learning tools. To enhance the biomedical reach of our research, we work in collaboration with clinical groups from different hospitals. As a result of these efforts, we have recently made significant advances in understanding the functional effect of BRCA1/2 protein variants underlying hereditary breast and ovarian cancers. Finally, mention that we are also devoting an important part of our work to the fundamental study of epigenetic processes, to reach a full picture of which phenomena contribute to the generation of phenotype and, more precisely, of clinical phenotype.

SCIENTIFIC HIGHLIGHTS

In addition to the standard scientific output, some of our results have deserved special recognition by the community. I want to mention the four most remarkable cases:

- Two of them are related to our work on the identification of pathogenic variants (Riera et al., 2016, Human Mutation):
  - In **2016**, it deserved the Editor's comment (Vihinen, 2016, Human Mutation) in the Human Mutation number where it was published
  - In **2018-2019** we presented our methodology to the international challenge CAGI, in the Hereditary Breast and Ovarian Cancer section where it ranked second in the groups' classification
- In **2015**, we were part of the team that discovered a novel, non-aggressive approach to the diagnosis of glioblastoma (De Mattos-Arruda et al., 2015, Nature Communications); this discovery was a breakthrough in the field and was awarded the price 'Vanguardia de la Ciencia'
- In **2019**, our first results on the suppression of disease-causing mutations were distinguished with the Best Poster Prize from the Editor of the Science journal, at the prestigious conference HGM 2018, Japan.

COLLABORATIONS

We see collaborations as a source of inspiration for our research and the best way to identify and approach the key problems in a field. For this reason, we have engaged ourselves in collaborative projects with different experimental groups, to sharpen our model-building and interpretational abilities, and, more recently, with clinical groups, to validate the applicability of the in silico tools we are generating.

Presently, we have strong (supported by articles either published or in preparation) collaborative links with the following groups:

- **Molecular Biology/Biomedicine:**
  - **Molecular signaling and chromatin (Consejo Superior de Investigaciones Científicas-CSIC),** Marian Martínez Balbás, Barcelona**.** Topic: Study of the molecular basis of epigenetic processes.
  - **Children's Hospital of Philadelphia (University of Pennsylvania)**, Elizabeth Bhoj, Pediatrics and Human Genetics. Topic: Characterization of a novel pediatric neurologic disorder.
  - **Hereditary Cancer Genetics (Vall d'Hebron Institute of Oncology-VHIO)**, Sara Gutiérrez-Orland Díez. Topic: Development of competitive in silico tools for the identification of Hereditary Breast and Ovarian Cancer high-risk variants.
  - **Diagnostic Immunology (Vall d'Hebron Institute of Research-VHIR)**, Roger Colobran. Topic: Understanding of the genetic basis of Primary Immunodeficiencies and use of experimental sequencing for diagnosis purposes.
- **Computational Biology:**
  - **Bioquímica y Biología Molecular y Celular (Universidad de Zaragoza, BIFI),** Javier Sancho. Topic: Development of computational models for understanding the impact of mutations on protein function.
  - **Bioinformática estructural para las ciencias del vino (Consejo Superior de Investigaciones Científicas-CSIC)**, Juan-Fernández Recio. Topic: Impact of genetic variants on protein-protein interactions.

STAYS AND FELLOSWHIPS

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STAYS AT DIFFERENT LABORATORIES

- **1999-2001**. **Universitat de Barcelona, Dep. de Bioquímica y Biología Molecular**. Investigador Reincorporado, lab. of M. Orozco. Research: bioinformatics studies of pathological mutations and alternative splicing; drug design against diabetes; dynamic properties of transcriptional factors and protease inhibitors.
- **1999. EBI-EMBL.** Invited post-doctoral researcher, lab. of J. M. Thornton. Research: protein structure prediction using neural networks.
- **1997-1999. University College London (UCL)**. Senior Post-doctoral, lab. of **J. M. Thornton**. Research: Protein functional annotation using structure-based tools.
- **1993-1997. National Institutes of Health (NIH, USA).** Junior Post-doctoral, lab. of B.K. Lee. Research: Structure prediction and functional studies of the anti-inflammatory protein uteglobin.
- **Spring 1992. ETH-Zürich.** Ph.D. student, lab. of W.F. van Gunsteren. Research: the interaction between a Rhinovirus serotype 2 peptide the corresponding antibody.
- **1990 – 1993. Universitat Politècnica de Catalunya (UPC).** Ph.D. student, lab. of Dr. **I. Fita**,. Research: Protein structure analysis and prediction.

FELLOWSHIPS AND CONTRACTS

Here I only describe the fellowships/contracts I won to support the aforementioned stays; research funding is shown in an independent section below.

- November 2001-Present. **ICREA Research Professor (Institució Catalana de Recerca i Estudis Avançats).**
- September 1999-November 2001. **Ministerio de Educacion y Ciencia: Contrato Reincorporación**. Dpto. Bioquímica y Biología Molecular, Universitat de Barcelona, lab. of M. Orozco.
- October 1997 - October 1999. **HFSP post-doctoral fellowship**. EBI-EMBL, Cambridge/UCL, London, lab. of J. Thornton.
- April 1997 - October 1997. **Ministerio de Educación y Ciencia: contrato formación de doctores y tecnólogos en el extranjero**. UCL, London, lab. of J. Thornton.
- 1/1/1994 - April 1997: **J. Fogarty Fellowship**. NIH, Bethesda USA, lab. of B. K. Lee
- 1/4/92 - 1/7/92 **EMBO Short Term Fellowship**, ETH-Zürich, Switzerland, lab. of W. F. van Gunsteren.
- 1/1/1990 – 31/12/1993: **FPI Fellowship, Generalitat de Catalunya**, Universitat Politècnica de Barcelona, lab. of I. Fita.

RESEARCH FUNDING

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GRANTS

- "Network for the interpretation of neonatal screening: from the mutation to the patient" EFA086/15 – PIREPRED. European Union, ERDEF. Duration: Sep. 2016-Sep. 2020. Amount 827008 euros. Coordinator: Javier Sancho Sanz. Role: Principal Investigator.
- "Aproximaciones para identificar variantes patogénicas en experimentos de secuenciación masiva basadas en la integración de impacto molecular e información biomédica" SAF2016-80255-R. Spanish Ministerio de Economía y Competitividad. Duration Dec. 2016- Dec. 2019. Amount: 96800 euros. Principal investigator: X. de la Cruz
- "Comprensión, predicción y validación del fenotipo de las mutaciones patológicas: transformando los resultados básicos en herramientas de diagnóstico" BIO2014-57314-REDT. Spanish Ministerio de Economía y Competitividad. Duration: 01/12/2014-30/11/2016. Amount: 25000 euros. Call: Redes de Excelencia. Coordinator: Javier Sancho Sanz. Role: Principal Investigator.
- "Desarrollo de herramientas bioinformáticas para la predicción y comprensión de dos rasgos fundamentales de las patologías humanas: severidad y fenotipo tisular". Funding Institution: Asociación Amigos del VHIR. Duration: 09/2014-09/2017. Amount: 60876 euros. Principal investigator: X. de la Cruz
- "Desarrollo de herramientas bioinformáticas para la predicción y comprensión de dos rasgos fundamentales de las patologías hereditarias: severidad y fenotipo tisular" BIO2012-40133. Spanish Ministerio de Economía y Competitividad. Duration Dec. 2012 – Dec. 2015. Amount: 105300 euros. Principal investigator: X. de la Cruz
- Genòmica Estructural i Aplicada. Ref. 2009SGR1222 AGAUR. Duration: 2010-2012. Amount: 43680 euros. Coordinator: J. Roca. Role: Principal Investigator.
- "Estudio bioinformático del papel biológico del splicing alternativo regulador" BFU2009-11527 Spanish Ministerio de Ciencia e Innovación. Duration 2009-2012. Amount: 151250 euros. Principal investigator: X. de la Cruz
- "Estudio de la conservación y convergencia funcional del splicing alternativo regulador" 200420E578 CSIC. Duration: 1/2009-5/2010. Amount: 50000 euros. Principal investigator: X. de la Cruz
- "Estudio bioinformático de la base molecular de las diferencias fenotípicas entre humano y modelos animales: comparación de la diversidad funcional de los proteomas" BIO2006-15557 Spanish Ministerio de Educación y Ciencia. Duration: 2007-2010. Amount: 157300 euros. Principal investigator: X. de la Cruz.
- "Mejora en la calidad de los modelos de baja resolución de la estructura de las proteínas mediante el uso de comparaciones estructurales y modelado por homología" BIO2003-09327 Spanish Ministerio de Investigación y Tecnología. Duration: 2003-2006. Amount: 139150 euros. Principal investigator: X. de la Cruz.
- "Use of protein structure comparison methods and homology modeling techniques to improve the quality of experimental and computational low-resolution models of protein structures" 069878/Z/02/Z Wellcome Trust. Duration: 2003-2006. Amount: 10931 euros. Coordinator: C. Orengo. Principal investigator: X. de la Cruz

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GRANTS FOR SUPERCOMPUTER TIME

- "Computational study of the molecular basis of allosteric mechanisms and its conservation among species" BCV-2008-1-0012, BCV-2009-1-0003 (Barcelona Supercomputing Center). Amount of supercomputer time: 896 Khours. NOTE: This project was the second highest-ranking project, in resources allowed, of the call. Principal Investigator: X. de la Cruz
- "Molecular Dynamics Simulation of the Folding/Unfolding Mechanism of Apoflavodoxin" BCV-2007-2-0003, BCV-2008-1-0014. BSC (Barcelona Supercomputing Center). Amount of Supercomputer Time: 350 Khours. Principal Investigator: X. de la Cruz.

GRANTS AS TEAM MEMBER

- "Design of new oligonucleotide-based antigene and antisense therapies" Fundación BBVA Duration: 2004-2005. Amount: 70000 euros. Principal investigator: Modesto Orozco.
- "Aproximación bioinformática a la selección de genes asociados a la diabetes de tipo 2" Ministerio de Ciencia y Tecnología. Duration: 2002-2005. Amount: 97000 euros. Principal investigator: Francisco Javier Luque.
- "Aproximación bioinformática al estudio de las mutaciones patológicas" Ramón Areces Foundation. Duration: 2002-2005. Amount: 60101 euros. Principal investigator: Modesto Orozco.
- "Ajuts per al desenvolupament i consolidació de xarxes tematiques" Generalitat de Catalunya, Duration: 2002-2004. Amount: 8414,17 euros. Principal investigator: Modesto Orozco.
- "Ciclo de Conferencias de Bioinformática 2002" DURSI, Generalitat Catalunya, Duration: 2002-2002. Amount: 1323,00 euros. Principal investigator: Modesto Orozco.
- "Ciclo de Conferencias de Bioinformática 2001" DURSI, Generalitat Catalunya, Duration: 2001-2001. Amount: 2854,81 euros. Principal investigator: Modesto Orozco.
- "Ciclo de Conferencias de Bioinformática 2000" DURSI, Generalitat Catalunya, Duration: 2000-2000. Amount: 2404,05. Principal investigator: Modesto Orozco.

DOCTORAL THESES

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- “A Machine Learning Model for Improving the Annotation of Protein Sequence Variants in Sequencing Projects” Elena Álvarez de la Campa Crespo, november 2019. Grade: Excelente.
- “Estudio de las propiedades conformacionales de las proteínas mediante el uso de los modelos de baja resolución basados en la discretización de las coordenadas internas” Francisco Martín Bandera, july 2018. Grade: Excelente.
- “Caracterització bioinformàtica de la relació entre l'impacte molecular de les variants patogèniques i el fenotip clínic” Oscar Marín i Sala, july 2017. Grade: Excelente.
- “Novel approaches in the identification of pathogenic variants in the clinical diagnosis” Casandra Riera Ribas, september 2016. Grade: Excelente Cum Laude.
- "Estudi bioinformàtic de la funcionalitat i conservació de l'splicing alternatiu" Jordi Morata Chirivella, june 2012. Grade: Excelente Cum Laude.
- "Análisis Bioinformático de los Reguladores Epigenéticos" Sergio Lois Olmo, july 2012. Grade: Excelente Cum Laude.
- “Caracterització i millora de models estructurals de baixa resolució” David Piedra García, january 2009. Grade: Excelente Cum Laude.
- “Caracterització bioinformàtica de la contribució de l’splicing alternatiu a la variabilitat del proteoma” David Talavera i Baró, july 2007. Grade: Excelente Cum Laude. **NOTE:** Awarded the “Premi Especial de Doctorat” from the Universitat de Barcelona.
- “Anàlisi Bioinformàtica de les mutacions puntuals patològiques” Carles Ferrer Costa, july 2005. Grade: Excelente Cum Laude.

PUBLICATIONS

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BOOK CHAPTERS

- "Alternative splicing as a source of phenotypic differences between species: protein-level mechanisms" Jordi Morata, Casandra Riera and **Xavier de la Cruz**. In "Evolutionary Biology: Mechanisms and Trends", edited by Pierre Pontarotti (2012). Chapter 19, pp343-356. Springer-Verlag.
- "Contributions of structure comparison methods to the protein structure prediction field" David Piedra, Marco d'Abramo and **Xavier de la Cruz**. In "Bioinformatics", edited by H.S.Lopes and L. Magalhaes (2011). Chapter 17, pp329-344. InTech.
- "Data Mining of Molecular Dynamic Trajectories of Nucleic Acids" Modesto Orozco, Agnes Noy, Tim Meyer, Manuel Rueda, Carler Ferrer, Antonio Valencia, Alberto Pérez, Oliver Carrillo, Juan Fernández-Recio, **Xavier de la Cruz**, Fco.Javier Luque. In "Computational Studies of RNA and DNA", edited by J.Sponer and F.Lankas (2006) pp121-145. Springer-Verlag.
- "Conformation of lysine in oligopeptides", Perello, M., **de la Cruz, X.**, Verdaguer, N., Urpi, L., Fita, I., Aymami, J., Lloveras, J. and Subirana, J.A. Proceedings of the Twenty-First European Peptide Symposium (1990) Ed. Giralt, E and Andreu, D., pp 456-457, ESCOM Science Publishers B.V.

JOURNALS: INTERNATIONAL (*Corresponding)

- "PHF2 histone demethylase prevents DNA damage and genome instability by controlling cell cycle progression of neural progenitors" Pappa S., Padilla N., Iacobucci S., Vicioso M., Alvarez de la Campa ., Navarro C., Marcos E., **de la Cruz X***., Martinez-Balbas MA*. Proc Natl Acad Sci U S A. (2019) 116:19464-19473.
- "BRCA1- and BRCA2-specific in silico tools for variant interpretation in the CAGI 5 ENIGMA challenge" Padilla N., Moles-Fernandez A., Riera C., Montalban G., Ozkan S., Ootes L., Bonache S., Diez O., Gutierrez-Enriquez S., **de la Cruz X***. Hum Mutat. (2019) 40:1593-1611. NOTE: JOURNAL COVER.
- "Compensated pathogenic variants in coagulation factors VIII and IX present complex mapping between molecular impact and hemophilia severity" Marin O., Aguirre J., **de la Cruz X***. Sci Rep. (2019) 9(1):9538.
- "Increased dNTP pools rescue mtDNA depletion in human POLG-deficient fibroblasts" Blazquez-Bermejo C., Carreno-Gago L., Molina-Granada D., Aguirre J., Ramon J., Torres-Torronteras J., Cabrera-Perez R., Martin MA., Dominguez-Gonzalez C., **de la Cruz X**., Lombes A., Garcia-Arumi E., Marti R., Camara Y. FASEB J. (2019) 33:7168-7179.
- "Epigenetic signature for attention-deficit/hyperactivity disorder: identification of miR-26b-5p, miR-185-5p, and miR-191-5p as potential biomarkers in peripheral blood mononuclear cells" Sanchez-Mora C., Artigas MS., Garcia-Martinez I., Pagerols M., Rovira P., Richarte V., Corrales M., Fadeuilhe C., Padilla N., **de la Cruz X**., Franke B., Arias-Vasquez A., Casas M., Ramos-Quiroga JA., Ribases M Neuropsychopharmacology. (2019) 44:890-897.

- "Structural and Computational Characterization of Disease-Related Mutations Involved in Protein-Protein Interfaces" Navio D, Rosell M, Aguirre J, **de la Cruz X**, Fernandez-Recio J. Int J Mol Sci. (2019) 20(7).
- "Assessment of blind predictions of the clinical significance of BRCA1 and BRCA2 variants" Cline MS., Babbi G., Bonache S., Cao Y., Casadio R., **de la Cruz X**., Diez O., Gutierrez-Enriquez S., Katsonis P., Lai C., Lichtarge O., Martelli PL., Mishne G., Moles-Fernandez A., Montalban G., Mooney SD., O'Conner R., Ootes L., Ozkan S., Padilla N., Pagel KA., Pejaver V., Radivojac P., Riera C., Savojardo C., Shen Y., Sun Y., Topper S., Parsons MT., Spurdle AB., Goldgar DE. Hum Mutat. (2019) 40:1546-1556.
- "Lineage specific transcription factors and epigenetic regulators mediate TGFbeta-dependent enhancer activation" Fueyo R., Iacobucci S., Pappa S., Estaras C., Lois S., Vicioso-Mantis M., Navarro C., Cruz-Molina S., Reyes JC., Rada-Iglesias A., **de la Cruz X**., Martinez-Balbas MA. Nucleic Acids Res. (2018) 46:3351-3365.
- "Improving the diagnosis of cobalamin and related defects by genomic analysis, plus functional and structural assessment of novel variants" Brasil S., Leal F., Vega A., Navarrete R., Ecay MJ., Desviat LR., Riera C., Padilla N., **de la Cruz X**., Couce ML., Martin-Hernandez E., Morais A., Pedron C., Pena-Quintana L., Rigoldi M., Specola N., de Almeida IT., Vives I., Yahyaoui R., Rodriguez-Pombo P., Ugarte M., Perez-Cerda C., Merinero B., Perez B. Orphanet J Rare Dis. (2018) 13:125.
- "PMut: a web-based tool for the annotation of pathological variants on proteins., (2017 update" Lopez-Ferrando V., Gazzo A., **de la Cruz X**., Orozco M., Gelpi JL. Nucleic Acids Res. (2017) 45:W222-W228.
- "The histone demethylase PHF8 is a molecular safeguard of the IFNγ response" Asensio-Juan, E., Fueyo, R., Pappa, S., Iacobucci, S., Badosa, C., Lois, S., Balada, M., Bosch-Presegué, L., Vaquero, A., Gutiérrez, S., Caelles, C., Gallego, C., de la Cruz, X., Martínez-Balbás, M. Nucleic Acids Res. (2017) 45:3800-3811.
- "Elucidating the molecular basis of msh2-deficient tumors by combined germline and somatic analysis" Vargas-Parra GM., Gonzalez-Acosta M., Thompson BA., Gomez C., Fernandez A., Damaso E., Pons T., Morak M., Del Valle J., Iglesias S., Velasco A., Solanes A., Sanjuan X., Padilla N., **de la Cruz X**., Valencia A., Holinki-Feder E., Brunet J., Feliubadalo L., Lazaro C., Navarro M., Pineda M., Capella G. Int J Cancer. (2017) 141:1365-1380.
- "Identification and characterization of the novel point mutation m.3634A>G in the mitochondrial MT-ND1 gene associated with LHON syndrome" Carreno-Gago L., Gamez J., Camara Y., Alvarez de la Campa E., Aller-Alvarez JS., Moncho D., Salvado M., Galan A., **de la Cruz X**., Pinos T., Garcia-Arumi E. Biochim Biophys Acta. (2017) 1863:182-187.
- "Development of pathogenicity predictors specific for variants that do not comply with clinical guidelines for the use of computational evidence" de la Campa EA., Padilla N., **de la Cruz X**. BMC Genomics. (2017) 18(Suppl 5):569.

- "Early Versus Late Diagnosis of Complement Factor I Deficiency: Clinical Consequences Illustrated in Two Families with Novel Homozygous CFI Mutations" Franco-Jarava C., Alvarez de la Campa ., Solanich X., Morandeira-Rego F., Mas-Bosch V., Garcia-Prat M., **de la Cruz X**., Martin-Nalda A., Soler-Palacin P., Hernandez-Gonzalez M., Colobran R. J Clin Immunol. (2017) 37:781-789.
- "Elucidating the clinical significance of two PMS2 missense variants coexisting in a family fulfilling hereditary cancer criteria" Gonzalez-Acosta M., Del Valle J., Navarro M., Thompson BA., Iglesias S., Sanjuan X., Paules MJ., Padilla N., Fernandez A., Cuesta R., Teule A., Plotz G., Cadinanos J., **de la Cruz X**., Balaguer F., Lazaro C., Pineda M., Capella G. Fam Cancer. (2017) 16:501-507
- "The Complementarity Between Protein-Specific and General Pathogenicity Predictors for Amino Acid Substitutions" Riera C., Padilla N., **de la Cruz X***. Hum Mutat. (2016) 37:1013-1024.
- "EZH2 regulates neuroepithelium structure and neuroblast proliferation by repressing p21" Akizu N., Garcia MA., Estaras C., Fueyo R., Badosa C., **de la Cruz X**., Martinez-Balbas MA. Open Biol. (2016) 6(4).
- "Clinical and structural impact of mutations affecting the residue Phe367 of FOXP3 in patients with IPEX syndrome" Colobran R., Alvarez de la Campa ., Soler-Palacin P., Martin-Nalda A., Pujol-Borrell R., **de la Cruz X**., Martinez-Gallo M. Clin Immunol. (2016) 163:60-65.
- "Novel Mutations Causing C5 Deficiency in Three North-African Families" Colobran R., Franco-Jarava C., Martin-Nalda A., Baena N., Gabau E., Padilla N., **de la Cruz X**., Pujol-Borrell R., Comas D., Soler-Palacin P., Hernandez-Gonzalez M. J Clin Immunol. (2016) 36:388-396.
- "Molecular damage in Fabry disease: Characterization and prediction of alpha-galactosidase A pathological mutations" Riera C., Lois S., Dominguez C., Fernandez-Cadenas I., Montaner J., Rodriguez-Sureda V., **de la Cruz X***. Proteins. (2015) 83:91-104.
- "Cerebrospinal fluid-derived circulating tumour DNA better represents the genomic alterations of brain tumours than plasma" De Mattos-Arruda L., Mayor R., Ng CK., Weigelt B., Martinez-Ricarte F., Torrejon D., Oliveira M., Arias A., Raventos C., Tang J., Guerini-Rocco E., Martinez-Saez E., Lois S., Marin O., **de la Cruz X**., Piscuoglio S., Towers R., Vivancos A., Peg V., Cajal SR., Carles J., Rodon J., Gonzalez-Cao M., Tabernero J., Felip E., Sahuquillo J., Berger MF., Cortes J., Reis-Filho JS., Seoane. Nat Commun. (2015) 6:8839. **NOTE: Awarded the Price 'Vanguardia de la Ciencia'**.
- "Functional consequences of transferrin receptor-2 mutations causing hereditary hemochromatosis type 3" Joshi R., Shvartsman M., Moran E., Lois S., Barque A., **de la Cruz X**., Bruguera M., Vagace JM., Gervasini G., Sanz C., Sanchez M. Mol Genet Genomic Med. (2015) 3:221-232.
- "Molecular dynamics study of naturally existing cavity couplings in proteins" Barbany M., Meyer T., Hospital A., Faustino I., D'Abramo M., Morata J., Orozco M., **de la Cruz X***. PLoS One. (2015) 10:e0119978.

- "Identification and characterization of a novel splice site mutation in the SERPING1 gene in a family with hereditary angioedema", Colobran, R., Lois, S., **de la Cruz, X.**, Pujol-Borrell, R., Hernández, M. and Guilarte, M. Clin Immunol. (2014) 150:143-148.
- "Prediction of pathological mutations in proteins: the challenge of integrating sequence conservation and structure stability principles" Riera, C., Lois, S. and **de la Cruz, X.*** WIREs Mol. Comp. Sci. (2014) 4:249–268.
- "Genome-wide study of the relationship between transcript diversity and *cis*-regulatory and protein divergence: linking the molecular sources of phenotypic differences" Morata, J., Béjar, S., Mas de Xaxars, G. and **de la Cruz, X.*** PLoS ONE, Vol. 8, Number 8, 2013.
- "JMJD3 activates neuronal differentiation program by allowing RNA Pol II elongation in response to TGFβ signaling" Estarás, C., Akizu, N., **de la Cruz, X.***, and Martínez-Balbás, M. Development (2012) 139:2681-2691.
- "Dynamics of glutathione S-transferase and ectodysplasin-A isoforms: the impact of alternative splicing on protein flexibility" Barbany, M., Morata, J., Meyer, T., Lois, S., Orozco, M. and **de la Cruz, X.*** Proteins (2012) 80:2235–2249.
- "Scoring by intermolecular pairwise propensities of exposed residues (SIPPER): a new efficient potential for protein-protein docking" Pons, C., Talavera, D., **de la Cruz, X.**, Orozco, M., Fernandez-Recio, J. Chem. Inf. Model. (2011) 51:370-377.
- "Characterization of structural variability sheds light on the specificity determinants of the interaction between effector domains and histone tails" Lois, M., Akizu, N., Mas de Xaxars, G., Vázquez, I., Martínez-Balbás, M. and **de la Cruz, X.*** Epigenetics (2010) 5:137-148. **NOTE:** JOURNAL COVER.
- "Autoacetylation regulates P/CAF nuclear localization" Blanco-García N., Asensio-Juan E., **de la Cruz X.** and Martínez-Balbás M.A. J. Biol. Chem. (2009) 284:1343-1352.
- "An atomistic view to the gas phase proteome" Meyer, T., **de la Cruz, X.** and Orozco, M. Structure (2009) 17:88-95.
- "Preservation of protein clefts in comparative models" Piedra, D., Lois, S. and **de la Cruz, X.*** BMC Struct Biol. (2008) 8:2.
- "A procedure for identifying homologous alternative splicing events" Talavera, D., Hospital, A., Orozco, M. and **de la Cruz, X.*** BMC Bioinformatics (2007) 8:260.
- "The functional modulation of epigenetic regulators by alternative splicing" Lois, S., Blanco, N., Martínez-Balbás, M. and **de la Cruz, X.*** BMC Genomics (2007) 8:252. **NOTE:** "HIGHLY ACCESSED".
- "Involvement of chromatin and histone deacetylation in the SV40 T antigen transcription regulation" Valls, E.; Blanco-García, N.; Aquizu, N.; Piedra, D.; Estarás, C.; **de la Cruz, X.**, Martínez-Balbás, M. Nucleic Acids Res. (2007) 35:1958-1968.
- "The (In)dependence of Alternative Splicing and Gene Duplication" Talavera, D., Vogel, C., Orozco, M., Teichmann, S. and **de la Cruz, X.*** PLoS Comp. Biol. (2007) 3(3):e33. **NOTE:** JOURNAL COVER.

- "Characterization of compensated mutations in terms of structural and physico-chemical properties" Ferrer-Costa, C., Orozco, M. and **de la Cruz, X.*** J.Mol.Biol. (2007) 365:249-256.
- "A fast method for the determination of fractional contributions to solvation in proteins" Talavera D, Morreale A, Meyer T, Hospital A, Ferrer-Costa C, Gelpi JL, **de la Cruz X**, Soliva R, Luque FJ, Orozco M. Protein Science. (2006) 15:2525-2533.
- "Data mining of molecular dynamics trajectories of nucleic acids" Noy A., Meyer T., Rueda M., Ferrer C., Valencia A., Perez A., **de la Cruz X.**, Lopez-Bes J.M., Pouplana R., Fernandez-Recio J., Luque F.J., Orozco M. J. Biomol. Struct. Dyn. (2006) 23:447-456.
- "Use of Bioinformatics Tools for the Annotation of Disease-Associated Mutations in Animal Models" Ferrer-Costa, Orozco, M. and **de la Cruz, X.*** Proteins (2005) 61: 878-887.
- "Exploring the Essential Dynamics of B-DNA" Perez, A., Blas, J. R., Rueda, M., Lopez-Bes, J. M., **de la Cruz, X.** and Orozco, M. J. Chem. Theory and Comput. (2005) 1: 790-800.
- "PupasView: a visual tool for selecting suitable SNPs, with putative pathological effect in genes, for genotyping purposes." Conde, L., Vaquerizas, J.M., Ferrer-Costa, C., **de la Cruz, X.**, Orozco, M. and Dopazo J. Nucleic Acids Res. (2005) 33(Web Server issue):W501-W505.
- "PMUT: A web-based tool for the annotation of pathological mutations on proteins" Ferrer-Costa, C., Gelpí, J.L., Zamacola, L., Párraga, I., **de la Cruz, X.** and Orozco, M. Bioinformatics (2005) 35: 3176-3180.
- "Do protein-motifs read the histone code ?" **de la Cruz, X.**, Lois, S., Sánchez-Molina, S. and Martínez-Balbás, M. Bioessays (2005) 27:164-175.
- "Partition of protein solvation into group contributions from molecular dynamics simulations" Morreale, A., **de la Cruz, X.**, Meyer, T., Gelpí, J.L., Luque, F.J. and Orozco, M. Proteins (2005) 58: 101-109.
- "Sequence-based prediction of pathological mutations" Ferrer-Costa, C., Orozco, M., **de la Cruz, X.*** Proteins (2004) 57: 811-819.
- "Linear-response theory: An alternative to PB and GB methods for the analysis of molecular dynamics trajectories?" Morreale, A., **de la Cruz, X.**, Meyer, T., Gelpí, J.L., Luque, F.J. and Orozco, M. Proteins (2004) 57: 458-467.
- "Exploring the binding mode of semicarbazide-sensitive amineoxidase/VAP-1: Identification of novel substrates" Marti, L., Abella, A., **de la Cruz, X.**, Unzeta, M., Carpene, C., Palacín, M., Testar, X., Orozco, M. and Zorzano, A. J.Med.Chem. (2004) 47: 4865-4874.
- "Triplex Targets Sequences in the Human Genome" Goñi, R., **de la Cruz, X.**, Orozco, M. Nucleic Acids Res. (2004) 32: 354-360.
- "Alternative Splicing mechanisms for the modulation of protein function: conservation between human and other species" Valenzuela, A., Talavera, D. Orozco, M., **de la Cruz, X.*** J.Mol.Biol. (2004) 335: 495-502.

- “The SV40 T-antigen modulates CBP Histone Acetyltransferase activity” Valls, E., **de la Cruz, X.**, Martínez-Balbás, M. Nucleic Acids Res. (2003) 31:3114-3122.
- “Towards Predicting Protein Topology: A Novel Approach to Identifying β-hairpins” **de la Cruz, X.***, Hutchinson, E.G., Shepherd, A. and Thornton, J.M. Proc.Natl.Acad.Sci. USA (2002) 99: 11157-11162.
- “Characterization of disease-associate single amino acid polymorphisms in terms of sequence and structure properties” Ferrer-Costa, C., Orozco, M., **de la Cruz, X.*** J.Mol.Biol. (2002) 315:771-786.
- “hSos1 Contains a New Amino-terminal Regulatory Motif with Specific Binding Affinity for Its Pleckstrin Homology Domain” Jorge, R., Zarich, N., Oliva, J.L., Azañedo, M., Martínez, N., **de la Cruz, X.**, Rojas, J.M. J.Biol.Chem. (2002) 277: 44171-44179.
- “Ligand-induced changes in the binding sites of proteins” Pradera, X., **de la Cruz, X.**, Silva, C.H.T.P., Gelpí, J.L., Luque, F.J., Orozco, M. Bioinformatics (2002) 18:939-948.
- "Use of Structure Comparison Methods for the Refinement of Protein Structure Predictions. I. Identifying the Structural Family of a Protein from Low Resolution Models", **de la Cruz, X.***, Sillitoe, I. and Orengo, C. Proteins (2002) 46: 72-84. **NOTE:** "HIGHLY ORIGINAL CONTRIBUTION IN BIOINFORMATICS" (Rost, B. 2002, The Scientist, section “New & Notable”. 16(6): 37).
- “Classical Molecular Interaction Potentials: An Improved Set-Up Procedure in Molecular Dynamics Simulations of Proteins” Gelpí, J.L., Kalko, S., Barril, X., Cirera, J., **de la Cruz, X.**, Luque, F.J. and Orozco, M. Proteins (2001) 45:428-437.
- "Use of surface area computations to describe atom-atom interactions" **de la Cruz, X.*** and Calvo, M. J.Comp-Aided Mol.Des. (2001) 15:521-532.
- "Export of a Cysteine-free Misfolded Secretory Protein from the Endoplasmic Reticulum for Degradation Requires Interaction with Protein Disulfide Isomerase" Gillece, P., Luz, J.M., Lennarz, W.J., **de la Cruz, X**. and Romisch, K. J.Cell Biol. (1999) 147, 1443 -1456.
- "Factors limiting the performance of prediction based fold recognition methods" **de la Cruz, X.** and Thornton, J., Protein Science (1999) 8, 750 - 759.
- "A new procedure for Constructing Peptides into a Given Ca-chain", Wang, Y., Huq, H.I., **de la Cruz, X**. and Lee, BK, Folding and Design (1997) 3, 1 - 10.
- "Discrete Representations of the protein Cα chain",**de la Cruz,X**. and Lee,BK, Folding and Design (1997) 2,, 223 - 234.
- "The structural homology between Uteroglobin and the pore-forming domain of Colicin A suggests a possible mechanism of action for Uteroglobin" **de la Cruz, X.,** and Lee, BK, Protein Science (1996) 5, 857-861.
- "A 15 amino acid stretch close to the Grb2-binding domain defines two differentially expressed hSos1 isoforms with markedly different Grb2 binding affinity and biological activity" Rojas, J.M., Coque, J.J.R., Guerrero, C., Aroca, P., Font de Mora, J., **de la Cruz, X.**, Lorenzi, M.V. and Santos, E., Oncogenes (1996) 12, 2291-2300.

- "Investigation of shape variations in the antibody binding site by molecular dynamics computer simulation" **de la Cruz, X.**, Mark, A.E., Tormo, J., Fita, I. and van Gunsteren, W.F. J.Mol.Biol (1994) 236, 1186 - 1195.
- "Representation of noncovalent interactions in protein structures" **de la Cruz, X.**, Reverte, J. and Fita, I. J.Mol.Graph. (1992) 10, 96 - 100.
- "Structure of trans-Diaquabis[(2'-acetamido)-2-oxopyrrolidine] Copper (II) Perchlorate" **de la Cruz, X**., Martinez-Balbas, A., Tormo, J. and Verdaguer, N. Acta Crys. (1992) C48, 118 - 121.
- "Structure of L-Lysinamide Dihydrochloride. A New conformation of the Lysine Side Chain" **de la Cruz, X**., Tormo, J., Fita, I. and Subirana, J.A. Acta Cryst. (1991) C47, 1705 - 1707.
- "Atomic accessible and contact surfaces as restraints in the Hendrickson-Konnert refinement program" **de la Cruz, X.** and Fita, I. J.Appl.Cryst. (1991) 24, 941 -946.

JOURNALS: NATIONAL

- "Modelització, bioinformàtica i supercomputació" Orozco, M., **de la Cruz, X.**, Luque, F.J. (2002). Teraflop 65:13-15.
- "El ADN de la Química a la Bioinformática" **de la Cruz, X.** and Subirana, J.A. Anal.Real Soc.Quim. (2000) 96, 7-12.
- "Evaluation of "Free Energy" for non-covalent interactions in protein structures" **de la Cruz, X**. and Fita, I. Butll.Soc.Cat.Cien. (1991) Vol.XII, 2, 479-485.

PERIODICALS

- "El misterio científico del plegamiento de las proteínas" **de la Cruz, X.**, Fita, I., 1989, La Vanguardia.

EVALUATOR/REVIEWER ACTIVITIES

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PROJECT EVALUATOR

For International Agencies. Worked for: EU (International), BBSRC (UK), HFSP (International), FRM (France), Foundation for Research and Technology (FORTH, Greece)) and the Mount Sinai School of Medicine (USA).

For National Agencies. Member of the ANEP's comisión de base, years 2008-2009. Current project evaluator for the Spanish evaluation agency ANEP (2005-present); evaluator of the Juan de la Cierva fellowhips (2007); evaluator of the Ramón y Cajal contracts (2008). Evaluator for the Servicio Galego de Saúde (2009) and the Agencia para la Calidad del Sistema Universitario de Castilla y León (2008). Evaluator of the Beatriu de Pinós fellowships for the AGAUR (2006).

REVIEWER

Has refereed articles for the following journals: PLoS Genetics, PLoS Comp Biol, Current Opinion in Structural Biology, Nucleic Acids Research, WIREs Computational Molecular Science, Human Mutation, Human Molecular Genetics, Bioinformatics, J.Mol.Biol., Febs. Letters, BMC Bioinformatics, BMC Genomics, BMC Medical Genomics, Proteins, Protein Science, Theoretical Chemistry Accounts, Plos One.

CONFERENCES/MEETINGS/COURSES

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A. Organization

- January **2018** - Scientific organizer. Meeting "The bench to bedside pathway: where are we now?" – 2nd PIREPRED Scientific Meeting.
- December **2017** - Co-organizer. Meeting "V Jornada de Bioinformàtica i Genòmica", Societat Catalana de Biologia, Barcelona.
- January, **2016** - Organizer. Course "Identificación y análisis de mutaciones en proyectos de secuenciación masiva (exomas y paneles) en biomedicina: una visión práctica" Specialized course given by my group at the Universidad Autónoma de Madrid.
- December, **2015** - Organizer. Course "Identificación y análisis de mutaciones en proyectos de secuenciación masiva (exomas y paneles) en biomedicina: una visión práctica" Specialized course given by my group at the Instituto de Investigación Sanitaria Aragón, Zaragoza.
- February, **2015** - Co-organizer. Course "Identification and analysis of sequence variants in sequencing projects: fundamentals and tools" VHIR-CNAG, Barcelona.
- October **2014** - Organizer. Conference "The impact of genomics in translational medicine: present view", Barcelona.
- June, **2008**. Co-organizer. BSC-IRB. "Grand Challenges in Computational Biology", Barcelona.
- September, **2007**. Programme committee. "5th International Workshop on Biological Data Management (BIDM'07)", Regensburg, Germany.
- July, **2006**. Scientific Commitee. "Current challenges in computational structural biology: improving model refinement for functional predictions - MODREF2006" Barcelona.
- June **2005** - Co-Organizer. Conference "II Reunión Nacional de Modelización Molecular y QuimioInformática", Barcelona.
- May, **2003**. Organizer/Scientific Responsible. ICREA Conference. "Bioinformatics: present applications and future challenges", Parc Científic Barcelona, Barcelona.
- **2002, 2003, 2005** - Co-Organizer. Conference "Jornades Xarxa Catalana de Bioinformàtica", Lleida.
- **2000, 2001, 2002, 2003**. Co-organizer. Talk Series. "Bioinformática 2000", Parc Científic Barcelona.

B. Invited talks and chairmanships

From 2019 to 2014

- "From Mutations to Disease Using Computers Only: Is This a Dream?", BIFI2019, Zaragoza, **Opening Lecture/Keynote Speaker**.
- "BRCA1- and BRCA2-specific in silico tools for variant interpretation in the CAGI 5 ENIGMA challenge" CAGI Workshop, San Francisco USA. **Co-Invited Flash talk**.
- "The molecular component in Genomic Medicine: laying the foundations for the identification of pathogenic variants", 3rd PIREPRED Scientific Meeting, Pamplona, 2018, **Invited talk**.

- "The clinical costs of in silico tools: a novel approach to chose the best pathogenicity predictor for healthcare applications" VI Jornada de Bioinformàtica i Genòmica, Barcelona, 2018, **Co-Invited talk**.
- "Reptes en Systems Biology", Fund. Acadèmica de Ciències Mèdiques de Catalunya i de Balears, 2018, **Discussion Panel**.
- "Cost: an (un)expected link between basic research and clinical applications?" 2nd PIREPRED Scientific Meeting, Barcelona, 2018. **Invited talk**.
- "The biomedical/clinical approach to Rare Diseases. An Overview." 2nd PIREPRED Scientific Meeting, Barcelona, 2018. **Chair**.
- "From measuring mutation impact to diagnostics yield: the path of translational research" 1st PIREPRED Scientific Meeting, Bilbao, 2017. **Invited talk**.
- "Los diferentes niveles de estructura en biología y su relación con las aplicaciones biomédicas" 10th Scientific Meeting, VHIR, Barcelona, 2016. **Invited talk**.
- "Aplicación de la secuenciación en un entorno biomédico/clínico: avances y desafíos" Meeting of the Red de Excelencia "Comprensión, predicción y validación del fenotipo de las mutaciones patológicas", Zaragoza, 2015. **Invited talk**.
- “Identification of pathological variants in sequencing projects: a practical view of the interpretation problem” IDIBAPS – CLINIC, 2015. **Invited seminar**.
- "Identification of pathological variants: successes, risks and the incidentalome" "The impact of genomics in translational medicine: present view", VHIR 20th Anniversary Meeting, Barcelona, 2014. **Invited talk**.
- "The challenge of improving the identification of pathological mutations beyond 80%",10th Workshop on Genomics and Proteomics - SCB, Barcelona, 2014. **Invited talk**.

Before 2014

- Session "Genome Evolution" 17th EBM Conference, Marseille, 2013, **Chair**.
- "The relationship between gene number of exons and protein divergence", 17th EBM Conference, Marseille, 2013, **Invited talk**.
- "Alternative splicing and stochastic gene expression", Global Questions on Advanced Biology, Centenary Societat Catalana de Biologia (1912-2012), Barcelona, 2012, **Invited talk**.
- "The functional role of alternative splicing: from protein to cell levels", ICGEB, Trieste, 2012, **Invited talk**.
- "Protein sequence mutations and severity phenotype in disease", 16th EBM Conference, Marseille, 2012, **Invited talk**.
- "From genotype to phenotype using computational tools", Frontiers of Molecular Biology, IBMB-CSIC, Barcelona, 2011, **Invited talk**.
- "Alternative splicing: its impact on protein diversity of specific gene families and its relationship with cis-regulatory and protein divergence" 15th EBM Conference, Marseille, 2011, **Invited talk**.

- Session "Evolutionary Biology Concepts" 15th EBM Conference, Marseille, 2011, **Chair**.
- "Stochastic gene expression and alternative splicing" ISMB/ECCB, Vienna, 2011, **Invited talk**.
- "Structural Analysis of the Specificity Determinants of the Interaction Between Histone Tails and Effector Domains" Epigenetics Europe, Dublin, 2010. **Invited talk.**
- "The regulatory role of alternative splicing" UCL, London, 2009. **Invited talk.**
- "Bioinformatics characterization of protein variability" IRB-PCB, Barcelona, 2008. **Invited talk.**
- "Alternative splicing at the protein level" Centro de Biología Molecular (CBM)-CSIC, Madrid, 2006. **Invited talk.**
- "Alternative splicing at the protein level. A view from bioinformatics" UCL, London, 2006. **Invited talk.**
- "SPLASH - A simple procedure for the annotation of alternative splicing events at the protein level" EBI-EMBL, Cambridge, 2006. **Invited talk.**
- "El impacto funcional del splicing alternativo a nivel de proteinas. Elcaso de las proteinas asociadas a los procesos epigenéticos" IDIBAPS-CLINIC, Barcelona, 2006. **Invited talk.**
- "Modulacion de la funcion de las proteinas mediante splicing alternativo" Centro de Investigación Príncipe Felipe, Valencia, 2006. **Invited talk.**
- "Base molecular de las mutaciones simultáneamente patológicas en humanos y neutras en otros organismos" Institut Cavanilles de Biodiversitat, Valencia, 2006. **Invited talk.**
- "Prediction of pathological mutations using bioinformatics tools". In "Protein Production and Bioinformatics", Barcelona, 2006. **Invited talk.**
- "II Reunión Nacional de Modelización Molecular y QuimioInformática", Barcelona, 2005. **Chair**, Session VII "Bioinformatics".
- "Nuevas tendencias en bioinformatica aplicada a la biomedicina" Universidad de Cantabria, may 2004. **Invited talk.**
- "Prediction of pathological mutations from sequence" In *SNPs analysis, tools and applications*, ESF Programme on Integrated Approaches for Functional Genomics, CNIO, Madrid, 2003. **Invited talk**.
- IV Jornadas de Bioinformática, La Coruña. 2003. **Chair**, Session "Bioinformática Estructural".
- "Predicción de mutaciones patológicas mediante redes neuronales" Round Table: *Tecnologías de la informática al servicio de la genética*, 22 Congreso Nacional de Genética Humana, Zaragoza, 2003. **Invited talk**.
- "Predicting pathological mutations from protein sequence" SYMPOSIUM *Relating molecular evolution and protein function*, Valencia, 2003. **Invited talk.**
- "Prediction of Pathological Mutations" ICREA-FCR Conference on Bioinformatics, Barcelona, 2003. **Invited talk**.

- “Análisis de la base estructural de la función de las proteínas y de sus alteraciones patológicas” MMQ 2002. Iª Reunión nacional de Modelización Molecular y Quimioinformática, Barcelona 2002. **Invited talk.**
- “Aspectos estructurales de la variabilidad genética asociada a patologías” “VIII Conferencia Española de Biometría”, Pamplona. 2001. **Invited talk**.
- “¿ Mutaciones patológicas: Una conexión secuencia-estructura ?” VII Jornades d’Investigació de Bioquímica i Biologia Molecular, Barcelona, 2001. **Invited talk**.
- “Protein structure and disease” II Jornadas de Bioinformática, Málaga 2001. **Invited talk.**
- "Métodos de comparación estructural aplicados a la predicción estructural en proteínas: una nueva aproximación a un viejo problema"en XXIII Congreso de la Sociedad Bioquímica Española, Granada, 2000. **Invited talk**.
- “Comparaciones estructurales y predicción estructural: un primer paso hacia la obtención de mejores modelos estructurales” Iª Jornadas de Bioinformática, Cartagena, 2000. **Invited talk**.
- “Bioinformática: de la secuencia del ADN a la estructura de las proteínas” V Jornadas Monográficas de la Sociedad Española de Química Terapéutica, Toledo, 2000. **Invited talk**.
- “Predicción de motivos estructurales en proteínas” XXII Congreso de la Sociedad Bioquímica Española, Pamplona, 1999. **Invited talk**.
- "Biomolecular Function & Evolution in the Context of the Genome Project", Newton Institute for Mathematics, Cambridge, United Kingdom. **Invited participant.**
- "Combining statistical potentials and sequence annotations to improve fold recognition reliability" In "To understand and predict the folding of a protein: experimental and theoretical strategies" Gif-sur-Yvette, Francia, 1997. **Invited talk**.
- “Aproximació a la predicció de l’empaquetament de les proteïnes” en VIIIas Jornades de la Secció de Biologia Molecular de la Societat Catalana de Biologia. 1991. **Invited talk**.

C. POSTERS

From 2019 to 2014

- "BRCA1- and BRCA2-specific in silico tools for variant interpretation in the CAGI 5 ENIGMA challenge" Padilla, N., Moles, A, Riera, C, Montalban, G, Özkan, S, Bonache, S, Díez, O, Gutiérrez, S, **de la Cruz, X.** CAGI Conference, San Francisco USA, 2019.
- "Co-location of paralogs in TADs may explain why the effect of some deleterious mutations is suppressed" Padilla, N. and **de la Cruz, X**. HGM2018, Yokohama, Japan. BEST POSTER PRIZE OF THE SCIENCE EDITOR, 2018.
- "Pushing the reach of present in silico tools for the annotation of pathogenic variants" de la Campa, E.A. and **de la Cruz, X**. Applied bioinformatics in Life Sciences (2nd edition), Leuven, Belgium, 2018.

- “The clinical cost of in silico tools: a novel approach to choose the best pathogenicity predictor for healthcare applications” Aguirre, J. and **de la Cruz, X**. VI Jornada de Bioinformàtica i Genòmica, 2018, Barcelona.
- "Using protein-protein interactions data to improve variant pathogenicity predictions and their interpretability" Padilla, N., Riera, C., Barradas, D., Fernández-Recio, J. and **de la Cruz, X**. HGM2017, Barcelona, 2017.
- "Introducing clinical costs considerations in the interpretation of sequence variants: moving closer to the needs of healthcare stakeholders" **de la Cruz, X**., Riera, C. and Padilla, N. HGM2017, Barcelona, 2017.
- Posters presented at the V Jornada de Bioinformàtica i Genòmica, 2017, Barcelona
    1. “Are TGFß-responsive genes confined into specific TADs?” de la Campa, E.A. and **de la Cruz, X**. (VHIR).
    2. “Characterizing the pathogenic landscape of cobalamin defects” Padilla, N., Riera, C., Pérez, B., and **de la Cruz, X**.
    3. “Towards a bets ‘per gene’ method to identify pathogenic variants associated with metabolic disorders” Aguirre, J., and **de la Cruz, X**.
- Posters presented at the IV Jornada de Bioinformàtica i Genòmica, 2016, Barcelona:
    1. "Finding an optimal combination of pathogenicity predictors for the clinical setting" de la Campa, E.A. and **de la Cruz, X**.
    2. "Characterizing the impact of the Incidentalome in clinical gene sequencing panels" Aguirre, J., Padilla, N., and **de la Cruz, X**.
    3. "Identification of causative mutations in Breast and Ovarian Inherited Cancers" Padilla, N., Riera, C., Montalbán, G., Bonache, S., Díez, O., Gutiérrez-Enríquez, S., **de la Cruz, X**.
- "Exploring the advance of protein-specific methods in the prediction of pathological mutations", Riera, C., Lois, S. and **de la Cruz, X**. HGM2014, Geneve (Switzerland), 2014.

Before 2014

- "Naturally existing cavity couplings in proteins and the origins of allostery", Barbany, M. and **de la Cruz, X**. Frontiers in Dynamics Simulations of Biological Molecules, Barcelona, 2013.
- "The contribution of alternative splicing to phenotypic differences" Morata, J., Béjar, Santiago and **de la Cruz, X.** The EMBO meeting 2010, Barcelona, 2010.
- "The relationship between alternative splicing and other sources of complexity differences between organisms" Morata, J., Béjar, Santiago and **de la Cruz, X**. SMBE 2010 - Annual Meeting of the Society for Molecular Biology and Evolution, Lyon, 2010.
- “Study of the Regulatory Alternative Splicing”. Morata, J. and **de la Cruz, X.** Memorial Ángel R. Ortíz(Asociado a las Jornadas de Bioinformática). Madrid, 2009.

- "Study of the Regulatory Alternative Splicing" Morata, J. and **de la Cruz, X.** International Workshop on High Throughput Technologies for Alternative Splicing, Valencia, 2009
- "Patterns of Alternative Splicing in Chromatin-Modifying Enzymes Unveil a New Complexity Level in the Regulation of Gene Expression" Lois, S., Blanco, N., Martínez-Balbás, M.A. and **de la Cruz, X.** VII Jornadas de Bioinformática, Zaragoza, 2006.
- "Conservation of the protein cavity pattern in predicted structures: From HIGH- to LOW-resolution homology models" Piedra, D. and **de la Cruz, X**. VII Jornadas de Bioinformática, Zaragoza, 2006.
- "Patterns of Alternative Splicing in Chromatin-Modifying Enzymes Unveil a New Complexity Level in the Regulation of Gene Expression" Lois, S., Blanco, N., Martínez-Balbás, M.A. and **de la Cruz, X.** I Biomedical Symposium Scientific Park of Barcelona and Université René Descartes-Paris 5, Barcelona. 2006.
- "A Comparative Study Of The Contribution Of Alternative Splicing And Gene Duplication To The Proteome Diversity" Talavera, D., Vogel, C., Orozco, M., Teichmann, S. and **de la Cruz, X.** ECCB'2005, Madrid, 2005.
- "Aspectos estructurales y evolutivos de las mutaciones puntuales patológicas" Ferrer-Costa, C., Orozco, M. and **de la Cruz, X.** "II Reunión Nacional de Modelización Molecular y QuimioInformática", Barcelona. 2005.
- "Comparative Study of MAPK 9 Alternative Splicing from Human and Mouse" Talavera, D., Ferrer-Costa, C., Orozco, M. and **de la Cruz, X.** V Jornadas de Bioinformática, Barcelona, 2004.
- "A Bioinformatics Approach to the Comparative Study of Human and Mouse Proteomes" Lois, S. and **de la Cruz, X.** V Jornadas de Bioinformática, Barcelona, 2004.
- "A Study of the Impact of Sequence Variability in Protein Cavities" Piedra, D., Calvo, M. and **de la Cruz, X.** V Jornadas de Bioinformática, Barcelona, 2004.
- "Annotation of Non-Human Pathological Mutations utilising Human-Parameterised Neural Networks" Ferrer-Costa, C., Orozco, M. and **de la Cruz, X.** V Jornadas de Bioinformática, Barcelona, 2004.
- "Hydration Free Energy in Macromolecules" Morreale, A., **de la Cruz, X.**, Meyer, T., Gelpí, J.L., Luque, F.J. and Orozco, M. V Jornadas de Bioinformática, Barcelona, 2004.
- "Scanning the genome for triplex-forming sequences", Goñi, R., **de la Cruz, X.** and Orozco, M., ECCB'2003, París, 2003.
- "Predicción del carácter patológico de las mutaciones puntuales", Ferrer, C., Orozco, M., and **de la Cruz, X.**, "III Jornadas de Bioinformática", Salamanca, 2002.
- "Mapping disease-causing single amino acid polymorphisms to structure", Ferrer, C., Orozco, M. and **de la Cruz, X.** "Workshop on Structural Genomics and Bioinformatics", Fundación Juan March, Madrid, 2001.

- "Estudios estructurales del "splicing" alternativo", Valenzuela, A., Orozco, M., and **de la Cruz, X**, "XXIV Congreso de la Sociedad Bioquímica Española", Valencia, 2001.
- "Variabilidad de la estructura de centros activos en función del ligando", Valenzuela, A., Orozco, M., and **de la Cruz, X**, "XXIV Congreso de la Sociedad Bioquímica Española", Valencia, 2001.
- "Mapping disease-causing SNPs to Protein Structure", Ferrer, C., Orozco, M. and **de la Cruz, X**., 2000, "Conference in Structural Genomics", Cambridge, United Kingdom.
- "Use of structural multiple sequence alignments to enhance prediction-based fold recognition methods" **de la Cruz, X**. and Thornton, J.M., "Bioinformatics 1999", Lund, Suecia.
- "Identification of Supersecondary Structure Motifs Combining Sequence-based predictions and Knowledge-based Potentials", **de la Cruz, X.** and Thornton, J.M., "Bioinformatics, 1999", Lund, Suecia.
- "Factors limiting the performance of prediction based fold recognition methods" **de la Cruz, X.** and Thornton, J.M, 1997, PMDG-4, Harlow, United Kingdom.
- "Discrete Representations of the Cα Chain" **de la Cruz, X.**, Mahoney, M. and Lee, BK. 10th Meeting of the Protein Society, 1996, San Jose, USA.
- "Discrete Representations of the Cα Chain" **de la Cruz, X**., Mahoney, M. and Lee, BK. "Protein Folding and Design Meeting", 1996, NIH, Bethesda, USA.
- "A Common Structural Motif between Uteroglobin and the C-terminal domain of Colicin A" **de la Cruz, X**. and Lee, BK. European Science Foundation Conference on "Protein Folding and Stability", April 1995, Sant Feliu de Guixols, Girona, España.
- "Energía libre de las interacciones no-enlazantes y plegamiento de proteinas", **de la Cruz, X.**, Fita, I. III Congreso de la Sociedad de Biofísica de España, 1991, Madrid.
- "Estimation of Interatomic Free Energies and Protein Folding", **de la Cruz, X.** and Fita, I. Expanding Frontiers in Polypeptide and Protein Structural Research,July 1990, Whistler, British Columbia, Canada.
- "Estimation of Interatomic Free Energies from Protein Crystal Structures" **de la Cruz, X.** and Fita, I. 32nd IUPAC Congress, August 1989, Stockholm, Suecia.

D. Attendance

- 2018 "3rd European Conference on Translational Bioinformatics: Biomedical Big Data supporting Precision Medicine"
- 2015 "3rd CNAG Symposium on Genome Research: Rare Diseases", Barcelona, Spain.
- 2014 "Secuenciación, Captura de Secuencia, y PCR a tiempo real: Aplicaciones" Roche Meeting, Barcelona, Spain.
- 2014 "Advances in Genome Science" Illumina's User's Day, Barcelona, Spain.
- 2014 "XXI Symposium on Bioinformatics", Sevilla, Spain.
- 2012 "Bayesian Methods in Biostatistics and Bioinformatics", IRB, Barcelona, Spain

- 2011 "Computational Biology of Molecular Sequences" CRG, Barcelona, Spain.
- 2011 "Macromolecular Dynamics" IRB-BBVA, Barcelona, Spain.
- 2009 "NGS2009. Next Generation Sequencing: Challenges and Opportunities" Hospital de la Santa Creu i Sant Pau, Barcelona, Spain.
- 2009 "Janet Thornton 60th birthday Symposium", Cambridge, UK.
- 2008 "Quasispecies: Past, Present and Future", Institut d'Estudis Catalans, Barcelona, Spain.
- 2008 " ICREA Conference on the Origin and Early Evolution of Metazoa" Parc de Recerca Biomedica de Barcelona, Barcelona, Spain.
- 2006 “Filogenias y Genealogías de DNA: Inferencia y Aplicaciones” Universitat de Barcelona, Barcelona, Spain.
- 2002 "Association Methods of Gene Mapping" Universitat Pompeu Fabra, Barcelona, Spain.
- 1999 “8th Alfred Spinks Symposium”, London, United Kingdom.
- 1999 “Effectively Applying Bioinformatics”, London, United Kingdom.
- 1998 "Wellcome Trust Genome Campus Inaugural Symposium", Cambridge, United Kingdom.
- 1998 “Getting the Most from Structure-Functions Based Genomics”, Harlow, United Kingdom.
- 1998 “The Third Johns Hopkins Protein Folding Meeting”, Coolfont, USA.
- 1997 "Statistical Analysis of DNA", Newton Institute, Cambridge, United Kingdom.
- 1991 NATO Advanced Research Workshop "The role of computational models and theories in Biotechnology", Sant Feliu de Guixols, Girona, España.
- 1990 "Advanced Methods in Protein Structural and Functional Analysis", Universitat Autonoma de Bellaterra, Barcelona.
- 1989 International Summer School on "Protein and Genetic Engineering", Spetsai, Grecia.
- 1989 “Conformational Analysis with the Consistent Force Field”, Dep. Química-Física, Fac. Química, Universitat de Barcelona.
- 1988 “Tècniques de representació grafica i disseny amb computador”, Dep. de llenguatges i sistemes informàtics, Universitat Politecnica de Barcelona.
- 1985 “Programador d’Aplicacions Científiques”, Centre d’ Informàtica, Universitat de Barcelona.

ACADEMIC ACTIVITIES

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MASTERS. ORGANISER

- Academic Committee member and Director's team member of the First Internacional Master "MSc on Bioinformatics for Health Sciences" organised by the Universitat de Barcelona and the Universitat Pompeu Fabra, **2005/2006, 2004/2005**.

TEACHING EXPERIENCE

- **Teacher** in the **"Setmana de la Ciència"** 2014, 2013, 2012, 2011, 2010, 2009, 2008, 2007, 2006 and 2004, organised by the FCR.
- **Coordinator of the Ph.D course** "Biomedicina III", from the Ph.D. program in biomedicine, Dpto. de Bioquímica from the Universitat de Barcelona, 2004.
- **Teacher** at the XXX Escola D'Estiu de Secundària para maestros, summer 2003.
- **Teacher** in the post-graduate course "Prediccion Estructural de Biomoleculas", Universidad de Extremadura, Caceres.
- 96 hours wet-laboratory teaching, second year of chemistry (University of Barcelona).
- 32 hours wet-laboratory teaching, Industrial Biochemistry, fourth year of biochemistry (University of Barcelona).
- 30 hours of structural biology and bioinformatics, in different Ph.D. courses.