



CURRICULUM VITAE ABREVIADO (CVA)

IMPORTANT – The Curriculum Vitae cannot exceed 4 pages. Instructions to fill this document are available in the website.

Part A. PERSONAL INFORMATION

First name	Francisco José		
Family name	Blanco Gutiérrez		
Gender (*)	Male	Birth date (dd/mm/yyyy)	03/10/1964
Social Security, Passport, ID number	50811287D		
e-mail	fj.blanco@ibv.csic.es	URL Web	https://www.ibv.csic.es/en/ibv/
Open Researcher and Contributor ID (ORCID) (*)	0000-0003-2545-4319		

(*) Mandatory

A.1. Current position

Position	Scientific Researcher-CSIC and Group Leader		
Initial date	12/03/2020		
Institution	Instituto de Biomedicina de Valencia-CSIC		
Department/Center	Molecular basis of disease		
Country	Spain	Teleph. number	963289680
Key words	Protein structure, molecular recognition, NMR, DNA replication, chromatin, cancer		

A.2. Previous positions (research activity interruptions, indicate total months)

Period	Position/Institution/Country/Interruption cause
1989-1992	Predoctoral Researcher, IEM-CSIC, Madrid, Spain
1993-1997	Postdoctoral Researcher, EMBL, Heidelberg, Germany
1997-2000	Visiting Fellow, NIH, Bethesda, USA
2000-2001	Postdoctoral Researcher, IEM-CSIC, Madrid, Spain
2002-2007	Ramón y Cajal Investigator and Group Leader, CNIO, Spain
2007-2020	Ikerbasque Research Professor, CIC bioGUNE

A.3. Education

PhD, Licensed, Graduate	University/Country	Year
Graduate in Chemistry	Complutense de Madrid	1988
PhD in Chemistry	Complutense de Madrid	1992

(Include all the necessary rows)

Part B. CV SUMMARY (max. 5000 characters, including spaces)

My PhD thesis was supervised by José L. Nieto at Instituto de Estructura de la Materia (IEM-CSIC), Madrid. We used **NMR** to study peptides in aqueous solution as models of the early stages of protein folding. We designed a linear peptide able to fold into a **β -hairpin**, providing a system to study this type of secondary structure (doi: [10.1021/ja00066a092](https://doi.org/10.1021/ja00066a092)).

As a Postdoctoral Researcher in the group of Luis Serrano at the European Molecular Biology Laboratory, we studied linear peptides and the spectrin protein SH3 domain as models for **protein folding**. We reported the first peptide with a native hairpin structure (doi: [10.1038/nsb0994-584](https://doi.org/10.1038/nsb0994-584)), designed peptides for hairpin and helix formation studies, and found that the appearance of a new protein fold from an existing one is unlikely to occur by evolution through a route of folded intermediate sequences (doi: [10.1006/jmbi.1998.233](https://doi.org/10.1006/jmbi.1998.233)).

In Robert Tycko's Lab at the National Institute of Diabetes, Digestive and Kidney Diseases (NIH, Bethesda, USA), as a Visiting Fellow. We developed a **solid-state NMR** method for protein structure investigation and applied it to the Rev protein of the Human Immunodeficiency Virus in its fibrillar state, supporting a helix-loop-helix structure at the N-terminal region (doi: [10.1006/jmbi.2001.5067](https://doi.org/10.1006/jmbi.2001.5067)).



After 8 years abroad I returned to the IEM with a CSIC contract to work with Manuel Rico, and participated in an international **structural genomics** project. We determined the NMR structure of a protein revealing a previously undescribed protein fold and a possible role in cell division (doi: [10.1110/ps.04620504](https://doi.org/10.1110/ps.04620504)).

I joined the CNIO in 2002 with a Ramón y Cajal contract, to establish and lead the NMR group. We studied the molecular recognition of small molecules by integrin proteins involved in cancer metastasis and unexpectedly found that they were **allosteric inhibitors** instead of competitive ones (doi: [10.1021/jm3016848](https://doi.org/10.1021/jm3016848)). We studied how ING tumor suppressor proteins recognize the N-terminal region of histone H3 methylated at K4 (doi: [10.1074/jbc.M710020200](https://doi.org/10.1074/jbc.M710020200)), and the structure-function of several native and engineered **meganucleases** (doi: [10.1038/nature07343](https://doi.org/10.1038/nature07343)).

After 6 years I moved to CIC bioGUNE as Ikerbasque Research Professor. We showed how the **ING tumor suppressor proteins** form dimers and bind DNA to recruit histone acetylation complexes to chromatin sites enriched in methylated histone H3 (doi: [10.1016/j.jmb.2019.04.018](https://doi.org/10.1016/j.jmb.2019.04.018)). We described how the ring-shaped protein PCNA embraces the DNA double helix, proposing a mechanism for sliding while coordinating **DNA replication** by polymerases (doi: [10.1038/ncomms13935](https://doi.org/10.1038/ncomms13935)). We characterized the **molecular recognition** of PCNA by regulatory proteins, including the **intrinsically disordered protein p15**, showing a unique mode of binding with the p15 chain traversing the ring (doi: [10.1038/ncomms7439](https://doi.org/10.1038/ncomms7439)). We prepared p15 in its ubiquitinated form and showed that while PCNA binding is unaffected, it acquires the capacity to recognize a DNA methyl transferase, recruiting it to the replication fork to restore the cytosine-methylation pattern of the parent DNA strand on the newly synthesized one (doi: [10.1021/acscchembio.9b00679](https://doi.org/10.1021/acscchembio.9b00679)).

In 2020 I was appointed Research Scientist at the Centro de Investigaciones Biológicas-CSIC and moved my lab to study the structure, function, and interactions of PCNA and other proteins involved in DNA replication and repair (doi: [10.1016/j.str.2023.03.004](https://doi.org/10.1016/j.str.2023.03.004)). Supported by an NIH-funded project, we have structurally characterized how small molecules target the cellular signaling triggered by a **G protein**, disrupting its interaction with an activating protein that is present at high levels in metastatic **breast cancer** cells (doi: [10.1073/pnas.2213140120](https://doi.org/10.1073/pnas.2213140120)).

I have mainly used NMR for the structural characterization of biomolecules and their interactions, incorporating complementary techniques (crystallography, small angle X-ray scattering, electron microscopy, or computation) through collaborators with expertise and access to equipment. I rely on collaborations to investigate the functional implications of the structural properties of the complexes. This **integrative approach** is indispensable for understanding complex systems.

I am member of 3 scientific societies, having served as coordinator of the Protein Structure and Function Group of the Spanish Society of Biochemistry and Molecular Biology, and currently as Vice-president of the NMR Group of the Royal Spanish Society of Chemistry.

I have participated in **outreach** activities (article in Investigación y Ciencia magazine, interviews in newspapers and TV), and have given talks at Semana de la Ciencia, and at elementary and high schools.

Statistics (<https://www.webofscience.com/wos/author/record/D-4401-2009>)

35 years of research (1989-2024), with 5 sexennia and 5 quinquennia.

10 Supervised PhD theses, with “Sobresaliente *cum laude*”, 3 with “Doctorado internacional”

133 scientific publications, more than 6400 citations, 1 international patent, h-index = 44 (Scopus).

Part C. RELEVANT MERITS (sorted by typology)

C.1. Publications (Corresponding authors are indicated with **asterisks**)

1. Ruiz-Albor A, Chaves-Arquero B, Martín-Barros I, Guerra-Castellano A, Gonzalez-Magaña A, Ibáñez de Opakua A, Merino N, Ferreras-Gutiérrez M, Berra E, Díaz-Moreno I, **Blanco FJ***. *PCNA molecular recognition of different PIP motifs: Role of Tyr211 phosphorylation*. (2024) **Int J Biol Macromol** 273, 133187. **IF 8.025**. Doi: [10.1016/j.ijbiomac.2024.133187](https://doi.org/10.1016/j.ijbiomac.2024.133187).
2. Ferreras-Gutierrez M, Chaves-Arquero B, González-Magaña A, Merino N, Amusatogui-Mateu I, Huecas S, Medrano FJ, **Blanco FJ***. *Structural analysis of ING3 protein and histone H3 binding* (2023) **Int J Biol Macromol** 242, 124724. **IF 8.025**. Doi: [10.1016/j.ijbiomac.2023.124724](https://doi.org/10.1016/j.ijbiomac.2023.124724).
3. Zhao J, DiGiacomo V, Ferreras-Gutierrez M, Dastjerdi S, Ibáñez de Opakua A, Park J-C, Luebbbers A, Chen Q, Beeler A, **Blanco FJ**, Garcia-Marcos M*. *Small-molecule targeting of*



GPCR-independent noncanonical G-protein signaling in cancer (2023) **Proc Natl Acad Sci USA** 120 (18) e2213140120. **IF 11.1**. Doi: [10.1073/pnas.2213140120](https://doi.org/10.1073/pnas.2213140120).

- Liu J, Chaves-Arquero B, Wei P, Tencer AH, Ruiz-Albor A, Zhang G, **Blanco FJ***, Kutateladze TG*. *Molecular insight into the PCNA-binding mode of FBH1* (2023) **Structure** 31, 511. **IF 5.7**. Doi: [10.1016/j.str.2023.03.004](https://doi.org/10.1016/j.str.2023.03.004).
- Chaves-Arquero B, Persson C, Merino N, Tomás-Cortazar J, Rojas AL, Anguita J, **Blanco FJ***. *Structural Analysis of the Black-Legged Tick Saliva Protein Salp15* (2022) **Int J Mol Sci**, 23,3134. **IF 5.6**. Doi: [10.3390/ijms23063134](https://doi.org/10.3390/ijms23063134).
- González-Magaña A, de Opakua AI, Merino N, Monteiro H, Diercks T, Murciano-Calles J, Luque I, Bernadó P, Cordeiro TN, Biasio A, **Blanco FJ***. *Double Monoubiquitination Modifies the Molecular Recognition Properties of p15(PAF) Promoting Binding to the Reader Module of Dnmt1* (2019) **ACS Chem Biol** 14, 2315-2326. **IF 4.4**. Doi: [10.1021/acscchembio.9b00679](https://doi.org/10.1021/acscchembio.9b00679).
- Ormaza G, Rodríguez JA, de Opakua AI, Merino N, Villate M, Gorroño I, Rábano M, Palmero I, Vilaseca M, Kypka R, Vivanco MD, Rojas AL, **Blanco FJ***. *The tumor suppressor ING5 is a dimeric, bivalent recognition molecule of the H3K4me3 mark* (2019) **J Mol Biol** 431, 2298-2319. **IF 5.6**. Doi: [10.1016/j.jmb.2019.04.018](https://doi.org/10.1016/j.jmb.2019.04.018).
- A de Biasio*, A Ibáñez de Opakua, MJ Bostok, D Nietlispach, T Diercks*, **FJ Blanco***. *A generalized approach for NMR studies of lipid-protein interactions based on sparse fluorination of acyl chains* (2018) **Chem Comm** 54, 7306-7309. **IF 4.9**. Doi: [10.1039/C8CC02483A](https://doi.org/10.1039/C8CC02483A).
- De March M, Merino N, Barrera-Vilarmau S, Crehuet R, Onesti S, **Blanco FJ***, De Biasio A* (2017) *Structural basis of human PCNA sliding on DNA*. **Nature Commun** 8, 13935. **IF 16.6**. Doi: [10.1038/ncomms13935](https://doi.org/10.1038/ncomms13935).
- De Biasio* A, Ibáñez de Opakua A, Mortuza GB, Molina R, Cordeiro TN, Castillo F, Villate M, Merino N, Delgado S, Gil-Cartón D, Luque I, Diercks T, Bernadó P, Montoya G, **Blanco FJ*** (2015) *Structure of the p15^{PAF}/PCNA complex and implications for clamp sliding on the DNA during replication and repair*. **Nature Commun** 6, 6439. **IF 16.6**. Doi: [10.1038/ncomms7439](https://doi.org/10.1038/ncomms7439).

C.2. Congress, indicating the modality of their participation (invited conference, oral presentation, poster)

- 11th Biennial meeting of GERMN-RSEQ**, Almería, 13th October 2022. *Molecular Recognition of DNA helicase FBH1 by PCNA*. **Oral presentation**.
- 20th KIAS Conference on Protein Structure and Function**, Seoul (Korea), 15th September 2022. *Interactions of the PCNA human DNA clamp in replication*. **Invited conference**.
- XVII Iberian Peptide Meeting**, Madrid, 6th February 2020. *Double monoubiquitination of the IDP p15 promotes recognition by Dnmt1*. **Oral presentation**.
- 5th Iberian NMR meeting and 8th Biennial meeting of Grupo de RMN-RSEQ**, Valencia, 28th June 2016. *Structure and interactions of the 90 kDa human DNA sliding clamp*. **Invited conference**.
- IX Reunión de la Red Nacional de Estructura y Función de Proteínas**, Sevilla, 13th November 2015. *Structure of the p15^{PAF}/PCNA complex and implications for clamp sliding on the DNA during replication and repair*. **Oral presentation**.
- XV Congress of the Spanish Biophysical Society**, Granada, 10th June 2015. *Structure of the p15^{PAF}/PCNA complex and implications for clamp sliding on the DNA during replication and repair*. **Invited conference**.
- 8th Iberian Biophysics Congress**, Bilbao 20-21st June 2022. *Structural Analysis of the black-legged tick saliva protein Salp15*. **Poster**.
- 9th Iberoamerican NMR meeting and 10th GERMN-RSEQ Biennial Meeting**, Vitoria, 26-29th July 2021. *Molecular recognition of histone H3K4me3 by Tumor suppressor ING3*. **Poster**.



9. **EUROISMAR 2019** (joint EUROMAR and ISMAR conference), Berlin, 25-30th August 2019. *Human and Yeats PCNA dynamics: A comparative study using NMR Methyl Relaxation dispersion. Poster.*
10. **8th Iberoamerican NMR meeting** and **9th GERMN-RSEQ Biennial Meeting**, Lisboa, 26-29th June 2018. *The metastasis suppressor Kiss1 is an intrinsically disordered protein slightly more extended than a random coil. Poster.*

C.3. Research projects, indicating your personal contribution. In the case of young researchers, indicate lines of research for which they have been responsible.

PID2020-113225GB-I00 (funded with 181,500 € plus 1 predoctoral contract).

Molecular recognition in DNA replication.

Spanish Government, September 2021-August 2024.

PI: **Francisco J Blanco** (*project direction, thesis supervision, co-writing of publications*)

1R01GM130120-Subaward 4500003608 (funded with 90,000 \$).

Targeting of non-canonical G protein signaling with small molecules.

National Institutes of Health (USA), July 2018 - June 2023.

PI of the R01 grant: Mikel García-Marcos, Boston University (funded with 369,000 \$).

PI of the subaward: **Francisco J Blanco** (*project direction and co-writing of publications*).

CTQ2017-83801-R (funded with 170,610 € plus 1 predoctoral contract).

Structure and molecular recognition of the p15 oncogen: ubiquitination and interaction with DNA and PCNA.

Spanish Government, January 2018 - December 2020.

PI: **Francisco J Blanco**: (*project direction, thesis supervision, and co-writing of publications*).

CTQ2014-56966-R (funded with 174,240 € plus 1 predoctoral contract)

Histone H3 methyl recognition by the tumor suppressor ING5

Spanish Government, January 2015 - December 2017

PI: **Francisco J Blanco** (*project direction, thesis supervision, and co-writing of publications*).

CTQ2011-28680 (funded with 143,990 € plus 1 predoctoral contract)

Molecular recognition of histone post-translational modifications by the tumour suppressor proteins ING4 and ING5

Spanish Government, January 2012 - December 2014

PI: **Francisco J Blanco** (*project direction, thesis supervision, and co-writing of publications*).

C.4. Contracts, technological or transfer merits,

Company: **LEADARTIS**, Madrid

Contract title: Estado de oligomerización de dos proteínas

Person in charge: **Francisco J Blanco** (*performing experiments and writing reports*)

11-January 2022 – 10-April 2022

Amount: 6,425.7 €

Company: **CELLECTIS**, Paris France.

Contract title: Structure-function relationship in homing endonucleases

Person in charge: **Francisco J Blanco** (*supervising experiments and writing reports*)

November 2009 - November 2013

Amount: 226,000 €