MARIA J. MACIAS

Professional category

ICREA Research Professor and GL at the IRB Barcelona since 2002

GOOGLE SCHOLAR: **hEI-QyIAAAA**, RESEARCHER ID **K-3898-2014**, ORCID: **0000-0002-6915-963X**

Past positions

1998-2002, Staff Scientist at the Structural and Computational Biology Programme, EMBL, Heidelberg (Germany)

EDUCATION

1989 Degree in Chemistry, 1993 PhD in Organic Chemistry, Universidad de Salamanca, Spain.

1993-1998 Postdoctoral researcher at the EMBL, Heidelberg, Germany.

RESEARCH INTEREST IN BRIEF

During my career as a scientist, my research interests have been focused on deciphering the mechanisms that correlate cell signaling with gene expression using high-resolution structural biology. With our structures, we aim at discovering how these biological processes are regulated -or misregulated-, and their consequent implications in human diseases. With this research, we intend to generate new knowledge to unveil how cells gain new roles or start to promote cancer progression and metastasis and key tools to treat diseases that have a common trait, namely the mis-regulation of TGFβ signaling.

Structural Characterization of Macromolecular assemblies lab

Our laboratory belongs to the Mechanisms of Disease Programme at the Institute for Research in Biomedicine, (IRB Barcelona) and The Barcelona Institute of Science and Technology (BIST). At present, our group comprises three research scientists (Dr. Eric Aragón, Dr. Pau Martin Malpartida and Lidia Ruiz, in the laboratory for the last 15 years), two post-doctoral researchers (Dr. Radoslaw Pluta and Dr. Tiago Gomes) and three PhD students (Błażej Bagiński, Míriam Condeminas and Carles Torner). Radoslaw and Błażej belong to the Marie Skłodowska-Curie Fellowship-Postdoctoral and Predoctoral BIST-COFUND programme, respectively. Carles has a FI fellowship (AGAUR) and Míriam an FPU (Ministerio de Educación y Universidades). Our skill sets combine expertise in NMR, X-ray, Chemistry, molecular biology, and bioinformatics, including artificial intelligence and machine learning. These are the essential pillars of knowledge required to carry out our research.

Research fields (key words):

Structural Biology, NMR, X-ray crystallography, Computational Biology, Signaling, Protein Folding/aggregation, SMAD proteins, WW domains, indicators of metastasis progression

EXECUTIVE summary of the *Curriculum Vitae*

SCIENTIFIC BACKGROUND

I obtained my PhD in 1993, in the field of Organic Chemistry and Natural Products (Supervisor: Prof. M. Grande, Universidad de Salamanca). In 1993, I moved to the EMBL in Heidelberg with a Post-doctoral research position in Prof. H. Oschkinat's group, where I stayed for five years. During this time, I developed a deep understanding of Structural Biology—in particular NMR—applied to the determination of protein and nucleic acid structures in solution. I also gained a solid knowledge of X-ray crystallography and Computational and Molecular Biology. During the years at the EMBL, we characterized the structures of several key signaling protein domains (PH and WW domains, Nature 1994, 1996) and of the double stranded RNA binding domain (EMBO J. 1995). These structures—the first ones of their kind—revealed how these domains adopted new folds, their interactions with ligands and their functional implications. We also succeeded in the *de novo* design of a WW domain, folded as the native counterpart (Nature Structural Biology 2000), and developed a protocol for the determination of protein structures in solution, named ARIA (JMB 1997), which is highly used worldwide.

In 1998, I started my career as an independent Staff-Scientist at the EMBL in Heidelberg. In 2002, my lab moved from Heidelberg to Barcelona, when I became an ICREA research professor and GL of the Macromolecular Assemblies Lab at IRB Barcelona. We then started our journey to figure out why human bodies develop life-threatening diseases and how to use the tools provided by Structural Biology and Artificial Intelligence to identify new targets and vulnerable sites for drug action, to deploy new therapies and treatments to improve the quality of life of patients.

RECENT AND CURRENT PROJECTS

TGFβ signaling operates in early embryogenesis and also in development, and unfortunately, it is also at the core of several life-threatening diseases such as cancer or the Myhre syndrome, a rare disease causing muscle hypertrophy, hearing loss and variable intellectual disability for which there is no cure or treatment to date. The mediators of the TGFβ signaling process are the SMAD transcription factors and a large part of our work is dedicated to clarifying the role of SMAD proteins in the TGFβ signaling network, in atomic detail. We have also contributed to defining WW domains as models for understanding folding, protein degradation through ubiquitin ligases and amyloid aggregation, a research line started when I was a Postdoc at EMBL. We also study the conformations in solution of peptide hormones that regulate the endocrine system and affect neurotransmission processes and cell proliferation to improve their stability and functionality to obtain analogs with pharmacological applications. Given the pivotal role of TGF-β in tumor progression and in other life threatening diseases, this pathway is an attractive target for therapy. However, targeting the TGF-β receptor has proven very difficult because its inhibition affects the entire pathway and causes severe side-effects. Last year, we started with a different approach to overcome these drawbacks, with the validation of SMADs as new viable targets to regulate TGF-β signaling. We have succeeded in the identification of 14 small molecules that interact with SMAD4. Recently, together with medical doctors and researchers at the Sant Pau Hospital in Barcelona, we have started to study the probability of relapse and metastasis of gynecological cancer patients. In this project we plan to empower doctors with new affordable diagnostic tools to provide the best possible care for these patients. The project is based on genomic and transcriptomic data retrieved from biopsies and combined with public data deposited in databases. We analyze this information using artificial intelligence. We train the software with validated data and apply it later to identify disease progression markers. Together with the clinicians, we are trying to identify sets of mutations that can be used as markers to describe disease progression.

To address these fundamental biological questions, our laboratory has secured continuous competitive financial support (all as PI) since we started in 2002, as well as through contracts with Pharma and Biotech companies. In addition to the research, I participate in several activities to promote Gender Equity in Research Centers and in training researchers in the field of structural biology, an essential tool to unlocking the secrets of protein function and one that provides new avenues for medical research.

Our main scientific contributions have been:

1. Description of the WW-domains, a new fold to study protein recognition (Nature 1996, Nature Structural & Molecular Biology 2000) and a model system for studying amyloid formation (PNAS 2001, 2014, 2015).

2. Definition of a phosphorylation-dependent mechanism that labels SMAD proteins, first for activation and then for degradation (Cell 2009, Mol. Cell 2009, Genes and Dev, 2011)

3. Determine the molecular basis for distinct roles of SMAD2 and SMAD3 in the regulation of progenitor differentiation genes. This result challenges an erroneous view that had prevailed in the field for two decades that SMAD2 does not interact with DNA (Genes and Dev, 2019).

4. Found that the formation of the SMAD-TGIF1 complex prevents the interaction of each partner with DNA, thus revealing the mechanism for transcriptional repression and paving the way for the development of molecules that can regulate this mechanism in situations associated with diseases (Nucleic Acid Research, 2018).

5. Identification of novel DNA motifs recognized by SMAD proteins (Nature Communications, 2017)

6. Elucidation of the rules that define the different composition of SMAD complexes in BMP and TGFβ pathways (Comput. Struct. Biotechnol. J 2021).

7. Characterization for the first time the conformational landscape populated by non-activated full-length SMAD proteins (Comput. Struct. Biotechnol. J. 2021).

8. Design of peptide analogs with therapeutic properties (ChemBioChem 2011, Angewandte Chemie 2012, Scientific reports 2016, Nature Communications, 2021).

Current Collaborations

Since 2008, with the group of Dr. J. Massagué in many fundamental aspects related to TGFβ signaling and SMAD function, and with Dr. Y. David, in NCP reconstitution and pioneer factor complexes (recently started). Both researchers work at the Sloan Kettering Cancer Center in NY, (USA).

Since 2014, with J.A. Márquez, EMBL (Grenoble) in topics related to HT crystallography.

Since 2018, with Tiago N. Cordeiro, SAXS studies of full-length SMAD proteins, Universidade NOVA de Lisboa (Portugal) and with M. Royo (IQAC-CSIC, Barcelona) and E. Vázquez, (CIQUS) / USC, peptides.

Previous Collaborations

From 2000 till 2017, with the groups of Prof. Alan Fersht (MRC Laboratory of Molecular Biology, University of Cambridge) and Prof. H. Scheraga (Cornell University, NY, USA) in studies on the WW domain folding mechanisms and their impact on amyloid formation.

Intramural collaboration supported by five COFUND postdoctoral grants, studies of somatostatin analogs thanks to a collaboration with Dr. A. Riera, and with Dr. C. González.

With researchers from nearby institutions. With Dr. M. Beato (CRG Barcelona), where we contributed with studies of the enzymatic activity of Nudix5 *in vitro*, (published in *Science*, 2016), and with Dr. J. Valcárcel, CRG Barcelona, Dr. E. Pedroso, (Universitat de Barcelona) and with Dr. E. Martínez (Centro de Biología Molecular Severo Ochoa, Madrid) in studies of RNA-protein interactions, their regulations, and their role in tumor biology through a collaboration supported by the RNAREG CONSOLIDER grant.

FUNDING & RESOURCES: CURRENT: GRANTS & CONTRACTS (2017-2021)

COMPETITIVE GRANTS

- **PDC_2021**-121162-I00**, financed by MCIN/AEI/10.13039/501100011033 and the European Union "NextGenerationEU"/PRTR, Ministerio de Ciencia e Innovación**, Proof of concept (two years, starting in December 2021). Targeting the SMAD4 transcription factor for drug discovery: applications in cancer and rare diseases; 129.950,00€; PI.

- **Ministerio de Educación y Ciencia**, FPU, M. Condeminas, 48 months, from **30/Nov/2021** till **30/Nov/2025**, 89,943,61€

- **Ministerio de Ciencia e Innovación** BFU 2017-82675-P (**2017-2021**, extended up to September **2022**) Deciphering the interaction sites of Smad proteins with cofactors using high resolution structural biology; 234.000€; PI. Contracts: T. Gomes 01/10/2019-31/03/2021 and M. Condeminas 15/09/2021-30/11/2021

- **H2020-SwafS-2019-1,** 873134, (**2020-2023**) CALIPER Linking research and innovation for gender equality, 2.896.475€, (243.625€ for the IRB Barcelona group, Researcher).
- **Maratό de TV3,** 300.000€, Genomic indicators for the prediction of recurrence and metastasis in Endometrial Cancer (**2020-2023**). Two partners: Gynecological oncology, Hospital Sant Pau and our laboratory, 125.000 € for our group. PI.
- Agaur SGR (since 2009). Co-PI. 1PhD fellowship (**2020-2023**, 74324,91€)
- **2 Marie Skłodowska-Curie Fellowships.** (1 Postdoctoral, Pluta, R. 9/Jul/2018-11/Jul/2022, 203, 240€, 1 PhD Baginski, B. 28/Dec/2018-27-12-2022, 162.176€)
- **Severo Ochoa award** to IRB Barcelona. (2020-2025, 2015-2020 and 2011-2015), "participation as selected researcher" twice.

TOTAL: 1018633.00€

Contracts, technological or transfer merits

~20,000 euros/year, Specific contracts with Biotech and Pharma companies (Apeptico, BCN peptides, Fresenius Kabi, Slack) and with CIBER projects to perform structural characterizations of peptides and the analysis of metabolomics data by NMR. The benefits of these contracts support the research of our laboratory (preliminary data for new projects and grants, salaries, etc).

-Convenio. 10.000€/year, Fundación BBVA, Advanced training and mobility (since 2014). for our laboratory. Co-PI

Grants in kind (competitive)

- OpenScreen grants PID 8591, through the EU-OPENSCREEN-DRIVE (GA No 823893) trans-national access program for small molecule screening financed through H2020. Title: Small molecule binders for SMAD4 MH2 domain. PI.
- Access granted to large facilities (ALBA and ESRF synchrotrons, ultra-high field NMR) and through INSTRUCT and iNEXT projects, since 2013. PI.

Under evaluation (competitive):

- **Ministerio de Ciencia e Innovación**, SMAD complexes with a functional role in development and cancer progression (SMAD_DC).
- **EU-OPENSCREEN-DRIVE Medicinal Chemistry Call** 2021 Proposal PID: 18247 has been Scientifically Approved on Dec 17th 2021. Pending final approval.
- **iNEXT-Discovery - Instruct-ERIC** Protein Production and Biophysical Characterisation of FL-SMAD proteins expressed in mammalian cells.

PREVIOUS COMPETITIVE GRANTS (2000-2017)

- **Ministerio de Ciencia e Innovación BFU 2014-53787-P,** 'Comunicación celular vía TGFbeta-Smads: estructuras de Smads/Foxh1 unidos al promotor Gsc. Análisis de polimorfismos y mutaciones tumorales' · **Role: PI** · **170.000€** · **01/Jan/2015 - 31/Dec/2017** (Contracts: Jordi Medina - 01/Jan/2015 - 29/Dec/2016 and Angela Vea Bárdenas - 01/Jan/2016 - 30/Apr/2017)

- **5 Marie Skłodowska-Curie Fellowships**, **2 La caixa PhD** fellowships, **1 FPUs**, **1 FIs**.
- **NIH-The National Cancer Institute Center for Bioinformatics (NCICB)** · The National Cancer Institute Center for Bioinformatics (NCICB), · 'Structural Study of Smad Proteins and DNA complexes' · **Role: PI** /Director · **03/Feb/2016 - 31/Dec/2017**. **Granted the access to tumor-mutated genomes.**
- **IRB Barcelona and supported by the Obra Social "la Caixa" technology transfer programme** *Internal BioMedTec Programme***,** 'A rapid fluorescent screening method to evaluate the effect of disease mutated proteins in ligand binding **Role: PI /Director** · 15.000€ · **01/Dec/2015 - 30/Jun/2016**
- **Ministerio de Ciencia e Innovación SAF2011-25119** 'NMR-based Structural analysis of Smad complexes' · **Role: PI** /Director · 103.000€ · **01/Jan/2012 - 01/Jun/2015** (extended six months)

- **Ministerio de Educación y Ciencia · CONSOLIDER, CSD2009-00080_RNAREG** · 'An integrated approach to post-transcriptional regulation of gene expression and its role in human disease. ' · **Role: PI** of our subproject. Director J. Valcarcel. Total amount· 4.700.000€ ·divided by 11 groups **31/Dec/2009 - 31/Dec/2015** (granted an extension of one year).
- **Ministerio de Ciencia e Innovación, FIDR13-4E-2721** – **Infrastructure 2013**: Upgrade of the Bruker Avance III spectrometer with the installation of a cryoprobe of four nuclei and an extra amplifier. **Role: PI** Maria J. Macias, Institute for Research in Biomedicine, 194.689,00 of the 389.378 required.
- **Agaur · SGR 00901** · 'Unitat de Recerca en Síntesi Asimètrica del Parc Científic de Barcelona' **· Role: Researcher** · 35.000€ · 05/Jan/2009 - 31/Dec/2014 and from 2014-2016, Síntesi i Estructura de Biomolècules (SINESBIO) **Role: Researcher**.
- **Ministerio de Educación y Ciencia, BFU 2008-02795/BMC**, · 'Conformational changes and ligand recognition of the E3 ubiquitin ligases Itch, WWP1 and Rsp5 using NMR' · **Role: Principal Investigator** · 105.000€ · 31/Dec/2008 - 31/Dec/2011
- **Ministerio de Ciencia e Innovación** BFU 2005-06276, Structure determination of FF domains and characterization of their interactions by multidimensional Nuclear Magnetic Resonance. (12/2005 a 12/2008), **Role: PI** Maria J. Macias, Institute for Research in Biomedicine, 85.860€.
- **Ministerio de Ciencia e Innovación** GEN2003-20642-C09-04/NAC Protein dynamics, ligand recognition and structural characterization of complexes applying Nuclear Magnetic Resonance (09/2004 a 08/2007), **Role: PI** of the subproject Maria J. Macias, Institute for Research in Biomedicine, 54.432€.
- **Human Frontier Science Program** RG0234/2000-M, The WW domains network in yeast: (09/2000-09 a 02/2004). The project was coordinated by Prof. Stanley Fields, (University of Washington, USA). **Role: PI** of one of the five subprojects (135.000€/subproject). The project was granted while the PI was working at the EMBL Heidelberg and was finished at the IRB Barcelona.

COMPETITIVE FELLOWSHIPS

FI, Predoc Torner, Carles. 2020-2023
FPU, Predoc Condeminas, Míriam. start: 2021-12-01, end: 2025-11-30
Marie Skłodowska-Curie Fellowship · Predoc Bagiński Błażej 2018-12-01 until 2022-12-21
Marie Skłodowska-Curie Fellowship · PostDoc ·Pluta Radosław, 2018-2023
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Marie Skłodowska-Curie Fellowship · PostDoc · Ewelina Guca · 20/Apr/2016 - 30/Dec/2018
Marie Skłodowska-Curie Fellowship · PostDoc · Regina Freier · 18/Apr/2016 - 18/Apr/2018
Marie Skłodowska-Curie Fellowship · PostDoc · Marco Jan Klein · 18/Apr/2016 - 19/Apr/2018
IRB Barcelona, one year Fellowship · ``Structural basis of the effect of transcription factor mediators in the TGF beta signaling cascade' Investigator Jordi Medina /Director MJ. Macias ·16.400€ 02/Sep/2013 - 31/Aug/2014
Severo Ochoa FPI · PhD · Tiago Gomes Lopes · 01/Jan/2013 - 31/Dec/2016
Marie Skłodowska-Curie Fellowship · PostDoc · Toni Todorovski, 12/Nov/2012 - 12/Nov/2014
Marie Skłodowska-Curie Fellowship · PostDoc · Mads Beich-Frandsen· 01/Oct/2012 - 15/Oct/2014
La Caixa · PhD · David Suñol Moreno · 01/Sep/2012 - 30/Sep/2016
(**FPU**) Ministerio de Educación y Ciencia 'Structural Studies on Conformational Changes of E3-Ubiquitin ligases using NMR' · Investigator Albert Escobedo /PhD supervisor MJ. Macias· 62.951€ · 01/Oct/2010 - 07/Jul/2014
La Caixa ·PhD Constanze Schelhorn, 01/Sep/2010 - 31/Aug/2014

HOST SUPPORT PROVIDED BY THE IRB BARCELONA

- **Core funding for the lab – 80.000,00€ - per year** (average since 2011). In kind: 75% of the NMR time available at the Avance III Bruker 600 MHz equipped with a four-channel cryoprobe.
- **Core funding up to 10.000,00€ - per year** to access IRB Barcelona research facilities, including the X-ray platform, Mass spectrometry and Protein expression facilities.
- **Core funding 35.000,00€ - per year (since 2015)** to partially support the contract of a research scientist to assist with the NMR spectrometer and to cover the costs of NMR consumables (He and N2).

The core funding as well as some additional external funding is used to finance three researchers needed due to the specific needs of the lab, which include the NMR spectrometer and a computer cluster for bioinformatics analysis, structural calculations and backups.

  - Staff Scientist - Lidia Ruiz 30/Dec/2005 (Laboratory)

- Staff Scientist – Dr. Eric Aragón Altarriba 30/Jan/2005 (Laboratory and NMR)
- Staff Scientist – Dr. Pau Martin Malpartida 30/Jan/2003 (NMR and informatics)

- Internal Fellowships Competitive: 1 PhD Severo Ochoa for T. Gomes, 2 La Caixa Fellowships, (C. Schelhorn and D. Suñol) 3 fellowships in the programme "A future in Biomedicine" - O. Gracia Carmona 15/Sep/2016 - 31/May/2017, J. Cordero 15/Sep/2017- 31/May/2018, M. Condeminas 01/Oct/2019- 10/Jul/2020

RELEVANT MERITS

In the last 10 years we have published 29 research papers and one review (22 as corresponding author) and in 67 publications since the start of my career. I have supervised 16 PhD Theses, 20 masters, 12 post-doctoral researchers and 4 research associates. We have determined 57 structures deposited in the PDB, 9 protein ensembles deposited in the PED and two software packages at Github repositories (**https://github.com/maciaslab**).

I participate in several activities to promote Gender Equity in Research Centers and to avoid gender bias. I participate in mentoring of STEM among female baccalaureate students (we also host them in the lab for short research stays) and young postdocs at our institution. I am a founding member of the Gender and Equality Committee at IRB Barcelona, which seeks to implement and develop Gender Equality Plans and actions. We have secured EU financial support for these actions through the CALIPER project (https://cordis.europa.eu/project/id/873134).

During the Open Days organized by IRB Barcelona in 2021, 2019, and 2018, our lab participated in outreach activities for the general public, and to disseminate our findings and increase the visibility of biomedical science we also participate in seminars with patient associations and inTwitter. I have appeared in IRB Barcelona's media programme "Meet our Scientists", and have also been interviewed on TV3 and Barcelona betevé.

PUBLICATIONS, OTHER RESEARCH ACTIVITIES LAST 10 YEARS

Note: corresponding authors are indicated with *

Following DORA recommendations, ten publications are highlighted according to the significance of the contribution to scientific knowledge, which is briefly explained.

2021

-Structure-based design of a Cortistatin analogue with immunomodulatory activity in models of inflammatory bowel disease

Rol, A.; Todorovski, T.; Martin-Malpartida, P.; Escolà, A.; Gonzalez-Rey, E ... Delgado, M.; Riera, A. and **Macias, M.J.***

Nature Communications 12 (1), 1-15

We designed and tested in cell lines and in animal models a new peptide analogue with therapeutic properties in bowel and Crohn's disease. Finding new treatments for patients suffering from inflammatory bowel diseases remains a major challenge and a health concern for society because in most instances, the absence of cures turns IBD into a chronic condition, which affects the quality of patients' life to different extents.

-Conformational landscape of multidomain SMAD proteins

Gomes, T.; Martin-Malpartida, P.; Ruiz, L.; Aragón, E.; Cordeiro, T.N.* and **Macias, M.J.***

Computational and structural biotechnology journal 19, 5210-5224

The first approach towards unveiling the Conformational landscape of full-length non-activated SMAD proteins. We developed an integrative structural approach using SAXS, X-ray, NMR and computational approaches to determine conformation ensembles for multi-domain proteins separated by intrinsically disorder and highly flexible linkers. The mixed architectures of folded and flexible regions are common among TFs but are often ignored due to technical difficulties when studying their structures.

-Unveiling the dimer/monomer propensities of Smad MH1-DNA complexes

Ruiz, L.; Kaczmarska,Z.; Gomes,T.; Aragón, E.; Torner,C.; Freier, R.; Baginski, B.; Martin-Malpartida, P.; de Martin Garrido, M.; Márquez, J.A.; Cordeiro, T.N.; Pluta R. and **Macias, M.J.***

Computational and Structural Biotechnology Journal 19, 632-646

We found that all R-SMADs and SMAD4 bind to both SBE and 5GC sites, against the prevailing view in the field that TGF-β-activated SMADs prefer SBE sites whereas BMP-activated SMADs prefer 5GC sites. The key difference between the different SMADs resides in the property that SMAD2/3/4 MH1 domains bind to the DNA as monomers, whereas SMAD1/5/8 form N-terminal helix-swapped dimers. Since full length SMADs are associated as heterotrimers, their

specific composition seems to be defined by those SMADs whose MH1 domains form either dimers or monomers (1 dimer+1 monomer or 3 monomers), answering a long-standing question in the field regarding the rules that define the formation of SMAD complexes.

-HTSDSF explorer, a novel tool to analyze high-throughput DSF screenings
Martin-Malpartida, P.*; Hausvik, E.; Underhaug, J.; Torner, C.; Martinez, A and **Macias, M.J.***
Journal of Molecular Biology, 167372

The identification of new drugs for novel therapeutic targets requires the screening of libraries containing tens of thousands of compounds. We developed the HTSDSF explorer, a versatile, all-in-one, user-friendly application suite implemented as a server-client application. HTSDSF explorer pre-analyzes and displays the results interactively, thereby allowing the user to study hundreds of conditions and select the primary hits in minutes. We believe that this software will help to speed up the process of drug discovery using libraries of compounds, allowing the identification of new molecules with pharmacological applications in a more systematic manner than manually analyzing thousands of datasets.

-Structures of the germline-specific Deadhead and Thioredoxin T proteins from Drosophila melanogaster reveal unique features among Thioredoxins
Freier, R.; Aragón, E.; Bagiński, B.; Pluta, R.; Martin-Malpartida, P.; Ruiz, L.; Condeminas, M.; González, C. and **Macias, M.J.***
IUCrJ Biology and Medicine 8

These structures revealed two major differences of these specific Drosophila germline Trxs with respect to Trx found in other organisms. These differences can also have applications for the design of inhibitory molecules to reduce and control fly plagues, avoiding the cross-over effect of drugs between the target species and other animals thereby mitigating the environmental impact of pesticides. Among the human plagues is that caused by the black fly, which spreads river blindness in Africa and the Americas (World Health Organization) and negatively affects the economies of many countries due to losses in fruit and vegetable production.

2020

-Synthesis of Stable Cholesteryl–Polyethylene Glycol–Peptide Conjugates with Non-Disperse Polyethylene Glycol LengthsCristóbal-Lecina, E; Pulido, D.; Martin-Malpartida, P.; **Macias, M.J.;** Albericio, F.; and Royo, M.
ACS omega 5 (10), 5508-5519

2019

-Structural basis for distinct roles of SMAD2 and SMAD3 in FOXH1 pioneer-directed TGF-β signaling
Aragón, E.; Wang, Q.; Zou, Y.; Morgani, S.M.; Ruiz, L.; Kaczmarska, Z.; Su, J.; Torner, C.; Tian, L.; Hu, J.; Shu, W.; Agrawal, S.; Gomes, T.; Márquez, J.A.; Hadjantonakis, A.-K.; **Macias, M.J.*** and Massagué, J.*
Genes & development 33 (21-22), 1506-1524
Here we determined the molecular basis for distinct roles of SMAD2 and SMAD3 in the regulation of progenitor differentiation genes and the specific role of FoxH1 in priming promoters for the activation of mesendoderm differentiation during development and cancer. Our results challenge an erroneous view that had prevailed in the field for two decades that SMAD2 does not interact with DNA.

-Binding site plasticity in viral PPxY Late domain recognition by the third WW domain of human NEDD4
Iglesias-Bexiga, M.; Palencia, A.; Corbi-Verge,C.; Martin-Malpartida, P.; Blanco, F.J.; **Macias, M.J.;** Cobos, E. S.; and Luque I.
Scientific reports 9 (1), 1-17

2018

TGIF1 homeodomain interacts with Smad MH1 domain and represses TGF-β signaling.
Guca, E.; Suñol, D.; Ruiz, L.; Konkol, A.; Cordero, J., Torner, C.; Aragon, E.; Martin-Malpartida, P.; Riera, A. and **Macias, M.J.***Nucleic Acids Research 46 (17), 9220-9235
We investigated how signal-activated SMADs cooperate with transcriptional repressors. We studied how the repressor TGIF1–Homeodomain (TGIF1–HD) binds its canonical DNA motif and showed how it interacts with the MH1 domain of SMADs. In fact, the formation of the HD-MH1 complex partially hinders the DNA-binding site of the complex, preventing the efficient interaction of TGIF1–HD and SMADs with DNA, thus revealing how the SMAD-TGIF1 complex acts as a transcriptional repression system

2017

-Structural basis for genome wide recognition of 5-bp GC motifs by SMAD transcription factors
Martin-Malpartida, P.; Batet, M; Kaczmarska, Z; Freier, R; Gomes, T; Aragón, E.; Zou, Y; Wang, Q.; Xi, Q; Ruiz, L; Vea, A; Márquez, J.A.; Massagué, J; **Macias, M.J.***
Nature communications 8(1),2070
We established new principles of how SMADs bind to DNA, defined the 5bp GC motif as a highly abundant motif in promoters and illustrate the molecular bases for its recognition by X-Ray. The existence of these GC sites has been predicted in the past but their precise sequence and the critical bases that interact with SMADs was impossible to define without the structural information.

-Synthesis of an EDTA-like Chelating Peptidomimetic Building Block Suitable for Solid-Phase Peptide Synthesis.
Spengler, J; Barker, M.; Schelhorn, C; Garcia, J; **Macias, MJ** ; Albericio, F.
Chem. Commun., 2017, 53, 2634-2636

2016

- Peptide aromatic interactions modulated by fluorinated residues: Synthesis, structure and biological activity of Somatostatin analogs containing 3-(3 ', 5 ' difluorophenyl)-alanine.
Martin-Gago, P.; Rol, A.; Todorovski, T.; Aragón, E.; Martin-Malpartida, P.; Verdaguer, X.; Valles Miret, M.; Fernandez-Carneado, J.; Ponsati, B.; **Macias, M.J.*** and Riera, A.*
***Scientific reports*,** 6, 27285.

-ADP-ribose-derived nuclear ATP synthesis by NUDIX5 is required for chromatin remodeling.
Wright, R.H.G.; Lioutas, A.; Le Dily, F.; Soronellas, D.; Pohl, A.; Bonet, J.; Nacht, A. S.; Samino, S.; Font-Mateu, J.; Vicent, G.P.; Wierer, M.; Trabado, M.A.; Schelhorn, C.; Carolis, C.; **Macias, M.J.;** Yanes, O.; Oliva, B. and Beato, M*.
Science, 352, 6290, 1221 - 1225.

2015

-Structure of the N-terminal domain of the protein Expansion: an 'Expansion' to the Smad MH2 fold
Beich-Frandsen, M.; Aragón, E.; Llimargas, M.; Benach, J.; Riera, A.; Pous, J. and **Macias M.J.***
Acta Crystallographica Section D: Biological Crystallography, 71, 844-853
-Structural determinants of Smad function in TGF-beta signaling
Macias, M.J.*; Martin-Malpartida, P. and Massagué J.*
Invited review, ***Trends in Biochemical Sciences***, 40, 6, 296-308.

This work synthesizes the extant mutational and structural data to suggest how genetic variation in SMAD may affect the structure, regulation, and function of these proteins. As part of this publication, we developed a web-app that compares SMAD sequences and interactively displays SMAD protein structures and their disease-associated variants.
-Preventing fibril formation of a protein by selective mutation
Maisuradze, G.G.; Medina, J.; Kachlishvili, K.; Krupa, P.; Mozolewska, M.; Martin-Malpartida, P.; Maisuradze, L.; **Macias M.J.*** and Scheraga H.A*.
Proc. Natl. Acad. Sci. U S A, 112(44): 13549-54.
Protein folding intermediates are associated with formation of amyloid fibrils, which are responsible for a number of neurodegenerative disorders, such as Alzheimer's, Parkinson's, Huntington's, and Creutzfeldt-Jakob's diseases. We used WW domains as models for fibril formation in amyloid diseases and found that three-state folding though an intermediate state is a major folding scenario for this model system although two-state and downhill folding scenarios were also identified. Our findings lead to an understanding of the structural mechanisms by which intermediates initiate fibril aggregation and might lead to a procedure for their prevention.
-Structural Analysis of the Pin1-CPEB1 interaction and its potential role in CPEB1 degradation
Schelhorn, C.; Martin-Malpartida, P.; Suñol, D. and **Macias M.J.***
Scientific reports, 5, 14990.
-Addition of HOBt improves the conversion of thioester-amine chemical ligation
Todorovski, T.; Suñol, D.; Riera, A. and **Macias M.J.***
Biopolymers, 104(6): 693-702.

2014

-Structural Basis of the Activation and Degradation Mechanisms of the E3 Ubiquitin Ligase Nedd4L
Escobedo, A.; Gomes, T.; Aragón, E.; Martin-Malpartida, P.; Ruiz, L.; **Macias, M.J.***
Structure, 22, 10, 1446-1457.

-Identification of novel non-canonical RNA-binding sites in Gemin5 involved in internal initiation of translation
Fernandez-Chamorro, J.; Pineiro, D.; Gordon, J.M.B.; Ramajo, J.; Francisco-Velilla, R.; **Macias, M.J.** and Martinez-Salas, E.*
Nucleic acids research, 42, 9, 5742-5754.

-A tetradecapeptide somatostatin dicarba-analog: Synthesis, structural impact and biological activity
Martin-Gago, P.; Ramon, R.; Aragón, E.; Fernandez-Carneado, J.; Martin-Malpartida, P.; Verdaguer, X.; Lopez-Ruiz, P.; Colas, B.; Cortes B.M; Ponsati, B.; **Macias, M.J.*** and Riera, A.*
Bioorganic & Medicinal chemistry letters, 24, 1, 103-107.

-RNA recognition and self-association of CPEB4 is mediated by its tandem RRM domains
Schelhorn, C.; Gordon, J.M. B.; Ruiz, L.; Alguacil, J.; Pedroso, E. and **Macias, M.J**.*
Nucleic acids research, 42, 15, 10185-10195.

Here, we have examined the RNA interactions of the cytoplasmic polyadenylation element binding protein (CPEB) using a combination of biochemical, biophysical and NMR-based techniques and proposed a model of the RRM1–RRM2–RNA complex. This model has been used as a platform for studies aimed at the design of protein–RNA inhibitors, targeted to the CPEB family of proteins to modulate translational activation.

-Folding kinetics of WW domains with the united residue force field for bridging microscopic motions and experimental measurements
Zhou, R.; Maisuradze, G.G.; Suñol, D.; Todorovski, T.; **Macias, M.J.**; Xiao Y.; Scheraga, H.A.*; Czaplewski, C.; Liwo, A.*
Proc Natl. Acad. Sci. U S A., 111(51): 18243-8.

2013

-Insights into Structure-Activity Relationships of Somatostatin Analogs Containing Mesitylalanine
Martin-Gago, P.; Aragón, E.; Gomez-Caminals, M.; Fernandez-Carneado, J.; Ramón, R.; Martin-Malpartida, P.; Verdaguer, X.; López-Ruiz, P.; Colás, B.; Cortes, M.A.; Ponsati, B.; **Macias, M.J.*** and Riera A.*
Molecules, 8(12), 14564-14584

2012

-Martín-Gago, P.; Gomez-Caminals ,M.; Ramón, R.; Verdaguer, X.; Martin-Malpartida, P.; Aragón, E.; Fernández-Carneado, J.; Ponsati, B.; López-Ruiz, P.; Cortes, MA.; Colás, B.; **Macias M.J.*** and Riera A.*
Fine-tuning the π-π aromatic interactions in peptides: somatostatin analogues containing mesityl alanine.
Angew. Chem. Int. Ed. Engl., Feb 20;51(8):1820-5.

-Structural basis for the versatile interactions of Smad7 with regulator WW domains in TGF-β Pathways
Aragón, E.; Goerner, N.; Xi, Q.; Gomes, T.; Gao, S.; Massagué, J.*and **Macias M.J.***
Structure, Oct 10;20(10):1726-36.

2011

Aragón, E.; Goerner, N.; Zaromytidou, AI.; Xi, Q.; Escobedo, A.; Massagué, J.*and Macias **M.J. *** A Smad action turnover switch operated by WW domain readers of a phosphoserine code.
Genes & Dev. Jun 15;25(12):1275-88.

We clarified the action-turnover switch that operates the activation and degradation cycle of R-SMAD proteins. This mechanism involves the interaction of Smads with transcription activators that modulate their function as well as with ubiquitin ligases that limit their amount in the nucleus. This process is regulated by a phosphorylation code that we have deciphered and described at an atomic detail using high-resolution NMR.

Conferences, Workshops and invited seminars

National and International conferences and workshops: Two to three invited seminars/workshops per year (on average). Selected meetings as speaker (last 5 years): iNEXT and INSTRUCT meetings (2017, 2018, 2020), SBE (2016, 2018), in 2019 at Weizmann's GHz-fest conference (Israel), at the CIC-Biogune (Bilbao, SPAIN) and at the IQAC-CSIC (Barcelona, SPAIN) and in the BMP and TGF beta symposia 2020 and 2021. We also presented ~ 20 posters and short talks in international and national conferences during the last five years.

Organisation of Scientific Meetings 03/Nov/2019 EMBL in Spain, co-organizer, 28/Nov/2016 From genomes to structures: looking at big data with an atomic perspective Barcelona BioMed Conferences. Co-Organized with D. H. Oschkinat, FMP Berlin (Germany).

RESEARCH MANAGEMENT ACTIVITIES

- 2020- Member of the Advisory Committee of The Francis Crick Institute UK, NMR Centre
- 2021 Jury of the National Research Award Santiago Ramón y Cajal, 2021.
- Since 2002– Reviewer for National and International Agencies (Grants and Fellowships), Agencia Estatal de Investigación, Wellcome Trust, (2010, 2012, 2016) NIH, USA, (2013, 2015, 2017), French National Research Agency (ANR) (2013-present), Swiss National Science Foundation (SNSF) (2014, 2018), EMBL (ARISE program 2021, 2022). Member of the IJMS Editorial Board and for several journals including Mol Cell, Nature Communications, PNAS, NAR, Angewandte Chemie.
- Member of Evaluation Panels for GL positions at the IRB Barcelona and programmes such as To the Mothers of Science Programme.
- EMBL alumni, Human Frontier Science Program alumni, Member, la Sociedad Española de Bioquímica y Biología Molecular y de la Sociedad Española de Biofísica, Instruct member, iNEXT.
- Member of the "Red en Péptidos, en Biomedicina y Nanociencia (BIONAPEP)-. MICINN (RED2018-102417-T)" Coordinator: Eugenio Vázquez
- Member of the Red Española de Metabolómica **MetaboRed** (RED2020, Coordinator: Oscar Yanes).

INSTITUTIONAL ACTIVITIES

- 02/May/2016- Present. Member of the Equality and Diversity Committee at IRB Barcelona.
- 01/Feb/2016 - 03/Feb/2016. Member of Evaluation Panel. GL position at the IRB Barcelona
- 28/Nov/2016 - 30/Nov/2016. Conference/workshops Organization. From genomes to structures: looking at big data with an atomic perspective Barcelona BioMed Conferences. Organized with D. H. Oschkinat
- Internal BioMedTec Programme**,** promoted by the IRB Barcelona and supported by the Obra Social "la Caixa" **technology transfer programme**, 'A rapid fluorescent screening method to evaluate the effect of disease mutated proteins in ligand binding ', Role: Principal Investigator·01/Dec/2015 - 30/Jun/2016

MANAGEMENT OF INFRASTRUCTURES: NMR AND ITC

Our group uses sophisticated biophysical techniques for the structural characterization of biomolecules. Since 2006, when the IRB Barcelona purchased the 600-MHz Bruker spectrometer, we have been responsible for setting up standard and new NMR experiments, for its maintenance, and for software and technical upgrades. At the end of 2013 it was upgraded and equipped with a four-channel cryoprobe. The spectrometer is used to determine structures of proteins and nucleic acids as well as their dynamical behavior in solution (75% of the time is for our group). We provide support to other users in the IRB Barcelona during the remaining 25% of the available measurement time.

Since the year 2010 we are also responsible for managing the nano Isothermal titration calorimetry system at IRB Barcelona. Our responsibility includes the design and analysis of the data to characterize the thermodynamic parameters of interactions in solution and providing support to other users from the IRB Barcelona and nearby institutions. In some cases, the projects are performed as collaborative projects.

ADDITIONAL INFORMATION

The IRB Barcelona is the recipient of the Severo Ochoa Award of Excellence, 2011-2014, 2015-2018 and 2019-2022. In the first two calls I participated as a "selected researcher". The institute belongs to the CERCA (centres de recerca de Catalunya) and to the Barcelona Institute of Science and Technology (BIST).

EDUCATIONAL ACTIVITIES

I have supervised 15 PhD Theses, 20 masters, 12 post-doctoral researchers and 4 research associates. Our group actively participates in scientific programmes aimed at approaching research to undergraduate and master students. We participate in local programmes such as *Passa l'estiu al Parc*, and we have also hosted students from abroad, performing similar studies (project Unipharma for Italian graduates in chemistry). I also participate in lectures for master students and our group receives master and bachelor students for practical courses from several universities, local and from abroad.

PHD THESES (2011-2021) TOTAL: 9

- **Date:** 05-Nov-2019**. Role:** Director**. Title: "**Into the structure of human full-length smad proteins and the impact of cancer mutations"**. Student: Tiago Gomes Lopes.** Universitat de Barcelona, Spain.
- **Date:** 12-Feb-2018. **Role**: Director. **Title**: "Structure, dynamics and complex formation of Eukaryotic Transcriptional Regulators" **Student: Jordi Medina**, Universidad de Barcelona, Spain.
- **Date**: 19-Dec-2016. **Role**: Director. **Title**: "Structural studies of recombinant TGIF1 and FBP28 WW domains using NMR and peptide ligation strategies" **Student: David Suñol Moreno**, Universidad de Barcelona, Spain.
- **Date**: 11-Dec-2015-**Role**: Co-Director (with Dr. A. Riera). **Title**: "Análogos de somatostatina y cortistatina. Efecto de las interacciones aromáticas en sus estructuras y en la actividad biológica". **Student: Álvaro Rol Rúa**, Universidad de Barcelona, Spain.
- **Date**: 04-Feb-2015. **Role**: Director. **Title**: "Structural studies on the N-terminal part and RNA binding domains of the CPEB family" **Student: Constanze Schelhorn**, Technische Universität München (Germany).
- **Date**: 06-Nov-2014. **Role**: Director. **Title**: "Structural Insights into Substrate Binding and regulation of E3 Ubiquitin ligases in the Nedd4 family using NMR spectroscopy" **Student: Albert Escobedo Pascual**, Universidad de Barcelona, Spain.
- **Date**: 13-Dec-2013. **Role**: Director. **Title**: "Smad binding codes broken by WW domain containing proteins" **Student: Eric Aragón Altarriba**, Universidad de Barcelona, Spain.
- **Date**: 02-Oct-2012. **Role**: Director. **Title**: "Automation of an NMR laboratory". **Student: Pau Martin Malpartida**. Universidad de Barcelona, Spain.
- **Date**: 15-Dec-2011. **Role**: Director. **Title**: "Interactions of Smads and WW domains of proteins involved in TGF beta signaling". **Student: Nina Goerner**, Freie Universität Berlin, Germany.

PHD THESES (2003-2010) TOTAL: 6

- **Date**: 17/12/2010 **Role**: Co-Director (with Dr. Anna Díez). **Title:** "Síntesi i aplicació de ψ-dipeptids amb estructura de 3-aminopiperidona. Síntesis de ψ-melanotans". **Student: Jordi Mas Pons**, Universidad de Barcelona, Spain.
- **Date**: 10/09/2009 **Role**: Director. **Title**: "Structural Studies on FF domains by NMR spectroscopy". **Student: Roman Bonet i Figueredo**, Universidad Autónoma de Barcelona, Spain.
- **Date**: 05/03/2009 **Role**: Director. **Title**: "Estudios de la regulación de las E3 ubiquitina ligasas Itch y WWP1". **Student: Begoña Morales**, Universidad de Barcelona, Spain.
- **Date**: 10/01/2007 **Role**: Director. **Title**: "NMR as a tool to elucidate the rules that govern WW domain binding specificity and stability". **Student: Ximena Ramirez-Espain**, Universidad Autónoma de Madrid, Spain.
- **Date**: 18/06/2004 **Role**: Director. **Title**: "Structural and Biochemical Characterization of the WW domains of Itch E3 ubiquitin ligase using NMR spectroscopy". **Student: Alison Zoe Shaw**, University of Manchester, UK.
- **Date**: 25/02/2003 **Role**: Co-Director (with Dr. M. Sattler). **Title**: "Yeast splicing factor Prp40: Structures and ligand recognition of a WW domain pair and an FF domain". **Student: Silke Wiesner**, Freie Universität Berlin, Germany.

PROFESSIONAL DEVELOPMENT OF FORMER PHD STUDENTS OF OUR LABORATORY

- **Pau Martín Malpartida and Eric Aragón,** currently working as **Research Associates of our Lab. Research team of this project**. **Tiago Gomes Lopes,** currently: **Postdoc, recently awarded a Margarita Salas postdoctoral grant.**
- **Silke Wiesner,** Postdoc with J. Forman-Kay in Canada. **Alison Shaw**, associate editor of the scientific journal BBMC, **Ximena Ramirez,** Quality Control Researcher. Merck Biosciences AG, (Germany), **Begoña Morales,** At present: Project

Manager, IQFR-CSIC. **Román Bonet,** Postdoc with I.D. Campbell, (Oxford, UK), Researcher at the IBMB-CSIC. At present: Prof. of biological sciences. **Jordi Mas,** postdoc in the CNRS Paris. At present: RES Project Officer, BSC-CNS. **Nina Goerner,** Biotech Company, Germany. **Albert Escobedo,** Novartis. At present Postdoctoral at Centre for Genomic Regulation, Barcelona. **Constanze Schelhorn,** Scientific Officer and JAMS Project Manager at MDPI. **James Gordon,** Postdoc MRC Laboratory of Molecular Biology, Cambridge UK. **Toni Todorovski,** Peptide medicinal chemist, At present: Universitat Pompeu Fabra. **Alvaro Rol,** At present: Farmacéutico Titular del Estado, Madrid. **David Suñol,** At present: Advanced Researcher at Eurecat - Technology Centre of Catalonia, Barcelona. **Jordi Medina,** High School teacher (Biological sciences) in Barcelona.

PROFESSIONAL DEVELOPMENT OF FORMER POSTDOCTORAL RESEARCHERS OF OUR LABORATORY

- **Concepción Civera,** At present: Professor, Faculty of Pharmacy, Universidad Complutense de Madrid (Spain)
- **Silke Wiesner,** At present: Max Planck Research Group Leader (Germany)
- **Alexander Gasch**, Researcher at Faculty of Medicine, Mannheim, University of Heidelberg (Germany)
    - **Alison Shaw**, associated editor of the scientific journal BBMC
    - **James Gordon,** MRC Laboratory of Molecular Biology, Cambridge UK
- **Toni Todorovski,** Senior Post-doctoral fellow (Department of Experimental & Health Sciences) Universidad Pompeu Fabra.
- **Ewelina Gucca**, currently a Postdoc INSERM: Bordeaux/Pessac, France
- **Marco Jan Klein**, currently a Business Development Manager for Pharma companies in Catalonia
- **Regina Freier**, currently a researcher in PROTEROS biostructures GmbH Germany.

OTHER PUBLICATIONS, 1991-2009

Alarcón C., Zaromytidou A.I., Xi Q., Gao S., Yu J., Fujisawa S., Barlas A., Miller A.N., Manova-Todorova K., **Macias M.J.**, Sapkota G., Pan D., Massagué J.***** Nuclear CDKs drive Smad transcriptional activation and turnover in BMP and TGF-beta pathways.
Cell. 2009 Nov 13;139(4):757-69.

Gao S., Alarcón C., Sapkota G., Rahman S., Chen P.Y., Goerner N., **Macias M.J.**, Erdjument-Bromage H., Tempst P., Massagué J.***** Ubiquitin ligase Nedd4L targets activated Smad2/3 to limit TGF-beta signaling.
Mol Cell. 2009 Nov 13;36(3):457-68. doi: 10.1016/j.molcel.2009.09.043.

Bonet R., Ruiz L., Morales B., **Macias M.J.*** Solution structure of the fourth FF domain of yeast Prp40 splicing factor.
Proteins 2009 Dec; 77(4):1000-3.

Bonet R., Ruiz L., Aragón E., Martin-Malpartida P., **Macias M.J.*** NMR structural studies on human p190-A RhoGAPFF1 revealed that domain phosphorylation by the PDGF-receptor alpha requires its previous unfolding.
Journal of Molecular Biology *2009 Jun 5;389(2):230-7.*

Bonet R., Ramirez-Espain X., **Macias M.J.*** Solution structure of the yeast URN1 splicing factor FF domain: comparative analysis of charge distributions in FF domain structures-FFs and SURPs, two domains with a similar fold.
Proteins*. 2008 Dec;73(4):1001-9.*

Ramirez-Espain X., Ruiz L., Martin-Malpartida P., Oschkinat H., **Macias M.J.*** Structural characterization of a new binding motif and a novel-binding mode in group 2 WW domains
Journal of Molecular Biology *2007 Nov 9;373(5):1255-68*

Morales B., Ramirez-Espain X., Shaw A.Z., Martin-Malpartida P., Yraola F., Sánchez- Tilló E., Farrera C., Celada A., Royo M., **Macias M.J.*** NMR structural studies of the ItchWW3 domain reveal that phosphorylation at T30 inhibits the interaction with PPxY-containing ligands.
Structure *2007 Apr;15(4):473-83*

Brucet M., Querol-Audí J., Serra M., Ramirez-Espain X., Bertlik K., Ruiz L., Lloberas J., **Macias M.J.**, Fita I., Celada A.***** Structure of the dimeric exonuclease TREX1 in complex with DNA displays a proline-rich binding site for WW Domains.
Journal of Biological Chemistry *2007 May 11;282(19):14547-57.* 10.-

Macias M.J., Teijido O., Zifarelli G., Martin-Malpartida P., Ramirez-Espain X., Zorzano A., Palacín, M., Pusch M., Estévez R.***** Myotonia-related mutations in the distal C-terminus of ClC-1 and ClC-0 chloride channels affect the structure of a poly-proline helix.
Biochemical Journal *2007 Apr 1;403(1):79-87.*

Gasch A., Wiesner S., Martin-Malpartida P., Ramirez-Espain X., Ruiz L., **Macias M.J*** The structure of Prp40 FF1 domain and its interaction with the crn-TPR1 motif of Clf1 gives a new insight into the binding mode of FF domains.
Journal of Biological Chemistry *2006 Jan 6;281(1):356-64.*

Civera C., Simon B., Stier G., Sattler M., **Macias M.J.***Structure and dynamics of the human pleckstrin DEP domain: distinct molecular features of a novel DEP domain subfamily.
Proteins. 2005 Feb 1; 58(2):354-66

Shaw AZ, Martin-Malpartida P, Morales B, Yraola F, Royo M, **Macias MJ*.**
Phosphorylation of either Ser16 or Thr30 does not disrupt the structure of the Itch E3 ubiquitin ligase third WW domain.
Proteins. 2005 Aug 15;60(3):558-60.

Macias, M.J, Wiesner S. and Sudol M. WW and SH3 domains, two different scaffolds to recognize proline-rich ligands.
Febs Letters 2002, 513, 30-37.

Wiesner, S., Stier, G., Sattler, M., and **Macias, M.J.*** Solution structure and ligand recognition of the WW domain pair of the yeast splicing factor Prp40.
Journal of Molecular Biology 324, 807-82 (2002)

Ferguson, N., Johnson C. M., **Macias, M.J.**, Oschkinat, H. and Ferhst A.*****Ultrafast folding of WW domains without structured aromatic clusters in the denatured state
Proceedings of the National Academy of Sciences USA 98,13002-13007 (2001).

Pires, J. R., Taha-Nejad, F., Töpert, F., Ast, T. Hoffmüller, U., Schneider-Mergener, J., Kühne, R., **Macias, M.J.**, and Oschkinat H.***** Solution structures of the YAP65 WW domain and the variant L30K in complex with the peptides GTPPPPYTVG, N-(n-octyl)- GPPPY and PLPPY and the application of peptide libraries reveal a minimal binding epitope.
Journal of Molecular Biology 314, 1147-115. 17-02-2011 (2001)

Fàbrega, C., **Macias M.J**. and Eritja, R.*****Synthesis and properties of oligonucleotides containing 8-bromo-2′-deoxyguanosine.
Nucleosides, Nucleotides and Nucleic acids 20, 251-260 (2001)

Macias M.J., Gervais, V., Civera, C., and Oschkinat H.***** Structural analysis of WW domains and design of a WW prototype.
Nature Structural Biology 7(5):375-9 (2000)

Cregut, D., Civera, C., **Macias, M.J.**, Wallon G. and Serrano L.*A tale of two secondary structure elements: when a beta-hairpin becomes an alpha-helix.
Journal of Molecular Biology (1999) 292(2):389-401

Liu, Z., **Macias, MJ**., Bottomley, M.J., Stier, G., Linge, J.P., Nilges, M., Bork, P. and Sattler M.*The three-dimensional structure of the HRDC domain and implications for the Werner and Bloom syndrome proteins.
Structure Folding and Design (1999) 7(12):1557-66

Bottomley M.J.*, **Macias, M.J,*** Liu, Z. and Sattler M.*A novel NMR experiment for the sequential assignment of proline residues and proline stretches in 13C/15N labeled proteins.
Journal of Biomolecular NMR (1999) 13, 381-385

Güimil-Garcia, R., Ferrer, E. **Macias, M.J.**, Eritja R. and Orozco M.*
Theoretical calculations, synthesis and base pairing properties of oligonucleotides containing 8-amino- 2'-deoxyadenosine.
Nucleic Acids Research (1999) 27, 1991-8

Schultz, J., Hoffmüller, U., Krause, G., Ashurst, J., **Macias, M.J**., Schmieder, P., Schneider-Mergener, J. and Oschkinat H.* Specific interactions between the syntrophin PDZ domain and voltage-gated sodium channels.
Nature Structural Biology (1998) 5, 19-24

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A small region in phosducin inhibits G-protein βγ-subunit function.
EMBO Journal (1997) 16, 4908-4915

Nilges, M., Macias, M.J., O'Donoghue, S.I. and Oschkinat H.* Automated NOESY interpretation with ambiguous distance restraints: the refined NMR solution structure of the pleckstrin homology domain from β-spectrin.
Journal of Molecular Biology (1997) 269, 408-422 17-02-2011

Macias, M.J., Hyvönen, H., Baraldi, E., Schultz, J., Sudol, M., Saraste, M. and Oschkinat, H.*
Structure of the WW domain of a kinase-associated protein in complex with a proline-rich peptide.
Nature (1996) 382, 646-649

Hyvönen, M., **Macias, M.J**., Nilges, M., Oschkinat, M., Saraste, M. and Wilmanns M.*
Structure of the binding site for inositol phosphates in a PH domain.
EMBO Journal (1995) 14, 4676-4685

Macias, M.J.* Kharrat, A*., Gibson, T.J., Nilges, M. and Pastore A.*
Structure of the double stranded RNA-binding domain from E. coli Rnase III
EMBO Journal (1995) 14, 3572-3584

Macias, M.J., Martin, V., Grande, M. and Kubeczka K.H.*Phenylpropanoids from Pimpinella villosa.
Phytochemistry (1994) 37, 539-542

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Structure of the pleckstrin homology domain from β-spectrin.
Nature (1994) 369, 675-677

Villalobos, N., Martin, L., **Macias, M.J.**, Mancheño, B. and Grande M.*
Gibberellin-like activity of some tetracyclic diterpenoids from *Elaeoselinum* species and their derivatives.
Phytochemistry (1994) 37, 635-639

Grande, M.*, Morán, J.R., **Macias M.J.** and Mancheño B.
13C-NMR spectra of some tetracyclic diterpenoids isolated from *Elaeoselinum* species.
Phytochemical Analysis (1993) 4, 19-24

Grande, M.*, **Macias, M.J, Mancheño**, B. and Zazo A.New kaurane diterpenoids from the aerial parts of *Distichoselinum tenuifolium*.
Journal of Natural Products (1991) 54, 866-869