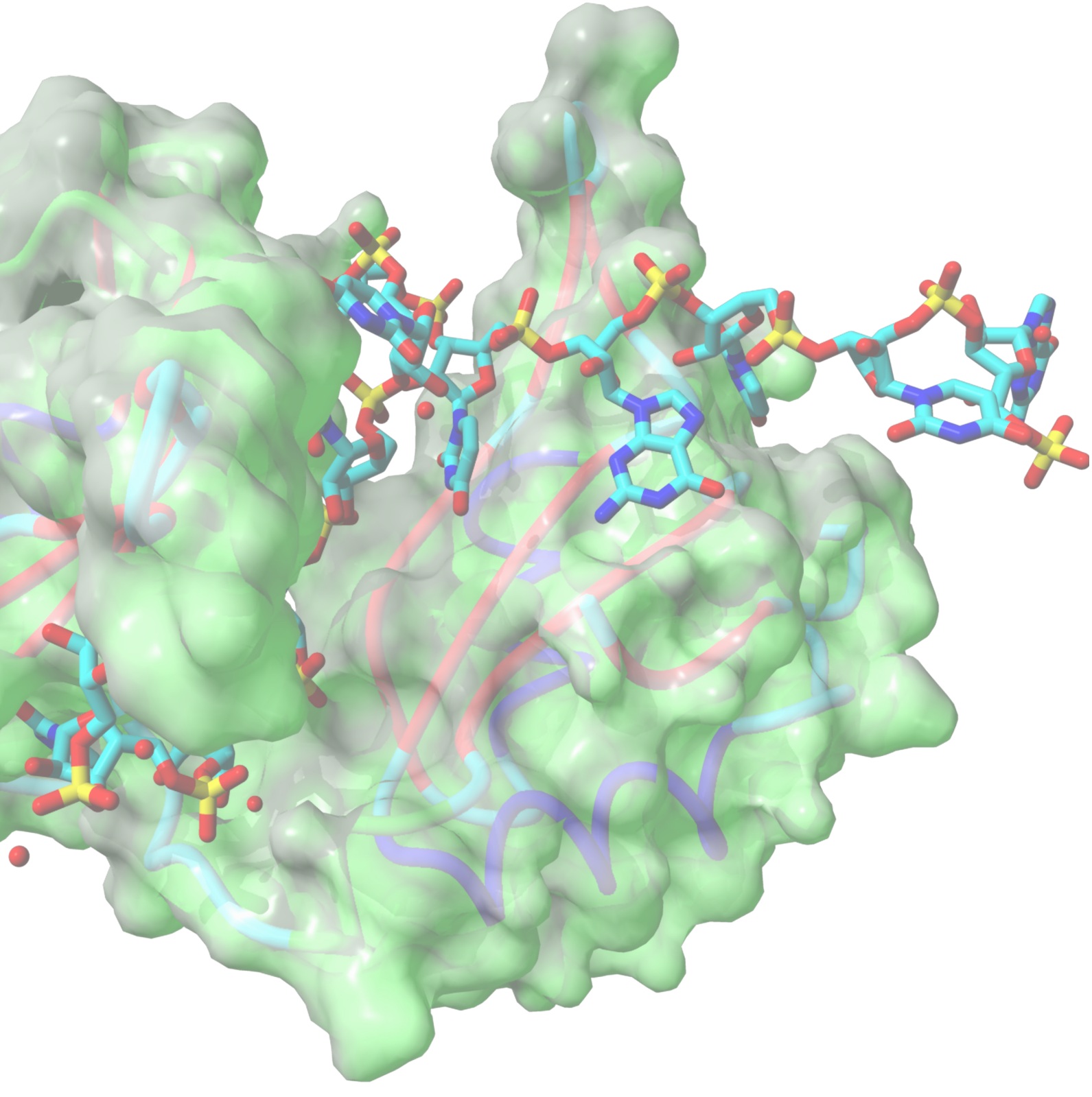
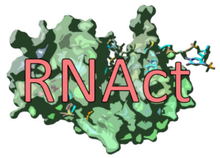
RNAct

Enabling proteins with RNA recognition motifs for synthetic biology and bio-analytics

March 2020





This issue of the newsletter has been edited by Anna Pérez i Ràfols (ESR 7) and Joel Roca Martínez (ESR 1).

ISSUE 1 **MARCH 2020**

TABLE OF CONTENTS

This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 813239. The responsibility of this publication lies with the author. The European Union is not responsible for any use that may be made of the information contained therein.

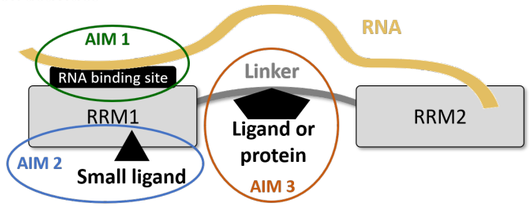
RNAct at a glance

The project in a nutshell

RNAct is a Marie Skłodowska-Curie Innovative Training Network (MSCA-ITN) project with the research aim of designing novel RNA recognition motif (RRM) proteins for exploitation in synthetic biology and bio-analytics. This is achieved through a design cycle that starts with computational approaches at the sequence and structure levels of proteins and RNA, in order to select amino acid positions and mutations for large-scale phage display experiments with RNA screening. Viable RRMs will be further investigated at the atomic level with integrative structural biology approaches, and will be applied in synthetic biology, to post-transcriptionally regulate fatty acid processing via RRMs, and in bio-analytics, to detect RNA in-cell and design RNA biochips.

RNAct creates a comprehensive, cross-disciplinary platform to train ten early-stage researchers (ESRs) with versatile computational and experimental skills, a high level of professional maturity, and an excellent academic and non-academic career opportunities. This platform includes:

- Training in molecular work for bio-analytics and synthetic biology
- Training on topical and transferable skills
- A buddy system to ensure links between computation and experiment
- Involvement in both academic and industry environments
- Engagement in dissemination and communication actions
- involvement in innovation activities



The project focuses on the following aims:

1. Modify the RNA specificity of single-domain RRMs by modulating their side-chain interactions with ssRNA motifs (3-5 nucleotides), so tuning or steering their RNA recognition while maintaining their other functions.

2. Allosterically control single-domain RRM-RNA binding via a small ligand that binds an RRM and either triggers RNA-recognition or modifies RNA specificity.

3. Design multi-domain RRM protein switches where allosteric changes in the domain linker change the RNA specificity, or where RNA binding changes the linker conformation.

The Network is organised into six Work Packages:

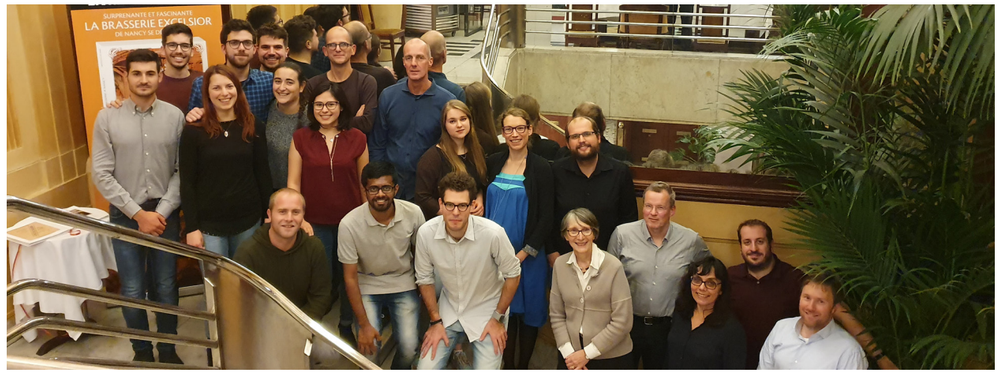
Work Package 1. Creation and characterisation of functional RRMs.
Work Package 2. Representation and design of dynamic proteins.
Work Package 3. Bio-analytics and synthetic biology.
Work Package 4. Training and education.
Work Package 5. Coordination and management.
Work Package 6. Dissemination and communication.

For more information, visit http://rnact.eu/workPackages/ .

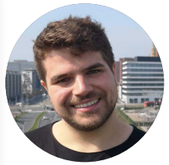
Consortium

RNAct brings together seven beneficiary institutions from five different European countries. Four academic organisations (VUB, CNRS, CSIC, and HMGU) and three companies (Giotto Biotech, Dynamic Biosensors and Ridgeview Instruments AB) join forces with the support of six partner universities (University of Liège, Lorraine University, Technical University of Munich, University of Florence, Polytechnic University of Valencia and Uppsala University) to build up a highly interdisciplinary network to tackle the ambitious goals of the project.

Beneficiaries	Partners
Vrije Universiteit Brussel (VUB) **Prof. Dr. Wim Vranken**	Université de Liège (ULG) **Prof. André Matagne / Dr. Marylène Vandevenne**
Centre National de la Recherche Scientifique (CNRS) **Dr. Isaure Chauvot de Beauchêne**	Université Lorraine (UL) **Prof. Malika Smaïl-Tabbone**
Helmholtz Zentrum München (HMGU) **Prof. Dr. Michael Sattler**	Uppsala Universitet (UU) **Prof. Helena Danielson**
Consejo Superior de Investigaciones Científicas (CSIC) **Dr. Guillermo Rodrigo**	Università degli studi di Firenze (UF) **Prof. Marco Fragai**
Ridgeview Instruments AB (RV) **Dr. Karl Andersson / Dr. Jos Buijs**	Universitat Politècnica de València (UPV) **Prof. Carmelo López**
Giotto Biotech Srl (GIO) **Dr. Tommaso Martelli**	Technische Universität München (TUM) **Prof. Dr. Martin Zacharias**
Dynamic Biosensors GmbH (DBS) **Dr. Ulrich Rant / Dr. Wolfgang Kaiser**	



Meet the ESRs



José Gavaldá-García
ESR1

Jose was born in Nules (Spain) and is 27 years old. He studied his bachelor in Biotechnology at the Polytechnic University of Valencia, where he learned about plant synthetic biology during his internship and iGEM participation. He moved to Amsterdam to study MSc Biomolecular Sciences and MSc Bioinformatics & Systems biology at the Vrije Universiteit Amsterdam, where he discovered his passion for protein biophysics and machine learning, and decided to redirect his career to that direction.

Currently, Jose holds the RNAct's computational ESR1 position at the Vrije Universiteit Brussel. His project aims to predict biophysical properties of proteins from their amino acid sequences. To do this, he trains classifiers with experimental data, to later predict properties of proteins that do not have such data. He works together with Joel for his main project, and has close interactions with Luca, Stefano and Hrishikesh. He will work with Anahí to tackle large-scale data collection and analysis in the RNAct project.

Jose's passions are sports and food, which luckily balance each other. He has competed at national level on swimming and wushu, for which he got a silver medal in the Dutch nationals. He also enjoys playing adventure videogames and singing with his ukulele.

Joel Roca Martínez
ESR2

Joel Roca was born in Mequinenza in 1995, a very small village in the northeast of Spain. He studied Biochemistry and Biotechnology at the University Rovira i Virgili (Tarragona, Spain) where he discovered bioinformatics by collaborating with the Cheminformatics and Nutrition Research Group. He then moved to Barcelona to study an MSc in Bioinformatics at the Autonomous University of Barcelona (UAB) and developed his master thesis at the Chemogenomics Research Group (University of Strasbourg, France). Then he came back to Spain and worked as bioinformatician in ProtoQSAR, developing machine learning QSAR models.

Currently, he is doing his PhD at the VUB (Brussels, Belgium) in the context of the RNAct project (ESR2). He will develop a framework to integrate different biophysical properties prediction tools with an improved *in-silico* structure representation to better understand the binding of RNA with RNA Recognition Motifs (RRMs). For that purpose, he will work together with Jose and learn experimental NMR methods from Stefano, Luca and Anna Pérez during his secondments.

When he is not sitting at the office, he does not like to stand around. He used to practice artistic skating but he has always loved most sports. Now he climbs outdoors whenever he can and indoors the rest of the time.

Hrishikesh Dhondge
ESR3

Hrishikesh is 23 years old and he is from Kandhar, India. Hrishikesh obtained his bachelor's and master's degree in Bioinformatics at the MGM's College of Computer Science & Information Technology (affiliated to Swami Ramanand Teerth Marathwada University), and at the Nanded and Pondicherry University, respectively. His master's thesis focused on DNA-based data storage systems and during this period he did an internship at Bose Institute (Kolkata, India), where he worked on next-generation sequencing (NGS) data analysis and machine learning.

Currently, he is enrolled as a PhD student at LORIA-INRIA in Nancy (France). His primary work is developing a database of available RRM information from the many available RRM data covering a broad range of behaviours. The second part of his thesis will include the computation of protein-RNA binding energies by molecular dynamics simulations of RRM-RNA models. Hrishikesh's main research interests are machine learning, structural biology and NGS data analysis.

Within RNAct, Hrishikesh will work with each ESR to understand the data they need and/or will generate from their projects. As a buddy ESR, he will work closely with Roswitha on how the RRMs can be used to create new pathways. During his spare time he enjoys playing videogames and reading novels.

Anna Kravchenko
ESR4

Anna is 23 years old and she is originally from Kyiv, Ukraine. Anna's background is primarily mathematical - she obtained both bachelor's and master's degree in Applied Mathematics at the National Technical University of Ukraine "Igor Sikorsky Kyiv Polytechnic Institute".

Currently, Anna holds the computational ESR4 position of the RNAct project. She is a PhD student in the "Lorraine Research Laboratory in Computer Science and its Applications" (LORIA), working in CAPSID team on the fragment-based modelling of protein-RNA complexes for protein design. Her nearest aim is to optimize algorithms for single-stranded RNA docking methodology. Further, she will incorporate new sources of information for data-driven docking and create an RNA–RRM model generation pipeline. Anna is collaborating with Hrishikesh in the frame of exchanging the data. Future mutual work with him will be held on the computation of the binding energies. She will also work with Jose and Joel to design a computational approach for modelling and predicting RRM-ssRNA interactions, and the results will be provided to Stefano for experimental validation.

Anna is enjoying horse riding and snowboarding. She prefers cold weather, listening to jazz music and taking photos. She also has a great love and curiosity associated with speleology.

Stefano Mocci
ESR5

Stefano was born in Oristano (Italy) and is 25 years old. He obtained his bachelor's degree in Biological Sciences at the University of Cagliari and his master's degree in Molecular Genetics at Sapienza University, where he started to be interested in protein structural biology.

He is now taking the opportunity to pursue his studies in this field through the PhD career. Currently, Stefano is working at Helmholtz Zentrum München in the BNMRZ, where he is designing new RRM domains in order to tune the RNA recognition capability.
To accomplish this goal, he will join the "Centre d'Ingénierie des Protéines" at the University of Liège to learn phage display screening. Moreover, within the ESRs he will collaborate with Jose, Joel and Hrishikesh as concerns the large-scale data analysis and with Luca and Anna Pérez for structural studies about RRM/RNA interactions.

Stefano loves being in the nature; in his free time he likes hiking, climbing and scuba diving during the summer.

Luca Sperotto
ESR6

Luca is 24 years old and he comes from Marostica, a small city in the north-east of Italy. After high school, he moved to Padua to study chemistry. Once he finished his bachelor, he decided to move in Florence to study biochemistry and NMR spectroscopy and he completed his MSc in biochemistry. One of his passions is listening to music, especially while chilling out under the sun! He likes playing sports, especially tennis and skiing, as well as hiking.

Currently, he is doing his PhD at the Helmholtz Zentrum München, working at the Bavarian NMR Center. The title of his project is "Biophysical characterisation and determination of single-domain RRM conformations". During his work he will use NMR spectroscopy and X-ray crystallography, alongside with biophysical techniques, to gain structural and dynamic information of RRMs and RNA binding.

In order to do this, he will collaborate with Anna Pérez, Stefano and Anahí during the characterization of RRM domains and with Jose, Joel and Hrishikesh during the process of data collection, helping the development of databases and computational approaches in order to study RRM domains. Finally, he will discuss different approaches to study RRM/RNA interactions together with Anna Kravchenko.

Meet the ESRs

Anna Pérez i Ràfols
ESR7

Anna was born in Barcelona, Spain, and she is 23 years old. She loves nature and enjoys playing sports, hiking and traveling. She studied her bachelor's degree in pharmacy at the University of Barcelona (UB) where she collaborated with the Organic Chemistry and the Biopharmacy and Pharmacokinetics departments.

Currently, she is doing an experimental PhD on "Expression of multi-domain RRMs for the characterization of protein dynamics by NMR" at Giotto Biotech, a spin-off CERM, the Magnetic Resonance Centre in the University of Florence. During her PhD she will focus on multi-domain RRMs, their interaction with RNA and the role of the linker on their orientation, using solution NMR with also paramagnetic probes. Furthermore, she will focus on the behavior of RRM domains with respect to each other, as well as influenced by RNA binding or small molecule binding.

She will collaborate with Luca and Stefano to analyze the data and define mutations, and with Hrishikesh and Anna Kravchenko for the collection of the data and improvement of the RNA fragment-based docking approach. Furthermore, she will spend three months in CNRS in order to learn about computational techniques for RNA/RRM interactions and how to apply them with the experimental structural biology data.

Roswitha Dolcemascolo
ESR8

Roswitha Dolcemascolo, was born in Palermo (Italy) in 1992. Her passion for research was developed at the University of Palermo where she obtained both the BSc and MSc degrees in Biotechnology. In March 2019 she participated in the Erasmus+ for traineeship project and she moved to Valencia (Spain).

There, she is currently doing her PhD in the synthetic biology field joining the RNAct consortium at the I2Sys-Bio-CSIC Institute. She is working on the experimental project entitled "Integrate RRMs in prokaryotes to create new pathways in synthetic biology" and focused on the development of synthetic circuits in *Escherichia coli* cells based on post-transcriptional regulation. She will mainly collaborate with Hrishikesh for their buddy project and will be trained at the Ridgeview Instruments AB company of Uppsala (Sweden) to improve quantitative methods for monitoring bacterial cells induced behavior.

In addition to science, she is interested in liberal arts, she likes learning new languages, travelling and meeting new people and their cultures.

Rosa Anahí Higuera
ESR9

Anahí was born in Mexico City and she recently turned 27 years old. She likes nature, hiking, cooking, dancing, travelling, entrepreneurship and technology transfer. She studied a BSc in Technology in Mexico, and she holds a MSc in Nanoscience and Nanotechnology from KU Leuven (Belgium) and UGA (France). Throughout her career, she has participated in numerous congresses and projects related to biosensors for the detection of analytes of interest in medicine and environment.

Currently she is doing an experimental PhD at Dynamic Biosensors GmbH (DBS) in Munich, Germany. Her project title is "Creating biochips to study RRM/RNA interactions", where she will focus on the development of DNA/RNA biochips and in vitro measurements of RRM-RNA interactions with the proprietary switchSENSE® technology DBS.

Within the RNAct, she will learn structured-based approaches to model RRM-RNA interactions at the CNRS in France. She will also have a collaboration with Jose at the VUB in Belgium, working in large-scale data collection analysis. Furthermore, she will support Stefano in phage display experiments for screening RNA sequences. Finally, she will team up with Anna Kravchenko, Luca and Anna Pérez, with the aim of obtaining valuable information about RRM/RNA molecular dynamics of binding.

Guillermo Pérez Ropero
ESR10

Guillermo Pérez was born in Soria (Spain) 26 years ago, but has lived almost his whole life in Madrid, where he studied Pharmacy at Complutense University of Madrid.

After working in several pharma companies in Spain and Germany, Guillermo moved to Sweden to start his PhD at Ridgeview Instruments AB (in collaboration with Uppsala University). Ridgeview Instruments is a Swedish biotech company focused on providing instruments and software for studying biological interactions in real-time, being the main aim of his PhD project the development of a method to detect RNA-protein interaction in living cells.

He will closely collaborate with Anna Pérez in protein binding characterization and with Roswitha Dolcemascolo in the development of real time assays with living bacteria. During his spare time, Guillermo enjoys reading and having fika, the Swedish habit he likes the most.

The fellows at Place Stanislas in Nancy (France).

Meet the PIs

Prof. Dr. Wim Vranken

Professor Dr. Wim Vranken started off with a degree in (organic) chemistry from the University of Gent, Belgium, and during his Ph.D., also in Gent, analysed the conformation of HIV V3 loop peptides using Nuclear Magnetic Resonance (NMR) experiments. He continued with the NMR analysis of peptides and proteins at McGill university and the Biotechnology Research Institute (BRI) in Montréal, Canada. During an in-between year at the Université Libre de Bruxelles (ULB), he rediscovered programming and moved towards computational aspects of NMR. This was the core of his work at the Protein Data Bank Europe (PDBe) at the European Bioinformatics Institute (EBI) at Hinxton, Cambridge, UK.
Now, he is a research professor at the VUB in Brussels, where they work on understanding and prediction biophysical characteristics of proteins. They focus especially on the dynamics of proteins, and on using only the protein sequence, so enabling them to gain information on the 'dark proteome' – the many proteins for which the sequences are available but have no idea what their behaviour is.

What was the idea behind the RNAct project? What made you want to focus the project on this field and not another?

The main aim of RNAct is to train ten ESRs! The ten of you should 'enable' RNA recognition motifs (RRMs) proteins for synthetic biology and for biosensing. This means we have to be able to design or modify RRMs with specific characteristics, such as recognising a particular RNA sequence, or responding to a small molecule signal. From my perspective, RRMs are very interesting because they are quite dynamic proteins, which is a problem for current structure-based methods for computational protein design. I think our dynamics prediction methods can make a difference there.

What is your role in this project?

I am the coordinator, so I hold the main responsibility for the project, and have to make sure problems get solved and that the work is done as promised to the EU.

Have you always focused your research on bioinformatics or when did you discover it?

I started off in chemistry and experimental structural biology, but realised that with computational approaches (and good experimental data!) it was possible to pursue more fundamental questions about protein behaviour. I only really got into bioinformatics proper after moving to the VUB, when we developed the DynaMine predictor of protein backbone dynamics.

Which scientific impact do you think this project may achieve? And how do you think it will help the ESRs to pursue their scientific careers?

I hope that with this project we will make headway in understanding RRMs and 'unlocking' their potential as bio-tools. For the ESRs, the computational/experimental tandem, the academic/commercial partners, and the manipulation at the molecular level to make these proteins work for us should give everyone a solid scientific background for participating in the bio-based economy and research, which is what Europe is moving towards.

Could you explain a little bit how all the collaborations will work (in a general sense)?

We have partners with very different expertise, and the collaborations bring together ESRs with the right expertise to tackle specific goals of the project. The aim is also to expose ESRs to different environments and ways of thinking; all this is supported by the secondments in the project.

Could you explain a little bit the purpose of the buddy system and how will it work?

The 'buddy system' is where two ESRs are 'paired up' with each other to do tasks together, which are not necessarily around a scientific collaboration. This is another way to encourage communication between the ESRs, in this case especially between people with computational and experimental backgrounds. It is intended more as a 'learning experience', we do not expect that buddies will produce scientific results together, although they might – sometimes such interactions can reveal interesting new avenues to explore. But it is mostly aimed at broadening everyone's horizon.

What do you think about the bioinformatics - experimental binomial that characterizes this project?

The combination of computational and experimental approaches is essential for modern science; many data are available, often of different origin and structure, and the only way to make sense of them is by using computational approaches (and machine learning). The computational results can then inform the planning of experiments, making those more targeted. If you get this synergy right, it is a very powerful combination, that is what we are trying to do in RNAct.

Bioinformatics used to be a reinforcement for the experimental research, but nowadays it has a main role in many different fields, why do you think it has evolved in this way?
Bioinformatics still depends on good experimental data, so that remains essential. The key reason is I think that there are now many more data available, also publicly, and that data has to be combined and analysed at a complexity and scale that is impossible for an experimentalist to do on their local desktop. The expertise required for bioinformatics has become very extensive, and it is a field in its own right, with many things to be discovered from (large scale) data.

About - Bio2Byte research group

Prof. Dr. Wim Vranken leads the Bio2Byte research group, focused on investigating how the dynamics, conformational states and available experimental data of proteins relates to their amino acid sequence. The team aims at unravelling underlying physical and chemical principles with statistics and informatics, and connect them to biological events in order to improve our understanding of how proteins work.

The main research lines in the group are:

- **Biophysical predictions**. Predicting biophysical characteristics of proteins from their amino acid sequence.
- **Amino acid mutations**. Assessing the likely effect of amino acid mutations on a protein (and the organism it is in).
- **Protein design**. Using computation to pre-screen the vast protein sequence space.
- **Protein similarity**. Determining similarity between proteins in biophysical space.
- **NMR**. Improving chemical shift-based methods in NMR.

The results of this research have lead to the development of several in-house software and tools such as DynaMine for the prediction of protein backbone dynamics from sequence only or DEOGEN2 to predict the effect of amino acid mutations in human proteins, among others. The full list of developed tools can be found here.

For more information on the group, please visit http://bio2byte.be/.

Meet the PIs

Dr. Tommaso Martelli

Dr. Tommaso Martelli is a chemist, with an MSc in Organic Chemistry and a PhD in Chemical Science. After his PhD he did a postdoc in CERM on Molecular Biology and protein NMR. Right now he is working as R&D area manager in Giotto Biotech. He takes care of the clients, trying to understand in deep their needs in order to provide them the best solution for their problems. He is also coordinating Giotto Biotech's specialists for the production of proteins and organic compounds and following the writing and development of their R&D projects.

Have you always been working in the NMR field? And how did you end up in Giotto Biotech?

Not really, I have started working using enzyme as catalysis for enantioselective chemical reactions, then I moved on to study protein-substrate and protein-ligand interaction and to structural biology by NMR. After some years in the Academia as a postdoc, I decided to move on to a different field. I wanted to test myself with something new and try to understand how my knowledge could be applied outside a lab. I was also interested in the economic aspects of the research and then I have decided to start at Giotto Biotech, a small company were both economic aspects and research are nicely balanced.

What is your role in this project?

I am the industrial supervisor of Anna Perez and the Research subcommittee manager. During the whole project we will experimentally study RRMs using a range of biophysical and structural biology techniques, in order to fully characterize and understand their binding with RNA at the atomic level. We will focus on multi-domain RRMs, their interaction with RNA and the role of the linker on their orientation, using solution NMR with also paramagnetic probes.

How do you think Giotto Biotech can contribute to this project? And what do you think the RNAct project can bring to your field?

As a spin-off company of the University of Florence, Giotto Biotech can bring to the project its particular point-of-view. As a company, Giotto can teach and show the importance of the economic aspects related to research, but since Giotto is still part of the University, can also bring its up-to-date knowledge. I think that RNAct will bring some new and valuable proteins to the market and also an important knowledge about protein-RNA interaction and, in a general way, RNA manipulation.

How do you think this project will be a positive thing for the ESRs?

I think that the fact that the project is multidisciplinary and involves students and supervisors with different background and skills, will give to the students a more complete perspective on the science field. Moreover, this project will create relationships (and I hope also friendships) between the next generation of scientists.

What is the thing you like the most about the RNAct project?

I really like the topic and the overall team. I think that the RNA is the real new target for the scientists and this projects aims to give a really interesting support to the field. Moreover, I think that all the supervisors have a great experience and capacity to be able to teach and supervise the students in this work.

In terms of protein structure determination of RNA recognition motifs, what can NMR bring that other techniques cannot?

Usually the most of the techniques show you a static and detailed picture of a protein or a complex, without taking care of the dynamic of the system or they show you the dynamics of the system without details of the interactions. NMR can show both the dynamic of the system that you are studying and the interaction details.

How do you think this project will be a positive thing for the ESRs?

I think that the fact that the project is multidisciplinary and involves students and supervisors with different background and skills, will give to the students a more complete perspective on the science field. Moreover, this project will create relationships (and I hope also friendships) between the next generation of scientists.

What is the thing you like the most about the RNAct project?

I really like the topic and the overall team. I think that the RNA is the real new target for the scientists and this projects aims to give a really interesting support to the field. Moreover, I think that all the supervisors have a great experience and capacity to be able to teach and supervise the students in this work.

In terms of protein structure determination of RNA recognition motifs, what can NMR bring that other techniques cannot?
Usually the most of the techniques show you a static and detailed picture of a protein or a complex, without taking care of the dynamic of the system or they show you the dynamics of the system without details of the interactions. NMR can show both the dynamic of the system that you are studying and the interaction details.

Do you think NMR will keep evolving or is it a well-established technique that will not change that much?
I think that it is impossible to predict the future. We are in an historical moment where every day new technologies arrive at the market and their prices always decrease. In 1783 there was the first flight of a man with an hot-air balloon and now, about 200 years later, we are sending satellites to the deep of the Solar system. Everyone, right now, has in its pocket a smartphone that is more powerful and more advanced than the computers that were used at NASA when the Apollo 11 landed on the moon about 50 years ago. This evolution is true for the smartphones but also for the scientific instrumentation.

Nuclear magnetic resonance was first described in 1938 and the first instrument dates back to 1952, that means only 70 years from now. For a variegate technique as the NMR, each small changes in the possibility to build an higher field magnet, to reduce the consumption of He and N2, to reduce the size of the instrument, to speed up the experiments and the calculation, but also the kind of material that is possible to work with, new pulse sequence, … everything will make this technique evolve.

About - Giotto Biotech

Giotto Biotech is a research-intensive SME founded in 2011 as a spin-off of the Magnetic Resonance Center (CERM) at the University of Florence. It was founded by a group of Florentine scientists with the aim of offering products and services to researchers in the biotech field.

The company specializes in technologies associated with nuclear magnetic resonance (NMR), providing biomolecules, organic synthesis, metabolomics, NMR access, and information technologies products and services to academic and industrial research groups. and provides NMR access, recombinant proteins, organic compounds, metabolomics services.

Thanks to a tight collaboration with CERM, Giotto Biotech has full access to a wide battery of NMR instrumentation ranging from 400 to 1200 MHz and it can provide a variety of services in NMR such as metabolomics, protein structure determination and screening of libraries against protein targets.

For more information, please visit https://www.giottobiotech.com/.

Project progress

Meetings

Kick-off meeting

The kick-off meeting took place on the 31st of January 2019 at VUB (Brussels). All the beneficiaries and two partner institutions (ULG and UF) were present. During the meeting, the members of the boards (management and supervisory) and subcommittees were appointed, and the main practical organisation and management topics were discussed and agreed.

Recruitment meeting

The recruitment meeting for RNAct took place in Brussels on the 10th of May 2019 and was preceded by an 'ice-breaker' socializing event the evening of the 9th of May 2019. A total of 25 excellent candidates were invited to the event; 18 of them attended the meeting in person and the other 7 were present virtually.

Board meetings

The supervisory and management boards met on the 10th of October 2019 during the 1st network-wide workshop held in Nancy (France). The meetings focused on the general management of the network, with special emphasis on the fellows' initial personal career plans (PCDPs). Subcommittee deputy managers were appointed during the meetings. Jose Gavaldá (ESR 1) was elected by peer fellows to act as ESR representative and thus to stand for the fellows in the board meetings.

Subcommittee meetings

The 4 dedicated subcommittes meet online montly or bimonthly since November 2019 to follow intermediate issues with regards to training, research, data management and dissemination. In order to have ESRs represented, Joel Roca (ESR 2) was appointed deputy manager of the dissemination subcommittee in November 2019.

Deliverables and milestones completed so far

Deliverables

D5.1 Advertising of all ESR positions
D6.1 RNAct website and social media networks online
D5.2 Supervisory board
D5.6 Consortium agreement
D5.7 Data management plan
D4.1 Initial personal career development plans (PCDPs)
D5.3 Signed common IP strategy
D7.1 EPQ - Requirement No. 1
D5.4 Progress report, year 1

Milestones

M17 Planned recruitment completed
M1 Prototype database useable for testing

Workshop 1 - RRMs, RNA and RNAct

The first workshop, "RRMs, RNA and RNAct", took place in October 2019 at *Laboratoire Lorrain de recherche en informatique et ses applications* (LORIA) in Nancy, France. The 10 ESRs attended for a week to seminars and courses aimed at providing them with skills and knowledge relevant to kick-start their individual projects and scientific careers. They also participated in team building activities in order to reinforce their bonds as their close collaboration is crucial for the project.

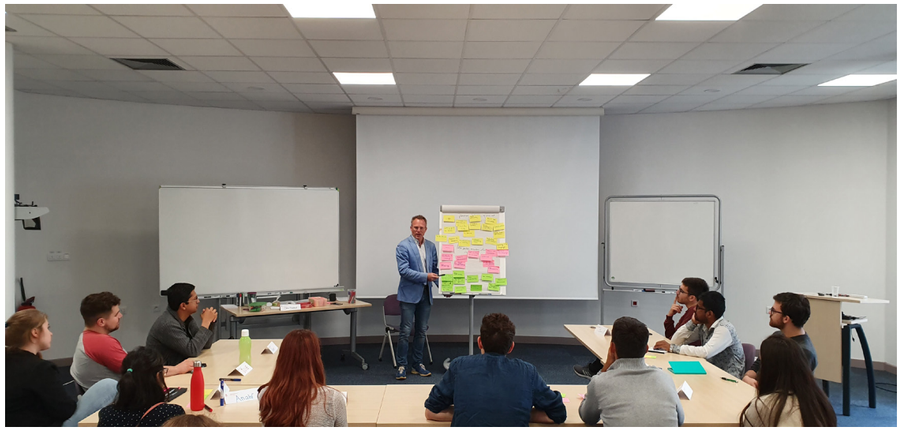
The seminars and courses included in the first workshop were:

- **Project Management**. Jan Pleter Weening (Weening Consult & Training, The Netherlands).
- **Scientific communication**. Dr. Katarzyna Szymanska (Science to the point, France).
- **Protein structure and dynamics**. Dr. Stéphanie Baud (Université de Reims Champagne-Ardenne, France).
- **Protein-RNA recognition**. Dr. Sylvain Maenner (CNRS – Université de Lorraine, France).
- **"Docking in Gle", and "Docking for RRM"**. Dr. Sjoerd de Vries (INSERM-Université Paris Diderot, France).
- **RRM-RNA what we know so far**. Prof. Dr. Michael Sattler (Technische Universität München, Germany).

During the project management session, the fellows learned how to improve the time management skills, with a focus on planning and prioritization. They also learned about emotional management, including how to identify their strengths and weaknesses. During the session on scientific communication, they focused on the different audiences they may have in a scientific presentation, learning how to change the level of detail, tone of voice and vocabulary.

The ESRs also attended scientific lessons covering a wide range of topics important for the smooth development of their individual projects: from experimental techniques such as NMR spectroscopy for protein structure elucidation to purely computational methods such as protein dynamics and docking, including the latest information about RRM-RNA recognition, keypoint in RNAct.

The project coordinator, Prof. Dr. Wim Vranken, gave an introductory presentation to provide ESRs with a clear vision of the global aims of RNAct and how the 10 indivual projects integrate to achieve these.



The fellows during the training on Project Management.

Project progress

Workshop 2 - Experiments and data

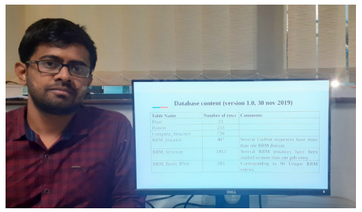
The second workshop, “Experiments and data”, will take place in March 2020 at the Centre for Fine Arts (BOZAR) in Brussels (Belgium). It will include the following seminars and courses:

- **Molecular interactions in drug development**. Dr. Jos Buijs (Ridgeview Instruments, Sweden).
- **Biophysical sample preparation, do’s and don’ts practical (hands-on session)**. Dr. Tommaso Martelli (Giotto Biotech, Italy).
- **Open science and FAIR data**. Dr. Surya Gupta (VIB-UGent Center for Medical Biotechnology, Belgium).
- **Presenting with impact**. Hans Van de Water (The Floor is Yours, Belgium).

In addition, the workshop will include ESRs progress presentations, the board meetings, and the mid-term check meeting with the Project Officer from the European Commission.

News

InteR3M: The RNAct database



We are glad to present the first version of the InteR3M, database for Interactions of RNA and RNA Recognition Motif, devoted to RRMs and developed by Hrishikesh Dhondge. This version contains all RRM-RNA interactions from the PDB database and its access has been provided to all RNAct consortium using pgAdmin interface . It is implemented in postgreSQL open-source database management system and it supports SQL queries.

Data for this version have been collected using Python scripts that parse the files downloaded from the public databases to extract relevant information. We checked that all the use-cases collected from other ESR fellows could be fulfilled by the database model and run on the database locally.

Contributions at scientific meetings

Gavalda-Garcia J., **Roca-Martinez J.**, **Vranken W**. RNAct: Enabling proteins with RNA recognition motifs for synthetic biology and bioanalytics. Poster presented at the (IB)2 Research Day, 25 October 2019, Brussels (Belgium).

Mocci S., Hyun-Seo K., **Sattler M**. Rational design of RNA binding by the multi-RRM protein Sex-Lethal. Poster presented at the 14th NMR Winter Retreat of Protein-RNA interaction, 14 January 2020, Perpan (Switzerland).

Sperotto L., Hyun-Seo K., **Sattler M.** Structural study of the role of SPF45 G-patch motif in the 3’ splice site regulation. Poster presented at the 14th NMR Winter Retreat of Protein-RNA interaction, 14 January 2020, Perpan (Switzerland).

Journal club

The fellows meet online every three months to discuss about articles relevant to the project.

1st Journal club session:

Date: 26th of November 2019
Article: A deep learning framework to predict binding preference of RNA constituents on protein surface
DOI: 10.1038/s41467-019-12920-0
Chair: Luca Sperotto (ESR 6)

2nd Journal club session:

Date: 11th of February 2020
Article: RNA recognition motifs: boring? Not quite
DOI: 10.1016/j.sbi.2008.04.002
Chair: Hrishikesh Dhondge (ESR 3)

Stay tuned!

Twitter
https://tinyurl.com/vuy5kup

Facebook
https://tinyurl.com/vrzjv97

Linkedin
https://tinyurl.com/tmeqjww

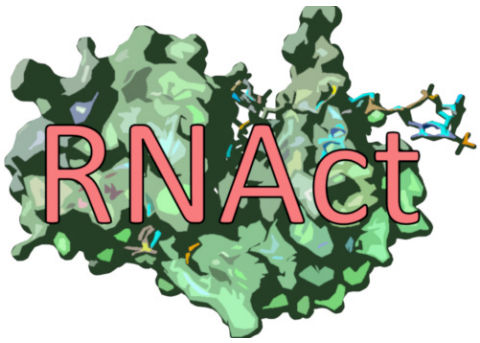
Instagram
https://tinyurl.com/utdvkb8

Discussion group in Linkedin
https://tinyurl.com/tx5z4bb

Youtube
https://tinyurl.com/s22x9x5

Researchgate
https://tinyurl.com/rdpogqb

RNAct Newsletters
https://tinyurl.com/wftv37p


RNAct