

Metalloproteins Investigation for the Development of new Inhibitors

Matteo Orlandi^{a,b}, Piero Procacci^a, Marina Macchiagodena^a, Fabrizio Carta^b, Claudiu T. Supuran^b and Marco Pagliai^a.

^aDepartment of Chemistry "Ugo Schiff", University of Florence, via della Lastruccia 13, 50119- Sesto F.no (FI), Italy

^bDepartment of NeuroFarBa, University of Florence, Via Ugo Schiff 6, 50019- Sesto Fiorentino, Italy

E-mail: matteo.orlandi1@unifi.it

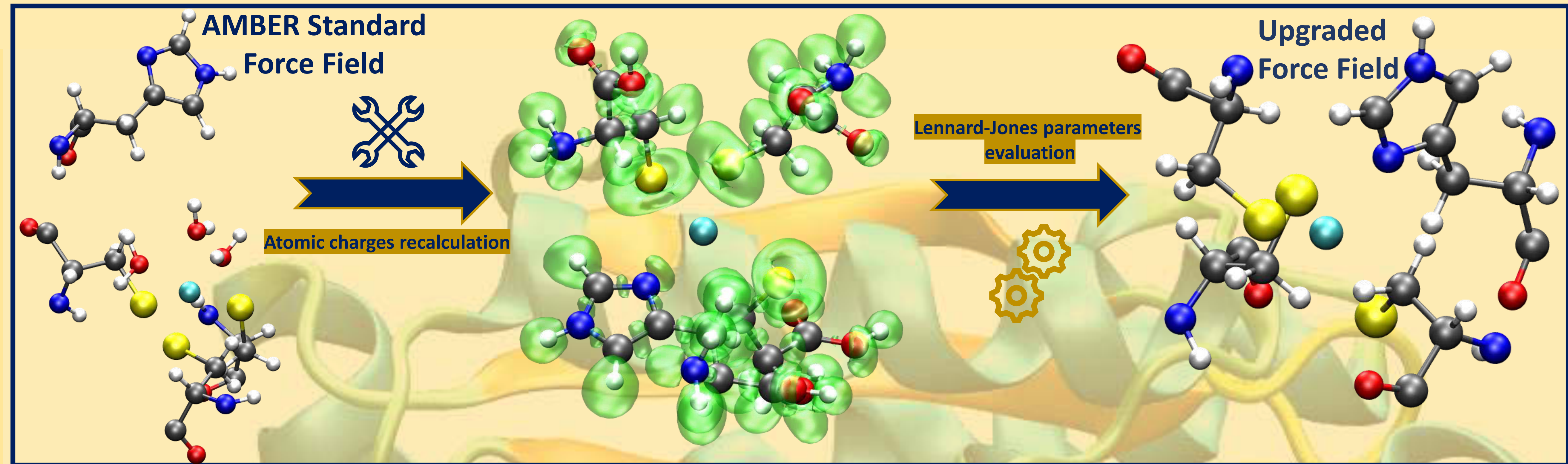
<https://doi.org/10.17952/37EPS.2024.P2274>



UNIVERSITÀ
DEGLI STUDI
FIRENZE
DICUS
DIPARTIMENTO DI CHIMICA
"UGO SCHIFF"

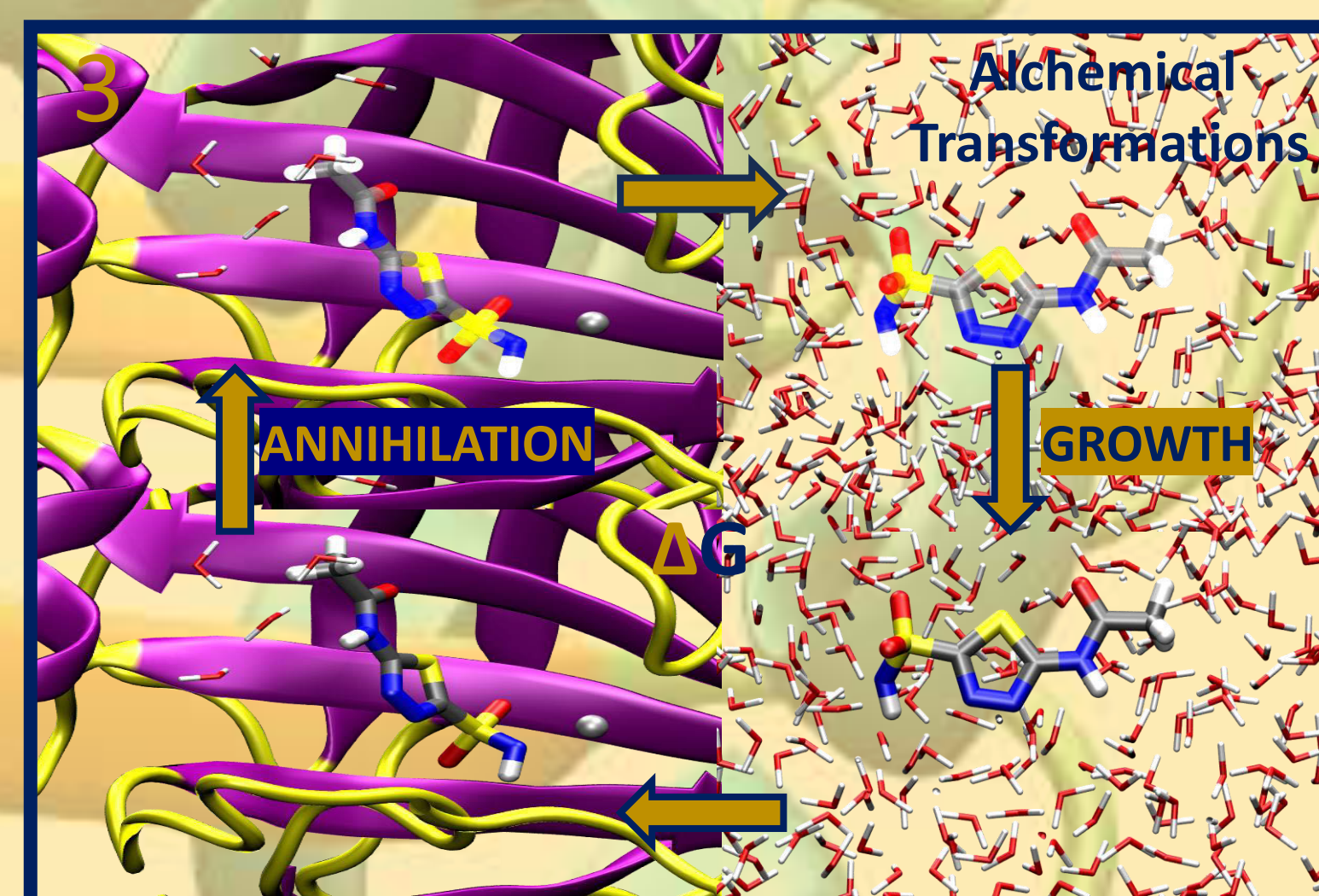
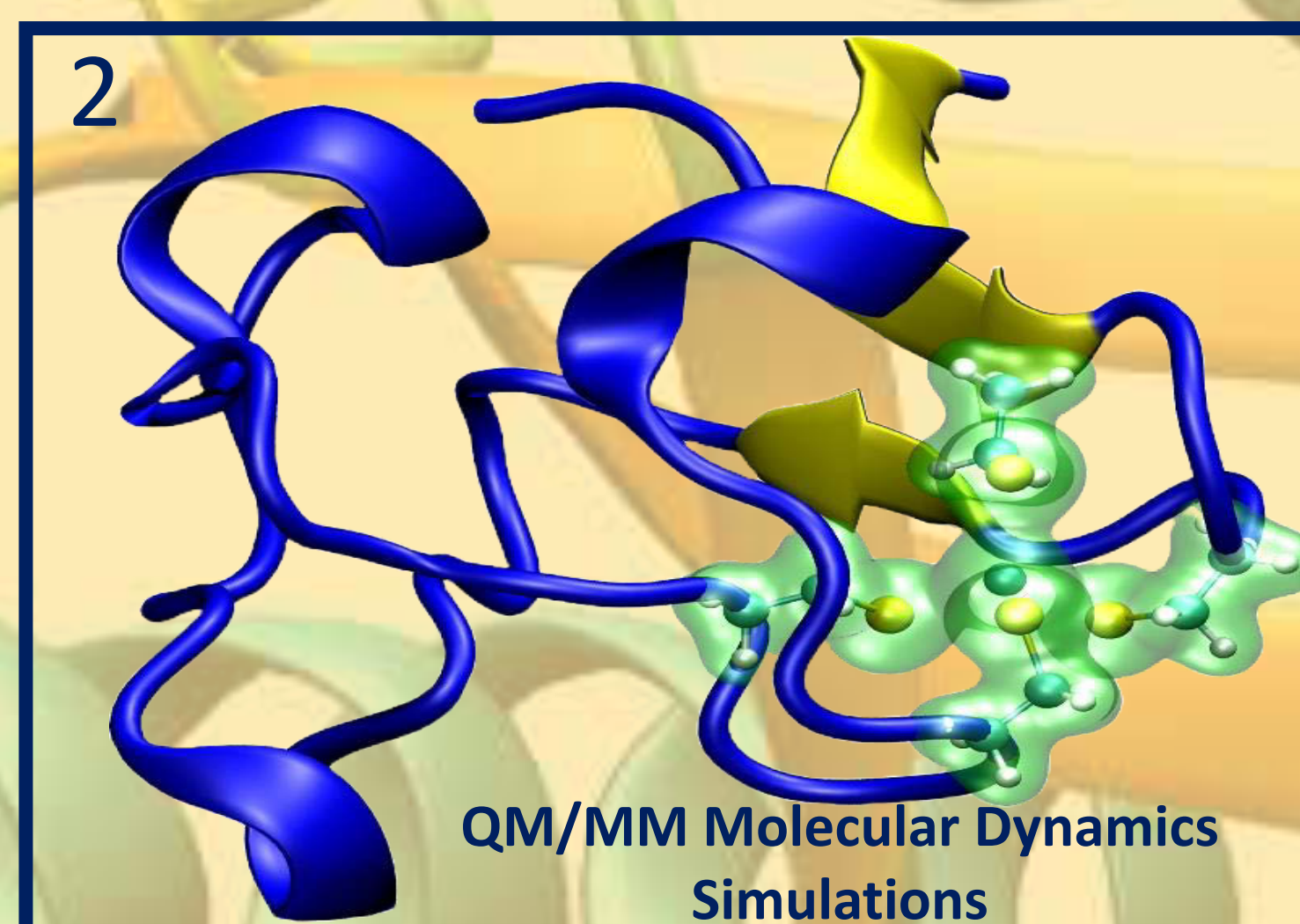
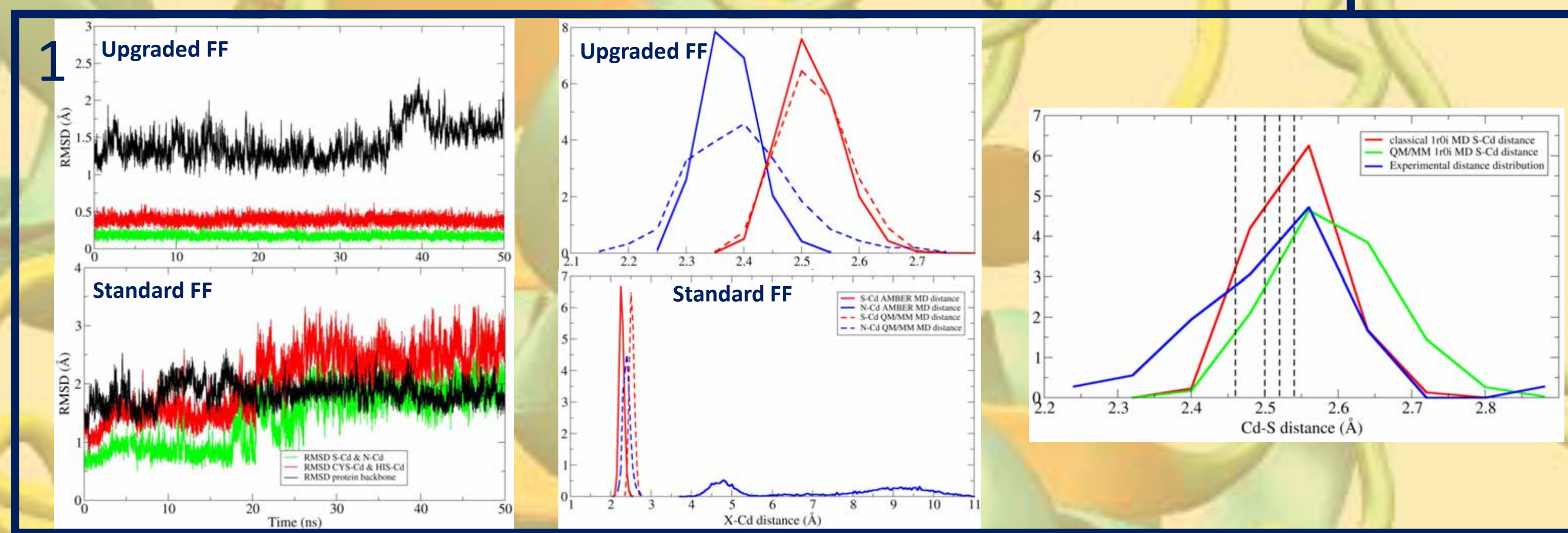
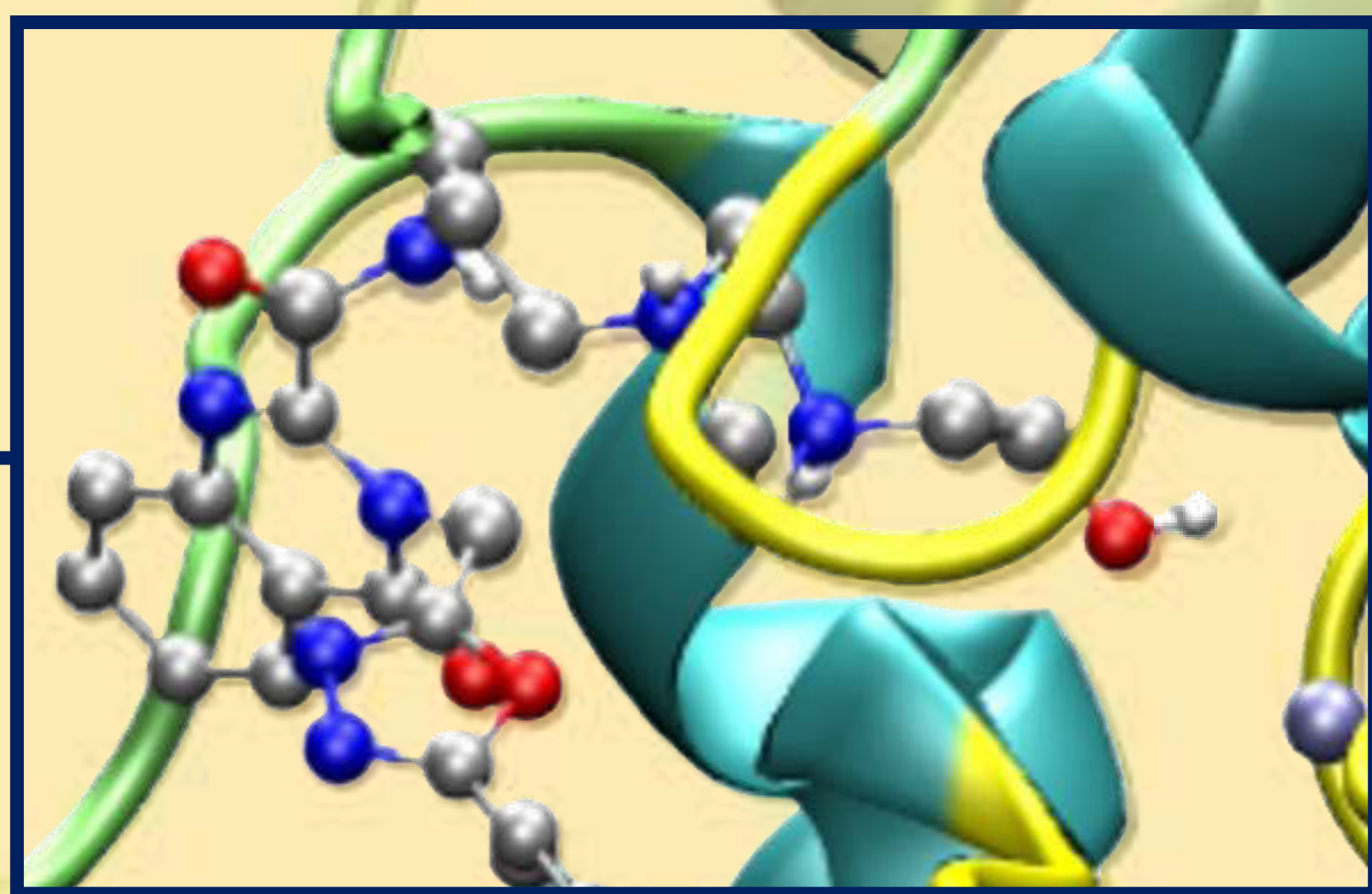
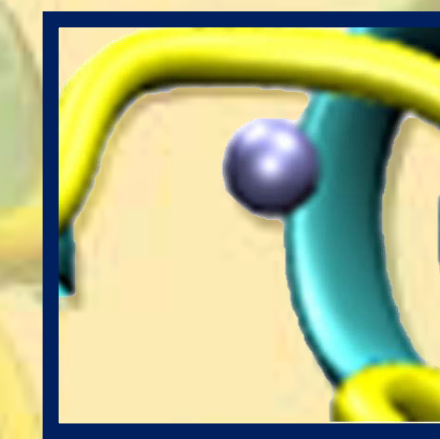


UNIVERSITÀ
DEGLI STUDI
FIRENZE
NEUROFARBA
DIPARTIMENTO DI NEUROSCIENZE,
PSICOLOGIA, AREA DEL FARMACO
E SALUTE DEL BAMBINO



Metalloproteins Modelling

Molecular Dynamics (MD) simulations are a pivotal tool in computational chemistry and biophysics that allow to study the behavior of molecules at the atomic level. The accuracy of these simulations heavily relies on the force fields used to model the interactions between particles. We focused on the development of tailored Force Fields (Fig. 1)[1] for the metal-ligand interactions to simulate more accurately the behavior of metalloproteins as potential drug targets and to computationally design innovative and effective inhibitors for these targets. Simulating metal-containing systems with MD is inherently challenging due to the complex electronic and bonding properties of metals. For example, we focused on capturing the polarization effect induced by the cations on the ligands surrounding through accurate QM/MM MD (Fig. 2) simulations (CP2K/GROMACS interface) to reparameterize their atomic charges and Lennard-Jones parameters.



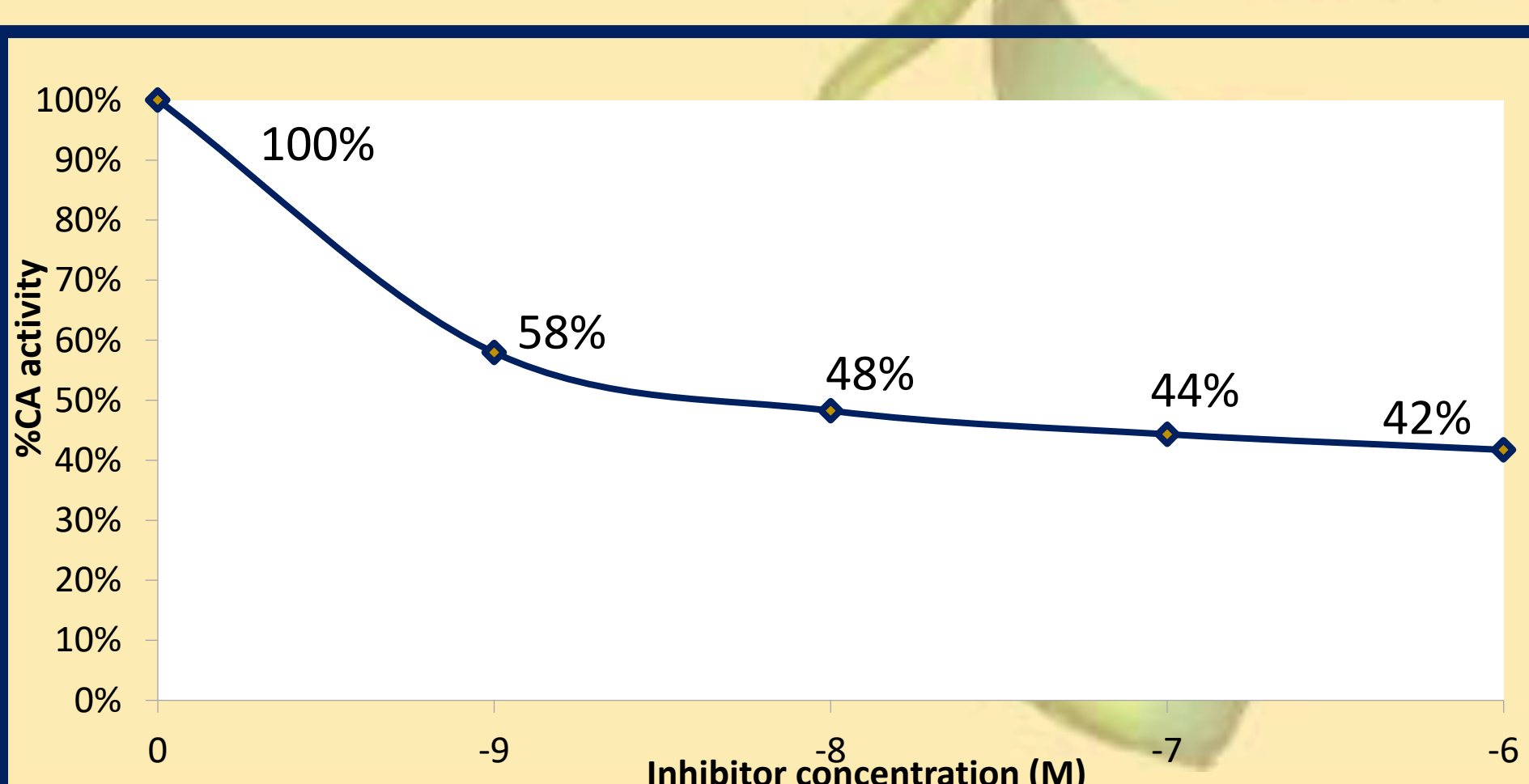
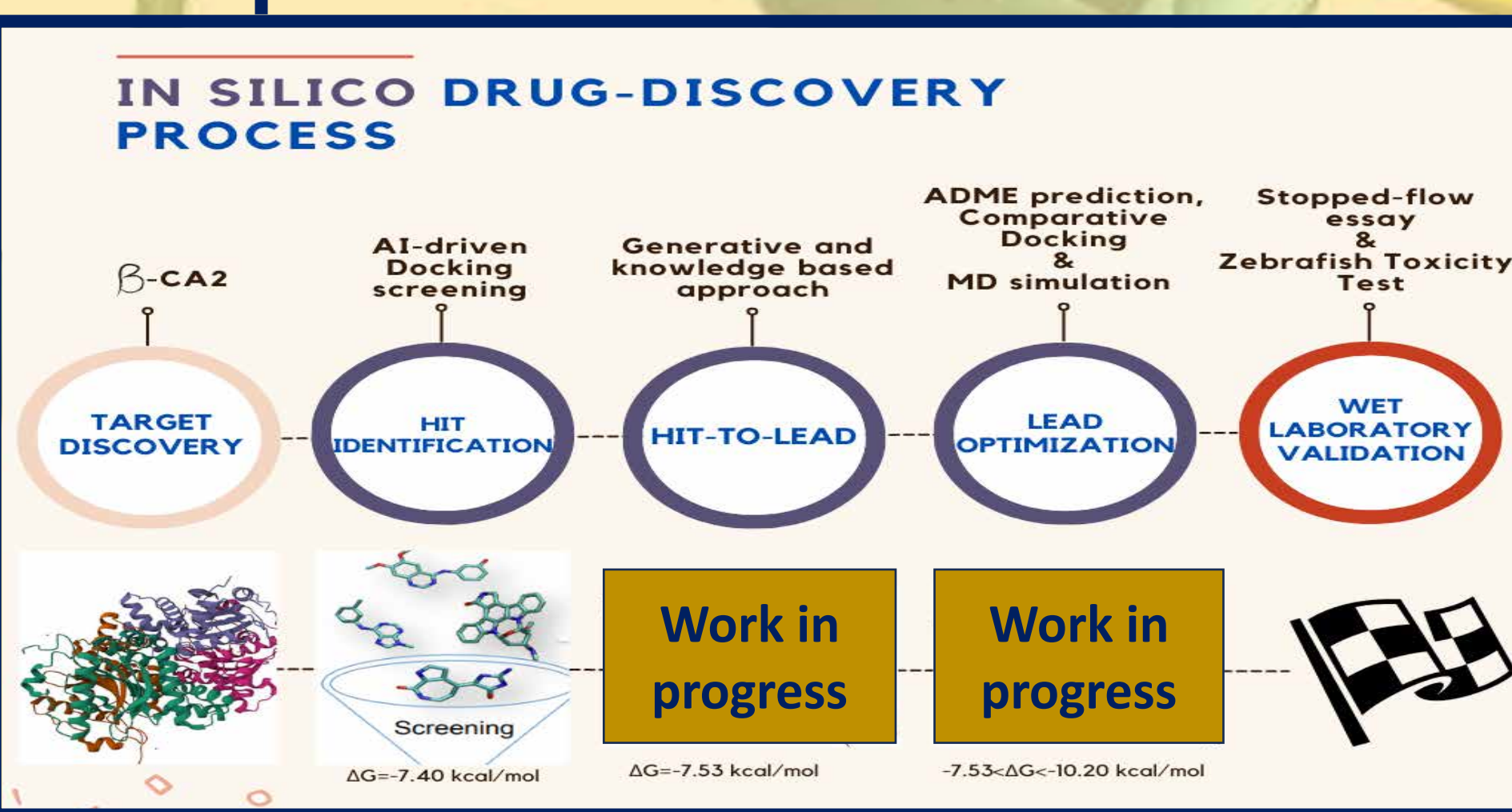
Drug Design

The drug discovery pipeline involves a multifaceted process, spanning from the validation of biological targets to in vivo testing. Computational chemistry tools play a crucial role in accelerating drug development. Their focus lies in minimizing false positive hits and lead compounds that may progress to in vivo experimentation, ultimately mitigating economic losses for the pharmaceutical industry. We focused on the design of a new class of antitubercular drugs effective against the β Carbonic Anhydrases of drug-resistant *Mycobacterium tuberculosis*[2]. To develop the new chemical entities both *deep learning generative models*[3] and chemical intuition were exploited. Binding affinities calculation schemes (Fig. 3) were also tuned on metalloproteins complex, since the modeling complexity of these systems poses arduous challenges in the feasibility of accurate predictions.

Acknowledgments

We acknowledge the CINECA under the IS CRA initiative (project IS CRA-C MIP), for the availability of high-performance computing resources and support.

EPS European Peptide Society is kindly acknowledged for the awarded registration grant to Mr. Matteo Orlandi.



[1] Macchiagodena, ... Upgrading and Validation of the AMBER Force Field for Histidine and Cysteine Zinc(II)-Binding Residues in Sites with Four Protein Ligands JCIF, 2021.

[2] Fabrizio Carta, ...Claudiu T. Supuran Carbonic anhydrase inhibitors. Characterization and inhibition studies of the most active β -carbonic anhydrase from *Mycobacterium tuberculosis*, Rv3588c, Bioorganic & Medicinal Chemistry Letters, 2009.

[3] Miha Skalic, ...Gianni De Fabritiis LigVoxel: inpainting binding pockets using 3D-convolutional neural networks, Bioinformatics, 2019