

**SAB 2020**

***Biofísica en tiempos de  
COVID-19***

**Libro de Resúmenes**



**3 y 4 de diciembre de 2020  
Argentina**

Sociedad Argentina de Biofísica

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### *Diagramación y Edición*

Ernesto Ambroggio, Soledad Celej, Axel Hollmann, Juan Pablo Acierno

### *Diseño de Tapa y Logo*

Comité Organizador

### *Asistencia Técnica Web*

Juan Pablo Acierno

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# Sociedad Argentina de Biofísica

*Member of the International Union for Pure and Applied Biophysics*



## Primeras jornadas virtuales de la Sociedad Argentina de Biofísica

**3 y 4 de diciembre 2020**

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## *Welcoming words*

Dear members, participants and friends,

This is a very special year in our lives. The Covid-19 pandemic has changed the way in how societies communicate, imposing modern modes of virtual interaction. Naturally, SAB was not unsympathetic to this turn of events and, therefore, in the spirit of maintaining our yearly gathering, we faced the challenge of organizing these first virtual sessions of the Argentinean Society of Biophysics.

We sincerely hope that during this two-day meeting, we enjoy this new proposal, where keynote lectures, lightning talks and round tables will be shared as open access events contributing to scientific outreach activities to the community. Not only these open sessions will be held, but also all registered participants (SAB members and invited colleagues) will be able to participate online in two workshops, presenting their scientific research as mini-videos and being able to discuss with pairs and mentors through separate virtual channels.

Lastly, we all know that this pandemic situation has already had a terrible impact on the economic situation of our country. Therefore, we thank in advance to all participants for their personal contributions along these days and to everybody for sharing their research and joining the scientific discussions.

*The SAB Executive Council*

## ***Scientific programme***

***Thursday, December 3***

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***9:45 – 10:00 h***      *Entry to virtual platform*

***10:00 – 10:10 h***      ***Opening Ceremony***

José María Delfino, IQUIFIB-CONICET, FFyB-UBA, Buenos Aires, Argentina

***10:15 – 12:15 h***      ***Poster session I***

Only for registered participants

***12:15 – 12:30 h***      ***Lightning talks***

*Chair: José María Delfino*

***Horizontal and Collaborative against the clock work in pandemic: Production, characterization and distribution of a low-cost SARS-CoV-2 antigen by the Argentinian AntiCovid Consortium***

María Florencia Pignataro, Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires, Buenos Aires, Argentina

***12:30 – 13:45 h***      *Lunch*

***13:45 – 14:00 h***      *Entry to virtual platform*

**14:00 – 16:00 h**      **Round Table 1 – Enseñanza virtual y presencial en biociencias**

*Chairs: Irene Mangialavori, Lía Pietrasanta and José María Delfino*

***Intervenciones educativas en línea: Desafíos y potencialidades***

Karina Alleva. Facultad de Farmacia y Bioquímica, UBA, Buenos Aires, Argentina

***Educomunicación ubicua para el nuevo escenario de convivencia***

Fernando Irigaray. Director de la Maestría Digital Interactiva, Facultad de Ciencia Política, UNR, Rosario, Argentina

***Los desafíos de evaluar con mediación tecnológica. Escenarios y propuestas***

Carina Lion. Facultad de Filosofía y Letras, UBA. Instituto de Investigaciones en Ciencias de la Comunicación, Buenos Aires, Argentina

***La enseñanza de ciencias experimentales en tiempos de pandemia: ¿es posible evaluar aprendizajes desde la virtualidad?***

Marcelo Mariscal. Vicedecano, Facultad de Ciencias Químicas, UNC, Córdoba, Argentina

**16:00 – 17:00 h**      **Keynote Lecture**

*Chair: José María Delfino*

***ECA2: ¿ángel o demonio?*** Mariela Gironacci. IQUIFIB, UBA, Buenos Aires, Argentina

## ***Friday, December 4***

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**8:45 – 9:00 h**                      *Entry to virtual platform*

**9:00 – 12:00 h**                      *Interactive workshops*

Only for registered participants

### ***Workshop 1: Uniprot: explorando secuencias y función de proteínas***

Cecilia Arighi. Department of Computer & Information Sciences, University of Delaware and Department of Biochemistry and Molecular & Cell Biology, Georgetown University Medical Center

### ***Workshop 2: Biofísica de Biomembranas***

Ernesto Ambroggio (CIQUIBIC-UNC, Córdoba), Luis Bagatolli (INIMEC-UNC, Córdoba), Laura Fanani (CIQUIBIC-UNC, Córdoba), Axel Hollmann (CIBAAL-UNSE, Santiago del Estero) and Natalia Wilke (CIQUIBIC-UNC, Córdoba).

**12:00 – 13:00 h**                      *Lunch*

**13:00 – 14:50 h**                      *Poster session II*

Only for registered participants

**14:50 – 15:00 h**                      *Entry to virtual platform*

**15:00 – 17:00 h**                      *Round Table 2 – Políticas integrales para la equidad de géneros en ciencia y técnica*



*Chairs: M. Natalia Lisa, Noelia Burgardt and M. Soledad Celej*

**Paula Lenguita.** Responsable del Programa de Género Agencia I+D+i, Argentina

**Victoria Prieto.** Comisión de Género y Comité de Calidad con Equidad Institut Pasteur de Montevideo, Comisión de Género Pedeciba (Programa de Desarrollo de Ciencias Básicas), Uruguay

**Erica Hynes.** Diputada provincial de Santa Fe por el Frente Progresista Cívico y Social. Especialista en tecnología de alimentos y política argentina, Argentina

**Victoria Tignino.** Secretaria ejecutiva del Programa Nacional para la Igualdad de Géneros en Ciencia y Tecnología del MinCyT, Argentina

**Azul Hermida.** Integrante del Observatorio de violencia laboral y de género (OVLG) y Comisión de Igualdad de Oportunidades y Trato (CIOT) de CONICET, Argentina

**17:00 – 18:00 h**      **Keynote Lecture**

*Chair: Lía Pietrasanta*

**Desarrollo de un suero equino hiperinmune para el tratamiento de COVID-19 en Argentina.** Fernando Goldbaum. CRIP, Inmunova, UNSAM, Buenos Aires, Argentina

**18:00 – 18:30 h**      **Poster Awards and Closing Ceremony**

*M. Soledad Celej and José María Delfino*



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## Inhibition of lanosterol 14 alpha-demethylase: Molecular modeling study of triazole derivatives acting against the phytopathogen *Botrytis cinerea*

Sirur Flores J<sup>a</sup>, Parravicini O<sup>a</sup>, Rojas S<sup>a</sup>, Gutiérrez LJ<sup>a</sup>, Herrera Cano N<sup>b</sup>, Feresin G<sup>b</sup>, **Andújar S<sup>a</sup>**

*a* - Facultad de Química, Bioquímica y Farmacia, Universidad Nacional de San Luis, Instituto Multidisciplinario de Investigaciones Biológicas (IMIBIO-SL)

*b* - Instituto de Biotecnología, Facultad de Ingeniería, Universidad Nacional de San Juan, CONICET-CCT

*Botrytis cinerea* is a phytopathogenic fungus that causes the gray mold disease. It is considered a main factor in post-harvest losses in fresh fruit crops, causing serious economic losses in the agricultural industry. In addition, it has become an important model for the molecular study of necrotrophic fungi. Although there are fungicides for its control, many of them have failed since *B. cinerea* has evolved a variety of infection mechanisms due to its genetic variability. In this regard, triazoles have been used for the control of several pathogenic fungi. These compounds act as inhibitor of the lanosterol 14 alpha-demethylase, a cytochrome p450 (CYP54B)-dependent enzyme system involved in the synthesis of ergosterol.

In order to explain the biological behavior of different CYP54B-triazole complexes we performed a combined molecular modeling study. In this way, we determined the conformational aspects of the currently available triazole antifungal agents when complexed with CYP54B. Furthermore, a new series of novel triazole derivatives was synthesized and their inhibitory activity was assessed. Some of them showed strong inhibitory effects comparable to that observed for commercial antifungal drugs. The molecular modeling study was carried out in three stages. First, we conducted molecular docking calculations. Next, we performed molecular dynamics (MD) simulations and free energy of the different complexes was calculated. Finally, we performed a per-residue analysis in order to identify the amino acids involved in the intermolecular interactions of the complexes.

Our molecular modeling study indicated that all active compounds are bounded in a similar spatial arrangement. Thus, it is reasonable to assume that the compounds studied here interact with the same region of the enzyme. MD simulations enable us to explain the different activities displayed by these compounds. The main stabilizing interactions are Tyr101, Thr105, Tyr115, Phe208, Ala287, His290 and Ile353.