**ESTRUCTURA DE MACROMOLECULAS**

Programa de seminarios del curso 2025-2026

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| **EQUIPO** | **SEMINARIO ESCOGIDO** | **Día** |
| María Millán  Anna Gallego  Andrea Lamata  Lucía Bas | [Salillas etal (2021)](https://jsancho.bifi.es/wp-content/uploads/Salillasetal2021.pdf) Selective targeting of human and animal pathogens of the Helicobacter genus by flavodoxin inhibitors: efficacy, synergy, resistance, and mechanistic studies |  |
| David Alija  Paula Martínez Adiego  Marta Monserrate  Lucas Gascón Zurita | [Conde-Giménez etal (2022)](https://jsancho.bifi.es/wp-content/uploads/Conde-Gimenezetal2022.pdf) Alchemical Design of Pharmacological Chaperones with higher Affinity for Phenylalanine Hydroxylase |  |
| Alejandro Alquezar Cañas  Pablo Daniel Martínez García  Sara Cortes Cubero  Catalina Jerez Losa | [Galano-Frutosetal (2024)](https://jsancho.bifi.es/wp-content/uploads/Galano-Frutosetal2024.pdf) L-Thyroxine and L-thyroxine-based antimicrobials against Streptococcus pneumoniae and other Gram-positive bacteria |  |
| Mario Iranzo  Marina Pérez  Marina GImeno  Pilar Gaspar | [Lamazares etal (2015)](https://jsancho.bifi.es/wp-content/uploads/Lamazaresetal2015.pdf) Rational stabilization of complex proteins: a divide and combine approach |  |
| Marina Salillas Rodés Verónica Martínez Luzón Andrea Esteban Blasco Inés Valiente Herrero | [Conde-Jiménez & Sancho(2021)](https://jsancho.bifi.es/wp-content/uploads/Conde-JimenezSancho2021.pdf) Unravelling the Complex Denaturant and Thermal-InducedUnfolding Equilibria of Human Phenylalanine Hydroxylase |  |
| Pablo Cartañá Polo  Iván Nogués Jové  Massimo Garcia Olivares  Daniel Torres Toro | [Galano-Frutoset al2022](https://jsancho.bifi.es/wp-content/uploads/Galano-Frutoset-al2022.pdf) A look at the face of the molten globule: structural model of the Helicobacter pylori apoflavodoxin ensemble at acidic pH |  |
| Violeta Serrano Gracia  Juan Moreno Muñoz  Martina Luzán Barrabés  Rubén Hernández Barón | [Galano-Frutos etal (2021)](https://jsancho.bifi.es/wp-content/uploads/Galano-Frutosetal2021.pdf) Molecular Dynamics Simulations for Genetic Interpretation in Protein Coding Regions: Where we Are, Where to Go and When |  |
| Iker Cortés  Nader Zapata  Kaitlyn Ramón  Eva Valero | [Alonso etal (2024).pdf](https://jsancho.bifi.es/wp-content/uploads/Alonsoetal2024.pdf) Association between missense variants of uncertain significance in the CHEK2 gene and hereditary breast cancer: a cosegregation and bioinformatics analysis |  |
| **Marina** Ramón Igea  Aimara Cuartielles Zalba  Sofia Martínez Cuartero Rocío Mañas Sicilia | [García-Cebollada etal (2022)](https://jsancho.bifi.es/wp-content/uploads/Garcia-Cebolladaetal2022.pdf) Protposer: the web server that readily proposes protein stabilizing mutations with high PPV |  |
| Lucía Castillo Peña  Alejandra Bartolomé Serrano  Andrea Megino Hernández  Naiara Aragón Doiz | [Galano-Frutos&Sancho(2024)](https://jsancho.bifi.es/wp-content/uploads/Galano-FrutosSancho2024.pdf) Energy, water, and protein folding: A molecular dynamics based quantitative inventory of molecular interactions andforces that make proteins stable |  |