**ESTRUCTURA DE MACROMOLECULAS**

Programa de seminarios del curso 2025-2026

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| **EQUIPO** | **SEMINARIO ESCOGIDO** | **Día**  |
| María MillánAnna GallegoAndrea LamataLucía 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 AlijaPaula Martínez AdiegoMarta MonserrateLucas 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 CañasPablo Daniel Martínez GarcíaSara Cortes CuberoCatalina 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 IranzoMarina PérezMarina GImenoPilar 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 PoloIván Nogués JovéMassimo Garcia OlivaresDaniel 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 PeñaAlejandra Bartolomé SerranoAndrea Megino HernándezNaiara 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 |  |