Session(*)			Posters and other abstracts
			Targeting the WNT signaling pathway: a novel predictive signature for neoadjuvant
1	Acedo Terrades	Ariadna	chemotherapy response in muscle-invasive bladder cancer
			Disentangling dynamic gene expression patterns from tissue movements: a
1	Aviñó	Laura	computational approach
			Personalized Medicine in Melanoma: biomarkers of prognosis and response to
1	Bagué	Jaume	immunotherapy, and its relation to dietary habits and physical exercise
_			Common genetic variants associated with urinary phthalate levels in children: a genome
1	Balagué Dobón	Laura	wide study
	Dalague Doboli	Luaru	Structural determinants of α-synuclein binding to an inhibitory peptide studied by
1	Bárcenas López	Oriol	molecular dynamics simulations
	barcenas Lopez	01101	Modeling the effects of circadian rhythm on the two alternative pathways for terpenoid
1	Basallo Clariana	Oriol	precursor biosynthesis in plants
	Butjosa Espín	Maria	Differences in silico in drug response between primary and metastatic cancer
	Cabrera Gumbau		Machine learning for early prediction of vibrio vulnificus infections in the US
	Cabrera Gumbau	Jordi Manu	
1	Canal Name	D-I	Methylation biomarkers for colorectal cancer early detection and survival prognostics
1	Canal Noguer	Pol	impact gene expression and link to cancer-related biological pathways
-	Casals Franch	Roger	Gene expression prediction under novel conditions using ATAC-seq-informed regulons
1	Casanova Suárez	Carla	Diet adaptations in anatomically modern humans
			Evaluating allele frequency trajectory and selection coefficient estimates from
	Colomer i Vilaplana	Aina	genealogies including ancient DNA
1	Diaz Hurtado	Marcos	Longitudinal segmentation of multiple sclerosis lesions
1	Diaz Ros	Maria	Conservation and evolution of human segmental duplications in mammal genomes
1	Engler	Camila	protAGOnist: an innovative NLS/NES prediction tool
			Pan-cancer vulnerability prompted by TGF -hypoxia-mediated suppression of
1	Espin Garcia	Roderic	alternative end-joining
			Epigenetic relationships to improve Synthetic Lethality prediction model for cancer
1	Fariña Morillas	Maria José	treatment
			In-silico simulation and efficacy evaluation of anti-PD1 treatment on 4 triple-negative
1	García Illarramendi	Juan Manu	breast cancer molecular subtypes
			Lipid mechanisms drive cerebrovascular disease in cognitively unimpaired individuals at
1	Genius Serra	Patricia	low risk for late-life dementia
1	Giné Bertomeu	Roger	Datoma: A cloud computing platform for high-performance metabolomics data analysis
1	González Barriada	Rubén	Deep Learning Based Methods for Fundus Image Quality Evaluation
			Bioactive peptides in Mediterranean plants: biological properties and pharmacological
1	Lisa Molina	Julia	implications
2	Llano Viles	Joshua	Identification of epigenetic biomarkers for molecular subgrouping of ependymoma
			Evolution of morphological complexity under development-based genotypephenotype
1	Loreto Velázquez	Antonio	maps
	'		Evolution of morphological complexity under development-based genotypephenotype
2	Marín Montes	Raúl	maps
	-		Multimodal data integration to model, predict, and understand changes in plant
2	Martinez	Emilce Sole	biodiversity
			dsFDL: DataSHIELD Federated Deep Learning for Secure and Collaborative AI in
2	Mateo Navarro	Ramon	Healthcare
	Mitjavila Ventura	Adrià	Transposons in the evolution of piRNA cluster expression in mice
			Molecular Dynamics study of the kynureninase enzyme: an approach for the design of
2	Moreno Farre	Javier	new therapeutic enzymes in cancer
			Prognosis of patient groups with COVID-19, chronic diseases and polypharmacy. Mixed
2	Muntañola Valero	Cristina	patient-centered approach
	TTTATICATION VAICTO	CHISCHIA	Evaluation of the msGBS methodology for the taxonomic identification and
2	Munzón Gil	Daniel	quantification of diatoms
	Muñoz López		Identification of clinical features associated with Sars-Cov-2 reinfections
	Nieto	Andrea	Characterising the regulation B cell differentiation at a single cell resolution
	Pelegrí	iviaria D010	BigDataStatMeth: An R package to implement statistical methods for Big Data
_	Dáras Lán	Coul	Aquasearch: a new software for fast proteomic characterization and classification of
	Pérez-López	Carlos	wastewater samples analyzed using MALDI-TOF
	Pintado Grima	Carlos	aSynPEP-DB: a database of biogenic peptides for inhibiting α-synuclein aggregation
2	Pose	Iria	Machine learning approaches for the characterization of COPD

			Fly wing development in silico: A computational investigation of morphological
2	Ratarac	Aleksa	plasticity in Drosophila wings
2	Ruiz	Gabriel	Extrapolation of pathogenicity between homologous variants
2	Sanchez Hernandez	Janet	Computational design of ganciclovir-dependent kinases for suicide cancer gene therapy
2	Sánchez Herrero	Sergio	Integrating Artificial Intelligence Methods in Pharmacokinetics & Pharmacodynamics Processes
			CADSETshield: Developing a secure and efficient platform for integrated medical
2	Sarrat González	David	imaging and genomic studies of COPD using DataSHIELD and OMOP CDM
2	Serrano Gómez	Gerard	Multi-omics microbiome dynamics in IBD
			Development and application of tools for automated integration and analysis of big data
2	Tejada Gutiérrez	Eva Luz	in forestry management
1	Tejero Laguna	Eudald	Reanalysis of next generation sequencing data from patients with cardiac diseases
2	Temprano Sagrera	Gerard	Identification of differential expressed genes between abdominal aortic aneurysm cases and controls in aortic tissue
			Discovering and tracking potential zoonotic species from metagenomic samples with a
2	Tarradas-Alemany	Maria	capture-based oriented pipeline
			Identification of new BCL-2 inhibiting small molecules using machine learning,
2	Tondar	Abtin	molecular docking, and MD simulation
2	Yakymenko	Illya	Characterization of strategies for structural variant imputation
2	Yang	Jing	A quantitative view of the heterogeneity-diversity axis in biological systems

^(*) Remind that for first years students it is not mandatory.