# Poster Presentation

| SYSTEM ID | AUTHOR NAME | ABSTRACT TITLE | PANEL SITE | TEMÁTICA |
|---|---|---|---|---|
| Bioinformática y Biocomputación / Bioinformatics and Biocomputation ||||
| (ID:104) | Alvarez | Computational optimization for signal processing and identification in metabolomics studies based on mass spectrometry | Pst-01 | **Bioinformática y Biocomputación** **Bioinformatics and Biocomputation** |
| (ID:117) | Botero, Osorio, Gonzalez, Pinzon-Velasco | Finding and filling gaps in metabolic networks through the 'g2f' R package | Pst-02 | |
| (ID:118) | Osorio, Botero, Gonzalez, Pinzon-Velasco | exp2flux: Convert Gene EXPression Data to FBA FLUXes | Pst-03 | |
| (ID:141) | Giraldo Torres, Segura Giraldo,... | Electrophysiological characterization of cognitive processes in the development of a motor task | Pst-04 | |
| (ID:190) | Marulanda | CINEMATIC MODEL OF COMPLETE AND PINCER GRIPS OF THE HUMAN HAND | Pst-05 | |
| (ID:194) | López, Ruíz, Castaño | DEVELOPMENT OF A TWO-DIMENSIONAL ANATOMICAL MODEL WITH REALISTIC MEASUREMENTS OF LACTIFEROUS CONDUIT OF HUMAN MAMMARY GLAND LACTATION FOR THE STUDY OF DUCTAL CARCINOMA IN SITU | Pst-06 | |
| Modelamiento y Simulación: Predictiva y Aplicada / Modeling and Simulation: Predictive and Applied ||||
| (ID:126) | Martinez, López-Kleine, Reyes | Graphing genomes in 2D, applications of multivariate statistics on the genomic composition | Pst-07 | **Modelamiento y Simulación: Predictiva y Aplicada** **Modeling and Simulation: Predictive and Applied** |
| (ID:62) | Carbajal-Tinoco, Granados-Ramírez,... | A coarse-grained model of circular dichroism | Pst-08 | |
| (ID:79) | Pinzón-Reyes, Sierra, Flórez, Rueda,... | DIRECTED EVOLUTION THROUGH DNA SHUFFLING: AN HEURISTIC APPROXIMATION | Pst-09 | |
| (ID:200) | Orozco-Ugarriza, Pedroza-Bedoya,... | A computational approach to molecular docking and ADME/Tox property of Murrayanina and enzyme phospholipase A2 | Pst-10 | |
| (ID:238) | Murgas, Martin | Development of a method for the inference of genes regulatory networks from time and specific data integration | Pst-11 | |
| (ID:86) | Suarez | Implementation of a Mixed Integer Linear programming approach to establish de novo synthesis routes of antioxidants derived from the fermentation of Theobroma cacao seeds | Pst-12 | |
| Ómica Vegetal, Descriptiva y Aplicada / Omics in plants, Descriptive and Applied ||||
| (ID:51) | Diaz-Riaño | Identification of differentially expressed genes in foliar tissue of Theobroma cacao under presence of Cadmium | Pst-13 | **Ómica Vegetal, Descriptiva y Aplicada** **Plant Omics, Descriptive and Applied** |
| (ID:76) | Bolivar, Caris-Maldonado, Molina,... | Panorama de los transcriptomas de Cannabis sativa por medio de métodos bioinformáticos | Pst-14 | |
| (ID:84) | Arcila Galvis, Arango Isaza, Arias... | The evolution of Mycosphaerellaceae mitochondrial genomes: Key insights in their molecular biology | Pst-15 | |
| (ID:115) | Rodríguez Cabal, Franco-Sierra,... | Transcriptome of Plukenetia volubilis reveals important genes in the Polyunsatturated Fatty Acid pathways during seed maturation | Pst-16 | |
| (ID:127) | López-Alvarez, Mosquera-Rendón,... | Reconstructing the pan-genome of Ralstonia solanacearum sensu lato and its applications in agriculture | Pst-17 | |
| (ID:143) | Orozco-Arias | Worldwide co-occurrence analysis of 17 species of the genus Brachypodium using data mining | Pst-18 | |
| (ID:146) | Orozco-Arias | Parallan: Parallel Analyzer and Classifier of LTR Retrotransposons. Application to study lateral transfer among plant genomes | Pst-19 | |
| (ID:153) | Carmona | Production and characterization in silico of the enzyme Hidrolasa papayae | Pst-20 | |
| (ID:180) | Pineda | Design of plasmids for CynD expression in Arabidopsis thaliana via A. tumefaciens | Pst-21 | |
| (ID:213) | Trujillo Posada, Bertel, Maldonado | A METHOD FOR IN-SILICO GENERATION OF SIMULATED SEGREGANT POPULATIONS IN PLANT BREEDING PROGRAMS OF ALLOTETRAPLOID SPECIES | Pst-22 | |
| (ID:220) | Garcia navarrete | evelopment of genomic resources in Lima beans (Phaseolus lunatus L.) for evolutionary studies and future breeding programs | Pst-23 | |
| (ID:223) | Céspedes Giraldo, Betancur Pérez | Development of a bioinformatic pipeline for reconstruction of evolutionary histories using mtDNA from 15 species of orchids Epidendroideae | Pst-24 | |
| Metagenómica, Ambiente y Biotecnología / Metagenomics, Enviroment and Biotechnology ||||
| (ID:56) | Chaves | ANÁLISIS BIOINFORMÁTICO DE SECUENCIAS NO CODIFICANTES EN METAGENOMAS: UNA REVISIÓN ACTUALIZADA | Pst-25 | **Metagenómica, Ambiente y Biotecnología** **Metagenomics, Enviroment and Biotechnology** |
| (ID:119) | Botero, Lopez, Cristanco, Alvarez | BIOPROSPECTING: CHALLENGES AND OPPORTUNITIES FOR BIODIVERSITY STUDIES USING COMPUTATIONAL BIOLOGY APPROACHES | Pst-26 | |
| (ID:305) | Bolaños | The importance of the bioinformatic predictions of the putative genes of enzymes for possible technological and industrial developments from microorganism associated to extreme Colombian environments. | Pst-27 | |
| (ID:121) | Serrano-Bermudez, Perez-Mancilla,... | Finding the metabolic potential of solventogenic Clostridium butyricum isolated from Colombian | Pst-28 | |
| (ID:178) | López Zuluaga | COMPARISON OF BIOINFORMATIC METAGENOMICS ASSEMBLY TOOLS | Pst-29 | |
| (ID:55) | Ramirez | Diagnóstico de la apropiación de la Biotecnología en la industria Colombiana | Pst-30 | |
| (ID:110) | Alvarez Yela, Alvarez Silva,... | Metagenomic study at dynamic state to analyze the influence of agricultural activities in the structure and metabolic functionality of soil ecosystems at the Parque Nacional de los Nevados in Colombia | Pst-31 | |
| (ID:154) | Mestanza, Figueroa-Galvis, G. Torres,... | Exploring the microbial functional potential from the Guajira's mangrove rhizosphere | Pst-32 | |
| (ID:187) | Mosquera-Rendón, López-Alvarez,... | Metagenomics analysis of microbial community changes in Fusarium wilt-infected banana crops from Colombia | Pst-33 | |
| (ID:189) | Alvarez-Yela, Noreña Puerta,... | Exploration of microbial diversity of marine ecosystems at the Seaflower Biosphere Reserve using metagenomics | Pst-34 | |
| (ID:227) | Niño Camacho | EFFECT OF THE MANAGEMENT AND USE OF THE GROUND (CONVENTIONAL VS AGROECOlOGY) ON THE FUNCTION OF THE MICROBIAL COMMUNITY IN TWO FARMS VALLE DEL CAUCA | Pst-35 | |
| (ID:106) | Hernández | Bacterial diversity of a ruminal sample fractionated using a sucrose gradient | Pst-36 | |

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| (ID:131) | Rocha | Hydroxylated Naftilchalcone derivatives as possible inhibitors of the polyphenol oxidase protein of the lulo (Solanum quitoense Lam.) Castilla variety. | Pst-37 | |

| **Ómicas, Biodiversidad y Bioprospección / Omics, Biodiversity and Bioprospection** | | | | |
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| (ID:108) | Gonzalez Muñoz, Mosquera Rendon,... | Transcriptional profiling of the coral Acropora tenuis(Cnidaria: Scleractinia) throughout early developmental stages: insights into the gastrulation process in a basal metazoan | Pst-38 | **Ómicas, Biodiversidad y Bioprospección** **Omics, Biodiversity and Bioprospection** |
| (ID:135) | Medina, Arenas, Ochoa, Delgado | In silico identification of antimicrobial and antitumoral peptides in the transcriptome of Bolitoglossa ramosi | Pst-39 | |
| (ID:139) | liscano martínez, Arenas, Delgado | Transcriptomic for peptides identification from Hypsiboas pugnax skin | Pst-40 | |
| (ID:155) | Romero Murillo, Icaza, Quezada, Orrego | Mitogenome annotation of Argopecten Purpuratus reveals the presence of atp8 gene: Use of Bioinformatics tools for protein modeling and functional identification | Pst-41 | |
| (ID:172) | MORENO, Cordoba, Caro Quintero, Reyes... | Detection of genetic variants of Anaplasma marginale in a bovine blood metagenome infected with hemoparasites. | Pst-42 | |
| (ID:191) | Sánchez Bermúdez, Franco-Sierra,... | Automated routine for vertebrate species identification with nanopore data. | Pst-43 | |
| (ID:196) | Erazo, Rosero, Mejia, Calderon, Castillo | STATUS OF CURRENT GENETIC VARIATION OF Diglossa albilatera and Diglossa lafresnayii (BIRDS: THRAUPIDAE) IN TWO BIOGEOGRAPHIC PROVINCES (ANDEAN AND ANDEAN-AMAZON) OF THE NARIÑO DEPARTMENT | Pst-44 | |
| (ID:230) | Arenas, delgado | De novo reference transcriptome of Bolitoglossa vallecula (Caudata:Plethodontidae) | Pst-45 | |
| (ID:231) | Arenas, Garza - Garcia, delgado | In silico analysis of Three Finger Protein Superfamily members in salamanders Bolitoglossa sp. (Caudata: Plethodontidae) | Pst-46 | |
| (ID:64) | Noreña | Colombia, an unknown diversity in the era of Big Data | Pst-47 | |
| (ID:216) | Mejía Bedoya, Corredor Rodriguez,... | Bioinformatics reconstruction on the metabolic network of Saccharomyces cerevisiae to modeling the metabolim of D-galacturonate for ethanol production in silico | Pst-48 | |
| (ID:70) | Borbón-García | Revealing the composition and metabolic potential of the gut microbiome of Andean Bears from 16S rDNA data: Application into ex-situ conservation plans | Pst-49 | |

| **Bioinformática de Virus: Descripciones y Métodos / Virus Bioinformatics: Description and Methods** | | | | |
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| (ID:33) | Arango Rodríguez | Implementación de reconocimiento de interacciones entre dominios del virus GBV-C por medio de herramientas bioinformáticas | Pst-50 | **Bioinformática de Virus: Descripciones y Métodos** **Virus Bioinformatics: Description and Methods** |
| (ID:184) | Becerra Sandoval, Moreno Tovar | Prediction of mimicked liner motifs used by viruses to enter the human cell | Pst-51 | |
| (ID:242) | Castillo | Bioinformatic and phylogenetic analysis of the L1 protein of papillomavirus in Colombian Bovines. | Pst-52 | |
| (ID:243) | Orozco-Ugarriza, Olivo-Martínez,... | In silico evaluation of antiviral activity of Nimbin from Azadirachta Indica against of dengue virus envelope protein | Pst-53 | |
| (ID:246) | Botero-Rodriguez | Computational tracing of protein and ncRNA epitovirome of Dengue virus. | Pst-54 | |

| **Diversidad Bacteriana, Mecanismo, infección y Ciencias Ómicas / Bacterial Diversity, Mechanisms, Infection and Omics Sciences** | | | | |
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| (ID:123) | López, Forero Rodríguez | Computational modeling of intestinal bacterial composition in relation to Parkinson's disease | Pst-55 | **Diversidad Bacteriana, Mecanismo, infección y Ciencias Ómicas** **Bacterial Diversity, Mechanisms, Infection and Omics Sciences** |
| (ID:129) | Duque Aldana, Restrepo Montoya, Pino,... | Some preliminary results on whole genome typing of Mycobacterium spp. | Pst-56 | |
| (ID:133) | TORO NAVARRO, Pinilla-Mendoza,... | A refined genome scale metabolic model of Streptomyces clavuligerus as a tool for metabolic target indentification | Pst-57 | |
| (ID:134) | Pinilla-Mendoza, Toro-Navarro,... | Comparative transcriptomic analysis of Streptomyces clavuligerus grown under different culture media conditions | Pst-58 | |
| (ID:152) | Solano, Pino, Robledo | variability of toxin-antitoxin systems in Mycobacterium tuberculosis lineages | Pst-59 | |
| (ID:206) | Franco-Sierra, Arteaga-Figueroa, Alvarez | Application of Oxford Nanopore sequencing data in bacterial genomics shows significant improvement in genome reconstruction | Pst-60 | |
| (ID:210) | Castaño, Corredor | Two components regulatory system genes from pathogens Gram-negative bacteria associated with colistin resistance. | Pst-61 | |
| (ID:218) | Pino, Niño | Topological Data Analysis for Gene Expression Network Modules Identification in Mycobacterium tuberculosis | Pst-62 | |

| **Parasitos y Bioinformática / Parasites and Bioinformatics** | | | | |
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| (ID:20) | Quiguanás | Modelamiento por Homología y Análisis Estereoquímico de la Proteína Hipotética PFDG_00307 de Plasmodium falciparum Dd2 | Pst-63 | **Parasitos y Bioinformática** **Parasites and Bioinformatics** |
| (ID:67) | Buitrago-López | In silico identification and description of hypothetical proteins related with adhesion in intestinal parasites: Cyclospora cayetanensis, Cryptosporidium parvum, y Giardia assemblage A and B. | Pst-64 | |
| (ID:102) | GARCIA LOPEZ | "Proteínas homologas a PD1-L1 y PD1-L2 humanas en Toxoplasma gondii" | Pst-65 | |
| (ID:114) | Hernandez, Marquez, Molina, Gomez,... | In silico study of molecules derived from the nucleus 4-thiazolidinone with anti-Toxoplasma gondii activity. | Pst-66 | |
| (ID:148) | Velasco velasquez, Velasco... | STRUCTURAL MODELING AND FUNCTIONAL ANALYSIS OF ROP4 PROTEIN OF Toxoplasma gondii | Pst-67 | |
| (ID:156) | Valencia, Acosta, Molina, Gomez | Computational Study of the Structure and Function of the Toxoplasma gondii SRS12B (TGGT1_321480) Protein. | Pst-68 | |

| **Ómicas, Enfermedad y Salud Humana / Omics, Disease and Human Health** | | | | |
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| (ID:36) | Orjuela Rodríguez | Filogenia molecular de subfamilias proteicas de canales transportadores de potasio voltaje dependientes e identificación de blancos para investigaciones oncológicas. | Pst-69 | |
| (ID:41) | Cardona-Londoño, Medina-Salcedo,... | Analysis of Gene expression profiles associated with neuroinflammatory pathways in Colombian patients with Alzheimer's disease | Pst-70 | |
| (ID:48) | Gaitán, Gaitán, Tamayo, López, Bermudez | Differential expressed genes in low and high grade gliomas: characterizing signaling networks involved in cancer progression. | Pst-71 | |
| (ID:95) | Velez Segura, Rojas Romero, León Guzmán | Exomic and clinical data management using Django | Pst-72 | |

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| (ID:125) | Villada Ramos | Structural and functional prediction of the calcium dependent pancreatic cytosolic phospholipase A2 protein present in Rattus norvegicus | Pst-73 | **Ómicas, Enfermedad y Salud Humana**<br><br>**Omics, Disease and Human Health** |
| (ID:136) | Medina | Conserved Protein-Ligand Interactions in Human CDK Family | Pst-74 | |
| (ID:147) | Pulido, Ramirez, Robledo, Correa, Pulido | In silico determination of the relevance of mutual exclusivity and concurrency patterns on the identification of driver genes from cancer public data | Pst-75 | |
| (ID:169) | Garcia | IDENTIFICATION OF GENETIC VARIANTS THROUGH WHOLE EXOMIC SEQUENCING IN A PATIENT WITH DISORDER OF SEXUAL DEVELOPMENT 46, XY. | Pst-76 | |
| (ID:173) | Alarcón | ESTUDIANDO EL BLOQUEO ELECTROSTÁTICO POR CA+2 EL HEMICANAL DE CONEXINA 26 HUMANA: UNA APROXIMACIÓN DESDE LA BIOLOGÍA COMPUTACIONAL | Pst-77 | |
| (ID:188) | Velarde Hoyos | Genetic variation in the human CYP2C19 subfamily in Colombian population | Pst-78 | |
| (ID:215) | Godoy Corredor, Lopez Kleine, Perdomo... | Statistical challenges in the integrated analysis of different sets of gene expression data for the understanding of lung carcinogenesis | Pst-79 | |
| (ID:228) | Bascur | The IDH1 and IDH2 cancerous mutants lose their inhibition because they have a different binding site than the wild types | Pst-80 | |