IX CRG Annual Symposium "Medical Genome Sequencing: Understanding the Genomes of Disease"

Abstract acceptance list

POSTERS

#	APPLICANT	Title
1	Abdullayev, Ilgar	MiR-155 target prediction in nasopharyngeal carcinoma
2	Ashraf, Sadia Ashraf	Adenine nucleotide transporters as potential targets for novel anti-chlamydial drugs
3	Dalton, James	Activ8: an integrated multi-layer modeling and visualization tool & networking environment for clinicians, patients and researchers
4	Dienstmann, Rodrigo	BRAF mutation status in a cohort of patients suitable for phase 1 trials with specific targeted agents
5	Fung, Y. Wendy	A study of tuberculosis infection in Hong Kong by metagenomics
6	Georgieva, Milena	Chromatin loop organization in normal and tumor cells
7	Glazkova, Slavyana	Sequence type determination of *Neisseria meningitidis*, isolated from patitents in Belarus
8	Kota Venkata, Naga Poojitha	Exome Sequencing: Approaches, Analysis and Validation in Relevance to Cancer
9	Mahfoudh, Wijden	BRCA1 mutation detection: the Tunisian experience.
10	Martsenyuk, Olga	Methylenetetrahydrofolate reductase polymorphism in human placenta and preeclampsia
11	Miloshev, George	Chromatin loop organization in normal and tumor cells
12	Mocan, Elena	Genetic polymorphism of 5-lipoxygenase activating protein and phosphodiesterase 4D in ischemic stroke Moldavian patients
13	Mukherjee, Bandhan	The evolutionary trends in the sequence of aminoacyl t-RNA synthatases: correlation with the structure
14	Nikolaou, Christoforos	A peak-hashing method for the fast analysis and clustering of ChIPSeq data
15	Oliva Virgili, Rafael	Epigenomics and Proteomics of the Human Sperm Chromatin
16	Ose, Sandra	SIMBIOMS: services for collaborative projects
17	Reimann, Ene	Whole transcriptome RNA-Seq of human dermal fibroblasts using SOLiD system
18	Rodriguez-Santiago, Benjamin	De novo copy number variations are mostly paternal in origin.
19	Saura i Manich, Cristina	PIK3CA mutation status in a cohort of patients suitable for phase 1 trials with specific targeted agents
20	Solovyev, Victor	A Tool for Reconstructing Sequences and Transcriptome Analysis using Next-Generation Sequencing Data
21	Tubio, Jose	Improving performance of paired-end mapping for the detection of chromosomal rearrangements induced by transposable elements
22	Vasli, Nasim	High throughput mutations screening for identification of novel genes in congenital myopathies

ORAL COMMUNICATIONS

APPLICANT	Title
Caceres Aguilar, Mario	Bioinformatic prediction of non-redundant polymorphic inversions in the human genome
Jorda Ramos, Mireia	Filling up gaps in epigenomic maps: the active Aluome
Pagani, Luca	Characterization, through re-sequencing, of genetic variants associated with high altitude adaptation in North Caucasian ethnic groups
Rabionet, Raquel	Using homozygosity mapping and exome sequencing to search for a gene causing a rare articular disease
Sardiello, Marco	Identification of disease genes through gene network analysis
Sun, Yu	Terminal Osseous Dysplasia is Caused by a Single Recurrent Mutation in the