www.TurkJBiochem.com

TÜRK BİYOKİMYA DERGİSİ

Turkish Journal of Biochemistry

ULUSLARARASI BİYOKİMYA KONGRESİ 2017

28. Ulusal Biyokimya Kongresi

19 - 23 Eylül 2017, Erzurum

INTERNATIONAL BIOCHEMICAL CONGRESS 2017

28th National Biochemistry Congress

19 - 23 September 2017, Erzurum

Türk Biyokimya Derneği'nin yayın organıdır.
[Published by the Turkish Biochemical Society]

2017
Volume 42
Supplement 1

YER ALDIĞI İNDEKSLER [INDEXED BY]

SCI Expanded, Journal Citation Reports/Science Edition, Chemical Abstracts, Index Copernicus, Embase, Scopus, Ulakbim Türk Tıp Dizini, Ulrich's Periodical Directory, EBSCO, Türkiye Atıf Dizini

2017 • VOLUME 42 • SUPPLEMENT ISSUE 1

TURKISH JOURNAL OF BIOCHEMISTRY

TÜRK BİYOKİMYA DERGİSİ

OFFICIAL JOURNAL OF THE TURKISH BIOCHEMICAL SOCIETY

DE GRUYTER

PP1-09

MEASUREMENT UNCERTAINTY, REFERENCE CHANGE VALUE, INDIVIDUALITY INDEX IN EVALUATION OF IMMUNOASSAY TEST RESULTS

Hakan Sayar, Mevhibe Balk, Gülsevim Saydam, Murat Keleş
Türkiye Yüksek İhtisas Research and Traning Hospital, Clinical Biochemistry Laboratory, Ankara

OBJECTIVES : Measurement Uncertainty is an indication of the confidence / quality level in measurement result. We aimed to assess Troponin -I, Prostate Specific Antigen (PSA), Thyroid Stimulating Hormone (TSH) Test Parameters Measurement Uncertainty , Reference Change Value (RCV) and Individuality Index (II) together with the test results due to value of Immunoassay Test Measurements quantities as picogram level, narrow limits of Reference Ranges and importance of Medical Decision point in the diagnosis and follow -up.
MATERIALS-METHODS: Each source that causes the measurement uncertainty was determined as mentioned in the Guide to Expression of Uncertainty in Measurement (GUM). Uncertainty Resources were identified including Internal Quality Control Source Uncertainty , External Quality Control Source Uncertainty , Repeatability Source Uncertainty , Recovery Source Uncertainty , Calibrator Source Uncertainty , and Calibration Sources Uncertainty . Relative Standard Uncertainty of each Source Uncertainty was calculated as proposed in the GUM. Individuality Index (II) were calculated from data of Intra-Individual Biological Variation (CVi) and Inter-Individual Biological Variation (CVg) in Ricos database, and Reference Change Value (RCV) was calculated based on 6 months the Analytical CV (CVA) data.
CONCLUSIONS : It is considered that the results of PSA and Troponin -I tests will be more reliable reporting together with Measurement Uncertainty and RDD because of the Individuality Index of PSA and Troponin-I tests is low.

Keywords: Measurement Uncertainty, Biological Variation, Immunoassay

PP1-10

IN SILICO IDENTIFICATION OF MICRORNAS IN 13 MEDICINAL PLANTS

Bihter Avsar, Danial Esmaeili Aliabadi
Sabanci University, Faculty of Engineering and Natural Sciences, İstanbul

OBJECTIVES : MicroRNAs are endogenous , non-coding small RNAs and they lay important roles in plant regulatory pathways , development , stress tolerance and growth . With the advent of next-generation sequencing technologies , the microRNA identification studies by computational methods have been increased and have become effective . In this study , we predicted microRNA repertoires from 13 medicinal plants by using their ranscriptome atlas .
MATERIALS -METHODS : The transcriptome sequences of 13 medicinal plants were retrieved and the miRNA identification was conducted based on homology conservation method . Phylogenetic tree was constructed to show the level of similarity /dissimilarity between 13 medicinal plants (Atropa belladonna , Camptotheca acuminate , Cannabis sativa, Digitalis purpurea , Dioscorea villosa, Echinacea purpurea , Ginkgo biloba , Hoodia gordonii , Hypericum perforatum , Panax quinquefolius , Rauvolfia serpentina , Rosmarinus officinalis , Valeriana officinalis) by MiniTab statistical software . The transcriptome of Arabidopsis thaliana organism was used as a model organism. Target annotations of predicted putative microRNAs was performed by psRNA target and Blast2Go softwares .
RESULTS: As a total number, 168 putative miRNAs were identified. The highest number of microRNAs were found in Camptotheca acuminate (28 miRNA families) transcriptome whereas Atropa belladonna had the lowest amount of putative miRNAs (three miRNA families) in its transcriptome. Digitalis purpurea and Rosmarinus officinalis showed the highest similarities . Targets of putative miRNAs in biological processes and molecular functions revealed us different profiles in different organisms .
CONCLUSIONS : Since medicinal plants have some important therapeutic properties , these findings might help to elucidate metabolic and regulatory pathways in medicinal plants to use them efficiently in biotechnological and pharmacological applications.

Keywords: Medicinal plants, microRNA identification, miRNA, transcriptome

PP1-11

2. TURKEY (IN VITRO) DIAGNOSTIC SYMPOSIUM-"BIOMARKERS" EVALUATION OF GENERAL PARTICIPANTS

Duygu Harmanci Karagülle[1],Zelih Kılıç[1], Ayşe Koçak[1], Nilgün Yener[2], Aysun Pabuççuoğlu[3], Ferhan Girgin Sağın[4], Hilal Koçdor[5]
1Dokuz Eylül University Institute of Health Sciences Department of Molecular Medicine, Izmir
2Dokuz Eylül University Faculty of Medicine Department of Medical Biochemistry, Izmir
3Ege University Faculty of Pharmacy, Department of Biochemistry, Izmir
4Ege University Faculty of Medicine, Department of Medical Biochemistry, Izmir
5Dokuz Eylül University Institute of Oncology, Izmir

OBJECTIVES: After the 1st in vitro Diagnostic (IVD) Symposium, invited speakers from abroad and domestic participated to the 2nd Turkey in vitro Diagnostic Symposium-BIOMARKERS organized in May this year and they discuOPed biomarkers; diagnosis, treatment, monitoring of treatment response of the diseases and the proceOP of using, medical laboratory tests and equipment together with topics public health and patient safety.The symposium organized by Dokuz Eylul University Health Sciences Institute and Turkish Biochemical Society Izmir Branch with the cooperation of Balçova Municipality to aim providing awareneOP to the latest developments in the biomarkers, clarifying basic questions such as future of biomarkers, infrastructure for innovative initiatives related to the effective use of biomarker.
MATERIALS -METHOD : 60 invited speakers attended the symposium , along with the participation Ministry of Health as a legal authority, representatives of manufacturers , scientists . In addition to the presentations , the participants ' views and suggestions regarding the symposium were also collected and a report was prepared.
RESULTS: 215 participants attended the symposium.The participant profile consists of many faculty members, ministry and company representatives, with intensive student (master's degree-doctorate-specialization).48% of the participants gave feedback.88% of the participants evaluated the symposium overall, as successful.78% of participants found successful in terms of scientific content.While 92% of the participants also found quite successful with regard to its social content 80% of them also stated that they would participate if the IVD symposiums to be organized.
CONCLUSION: II. Turkey IVD Symposium-BIOMARKERS was carried out as a successful activity in terms of satisfaction with scientific program, participant profile from different sections andfeedbackreceived.

Keywords: information, biomarkers, in vitro diagnostic

PP1-12

IN SILICO MOLECULAR DOCKING ANALYSIS OF HUMAN CARBONIC ANHYDRASE II TRP209 MUTANT ENZYMES

Deryanur Kılıç[1], Ömer İrfan Küfrevioğlu[2]
1Aksaray University, Faculty of Science and Art, Department of Chemistry, Aksaray
2Atatürk University, Faculty of Science, Department of Chemistry, Erzurum

OBJECTIVES: Recombinant human carbonic anhydrase II enzyme (hCA II) was obtained in our previous study using the SUMO expression system, an aromatic amino acid in its active site was replaced by some aliphatic amino acids (W209V, W209L, W209I, W209P) and mutant proteins were obtained using the same expression system . The activities of these mutant proteins and affinities for some benzenesulfonamides are experimentally compared to the wild type . In this work , our goal is to investigate the affinity of some benzenesulfonamides to these mutant and wild type as in silico .
MATERIALS -METHODS : The crystal structure of hCA II (PDB ID: 2WEJ) was download from the protein data bank and the structure was constructed using the protein preparation wizard of Schrödinger . Mutants of Trp 209 were then obtained by performing computational mutagenesis . Glide XP docking analyzes were performed to determine the affinity of the some benzenesulfo namides to the mutant protein and wild type .
RESULTS : Glide scores were obtained at the end of the docking study and these scores were compared . The best XP poses of the ligands binding to the proteins were taken and analyzes of the binding sites were performed.