

Sample Records from Analytical Abstracts Online

Record 1 of 4

Title:

Bioanalysis of drugs by liquid-phase microextraction coupled to separation techniques.

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Source:

Journal of Chromatography, B: Analytical Technologies in the Biomedical and Life Sciences , 5 Mar 2005 , **817** (1), 3-12

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Language:

English

Publication Type:

Journal

Analyte:

amitriptyline [50-48-6]
amphetamine [300-62-9]
atenolol [29122-68-7]
butylamine, s-, 1-(1,3-benzodioxol-5-yl)-*N*-methyl- [103818-46-8]
citalopram [59729-33-8]
clomipramine [303-49-1]
doxepin [1668-19-5]
drugs - analysis of, in biological fluids, by chromatography, LPME in, review
fluoxetine [54910-89-3]
fluvoxamine [54739-18-3]
haloperidol [52-86-8]
ibuprofen [15687-27-1]
ketoprofen [22071-15-4]
methadone [76-99-3]
methylamphetamine [537-46-2]
methylenedioxymetamphetamine [42542-10-9]
mianserin [24219-97-4]
naproxen [22204-53-1]
norephedrine [492-41-1]
paroxetine [61869-08-7]
pethidine [57-42-1]
pindolol [13523-86-9]
promethazine [60-87-7]
tenamphetamine [4764-17-4]
tenamphetamine, *N*-ethyl- [82801-81-8]
trimipramine [739-71-9]

Matrix:

biological fluids - analysis of drugs in, by chromatography, LPME in, review
blood - analysis of drugs in, by chromatography, LPME in, review
blood plasma - analysis of drugs in, by chromatography, LPME in, review
milk, human - analysis of drugs in, by chromatography, LPME in, review
urine - analysis of drugs in, by chromatography, LPME in, review

Technique:

chromatography - in analysis of drugs, in biological fluids, LPME in, review
extraction, micro-, liquid-phase (LPME) - hollow fibre, of drugs, from biological fluids, for analysis by chromatography, review

Abstract:

The demand for automation of liquid-liquid extraction (LLE) in drug analysis combined with the demand for reduced sample preparation time has led to the recent development of liquid-phase microextraction (LPME) based on disposable hollow fibres. In LPME, target drugs are extracted from aqueous biological samples, through a thin layer of organic solvent immobilised within the pores of the wall of a porous hollow fibre, and into an μ l volume of acceptor solution inside the lumen of the hollow fibre. After extraction, the acceptor solution is subjected directly to a final analysis either by high performance liquid chromatography (HPLC), capillary electrophoresis (CE), mass spectrometry (MS), or capillary gas chromatography (GC) without any further treatments. Hollow fibre-based LPME may provide high enrichment of drugs and excellent sample clean-up, and probably has a broad application potential within the area of drug analysis. This review focuses on the principle of LPME, and recent applications of three-phase, two-phase, and carrier mediated LPME of drugs from plasma, whole blood, urine, and breast milk. (33 references).

Record 2 of 4**Title:**

A new two-chip concept for continuous measurements on PMMA-microchips.

Author:

Vogt, O.; Pfister, M.; Marggraf, U.; Neyer, A.; Hergenroeder, R.; Jacob, P.

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Source:

Lab on a Chip , 25 Jan 2005 , 5 (2), 205-211

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Language:

English

Publication Type:

Journal

Analyte:

ions - sepn. of, by capillary electrophoresis, microfluidic systems for
lithium ion (Li^+) [17341-24-1]
potassium ion (K^+) [24203-36-9]
sodium ion (Na^+) [17341-25-2]

Technique:

electrophoresis, capillary
fluidic systems, micro- - for sepn. of ions, capillary electrophoretic, two-chip electrophoretic-hydrodynamic system for

Abstract:

A new concept for continuous measurements on microchips is presented. A PMMA (polymethylmethacrylate) based capillary electrophoresis chip with integrated conductivity detection is combined with a second chip, which undertakes the task of fluid handling and electrical connections. The combination of electrokinetic and hydrodynamic flows allows long-term continuous stable analyses with good reproducibilities of migration time and peak heights of analytes. The two-chip system is characterized in terms of stability and reproducibility of separation and detection of small ions. Relative standard deviations of <1% and 3% respectively for retention times and peak heights during long-term measurements can be achieved. The new system combines simple handling and automated analysis without the need for refilling, cleaning or removal of the separation chip after one or several measurements

Record 3 of 4**Title:**

A global approach combining proteome analysis and phenotypic screening with RNA interference yields novel apoptosis regulators.

Author:

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Source:

Molecular and Cellular Proteomics , Jan 2005 , 4 (1), 44-55

ISSN:

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Publication Year:

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Language:

English

Publication Type:

Journal

Analyte:

proteins - identn. of, involved in apoptosis regulation, by bioassay, digestion, gel electrophoresis, MALDI MS, PCR and Western blotting

Technique:

bioassay
digestion
electrophoresis, gel
mass spectrometry, matrix-assisted laser desorption-ionization (MALDI MS)
polymerase chain reaction (PCR)
Western blotting

Abstract:

Global approaches like proteome or transcriptome analyses have been performed extensively to identify candidate genes or proteins involved in biological and pathological processes. Here we describe the identification of proteins implicated in the regulation of apoptosis using proteome analysis and the functional validation of targets by RNA interference. A high-throughput platform for the validation of synthetic small interfering RNAs (siRNAs) by quantitative real-time PCR was established. Genes of the identified factors were silenced by automated siRNA transfection, and their role in apoptotic signaling was investigated. Using this strategy, nine new modulators of apoptosis were identified. A subsequent detailed study demonstrated that hepatoma-derived growth factor (HDGF) is required for TNF α -induced release of pro-apoptotic factors from mitochondria. The strategy described here may be used for hypothesis-free, global gene function analysis.

Record 4 of 4**Title:**

Addressing analytical uncertainties in the determination of trichloroacetic acid in soil.

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Source:

Journal of Environmental Monitoring , 3 Feb 2005 , 7 (2), 137-144

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Language:

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Publication Type:

Journal

Analyte:

acetic acid, trichloro- [76-03-9] - detmn. of, in soil, by headspace analysis-GC-ECD, extraction in, chemometrics in

Matrix:

soil - detmn. of trichloroacetic acid in agricultural and forest, by headspace analysis-GC-ECD, extraction in, chemometrics in

Technique:

chemometrics - error analysis, in detmn. of trichloroacetic acid, in soil, by headspace analysis-GC-ECD, extraction in

chromatography, gas (GC)

electron capture detection (ECD)

extraction - of trichloroacetic acid, from soil, for detmn. by headspace analysis-GC-ECD, chemometrics in headspace analysis

Abstract:

Soil is an important compartment in the environmental cycling of trichloroacetic acid (TCA), but soil TCA concentration is a methodologically defined quantity; analytical methods either quantify TCA in an aqueous extract of the soil, or thermally decarboxylate TCA to chloroform in the whole soil sample. The former may underestimate the total soil TCA, whereas the latter may overestimate TCA if other soil components (e.g. humic material) liberate chloroform under the decarboxylation conditions. The aim of this work was to show that extraction and decarboxylation methods yield different TCA concentrations because the decarboxylation method can also determine "bound" TCA. Experiments with commercial humic acid solutions showed there was no additional chloroform formation under decarboxylation conditions, and that all TCA in a TCA-humic acid mixture could be quantitatively determined ($108 \pm 13\%$). Anion exchange resin was used as a provider of solid-phase TCA binding; only $5 \pm 1\%$ of a TCA solution mixed with the resin was present in the aqueous extract subsequently separated from the resin, yet the decarboxylation method yielded mass balance ($123 \pm 22\%$) with TCA remaining in the resin. In aqueous extraction of a range of soil samples (with or without added TCA spike), the decarboxylation method was able to satisfactorily account for TCA in the extractant + residue post-extraction, compared with whole-soil TCA (+ spike) pre-extraction: e.g. mass balances for unspiked soil from Sikta spruce and larch forest were $99 \pm 8\%$ and $93 \pm 6\%$, respectively, and for TCA-spiked forest and agricultural soils were $114 \pm 13\%$ and $102 \pm 2\%$. In each case recovery of TCA in the extractant was substantially less than 100% (<20% for unspiked soils, <55% for spiked soils). Extraction efficiencies were generally lower in more organic soils. The results suggest that analytical methods which utilise aqueous extraction may underestimate whole-soil TCA concentrations. Application of both methodologies together may enhance insight into TCA behaviour in soil.
