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**Pharmacometabolomic approach in the investigation of the effects  
of physiologically active substances using *Danio rerio***

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## 1. Introduction

### 1.1. Pharmacological investigations: classic models and tests

In the scientific field of drug research and development and organism chemical exposure studies, traditional methods of pharmacological research are used. They are usually based on phenotypic screening of a response to a compound to receive a specific or a predicted effect. The most common animal models and methods are applied to achieve those goals.

The use of animal models allows a comprehensive perspective on underlying pathological disease mechanisms via a variety of visualization approaches and in vivo tests [260]. In addition, animal genetic manipulations, as well as disease modeling, can provide an insight into new drug targets. For instance, genetic alterations were used to cause type 1 diabetes to investigate new therapeutic targets [243]. Currently, transgenic animal lines are used to study various pathologic processes, including immune, neurological and hematologic diseases and tumors [253]. Animal drug research also includes pharmacokinetic (ADME) and pharmacodynamic studies.

At present, animal models are casually involved in lead compounds tests and interrogation of specific chemical activity or toxicity of candidate drugs [136, 223, 315, 316]. These studies include biochemical (e.g., levels of glucose, amino acids, fatty acids, etc.), physiological and morphological (heartbeat frequency, ECG and MRT assays, embryotoxicity, fetotoxicity, teratogenic effect, etc.), behavioral tests (open field test, light/dark test, etc.) and, additionally, determination of effective and lethal doses (ED50 and LD50, respectively) [27, 51].

The use of animals for pharmacological studies is carried out by implementing animal research replacement, reduction, and refinement (3R) measures. According to these principles, researchers attempt to develop new methods and models.

## **1.2. Metabolomics as a research field: definition, analytical strategies and applications**

### **1.2.1. Metabolomics in systems biology**

Metabolomics is the high-throughput study of small endogenous organic molecules (<1500 Da) called metabolites in various biological samples [318]. Complete coverage of endogenous metabolites that can be identified in a cell, bodily fluid, or an entire organism is a metabolome [317]. Metabolome consists of a diverse number of chemical classes (e.g., lipids, amino acids, short-chain peptides, nucleic acids, sugars, alcohols, and organic acids) that are in the process of continuous synthesis and degradation [322]. DNA, RNA, and proteins trigger different pathways via changes in metabolites level. Also, metabolites themselves can play the roles of endpoints, describing an organism's phenotype at a specific time point [322].

Metabolomics studies are highly complex since they capture a wide variety of metabolites related to different pathways, compared to traditional analytical strategies focused on specific endogenous metabolite annotation and its derivatives in a single pathway study [8, 88]. Metabolome content is dependent on a multitude of internal factors such as the genome, physiological factors, age, sex, diet, or current state of gut microbiota and external factors such as environment [167]. Therefore, the metabolome can reflect any changes in the organism's metabolism.

### **1.2.2. Analytical strategies in metabolomics**

Metabolomics studies can be carried out using different analytical platforms, including chromatography based on mass-spectrometry (e.g., high-performance liquid and gas chromatography-mass spectrometry, HPLC-MS and GC-MS) and nuclear magnetic resonance (NMR).

Mass-spectrometry (MS) is utterly different from NMR. In MS analysis, the sample undergoes ionization, then fragmentation and separation based on  $m/z$ . Annotation of mass-spectral characteristics (e.g., parent ion  $m/z$  and fragmentation spectra) to the compound libraries data can lead to identifying a molecular structure.

Additional chromatographic data such as retention time can also help to define an unknown molecule. Mass-spectrometry is a highly sensitive tool, resulting in even a small amount of a sample being enough to perform an analysis [12, 63, 238]. Since mass-spectrometry is a destructive assay method, analyzed chemicals can't be restored.

NMR detection involves determining the excess absorption or emission of electromagnetic energy of atomic nuclei of the sample. The perturbation of magnetic nuclear spins changes the resonance frequency, especially in  $^1\text{H}$  atoms, that creates characteristic NMR spectra that correlate with chemical structure level and location of  $^1\text{H}$  in the molecule. In contrast to mass-spectrometry, NMR analysis doesn't destroy the sample so that it can be analyzed again [319]. MS detection yielded much higher sensitivity than the NMR [321]. Modern NMR and MS analytical platforms can separate, detect, and define hundreds and thousands of molecules through one analytical cycle [103, 320]. When the analysis is done, peak picking identifies the sample components, and then data analysis is performed.

Metabolomics studies can be categorized into four workflows: 1) untargeted or high-resolution metabolomic profiling; 2) targeted analysis; 3) fluxomics; 4) imaging metabolomics.

Untargeted metabolomic profiling provides broad metabolites coverage (e.g., ~10000 compounds for one analytic cycle). The untargeted metabolomics method is considered inappropriate for specific metabolite quantification; however, it can be used as a first screening approach for biomarker discovery or a hypothesis-generating strategy [28, 246, 323].

Targeted metabolomics studies are shaped towards identifying specific metabolites classes that are present in low concentrations (e.g., 10 to 500 for one analytic cycle). Targeted metabolomic profiling showed promising results in proof-of-concept studies and biomarker validation; also, it is most commonly used [200, 267].

Fluxomics (or fluxomics studies) is a kind of targeted metabolomic analysis that allows performing metabolites quantification via HPLC-MS and NMR methods

in real-time [170]. Fluxomics is used to investigate dynamic underlying metabolic processes in cells and tissues; hence it can provide a detailed understanding of biochemical pathways [44].

Imaging metabolomics is one of the workflows within metabolomics studies that include both in vivo and in vitro evaluation and imaging of endogenous metabolites in tissue samples by applying the NMR method, positron emission tomography (PET), and matrix-activated laser desorption/ionization (MALDI) [117, 296]. Imaging metabolomics is used to study the metabolism of a specific cell, tissue, or organ and to differentiate a patient's tissue in real-time when surgery is performed [130, 296, 301].

### **1.2.3. Metabolomics applications in systems biology studies**

The main feature of metabolomic profile is its sensitivity to either exogenous exposure from the environment or endogenous characteristics of an organism itself (e.g., a physiological condition or a current state of intercellular interaction) [322]. The role of genotype is to predict an organism's possibilities. However, it's the role of the metabolome to reflect the organism's phenotype at the time of sampling [317]. Metabolomics gives an insight into the current state of an organism that can be integrated into several scientific fields, such as fundamental studies in physiology and pathophysiology, nutraceuticals, microbiology, plant studies, and, additionally, drug research and development [30, 140, 168, 305, 306, 318].

At first, metabolomics was used for diagnostic purposes to detect a disease or any other pathological state of an organ [66, 122, 183, 204]. Therefore it was considered an application of chemical analysis in clinical practice [322]. As the capabilities of analytical methods increased, the number of compounds that can be identified simultaneously enlarged. Since biochemical studies can identify a small number of chemicals, metabolomic profiling allows characterizing tens to hundreds of compounds for one assay. Metabolomic methods showed promising results in diagnostic and prognostic biomarker discovery and could provide mechanistic information on associated biochemical processes.

Metabolomic methods were used to investigate development mechanisms and consequences of chronic renal failure that is associated with the development of a large number of other chronic diseases, such as atherosclerosis, cardiovascular diseases, hypertension, stroke, infraction, cachexia, diabetes mellitus, tumor, dementia, gout and anemia [187]. The reason behind these conditions is urinary toxins, i.e., specific compounds that accumulate in blood and tissues due to chronic kidney disease [113, 187]. Several researchers described such endogenous substances, including acrolein, asymmetric dimethylarginine, creatinine, guanidino succinic acid, homocysteine, indoxyl sulfate, uric acid, urea, etc. as toxic chemicals that can cause cardiovascular [113, 288], bone [113] diseases, gout [298], cachexia [264], atherosclerosis [150, 284], stroke and infarction [50], dementia [50], diabetes mellitus [173], hypertension [202] and anemia [84].

Metabolomics application in normal physiology studies is commonly related to endogenous substances with regulatory and physiological activity. These substances have non-peptide structural characteristics, including amino acids, biogenic amines, eicosanoids, organic acids, steroids, and sugars [322].

Since the 80s, there have been studies on amino acids' role in human physiology. It has been proven that amino acids, especially branched-chain ones, play an essential role in insulin secretion [146, 185]; glutamine induces the secretion of glucagon-like peptide-1 [297]; arginine affects the secretion of both insulin and growth hormone [91, 104]. Amino acids derivatives also are important in the human organism. For example, thyroid hormones (thyroxine and triiodothyronine) are critical for carbohydrate, lipid, and protein metabolism [86]. Those findings influenced their role in insulin resistance and carbohydrate, lipid, and protein metabolism [137, 148, 177, 178].

Eicosanoids include prostaglandins, thromboxanes, leukotrienes, lipoxins, and resolvins. They are the polyunsaturated fatty acids metabolism product that can induce or inhibit inflammation and affect cell growth and blood pressure via changes in blood flow [272]. Due to the recent development of metabolomics methods, new



species of eicosanoids and oxylipins are being discovered, some of which carry previously unknown functions [115, 205].

Special attention is now given to organic acids. For instance, it has been established that lactic acid supports tumor growth and suppresses immune response [85]; succinic acid induces IL-1 $\beta$  and TNF- $\alpha$  secretion through specific SUCNR1 receptor activity that is primarily expressed in macrophages; hence it regulates the intensity of immune response [192, 208, 256]; citric acid is known to be responsible for bone structure formation involving osteoblasts [94]. Meanwhile, 2-ketocaproic and retinoic acids are known to induce insulin secretion and cell growth and development [115, 254]; more recently, new studies have unveiled other organic acids' functions.

Metabolomics also found its place in research on human gut microbiota biochemical processes. Since 2016, the complex of microorganisms that live in the digestive tracts of humans should be called microbiome [120]. In correlation with the fact that the human microbiome consists of many various molecules, science focus has shifted to the study of metabolomics of human microbiota. Currently, there were over 100 articles on metabolomic studies of the human microbiome that led to the discovery of 6700 unique metabolites from different chemical classes [166].

Gut microbiota metabolites (e.g., indole acids, tryptophan derivatives) play a considerable role as signal molecules that modulate or regulate several physiological processes. Their functional value was that predominant, so to describe their interaction with other organs, the new term "interaction axis" was implied. There are four "interaction axes" known: gut-brain axis, gut-liver axis, gut-lungs axis, and gut-kidneys axis [166]. It was found that changes in metabolites levels within these axes correlate with autism [118], schizophrenia [270], Parkinson's disease [77], and asthma [295]. It was also found that gut microbiota metabolites can regulate liver [128, 135] and kidney [181, 314] function.

As a result, metabolomics development influenced the successful application of its methods in drug discovery, pharmacological studies, and xenobiotic exposure studies.

#### **1.2.4. The use of metabolomics analysis of biological samples in the investigation of pharmacological effects of physiologically active substances**

Recently metabolomic analysis has been applied to study various chemical exposures on the human organism. It is also involved in drug development studies and research on its adverse effects. The application of metabolomics in the drug research pipeline developed a new workflow called pharmacometabolomics.

Pharmacometabolomics is a scientific field that studies drug or other substance mechanisms of action at a molecular level to predict organism's response to their exposure in correlation with patient's phenotype based on metabolomic profiles before and after the exposure [160]—in particular, measuring endogenous metabolites level after xenobiotic exposure provides detailed information on chemical's effect on specific metabolic pathways that can support traditional assays on pharmacodynamic liabilities to understand better main therapeutic and adverse impact of a drug [160, 162].

The pharmacometabolomic approach can be applied to every stage of drug development and candidate selection pipeline. Most of the most common diseases (e.g., cardiovascular diseases, diabetes mellitus, obesity, depression) are associated with metabolic alterations [209, 241]. Moreover, discovering new metabolic pathways results in the investigation of new drug targets.

Recent findings of trimethylamine synthesis from choline and carnitine by gut microbiota [171, 311] in correlation with the fact that trimethylamine is a precursor for trimethylamine oxide (a metabolite causing atherosclerotic lesions) led to the discovery of two potential drug targets against atherosclerosis – flavin-containing monooxygenase-3 and bacterial choline trimethylamine-lyase that are in charge for trimethylamine oxide synthesis [68]. Later, researchers Hazen et al. proposed a potential inhibitor for the enzymes mentioned above – 3,3-dimethyl-1-butanol naturally occurring in olive oil [311]. Then preclinical studies took place, and new enzyme inhibitors were discovered and later approved for medical use [229].

A prime example of pharmacometabolomics application for investigation of disease mechanisms and further target detection would be a recent invention of two

new drugs to treat relapsed acute myeloid leukemia – ivosidenib and enasidenib. Metabolomics application in relapsed myeloid leukemia studies can be found in Dang et al. [96] and Ward et al. [312]. Findings showed that mutated forms of isocitrate dehydrogenase 1 and 2 were present in patients who have that kind of leukemia. That enzyme turned  $\alpha$ -ketoglutaric acid into  $\alpha$ -hydroxyglutaric acid, which was elevated in patients [250]. Later it was proven that isocitrate dehydrogenase 1 and 2 inhibitors showed promising results in decreasing the level of  $\alpha$ -hydroxyglutaric acid and tumor growth in vitro and in vivo studies [325]. Confirmation studies in vitro and in vivo [277] led to the development and later regulatory approval of enasidenib in the United States in 2017 [196, 219].

In terms of clinical studies, pharmacometabolomics can be used in drug metabolism discovery [9, 82, 308], measuring therapeutic response [10, 31, 95], rational dosing prediction [34, 35, 217, 234], and achieving optimal response for therapy [142]. Pharmacometabolomics is a promising tool for establishing a personalized approach to patient care and personalized medicine.

Personalized medicine aims to select a specific therapy considering the individual characteristics of every patient. A prime example of applying the pharmacometabolomic approach to manage disease would be therapy personalization in inborn errors of metabolism. Screening for metabolites related to inborn errors of metabolism is used not only to diagnose a disease but to choose personalized drug therapy and to monitor therapy response [124, 180]. In addition, there are other scientific approaches and initiatives developed for prospective longitudinal studies in large cohorts (over a few thousand participants) to determine their health status and control changes in metabolome to diagnose altered health conditions and evaluate therapy efficiency [83, 111].

Another pharmacometabolomic application in personalized medicine is therapeutic response monitoring. Response to therapy varies greatly depending on the organism's features, and the most common of them is the expression of different cytochrome P450 genes [1, 7, 26, 32, 302]. While pharmacogenomics shows promising results in personalized pharmacotherapy [33, 36],

pharmacometabolomics can provide data to support genomics [17, 18, 161]. Studies on drug metabolism showed that it depends not only on genetic features but also on ethnic origin, age, sex, weight, diet, etc. However, their impact is impossible to predict by genomics data [37, 116, 161]. Hence, Clayton et al. proposed a pharmacometabolomic approach to predict the metabolomic rate and rational dosing of a drug in individual recipients [87].

More recent articles on pharmacometabolomic application provide data to predict individual drug response. For instance, it has been observed that endogenous metabolites levels significantly correlate with therapeutic response to simvastatin [158, 159]. The pharmacometabolomic approach is a promising tool to select a drug therapy in the case of organ transplantation [258], treating Alzheimer's disease [236], personal statins dosing [175], and special drug groups, e.g., antidepressants [335] and other [105, 326]. For example, Kaddurah-Daouk et al. found changes in phosphatidylethanolamine and other lipids concentrations after olanzapine and risperidone 3-week therapy in schizophrenia patients [157]. As discovered by Krause et al. in a recent article, changes in kynurenine pathway metabolites of tryptophan metabolism correlate with therapy response on celecoxib in patients with the major depressive disorder [174].

Metabolomic analysis is also used to efficiently evaluate drug therapy to study the impact of neurotropic substances on endogenous metabolites levels. Kaddurah-Daouk et al. used citalopram to study a depressive state therapy and found that the serotonin level decreases while 5-hydroxytryptophan and 5-hydroxyindole acetic acid levels significantly increase in human plasma [57]. They also observed a change in catecholamines levels, oxidative stress metabolites, and gut microbiota metabolites levels [57]. Moreover, there was a correlation between the change and therapeutic success [255]. A change in indole acids metabolic profile in major depressive disorder patients who underwent ketamine therapy was described in Rotroff et al.

First attempts to benchmark the InnoMed PredTox Consortium performed data provided by traditional analytical methods to "omics" data. Their results

highlighted good translatability between metabolomics data and traditional methods data and its supportive role in existing drug toxicity knowledge [201]. Currently, some clinical studies imply the pharmacometabolomics approach. For example, Burt and Nandal's systematic research reported that 99 clinical drug trials performed in 2004-2015 used pharmacometabolomic analysis [71].

Studies in animal models provided data on abuse substances exposure on neurotransmitters levels. The use of methamphetamine increased dopamine, tryptophan, and phosphatidylcholine levels in the rat brain [203]. Heroin and morphine exposures caused serotonin synthesis disorder and harmed dopaminergic pathways [330, 333].

Pharmacometabolomics can also be integrated into preclinical trials in drug research and pharmacological and adverse effects study activities. Its use in the research on remoxipride (i.e., dopamine D2 receptor antagonist) revealed the correlation between amino acids and biogenic amines levels and pharmacological features on the drug itself; hence it allowed to expand drug-related toxicity knowledge [67].

Safety testing is essential in the drug development pipeline and post-marketing studies [309]. Investigating metabolic pathways related to drug-induced toxicity is a forward-looking tool that overcompensates specific target organ toxicity studies [131, 132] and general toxicity studies [56, 61].

### **1.3. Pharmacological effects assessments using a new animal model – *Danio rerio***

Research on new biological models to study the pharmacological impact of compounds is still in progress. Apart from the shift of the preclinical studies towards in vitro models, there is also a need for new animal models which allow better translatability, higher throughput, and cost-saving properties [247]. Recently, *Danio rerio* (or zebrafish) caught researchers' attention.

*Danio rerio* (zebrafish) is a small freshwater fish belonging to the minnow family Cyprinidae [169]. *Danio rerio* is used in developmental biology and

pathophysiology studies. Their physiological features were firstly described in 1995, and since then, they have been established as an alternative *in vivo* model in scientific research [13, 20, 169].

The main advantages of *Danio rerio* species compared to other models are:

- i) their genome and physiology is highly conserved with humans (e.g., brain, intestinal, muscle structure, and immune system) [121, 127, 164, 165];
- ii) conservation in pathogenesis (i.e., ~ 80% of genes related to diseases in humans are observed in zebrafish) [261];
- iii) zebrafish reach maturity in 3-5 months, and then female zebrafish is capable of bearing ~200 eggs per spawning [65, 76];
- iv) embryo development is quick, i.e., blastulation and gastrulation stages last five hours. An embryo is considered fully formed in 24h post-fertilization (hpf) and leaves its chorion and enters a free-feeding stage until 72 hpf [221];
- v) zebrafish maintenance doesn't require significant expenses and free space [184].

*Danio rerio* application in developmental biology studies includes research on the nervous system and angiogenesis. Zebrafish embryos are transparent what allowed studies on gastrulation [249], angiogenesis [81, 149], blood flow [106, 176], and the development of peripheral and central nervous systems [52, 182, 329, 332] to be performed.

Most tissues and organs, except for lungs, prostate, and mammary glands, are present in *Danio rerio* and conserved with humans [240]. The availability of transgenic lines facilitates observing neurodegenerative disorders [2, 275], blood diseases [55], cardiovascular diseases [269], tumor [190], Parkinson's disease [263] and stress disorders [11, 80].

Many scientists worldwide have investigated the similarities between the fish species *Danio rerio* and humans. In 2013 Howe et al. sequenced the fish genome and concluded that 70% of its genome, including amino acids sequence coding genes for CYP450 protein, is either conserved or homologous with humans [143]. Also,

protein composition studies of zebrafish blood plasma and organs revealed a high grade of similarity with mammals and humans, specifically [53, 186, 189].

Zebrafish brain structure was also studied and conserved with mammals [4, 16, 257]. There are medial, dorsal, and lateral pallial portions in the zebrafish brain that are relevant to the amygdala, cerebral cortex, and hippocampus in mammals, respectively [64, 213]. It has been proven that essential enzymes are critical to neurotransmitter synthesis and metabolism, such as tyrosine hydroxylase [75], monoamine oxidase [48], catechol-O-methyltransferase [228], and choline acetyltransferase [214], are also present in zebrafish.

Zebrafish neurotransmitter systems are also conserved with humans. GABAergic, dopaminergic, adrenergic, serotonergic, cholinergic systems and glycine, glutamate, and aspartate binding sites are present in *Danio rerio* [141, 228].

*Danio rerio* species fish is a suitable model for uncovering pharmaceutical substances, cosmetics, nanoparticles, and pesticides [14, 294]. A number of toxicological studies using zebrafish grow exponentially due to the low amount of substance needed for an assay [21, 220], high reproduction rate [300], and good data translatability to mammal models [134]. The most common testing performed in zebrafish is sublethal dose determination (LD50) to study acute toxicity. In Russia, acute toxicity testing in *Danio rerio* species fish is described in GOST 33774-2016 "Analytical methods for substances that are hazardous to the environment. Acute toxicity in fish embryos". Chemical-induced lethality is measured every 24h for 96h. Lethality is based on the abundance of coagulated embryos, a lack of somites, tail detachment, or a heartbeat and inspected visually [273]. While zebrafish embryos are not considered laboratory animals until six days post-fertilization (dpf), acute toxicity tests in fish embryos are seen as an alternative to adult fish tests since the latter requires an ethical committee approval according to international laws [283]. The use of zebrafish embryos reduced the number of animal models involved in lethality studies and potentially replaced traditional test models.

Fish species *Danio rerio* is also used to assess morphological changes caused by chemical exposure. Morphological changes include developmental heart and

swim bladder disorders, body structure (e.g., somites, tail or fins), nervous system (e.g., brain, notochord, or eyes) disturbances. These effects can be measured via visual inspection or light microscope [230] and accessible to be differentiated compared to controls. This kind of study is considered a substitute for traditional mammal model testing [226, 313].

Spontaneous and drug-stimulated locomotor activity studies in *Danio rerio* can reveal chemicals exposure on the central nervous system [19, 38, 179]. Zebrafish have a fully functioning blood-brain barrier [69, 163]; hence behavioral tests in it are available to perform to study presumably neurotoxic substances. For example, spontaneous movements (e.g., speed, longitude, and length while swimming) significantly decrease due to pesticide [156] and industrial chemicals [304] exposure in zebrafish. A change in behavioral activity as a response to visual stimulations (e.g., dark-light task and light stimulus test) can be applied to study pharmaceutical substances [195] and neurotoxins [172] exposure on CNS.

Promising results of traditional methods in investigating substances exposure in *Danio rerio* species prompted the development of a metabolomic and pharmacometabolomic approach for their implication in chemicals study in zebrafish. The most prominent example of metabolomic approach application is a study of polystyrene microplastic impact on zebrafish. These compounds caused changes in amino acids, including proline, leucine, lysine, threonine, and lipid (linolenic acid and palmitic acid) levels that indicate liver dysfunction [239].

Pharmacometabolomic studies in zebrafish showed promising results in the annotation of pesticides and insecticides as environmental pollutants and hazardous molecules for humans. Studies on bisphenol A [222], chlorpyrifos [144], fipronil [324], flutolanil [291], and isocarbophos [155] showed their significant impact on zebrafish metabolomic profile, proving their cardio-, liver-, brain- and muscle toxic attributes.

Studies of pharmacometabolomic changes in exposure to pharmaceutical substances on fish of *Danio rerio* species are just beginning to gain popularity. Using the pharmacometabolomic approach, it has been proven that fungicides,



diniconazole, and difenoconazole, induce serious lipids, amino acids, sugars, and nucleotides metabolism disturbances [291, 309]. Antimicrobial agent triclosan caused urea, citric acid, galactose, glucose, stearic acid, proline, phenylalanine, and glutamine changes [111]. Exposure to citalopram, fluoxetine, amitriptyline changes levels of glutamate, tryptophan, acetylcholine, and serotonin in zebrafish brain [97].

### **Aims and scope of the study**

To summarize, it can be concluded that the use of the pharmacometabolomic approach in the investigation of pharmacological effects of physiologically active drugs is a field of great scientific interest. The use of zebrafish as an alternative animal model for this type of the studies may also be very promising.

There are studies in the field of the investigation of the effects of different drugs using zebrafish as a model organism. But there is a lack of studies in the field of pharmacometabolomic investigations using *Danio rerio*. Also, these sporadic studies do not follow the same methodology to form a unified approach in these investigations.

In this regard, an urgent task is to develop the methodical and methodological basis of the pharmacometabolomics approach in the investigations of the pharmacological effects of physiologically active drugs using zebrafish as a model organism.

The aims of this study were:

1. To identify the most relevant metabolic pathways for investigating the pharmacological effects of physiologically active drugs of neurotropic action based on untargeted metabolomics profiling.
2. To develop and validate analytical methods of the quantitative determination of endogenous metabolites of specific biochemical pathways of neurotransmitters metabolism (to develop a targeted metabolic panel).
3. To determine specific quantitative characteristics of the metabolomics profile of zebrafish larvae after the exposure to a pharmacological substance of neurotropic action with a well-studied model of action using targeted metabolomics.

4. To determine specific quantitative characteristics of the metabolomics profile of zebrafish larvae after exposure to a novel psychoactive substance of the cannabimimetic family.

5. To investigate the behavioral changes caused by the novel psychoactive substance to find a correlation between metabolomics and behavioral changes.

## 2. Materials and methods

### 2.1. Chemicals and equipment

#### 2.1.1. Pharmacologically active substances

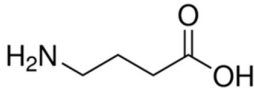
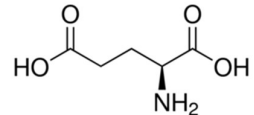
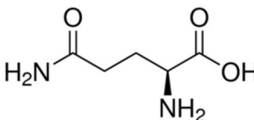
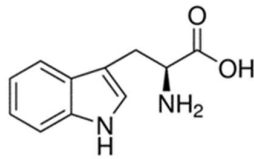
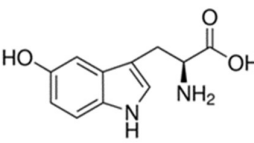
Diazepam (7-chloro-1-methyl-5-phenyl-1,3-dihydro-2H-1,4-benzodiazepine-2-one) was purchased from Sigma-Aldrich (Darmstadt, Germany). Diazepam is a pharmacologically active substance with a well-defined mechanism of action. Diazepam exposure leads to the allosteric modification of the GABAA receptors, increasing the affinity of the receptors to GABA [5]. Diazepam is used as a "golden standard" in assessing the pharmacological investigations of the anxiolytic action of lead compounds [41, 42]. There are scientific studies that describe the action of diazepam on the different neurotransmitters systems, including the GABAergic system [72, 244], serotonergic system [62, 192, 236], dopaminergic/adrenergic system [273, 281], and cholinergic system [93, 231]. According to this data, diazepam was chosen as a primary compound in investigating the effects of pharmacologically active substances on neurotransmitters metabolomics using zebrafish larvae.

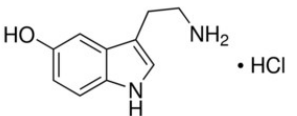
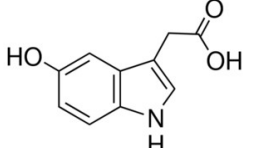
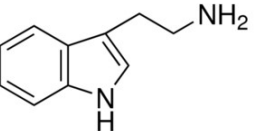
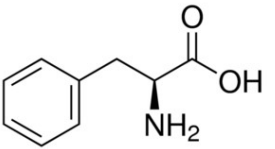
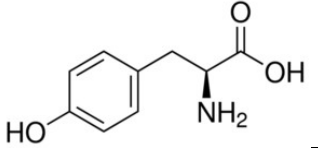
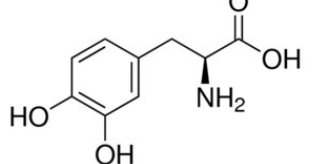
5F-APINAC (adamantane-1-yl-1-(5-fluoropentyl)-1H-indazole-3-carboxylate) was obtained from Cayman Chemicals (Michigan, USA). According to its' chemical structure, 5F-APINAC is a synthetic cannabinoid – a class of pharmacologically active substances whose main mode of action is realized through the affinity to the type 1 and 2 cannabinoid receptors in the central nervous system [49, 150]. The mechanistic reason for their action is the depolarization-induced suppression of inhibition and excitation of neurons, which is realized through the lowering of the presynaptic neurons firing rate [79, 286]. Although there are studies in the field of the effects of cannabimimetics on the different neurotransmitter systems, there were no complex metabolomics studies conducted [58, 98, 100, 107, 118]. 5F-APINAC was chosen as a pharmacologically active substance with a relatively unknown mode of action on the neurotransmitter systems.

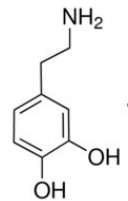
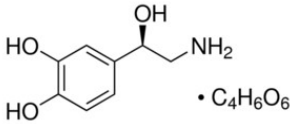
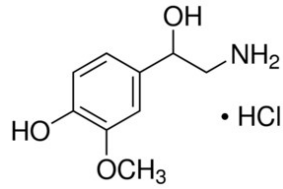
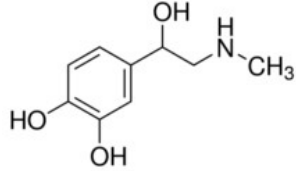
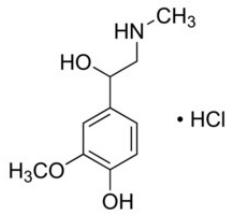
### **2.1.2. Standard substances**

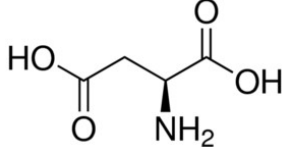
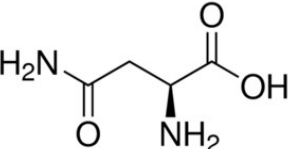
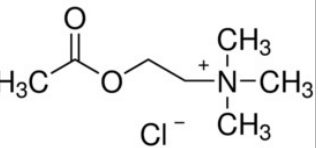
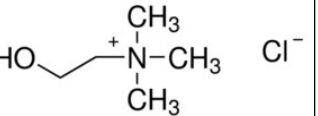
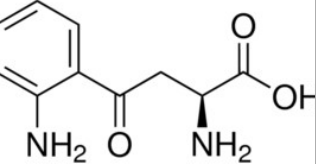
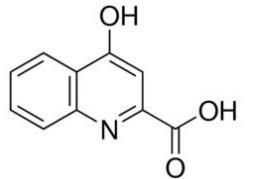
The standard substances of GABAergic, serotonergic, dopaminergic/adrenergic, cholinergic, aspartic acid systems, kynurenine and indole pathways, and other metabolites, connected to neurotransmission, were purchased from Sigma-Aldrich (Darmstadt, Germany) and Honeywell Fluka (Leicestershire, UK). Isotopically-labeled standards were purchased from Sigma-Aldrich and Toronto Research Chemicals (Toronto, Canada). The purity of all standards was >99%. The list of the compounds is presented in Table 1.

Table 1 – Analytical standards

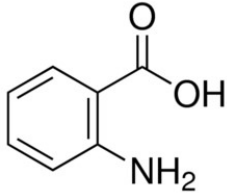
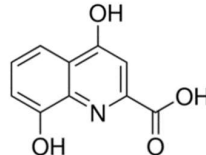
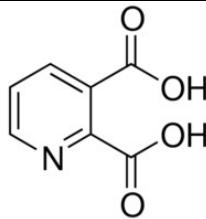
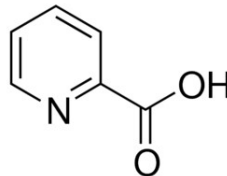
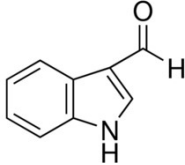
Neurotransmitter system or metabolic pathway	Metabolite	Role	Formula	Molar mass, g/mol	Cas№
GABAergic system	Gamma-aminobutyric acid	Neurotransmitter		103,12	56-12-2
	Glutamic acid	Neurotransmitter, precursor		147,13	56-86-0
	Glutamine	Precursor		146,12	56-85-9
Serotonergic system	Tryptophan	Precursor		204,23	73-22-3
	5-hydroxytryptophan	Precursor		220,22	4350-09-8

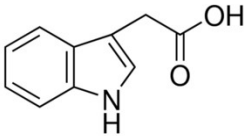
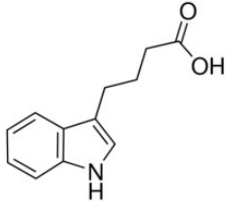
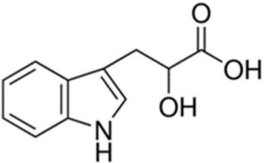
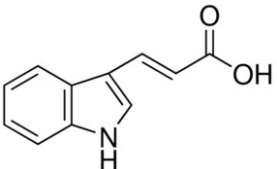
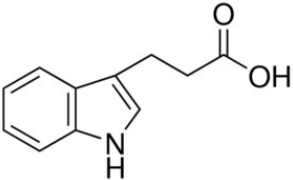
	Serotonin	Neurotransmitter		212,68 (HCl)	153-98-0
	5-hydroxyindole acetic acid	Metabolite		191,18	54-16-0
	Tryptamine	Alternative metabolite of tryptophan conversion		160,22	61-54-1
Dopaminergic/ adrenergic system	Phenylalanine	Precursor		165,19	63-91-2
	Tyrosine	Precursor		181,19	60-18-4
	L-DOPA	Precursor		197,19	59-92-7

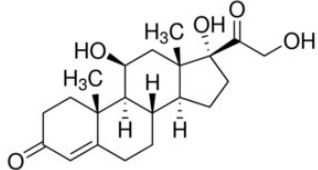
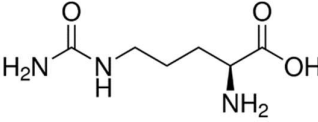
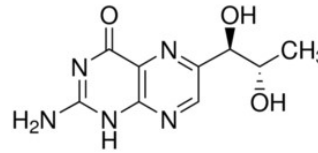
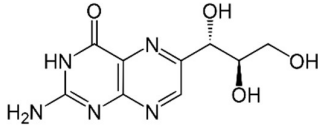
	Dopamine	Neurotransmitter, precursor	 • HCl	189,64 (HCl)	62-31-7
	Norepinephrine	Neurotransmitter, precursor	 • C <sub>4</sub> H <sub>6</sub> O <sub>6</sub>	319,26 (tartrate)	3414-63-9
	Normetanephrine	Metabolite	 • HCl	219,67 (HCl)	1011-74-1
	Epinephrine	Neurotransmitter		219,67 (HCl)	329-63-5
	Metanephrine	Metabolite	 • HCl	233,69 (HCl)	881-95-8

Aspartic acid system	Aspartic acid	Neurotransmitter		133,10	56-84-8
	Asparagine	Precursor		132,12	70-47-3
Cholinergic system	Acetylcholine	Neurotransmitter		181,66 (Cl <sup>-</sup> )	60-31-1
	Choline	Precursor		139,62 (Cl <sup>-</sup> )	67-48-1
Kynurenine pathway	Kynurenine	Tryptophan catabolism		208,21	2922-83-0
	Kynurenic acid	Tryptophan catabolism		189,17	492-27-3



	Anthranilic acid	Tryptophan catabolism		137,14	118-92-3
	Xanthurenic acid	Tryptophan catabolism		205,17	59-00-7
	Quinolinic acid	Tryptophan catabolism		167,12	89-00-9
	Picolinic acid	Tryptophan catabolism		123,11	98-98-6
Indole pathway	Indole-3-carboxaldehyde	Tryptophan catabolism		145,16	487-89-8

	Indole-3-acetic acid	Tryptophan catabolism		175,18	87-51-4
	Indole-3-butyric acid	Tryptophan catabolism		203,24	133-32-4
	Indole-3-lactic acid	Tryptophan catabolism		205,21	832-97-3
	Indole-3-acrylic acid	Tryptophan catabolism		187,19	1204-06-4
	Indole-3-propionic acid	Tryptophan catabolism		189,21	830-96-6

Others	Cortisol	Stress biomarker	 <p>The chemical structure of cortisol is a steroid with a four-ring nucleus. It features a ketone group at C3, a double bond between C4 and C5, and hydroxyl groups at C11, C14, and C17. Two methyl groups are attached at C13 and C14. A hydroxyl group is attached to C20, and a hydroxymethyl group is attached to C21.</p> <chem>CC12CCC3=C1C(=O)CC4=C3C(=C(C=C4)O)C(O)C2O</chem>	362,46	50-23-7
	Citrulline	Glutamine metabolite	 <p>The chemical structure of citrulline is a linear amino acid derivative. It consists of a central carbon chain with an amino group (NH<sub>2</sub>) at one end, a carboxylic acid group (COOH) at the other, and a side chain containing a secondary amide group (NH-CO-NH<sub>2</sub>).</p> <chem>NC(=O)NCCCC(N)C(=O)O</chem>	175,19	372-75-8
	Biopterin	Cofactor of enzymes responsible for monoamines biosynthesis	 <p>The chemical structure of biopterin is a pteridine ring system. It has a carbonyl group at C6, an amino group at C7, and a side chain at C8 consisting of a hydroxyl group and a methyl group.</p> <chem>CC(O)C1=NC2=C(N1)C(=O)N=CN=C2N</chem>	237,22	22150-76-1
	Neopterin	Metabolites of extensive biopterin elimination	 <p>The chemical structure of neopterin is a pteridine ring system. It has a carbonyl group at C6, an amino group at C7, and a side chain at C8 consisting of two hydroxyl groups and a hydroxymethyl group.</p> <chem>OC(O)C1=NC2=C(N1)C(=O)N=CN=C2N</chem>	253,21	2009-64-5

### 2.1.3. Reagents

The following reagents were used in the study: dimethyl sulfoxide (DMSO) (ACS reagent, >99.9%, Merck, Germany), sodium chloride (pure, Prime Chemicals Group, Russia), potassium chloride (pure, Prime Chemicals Group, Russia), calcium chloride\*2H<sub>2</sub>O (pure, Prime Chemicals Group, Russia), magnesium sulfate\*7H<sub>2</sub>O (pure, Prime Chemicals Group, Russia), methylene blue (>97%, Prime Chemicals Group, Russia), ethanol (puriss, Merck, Germany), sodium metabisulfite (puriss, Merck, Germany), methanol (puriss, Chimmed, Russia), ascorbic acid (99%, Merck, Germany), acetonitrile (HPLC, Fisher Chemical, USA), formic acid (99%+, Optima LC-MS grade, Fisher Chemical, USA), methoxyamine hydrochloride (98%, Sigma-Aldrich, Germany), pyridine anhydrous (99.8%, Sigma-Aldrich, Germany), MSTFA (for GC, Sigma-Aldrich, Germany), toluene anhydrous (99.8%, Sigma-Aldrich, Germany). Water was obtained using the Millipore Direct Q3-UV system (Merck-Millipore, USA).

### 2.1.4. Equipment

The following equipment were used in the study: Agilent 1290 II Infinity high-performance liquid chromatographer coupled to triple quadrupole mass-spectrometer Agilent 6470 (Agilent Technologies, USE); Discovery HS F5-3 PFP (150 mm, 2.1 mm, 3 um) analytical column for liquid chromatography (Supelco, Germany); Agilent 7820A gas chromatographer coupled to mass-selective detector MSD 5977 (Agilent Technologies, USA); Agilent HP-5MS (30 m, 0,25 mm, 0,25 mm) analytical column for gas chromatography (Agilent Technologies, USA); Adventurer AR 1530 analytical scales (Ohaus Corporation, Switzerland); coolable centrifuge 5418R (Eppendorf AG, Germany); Genius 3 vortex shaker (BioSan, Latvia); MiVac Quattro Concentrator heated vacuum concentrator (Fisher Scientific, USA); DT 255 H ultrasonic bath (Bandelin, Germany); adjustable volume Eppendorf pipets (Eppendorf AG, Germany); Millipore Direct Q3-UV water purification system (Merck-Millipore, USA); Leica DM2000 light microscope

(Leica Microsystems, Germany); high-performance video tracking system (DanioVision, Noldus, Netherlands); 6-, 12-, and 96-well plates (Corning, USA).

## 2.2. Animals

Zebrafish were housed according to the GOST 33219-2014 "Guidelines for accommodation and care of laboratory animals. Species-specific provisions for fish, amphibians, and reptiles" and ETS 123 "European convention for the protection of vertebrate animals used for experimental and other scientific purposes" [23, 70].

Wild-type adult zebrafish for obtaining eggs were purchased from a local pet shop (Moscow, Russia). Males and females were housed separately to prevent uncontrollable breeding. The fish were housed in the water tanks with the density of 1 fish per 2 liters of water; the water in the tank was constantly changing with a rate of 4-6 tank volumes per hour. The light/dark cycle was set at 14/10 hours, respectively. The temperature of the water and air was constant ( $26\pm 0,5^{\circ}\text{C}$  and  $25^{\circ}\text{C}$ , respectively) [23]. Fish were fed twice a day with dry food (TetraMin, Tetra GmbH, Германия) and thrice a week with a portion of live food (*Artemia salina* nauplii).

To obtain fertilized eggs, the following scheme of the shoal breeding was used: males and females in a ratio of 2:1 were transferred into the breeding tank; the bottom of the tank was covered with a net frame; the tank was filled with E3 medium in such a way that the water level was 4-5 cm above the frame (the placement of the net frame, as well as low water level, prevents the eggs from being eaten by the parents). The temperature of the water was set at  $28\pm 0,5^{\circ}\text{C}$  ( $2^{\circ}\text{C}$  higher than the one for housing) in order to initiate the maturation of the eggs in females. The spawning takes place in the early morning and lasts for approximately 30 min. After the spawning is finished, the parent flock is transferred back into the aquaria connected to the filtration system; after that, the net frame was pulled out from the breeding tank, the water containing eggs were filtered through mesh net; then, the eggs were washed twice using E3, the unfertilized eggs were separated; the fertilized eggs were then held for one day at a temperature of  $28\pm 0,5^{\circ}\text{C}$  to separate the unfertilized eggs

again; the viability of the eggs was assessed visually using Leica DM2000 light microscope.

## **2.3. Preparation of the working solutions and buffers**

### **2.3.1. Preparation of the solutions of the pharmacologically active substances**

Stock solutions of diazepam and 5F-APINAC were prepared by dissolving a precisely weighted standard substance in ethanol or DMSO of HPLC. Working solutions were made utilizing dilution. The diluent was medium for zebrafish larvae (E3) in order to have a correct ion balance in the working solution. The concentration of the carrier solvent was held at 0.1%. The working solutions were stored in the fridge for longer than one day.

### **2.3.2. Preparation of the working solution of zebrafish embryo medium (E3)**

To maintain the normal functioning and viability of the embryos, they should be kept in a saline solution with well-defined ions concentrations. For this purpose, a series of the E3 medium stock solution was made: the starting 50x E3 solution consisted of 14.6 g of NaCl, 0.63 g of KCl, 2.43 g of CaCl<sub>2</sub>\*2H<sub>2</sub>O, and 4.07 g of MgSO<sub>4</sub>\*7H<sub>2</sub>O per 1 liter of deionized water. After that, the solution is diluted to obtain 1x E3 medium, and 5 l of this solution is spiked with 100 ul of 1% aquatic solution of methylene blue. The stock and working E3 solutions were stored in the fridge for longer than a week.

## **2.4. Concentration ranges for diazepam and 5F-APINAC assessments**

### ***Experimental design***

All of the experiments were conducted in correspondence with the GOST 33774-2016 "Testing of chemicals of an environmental hazard. Fish embryo acute toxicity" and ETS 123 "European convention for the protection of vertebrate animals

used for experimental and other scientific purposes". All of the experiments were approved by the Local Ethical Committee of the Sechenov University.

***Evaluation of the diazepam solutions concentration range***

The doses of exposure concentrations were exponentially increased, starting from 0.8 µg/L to 160 µg/L. A 0.8 µg/L concentration has been reported to be the highest environmental concentration of diazepam, while the maximum dose of 160 µg/L has been shown to cause behavioral effects in 100% of zebrafish larvae [232].

***Evaluation of the 5F-APINAC concentration range (determination of LC<sub>50</sub> of 5F-APINAC)***

To evaluate the concentration range of 5F-APINAC, the investigation of its' half-lethal concentration (LC<sub>50</sub>) was conducted; the concentration range was also dependent on the data about the toxicity of APINAC – defluorinated analog of 5F-APINAC [23, 39, 210].

The assessment was carried out right after the spawning and lasted for 96 h; in the experiment, 40 zebrafish eggs were transferred in the 12-well plates. The use of the double amount of the eggs is explained by the unavailability of determination of fertilized eggs before 6 h post-fertilization. The unfertilized eggs separated, and 20 eggs per concentration were used in the experiment. The experiment was conducted using the following groups: 5 experimental groups that were exposed to 10, 20, 40, 80, and 100 µM solutions of 5F-APINAC in 1% DMSO in E3 medium; the carrier solvent control group – 20 zebrafish eggs in the 1% solution of DMSO in water; positive control group – 4 µg/l solutions of 3,4-dichloroaniline in 1% DMSO in water; negative control group, that were contained in E3 medium. The viability assessment included the fixation of the following parameters: coagulation, the absence of somite formation, the lack of heartbeat, and the absence of tail detachment. If one of the parameters were present, the embryo was considered dead. The observations were made after each 24 h. The calculation of LC<sub>50</sub> was created using the probit model.

## 2.5. Untargeted metabolomic profiling

### *Experimental design*

In this assessment, six days post-fertilization (dpf) larvae were used. The experiment was done in six replicates. In each experiment, 20 embryos were transferred into each well of the 6-well plates, each plate containing 5 ml of E3 medium. The experimental groups were exposed to diazepam solution with a concentration of 160 µg/l for 2.5 h.

The scheme of the experimental design is presented in the Figure 1.

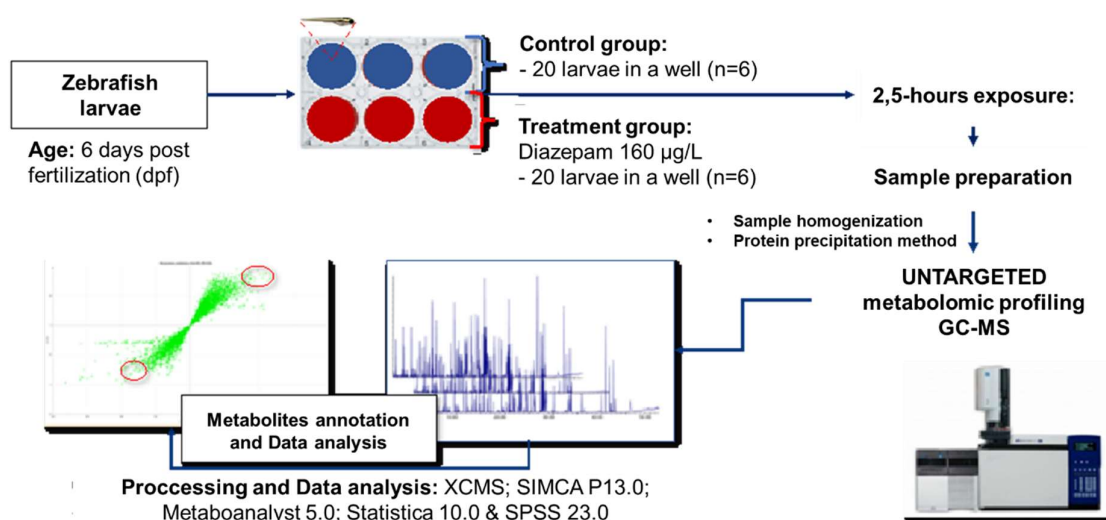


Figure 1 – Design of the experiment of the exposure of diazepam on the zebrafish larvae for untargeted metabolomics

### *Sample preparation*

The following sample preparation method was used: zebrafish larvae were transferred into 1.5 ml microtubes. The aqueous phase was removed, and 10 µL of cold 13 mM aqueous solution of sodium metabisulfite was added to the sample to prevent metabolite oxidation and to euthanize the fish. Then, 10 µL of the internal standard mixture was added, and the samples were vortexed. After, 450 µL of cold methanol was added, vortexed for 20 s. Subsequently, the mixture was sonicated in an ice bath for 15 minutes and centrifuged for 5 minutes at 16.900 rcf at 4°C.



Afterward, 200  $\mu$ L of the supernatant was transferred to a new microtube and evaporated to dryness.

After that, 20  $\mu$ L of 40 mg/ml solution of methoxyamine hydrochloride in pyridine was added, the samples were vortexed and heated for one h at a temperature of 60°C. Then, 70  $\mu$ L of toluene and 30  $\mu$ L of MSTFA were added, the samples were shaken and heated for 50 min at a temperature of 70°C. After cooling down, the samples were transferred into GC vials, and 1  $\mu$ L of the samples were injected into the system.

### ***GC-MS analysis***

The instrumental analysis was performed using an Agilent 7820A (Agilent Technologies, USA) coupled to Agilent 5850 single quadrupole mass spectrometer (Agilent Technologies, USA). The chromatographic separation was achieved using Agilent HP-5MS column; the column parameters were: length – 30 m, internal diameter – 250  $\mu$ m, solid-phase particles size – 0.25  $\mu$ m; chromatographic conditions were: injection in the split mode (1:5), helium as a carrier gas was used at a constant flow rate of 1 ml/min; the interface temperature – 290°C. The oven temperature was ramped from 70°C with 2 min hold to 310°C with 5°C/min. The transfer line temperature was 280°C, and the electron ionization voltage was 70 eV. The identification of metabolites was made using Human Metabolome Database and METLIN Metabolite through NIST mass-spectral library.

### ***Quality control***

Quality control samples (QC) were used to confirm the sample preparation and instrumental analysis validity. The preparation of the QC samples consists of mixing the aliquots of the similar volumes of each zebrafish sample. Sample preparation of the QC is similar to this for a regular sample. Besides that, to exclude carryover and batch effect, the obtained experimental samples were analyzed in a random order, while QC samples were analyzed before, in the middle, and at the end of the GC-MS assessment.

### ***Untargeted data preprocessing***

To complete data preprocessing, the chromatograms were converted into the appropriate format using Proteowizard software (ProteoWizard Software Foundation, CA, USA). These chromatograms were processed with XCMS software (<https://xcmsonline.scripps.edu/>, CIIIA) to obtain a database consisting of the mass fragments of the compounds, their retention time and intensity. The data were checked for the presence of blank cells; if the metabolite had more than 20% of the data missing, it was excluded from further analysis. Deconvolution and smoothing the peaks were made using the following parameters: slope – 2000 l/min, intensity threshold – 20000, mass tolerance – 0.7 Da, retention time delta – 0.2 min. Each feature in the obtained matrix had its specific m/z, retention time, and intensity in each of the samples. The features that presented more than 30% of the relative intensity deviation in the QC samples were also excluded from the analysis. The resulting matrix was converted into an appropriate electronic table for further statistical analysis.

Samples chromatograms were also processed using AMDIS software; this assessment aimed to juxtapose the unknown features with mass-spectral libraries to identify metabolites' names. After identifying the metabolites, features were matched with those obtained from XCMS. Thus, the untargeted dataset containing the names of the metabolites and their intensities in the samples was obtained.

## **2.6. Targeted metabolomic profiling**

### ***Method validation***

The validation of the developed HPLC-MS/MS method was made according to FDA and ICH guidelines on the validation of bioanalytical methods [27, 109, 146]. In the validation process, it was proven that the developed method is capable of measuring the concentrations of target endogenous metabolites of interest. For each of the metabolites, the acceptance criteria were measured. The method's suitability was evaluated using such parameters as selectivity, linearity, calibration curve, lower limit of quantification (LLOQ), carryover, within- and between-run precision and accuracy, extraction coefficient (recovery), matrix effect, and stability.

### ***Experimental designs***

During targeted metabolomics study, the profiles of GABAergic, serotonergic, dopaminergic/adrenergic, cholinergic, aspartic acid systems, kynurenine, indole pathways of tryptophan metabolism were investigated to evaluate the effect of diazepam or 5F-APINAC on these neurotransmitter systems in zebrafish larvae.

### **Short- and long-term exposure to diazepam**

Two independent metabolomics studies were performed on zebrafish (short- and long-term exposure). In the two experiments, zebrafish embryos were transferred into 12-well plates (20 embryos per well, each containing 5 mL E3 medium without methylene blue). Experiment I (2.5 h exposure) was designed to assess the influence of the drug 2.5 h after administration on the sixth dpf (at 11 am). In this experiment, four intervention groups at concentration doses equal to 0.8, 1.6, 16, and 160 µg/L, and a vehicle control group (0.1% ethanol in E3 medium) were used. Experiment II (96 h exposure) was similar to experiment I, the only difference being that diazepam started to be administered from the second until the sixth dpf.

The scheme of the experimental design is presented in the Figure 2.

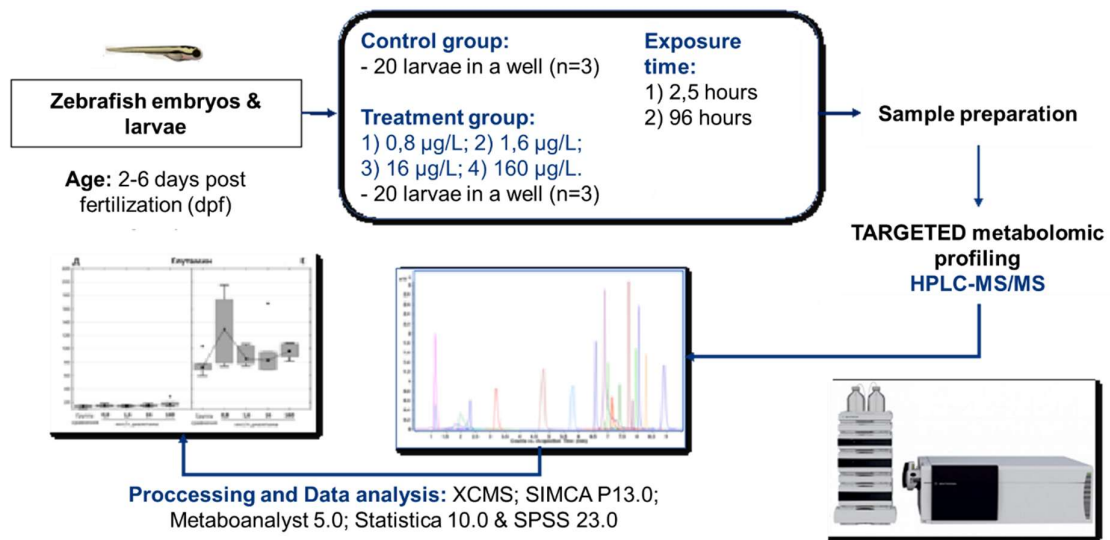


Figure 2 – Design of the experiment of the exposure of diazepam on the zebrafish larvae for targeted metabolomics

## Short- and long-term exposure of 5F-APINAC

Two independent studies were performed on zebrafish larvae/eggs (acute and chronic exposure). In the two experiments, zebrafish embryos were transferred into 12-well plates (20 embryos per well, each containing 5 ml E3 medium without methylene blue). Experiment I (acute exposure) was designed to assess the influence of the drug 4 h after administration on the sixth day postfertilization (dpf) at 11 am. In this experiment, five intervention groups at concentration doses equal to 0.001, 0.01, 0.1, 1.0, and 10  $\mu\text{M}$ , and a vehicle control group (0.1% DMSO in E3 medium) were used. Experiment II (chronic exposure) was similar to experiment I, the only difference being that 5F-APINAC started to be administered from the second until the sixth dpf.

The scheme of the experimental design is presented in the Figure 3.

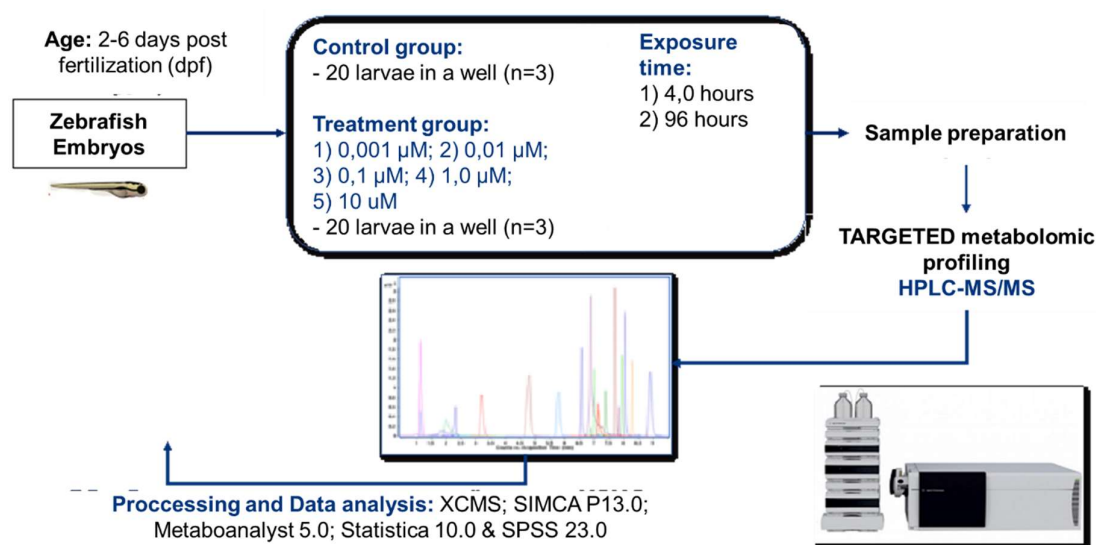


Figure 3 – Design of the experiment of the exposure of 5F-APINAC on the zebrafish larvae for targeted metabolomics

### *Sample preparation*

Larvae were transferred into 1.5 ml microtubes. The aqueous phase was removed, and 10  $\mu\text{l}$  of 13 mM cold aqueous solution of sodium metabisulfite was added to the sample to prevent metabolite oxidation. Then, 10  $\mu\text{l}$  of the internal standard solution were added, and the sample was vortexed for 10 s. Next, 450  $\mu\text{l}$  of

cold methanol was added, vortexed for 20 s. Then the mixture was sonicated in an ice bath for 15 min and centrifuged for 5 min at 16.900\*g at 4 °C. Subsequently, 200 µl of the supernatant were transferred to a new microtube and evaporated to dryness. The dried sample was reconstituted in 50 µl of 0.02% solution of ascorbic acid in 1:1 (v/v) water:methanol mixture and 2 µl of the solution were injected into the UPLC-MS/MS system.

### *HPLC-MS/MS analysis*

Chromatographic separation was conducted using the Agilent 1290 Infinity II UPLC system coupled to the Agilent 6470 Triple Quad tandem mass spectrometer equipped with an electrospray ionization source (Agilent Technologies, Santa Clara, CA, USA). The liquid chromatograph was equipped with a Discovery HS F5-3 PFP column (150 mm × 2.1 mm × 3 µm) (Supelco, Inc., Darmstadt, Germany). The column oven temperature was set at 45 °C. Gradient elution was used (eluent solution A - 0.1% formic acid in water, eluent solution B - 0.1% formic acid in acetonitrile), as described in Table 2.

Table 2 – HPLC gradient conditions

Time, min	Flow, ml/min	% mobile phase	
		A	B
0	0,4	90	10
4	0,4	90	10
9	0,4	10	90
10	0,4	10	90
10,10	0,4	90	10
12	0,4	90	10

Metabolite determination was performed in positive ionization mode with multiple reaction monitoring (MRM). Mass-spectrometer parameters were: capillary voltage – 1.5 kV, source temperature - 150 °C, evaporation gas – nitrogen, gas temperature – 300 °C, gas flow – 3 l/min. MRM parameters and retention times for all metabolites were optimized separately.

## 2.7. Behavioral studies

### *Experimental design*

Zebrafish larvae were exposed to a wide range of 5F-APINAC concentrations (0.001-10  $\mu\text{M}$ ). The control group was exposed to the carrier solvent (0.1% DMSO in E3). Zebrafish larvae at the age of 5 dpf were set into the wells of 96-well plate (1 larva per well). The exposure began at the sixth dpf at 11 am [197].

The locomotor activity of zebrafish was registered for full two days (48 h). This assessment allows investigating the acute response to 5F-APINAC and the long-term exposure on the locomotor activity of zebrafish larvae. The activity was recorded at a frame rate of 25 fps under a constant infrared light using the high-throughput video tracking system DanioVision (Noldus, Netherlands). The activity of each fish was calculated as the total distance traveled by a fish for 10 min. The scheme of the experimental design is presented in the Figure 4.

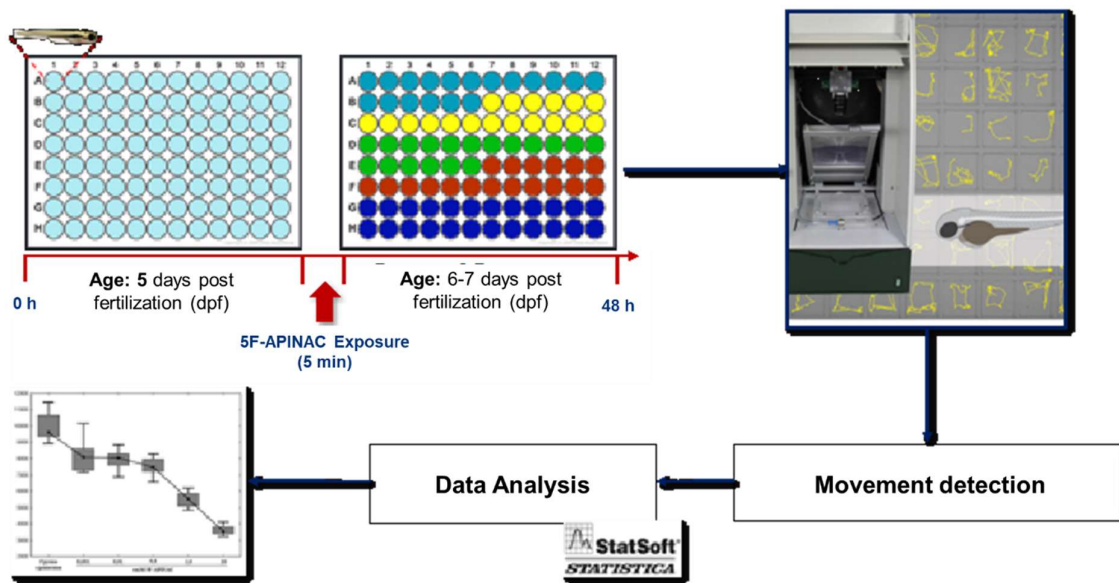


Figure 4 – Design of the experiment of the exposure of 5F-APINAC on the zebrafish larvae for behavioral studies

## 2.8. Statistical analysis

### *Statistical analysis of the data from the behavioral study, correlation search and LC<sub>50</sub> determination*

Statistical analysis of the behavioral data was conducted using a one-way ANOVA with Tukey posthoc assessment. The correlation coefficients between behavioral and metabolomics data were calculated using nonparametric Spearman's ranking. The analyses were carried out using Statistica 10.0 software (Statsoft, USA). LC<sub>50</sub> was calculated with the probit method regression model. This analysis was carried out using SPSS 23.0 (SPSS Inc., USA).

### *Untargeted metabolomics profiling*

The data obtained from the untargeted profiling was log-normalized, mean-centered, and Pareto scaled. Then, it was uploaded into the SIMCA-P 13.0 (Umetrics, Sweden) for further search for significant metabolites. Variance importance in the projection (VIP, VIP-score) represents the value of the feature in the discriminant analysis as a correlation factor. This analysis coupled with S-plot helps to evaluate the most significant metabolites in the dataset. Features with a VIP score of more than one were considered to have discriminative power across groups.

To evaluate the trending of concentrations between the two groups and also to exclude the outliers, principal component analysis was made. Further, orthogonal projection to latent structures-discriminant analysis was made to evaluate the features with the most statistical potency, and an S-plot was made using these metabolites. For the potentially significant features, depending on the normality of the data, the Student t-test or Mann-Whitney U-test were made.

After that, the Metaboanalyst 4.0 online platform was used to obtain the data about the metabolic pathway enrichment analysis. This analysis allows us to identify the metabolic pathways most affected by the substance exposure to form a targeted metabolomic panel of metabolites.

### *Targeted pharmacometabolomic profiling*

Data were inspected to detect extreme values. Extreme values were defined as concentrations higher than the 75th percentile +3 interquartile ranges (IQR).

These values were replaced by the corresponding concentrations for the 75<sup>th</sup> percentile +1.5 IQR (winsorization). The normality of the data was evaluated using the Shapiro-Wilk test. Most of the data was non-normally distributed. The nonparametric Kruskal-Wallis one-way ANOVA test was used to compare central tendencies among groups exposed to different diazepam and 5F-APINAC concentrations, followed by Dunn's post hoc correction. Statistical analyses were performed using the STATISTICA software version 10.0 (data analysis software system, Tulsa, Okla, USA).

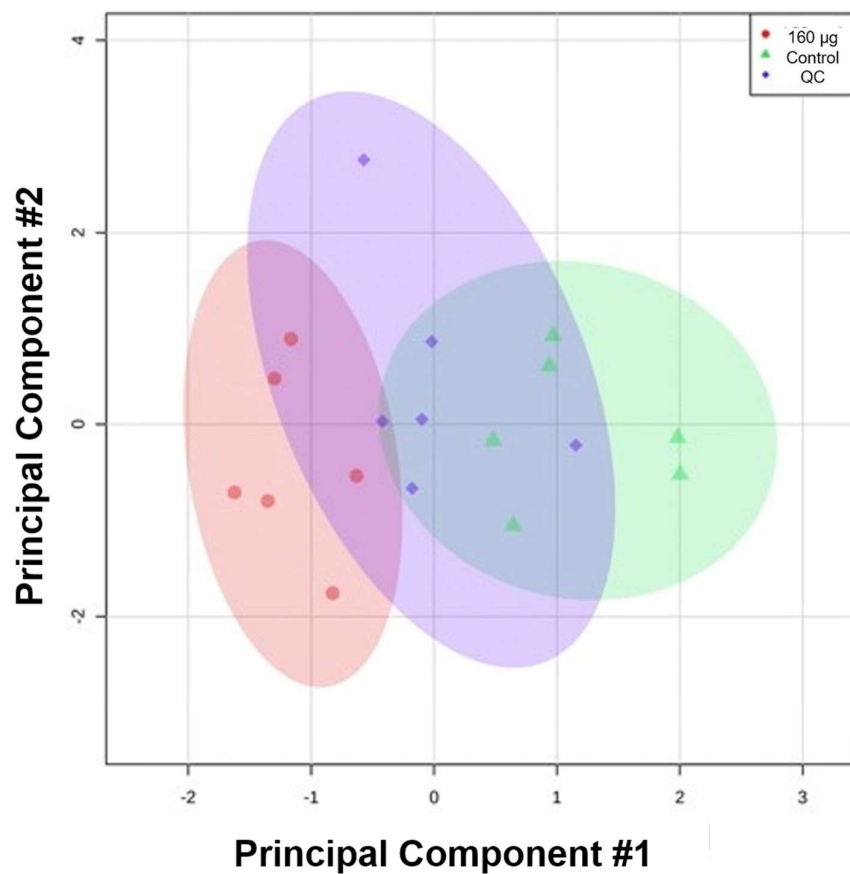


### 3. Results

#### 3.1. Untargeted metabolomics profiling of zebrafish larvae after diazepam exposure

GC-MS untargeted metabolomics profiling was made to identify the panel of endogenous metabolites necessary to investigate the pharmacological effects of physiologically active drugs of neurotropic action using *Danio rerio* as a model organism. To conduct the untargeted profiling, zebrafish exposed to 160 ug/L of diazepam and a control group were used. One thousand three hundred fifty-six features were identified during the untargeted approach. Principal component analysis (PCA) and orthogonal projections to latent structures-discriminant analysis (OPLS-DA) were used to detect significant metabolites.

PCA showed that there were metabolites significantly changed in the exposure group versus the control group (Figure 5A). According to OPLS-DA data (Figure 5B), the explained variation ( $R^2$ ) was 0.91 what indicates that there are components capable of discriminating the groups in the model. The test-model variability ( $Q^2$ ) was 0.63, which tells about the high predictive power of the model. Generally, the analyses showed good discrimination of the groups, which means suitable method reproducibility.

(A) **Principal Component Analysis (PCA)****Orthogonal Projections to Latent Structures  
Discriminant Analysis (OPLS-DA)**

(B)

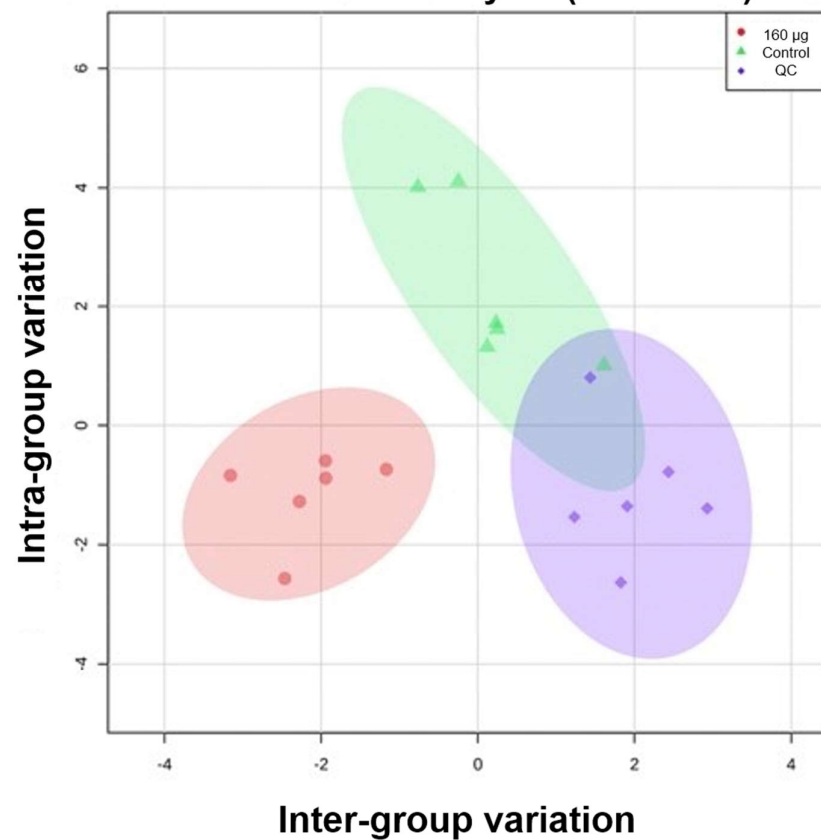


Figure 5 – Principal component analysis of the investigated groups (A). Orthogonal projections to latent structures-discriminant analysis (B).

S-plot had shown statistically significant metabolites that could be used to discriminate between exposure and control groups (Figure 6).

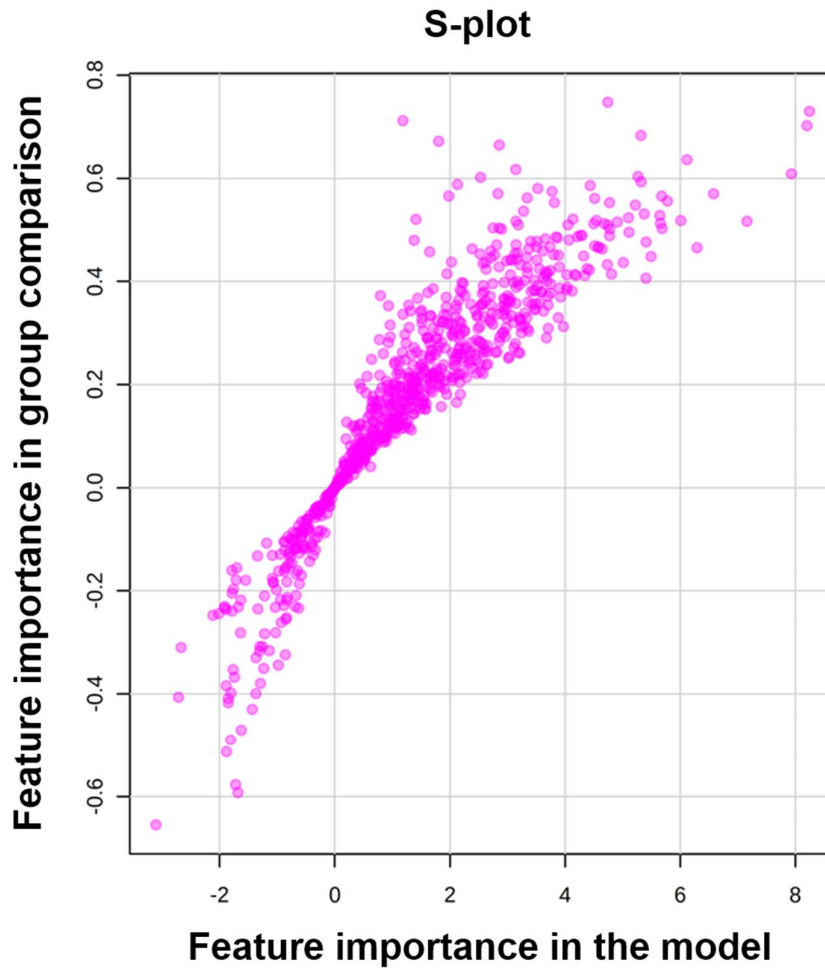


Figure 6 – S-plot, based on the OPLS-DA model from untargeted metabolomic data.

Based on the acquired data, statistically significant metabolites were identified. Twenty-five metabolic pathways associated with diazepam exposure were identified (Figure 7).

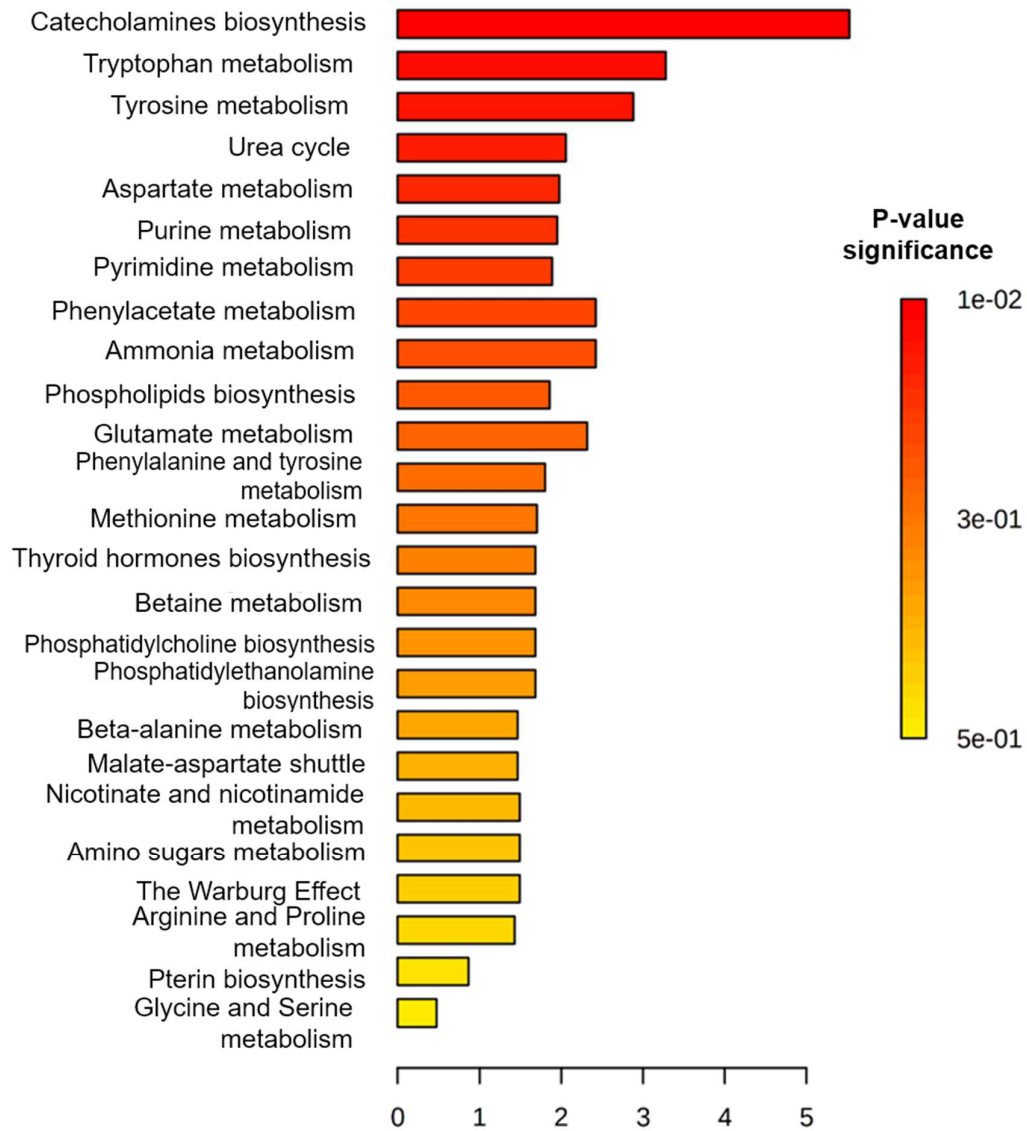


Figure 7 – Metabolomic set enrichment analysis.

The acquired data had shown that diazepam exposure led to alterations in the catecholamine biosynthesis, tryptophan metabolism, and tyrosine metabolism biochemical pathways (Table 3). Based on the results, it can be postulated that diazepam exposure led to the alterations in the concentrations of metabolites related to neurotransmission.

Table 3 – Metabolic pathways associated with the diazepam action on the zebrafish larvae

Metabolic pathway	<i>p</i> -value*	Metabolites	Direction
Catecholamine biosynthesis	0,013	Dopamine	↓
		Norepinephrine	↑
		Tyrosine	↑
		L-DOPA	↓
Tryptophan metabolism	0,081	Tryptophan	↑
		Serotonin	↑
		Kynurenine	↓
Tyrosine metabolism	0,097	Tyrosine	↑
		Homogentisic acid	
		L-aspartic acid	
Urea cycle	0,202	Arginine	↑
		Citrulline	
Aspartate metabolism	0,217	L-Aspartic acid	↑
		L-glutamic acid	↑
Purine metabolism	0,235	Guanine	↓
		Inosine	
Pyrimidine metabolism	0,246	Uridine	↓
		Citidine	
Phenylacetate metabolism	0,251	Phenylacetic acid	↓
		L-glutamic acid	↑
Ammonia metabolism	0,269	L-serine	↑
		L-aspartic acid	
		Oxoglutaric acid	↑
		Glycine	↓
Phospholipid biosynthesis	0,272	Palmitic acid	↑
Glutamate metabolism	0,273	GABA	↓
		L-cysteine	↑
		L-Aspartic acid	↑
Phenylalanine and tyrosine metabolism	0,280	Tyrosine	↑
		Phenylalanine	
		Oxoglutaric acid	
Methionine metabolism	0,281	L-methionine	↓
Thyroid hormones synthesis	0,296	Tyrosine	↑
Betaine metabolism	0,306	Adenosine	↑
		L-methionine	↓
Phosphatidylcholine biosynthesis	0,315	Cytidine	↓
		Ethanolamine	↑
Phosphatidylethanolamine biosynthesis	0,315	Cytidine	↓
		Ethanolamine	↑
Beta-alanine metabolism	0,324	Alanine	↑
Malate-aspartate shuttle	0,335	Malic acid	

Metabolic pathway	<i>p</i> -value*	Metabolites	Direction
		Aspartic acid	↓
Nicotine and nicotinamide metabolism	0,384	L-glutamic acid	↑
		Nicotinamide	
Amino sugars metabolism	0,421	D-fructose	↓
Warburg effect	0,457	Succinic acid	↑
Arginine and proline metabolism	0,469	Arginine	↑
Pterin biosynthesis	0,478	Neopterin	↑
Glycine and serine metabolism	0,512	Glycine	↓

\* *P*-values represent the strength of the metabolite's contributions into the pathway. *P*-values were calculated based on the number of metabolites that are engaged in the certain pathway.

Thus, to investigate the pharmacological effects of the neurotropic drugs, based on the untargeted metabolomics profile, the targeted metabolic panel was made. The panel included the metabolites of the dopaminergic/adrenergic system and serotonergic system. Also, the metabolites of the main neurotransmission systems (GABAergic, cholinergic, aspartic acid) were included in the study [140]. Also, the metabolites of the concomitant pathways were included in the study. Such pathways were: kynurenine pathway, which is the primary biochemical pathway of tryptophan catabolism [265]; indole (microbiota) pathway of tryptophan conversion through microbial reactions [144]; biopterin and neopterin, which are the metabolites of cofactors of the enzymes related to monoamines synthesis [138]; cortisol as one of the principal stress biomarkers [292].

### **3.2. Development and validation of the targeted HPLC-MS/MS method for the determination of the neurotransmitters and their metabolites in zebrafish larvae**

During the validation process, the applicability of the developed method was proven. The results of the method validation are represented below.

#### **3.2.1. Mass-spectrometry parameters and selectivity**

By analyzing the mass-spectrometry data of the individual solutions of the studied compounds and internal standards, MS/MS parameters of the compounds

were optimized. The parameters of ionization, the retention time were also optimized. The results are shown in Tables 4 and 5.

Table 4 – HPLC-MS/MS MRM parameters for targeted metabolites

Metabolite	Precursor ion ( <i>m/z</i> )	Product ion ( <i>m/z</i> )	Fragmentor (V)	Collision energy (V)	Retention time (min)	Polarity
GABA	104	87	90	10	1,2	Positive
		69	90	15		
5-hydroxytryptophan	221	162	90	20	3,8	Positive
		160	90	20		
Acetylcholine	146	87	90	15	3,8	Positive
		60	90	10		
		43	90	30		
Anthranilic acid	138	120,1	95	10	6,2	Positive
		92	95	20		
Asparagine	133	87	100	10	1,0	Positive
		74	100	20		
Aspartic acid	134	88	100	10	1,0	Positive
		74	100	15		
Biopterin	238	194	90	20	1,9	Positive
		178	90	20		
Choline	104	60	90	20	1,2	Positive
Citrulline	176	113,1	90	20	1,1	Positive
		70,1	90	30		
Cortisol	363	327	120	10	7,3	Positive
		121	120	20	7,3	
Dopamine	154	91	90	30	1,7	Positive
		137	90	10		
	137	91	90	10		



Metabolite	Precursor ion ( <i>m/z</i> )	Product ion ( <i>m/z</i> )	Fragmentor (V)	Collusion energy (V)	Retention time (min)	Polarity
Epinephrine	184	166	90	5	1,9	Positive
		151	90	25		
	166	151	110	20		
Glutamic acid	148	84	100	15	1,0	Positive
		56	100	30		
Glutamine	147	130	100	10	2,0	Positive
		84	100	15		
5-hydroxyindole acetic acid	192	146	100	20	5,9	Positive
Indole-3-acetic acid	176	130	95	20	7,1	Positive
Indole-3-acrylic acid	188	170	100	20	7,4	Positive
		115	100	25		
Indole-3-butyric acid	204	144	100	25	7,7	Positive
		130	100	25		
Indole-3-carboxaldehyde	146	118	95	15	7,2	Positive
		91	95	30		
Indole-3-lactic acid	206	118	95	22	6,8	Positive
Indole-3-propionic acid	190	130	95	20	7,5	Positive
Kynurenic acid	190	144	95	20	7,8	Positive
Kynurenine	209	146	95	30	3,3	Positive
		94	95	10		
L-DOPA	198	181	100	10	1,9	Positive
		152	100	10		
Metanephrine	198	180	90	5	3,5	Positive
		165	90	20		
		148	90	25		

Metabolite	Precursor ion ( <i>m/z</i> )	Product ion ( <i>m/z</i> )	Fragmentor (V)	Collision energy (V)	Retention time (min)	Polarity
Neopterin	254	206,1	100	20	1,3	Positive
		190,1	100	20		
Picolinic acid	124	78,1	90	20	1,7	Positive
		53,1	90	20		
Norepinephrine	170	152	90	5	1,4	Positive
	152	107	110	20		
Normetanephrine	166	134	100	15	2,3	Positive
Phenylalanine	166	120	100	15	3,8	Positive
Quinolinic acid	168	106,1	95	15	3,2	Positive
		78,1	95	30		
Serotonin	160	132	120	20	3,5	Positive
		105	120	30		
Tryptamine	161	144,1	95	10	6,3	Positive
		115,1	95	30		
Tryptophan	205	188	100	10	5,2	Negative
		146	100	20		
Tyrosine	182	165	90	5	2,5	Positive
		136	90	10		
Xanthurenic acid	206	160	95	20	7,6	Positive
		132,1	95	30		

Table 5 – HPLC-MS/MS MRM parameters for internal standards

Standard	Precursor ion ( <i>m/z</i> )	Product ion ( <i>m/z</i> )	Fragmentor (V)	Collision energy (V)	Retention time (min)	Polarity	Concentration in the sample (ng/ml)
GABA-d6	110	93	90	10	1,2	Positive	200
		73	90	15			
Dopamine-d4	158	123	90	10	1,7	Positive	20
		95	90	30			
5-hydroxyindole acetic acid-d5	197	150	100	20	5,9	Positive	20
Indole-3-acetic acid-d4	180,1	133	95	20	7,1	Positive	20
Indole-3-butyric acid-d4	208	132	100	25	7,7	Positive	200
Indole-3-carboxaldehyde- <sup>13</sup> C8	154	126	95	30	7,2	Positive	20
		98	95	30			
Indole-3-lactic acid-d5	211	122	95	22	6,8	Positive	200
Indole-3-propionic acid-d2	192	130	95	20	7,5	Positive	200
Kynurenic acid-d5	195	149	95	30	7,8	Positive	20
Kynurenine-d4	213	98	95	10	3,3	Positive	200
Tryptophan-d5	208	164	100	15	5,2	Negative	20000
		120	100	15			
Normetanephrine-d3	187	137	100	15	2,3	Positive	20
Quinolinic acid-d3	171	109	95	15	3,2	Positive	200

Standard	Precursor ion ( <i>m/z</i> )	Product ion ( <i>m/z</i> )	Fragmentor (V)	Collision energy (V)	Retention time (min)	Polarity	Concentration in the sample (ng/ml)
		81	95	30			
Serotonin-d4	181	164	90	7	3,5	Positive	200
		136	120	20			
Xanthurenic acid-d4	210	164	95	20	7,6	Positive	20
		136	95	30			
Neopterin- <sup>13</sup> C5	259,1	211	100	20	1,3	Positive	20
Cortisol-d4	367	331	120	10	7,3	Positive	20

The selectivity of the developed method was assessed by analyzing the interference strength in the blank samples compared to quality control (QC) samples. Six blank samples were used (blanks were 5% solution of bovine serum albumin in 0.9% NaCl).

The method's selectivity was acceptable when the investigated blank samples have not had the peaks that interfere with the retention time of the peaks corresponding to the targeted metabolites. The selectivity was fine if the level of interference in the blank sample was less than 20% of the LLOQ.

For all of the investigated analytes, the selectivity assay was acceptable. The chromatograms of the blank samples, QC chromatograms, and internal standard chromatograms are represented in Figure 8.

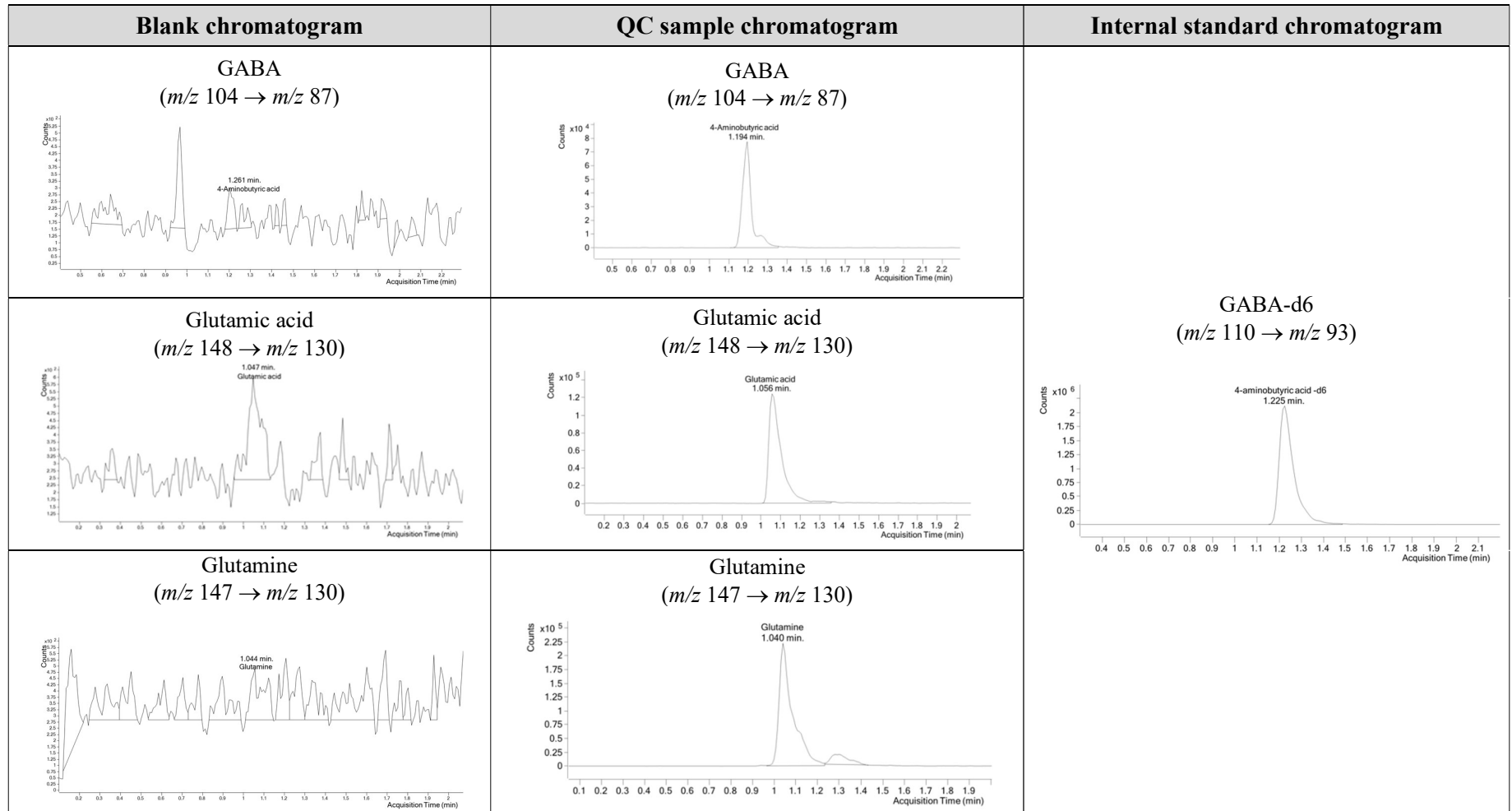


Figure 8 – Mass-chromatograms of the blank samples, QC samples, and internal standards

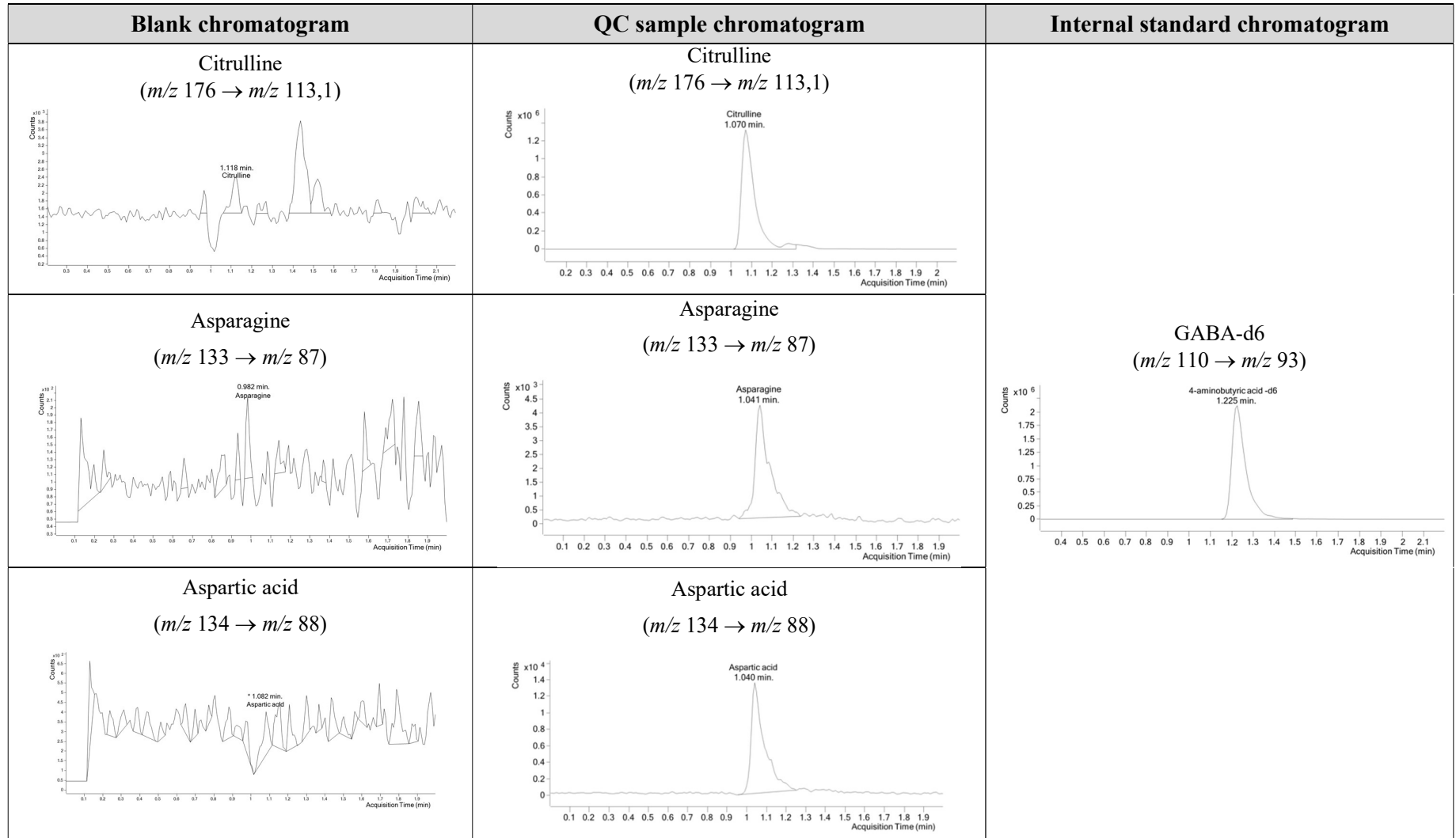


Figure 8 – Mass-chromatograms of the blank samples, QC samples, and internal standards (cont.)

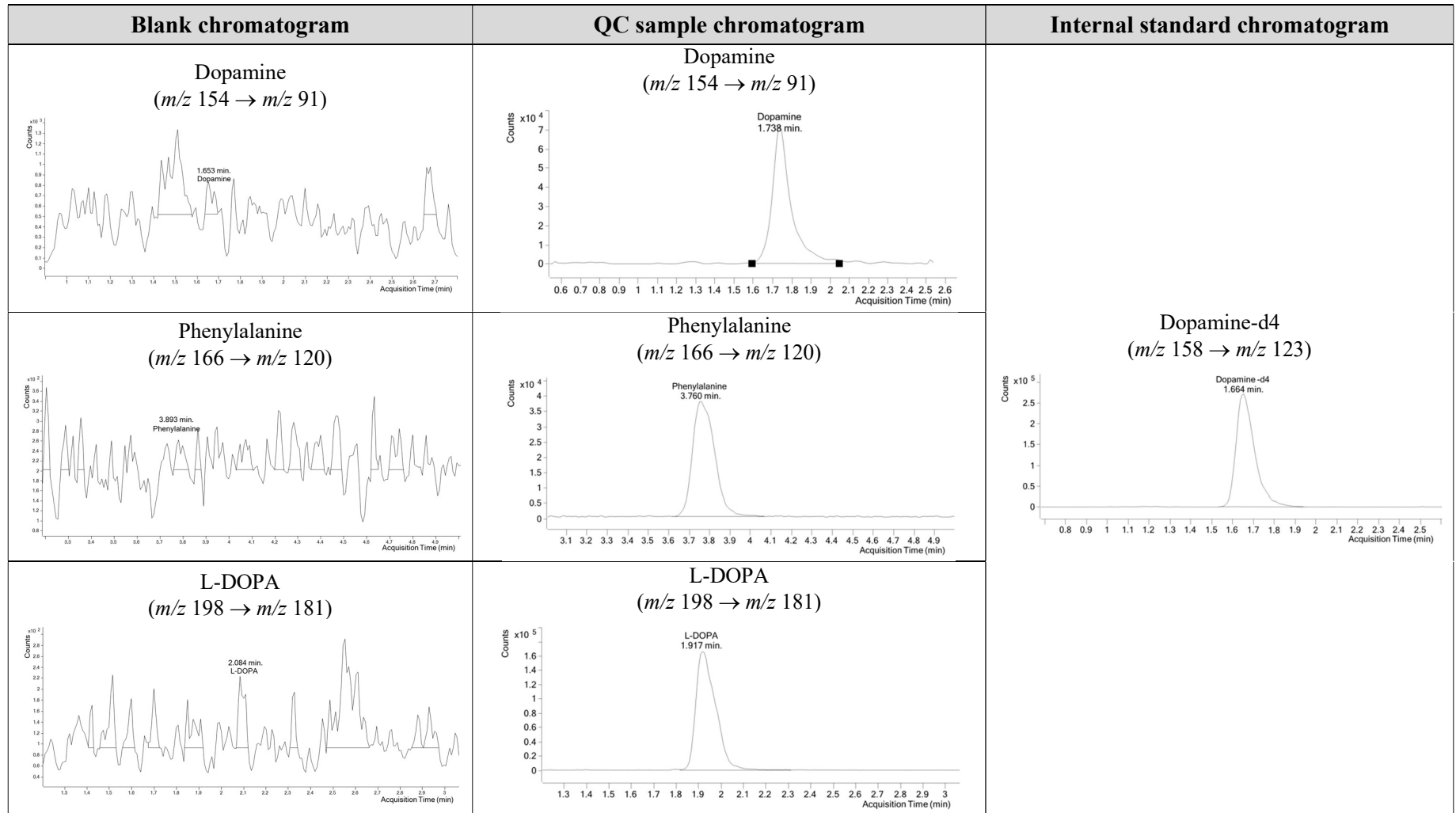


Figure 8 – Mass-chromatograms of the blank samples, QC samples, and internal standards (cont.)



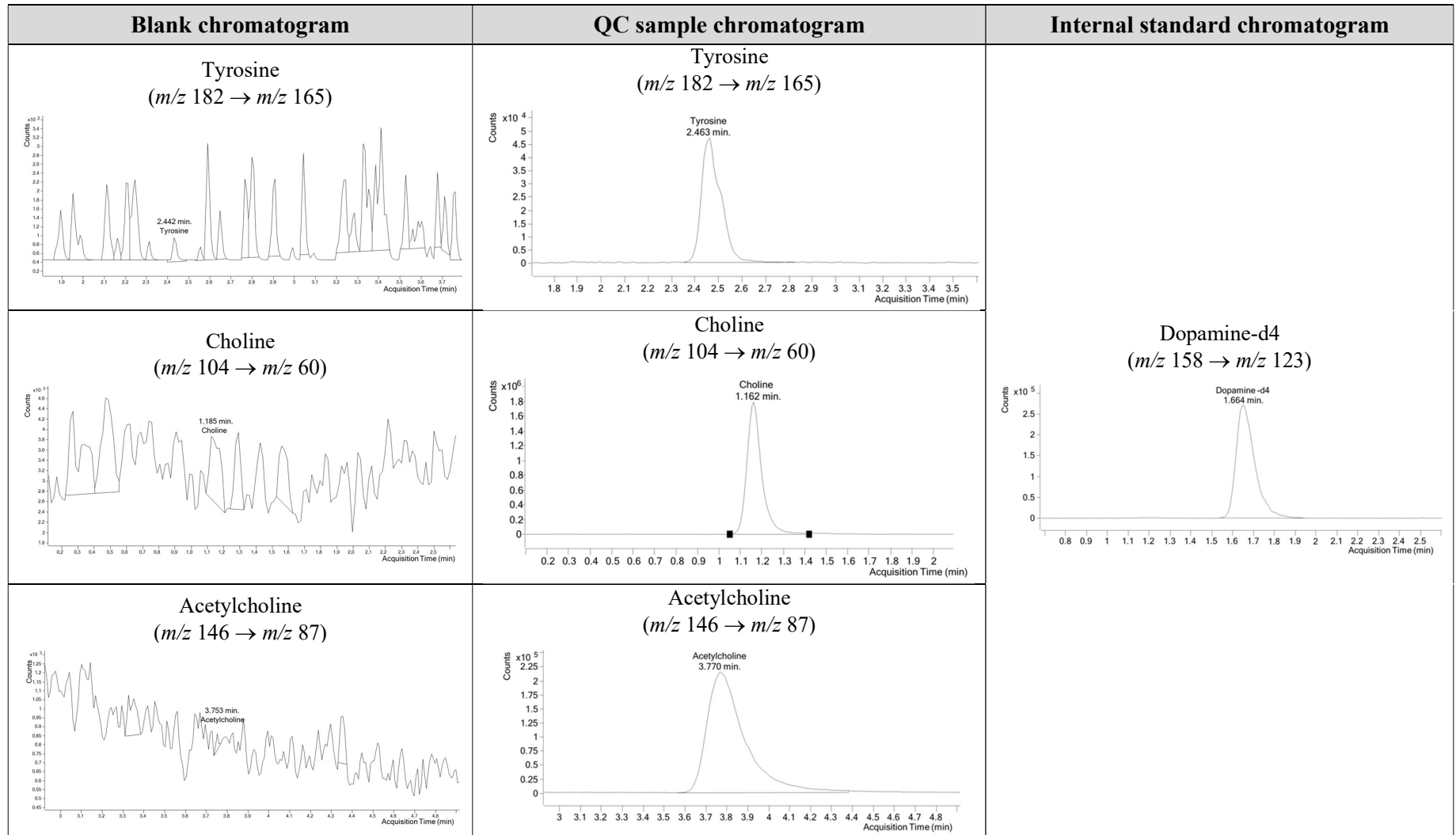


Figure 8 – Mass-chromatograms of the blank samples, QC samples, and internal standards (cont.)

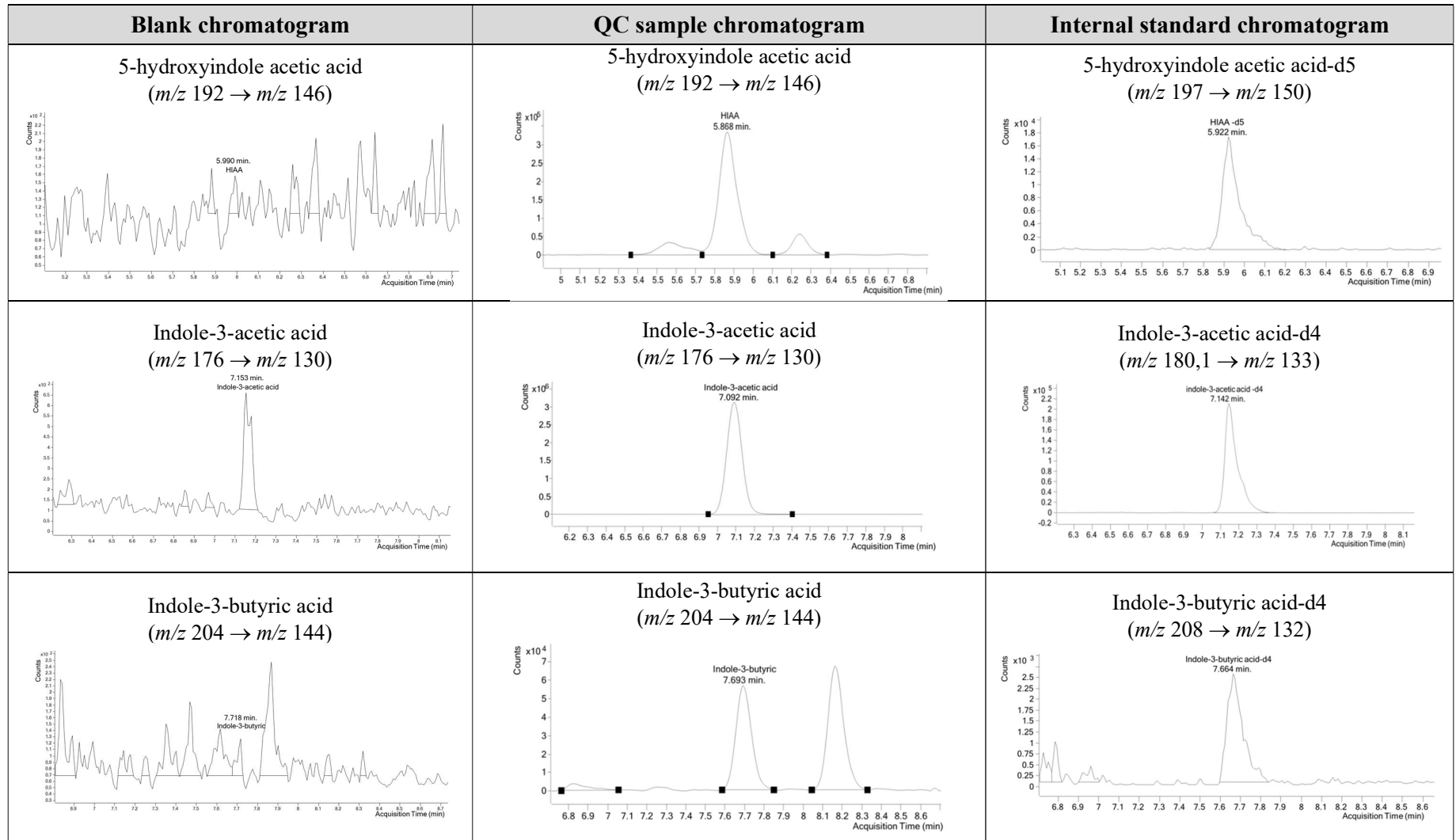


Figure 8 – Mass-chromatograms of the blank samples, QC samples, and internal standards (cont.)

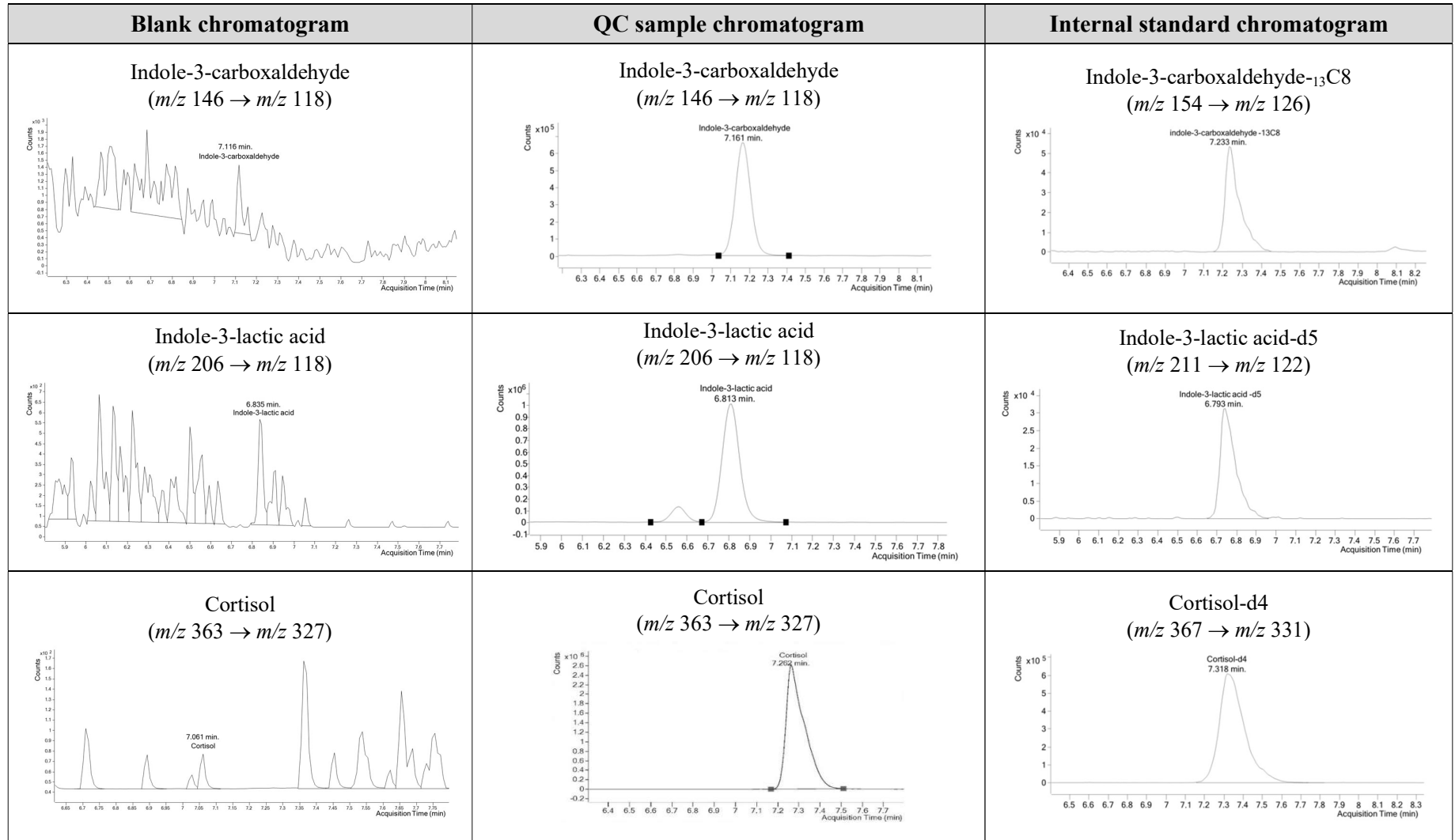


Figure 8 – Mass-chromatograms of the blank samples, QC samples, and internal standards (cont.)

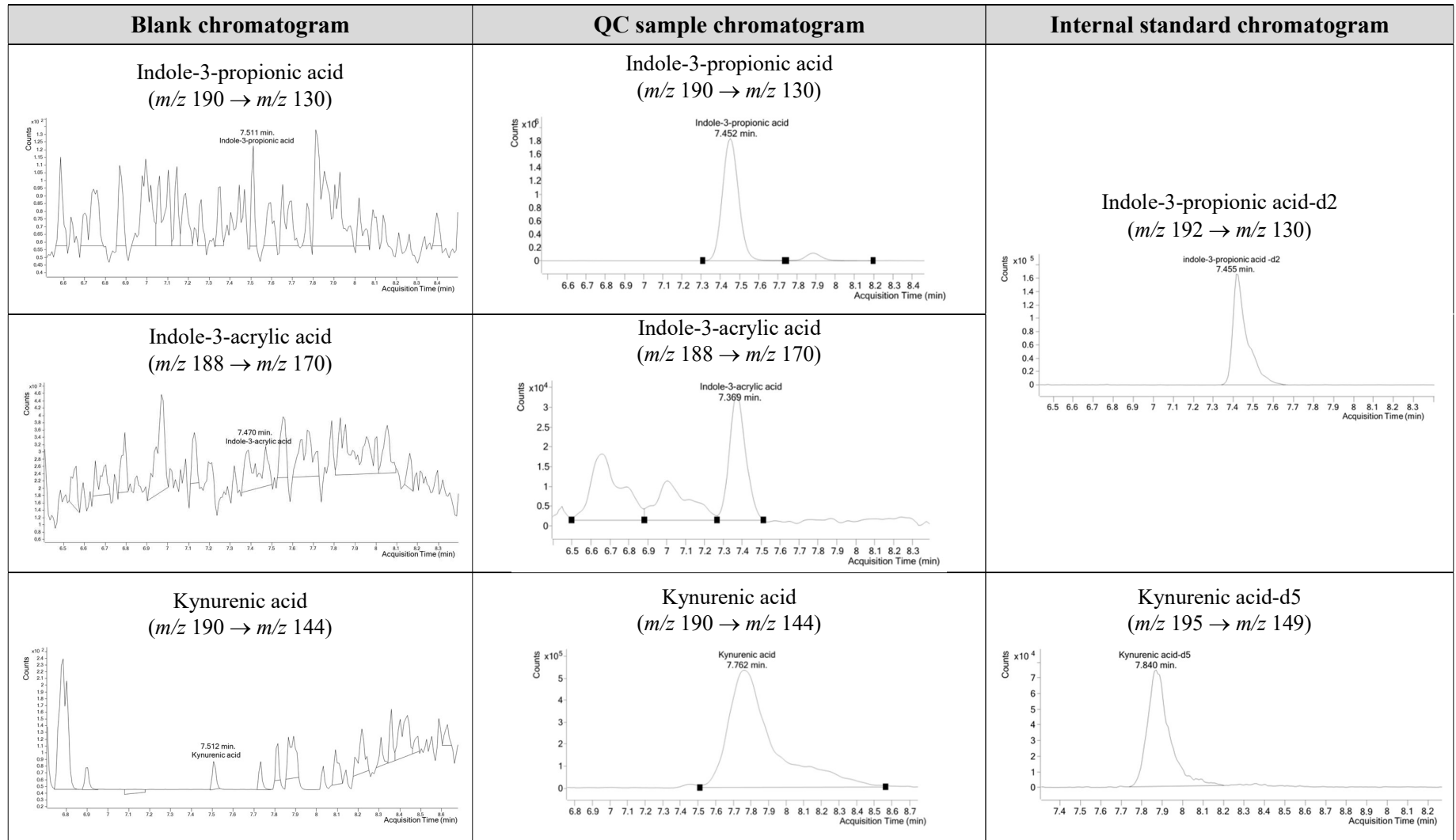


Figure 8 – Mass-chromatograms of the blank samples, QC samples, and internal standards (cont.)

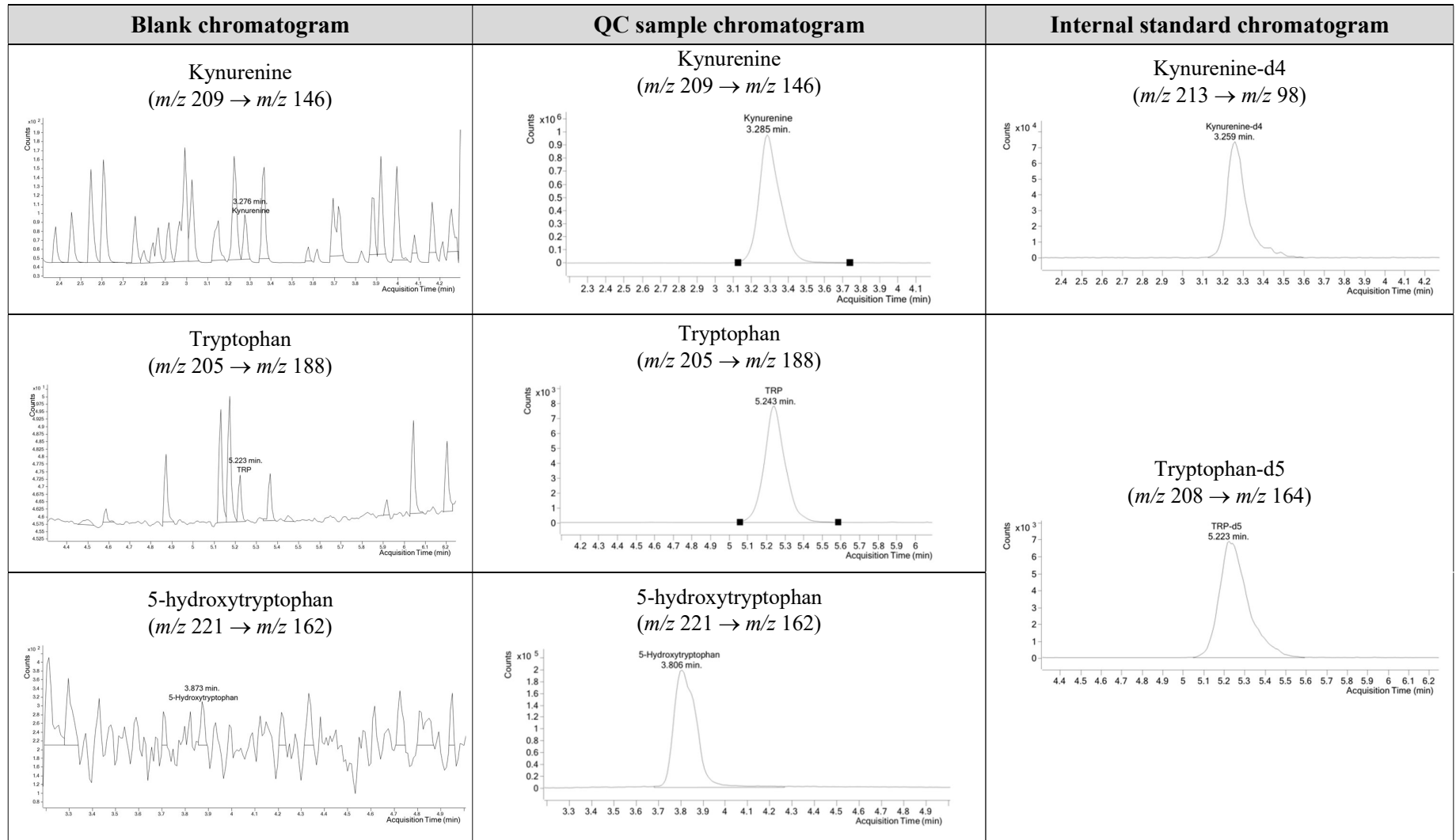


Figure 8 – Mass-chromatograms of the blank samples, QC samples, and internal standards (cont.)

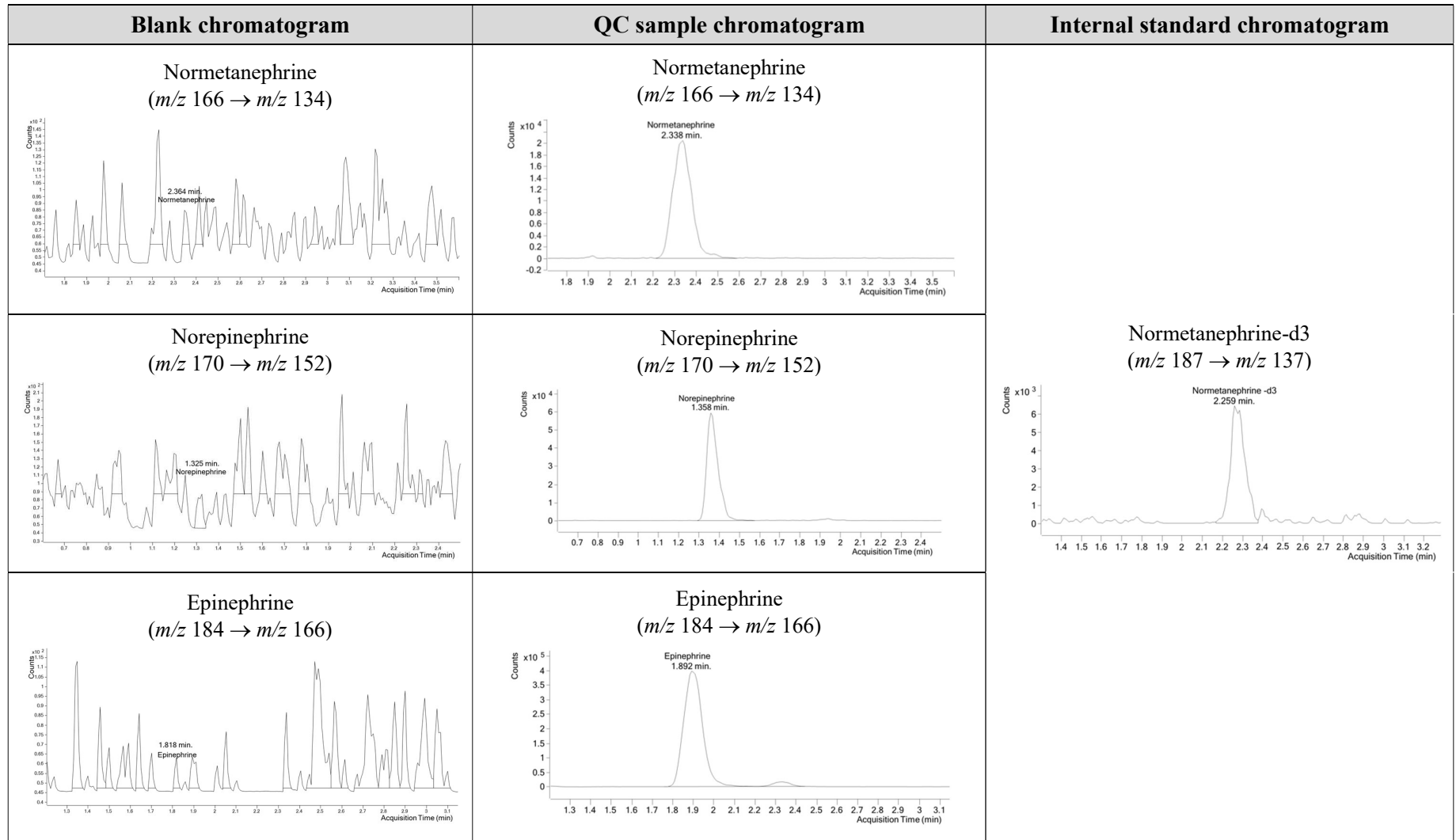


Figure 8 – Mass-chromatograms of the blank samples, QC samples, and internal standards (cont.)

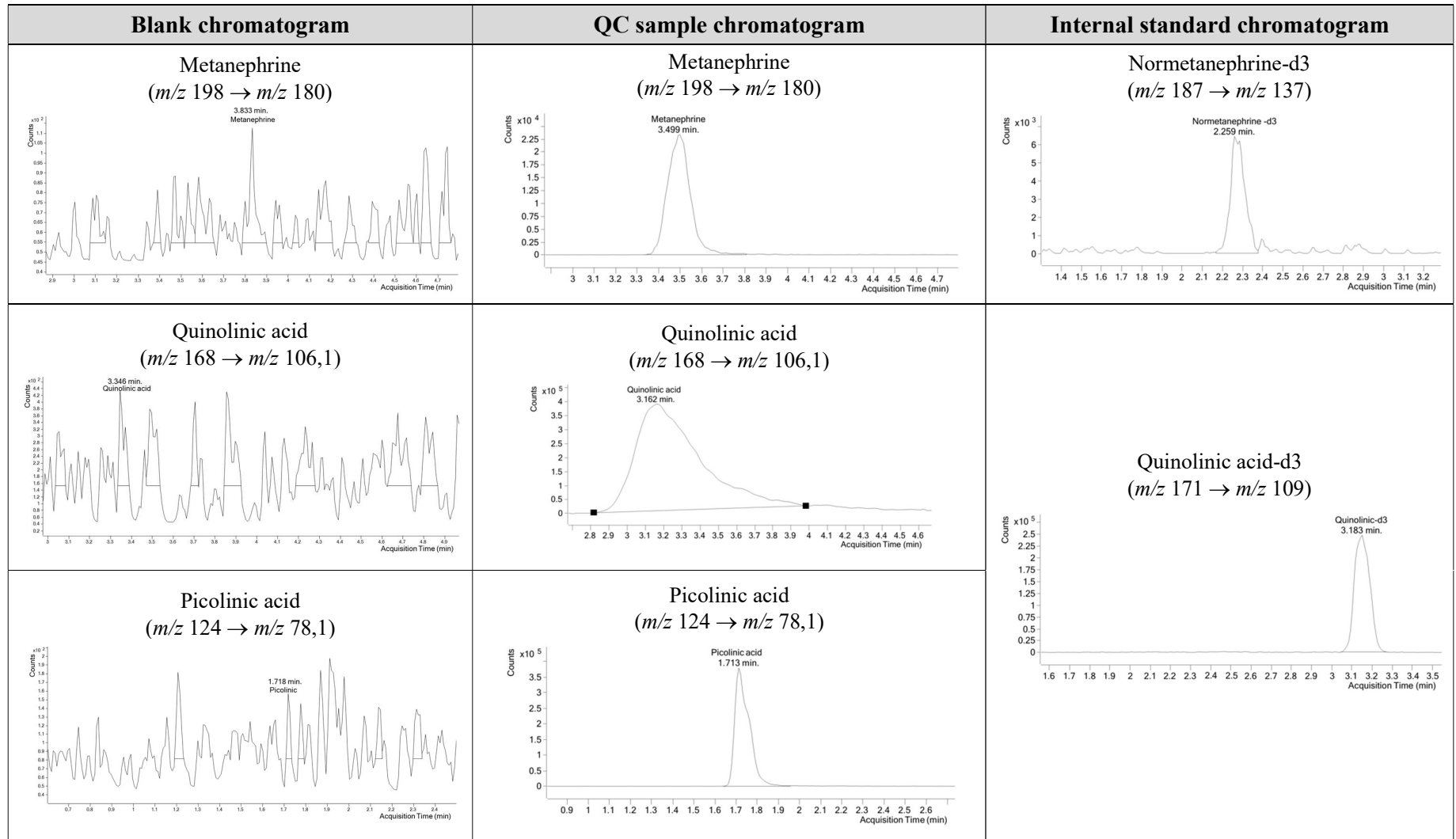


Figure 8 – Mass-chromatograms of the blank samples, QC samples, and internal standards (cont.)

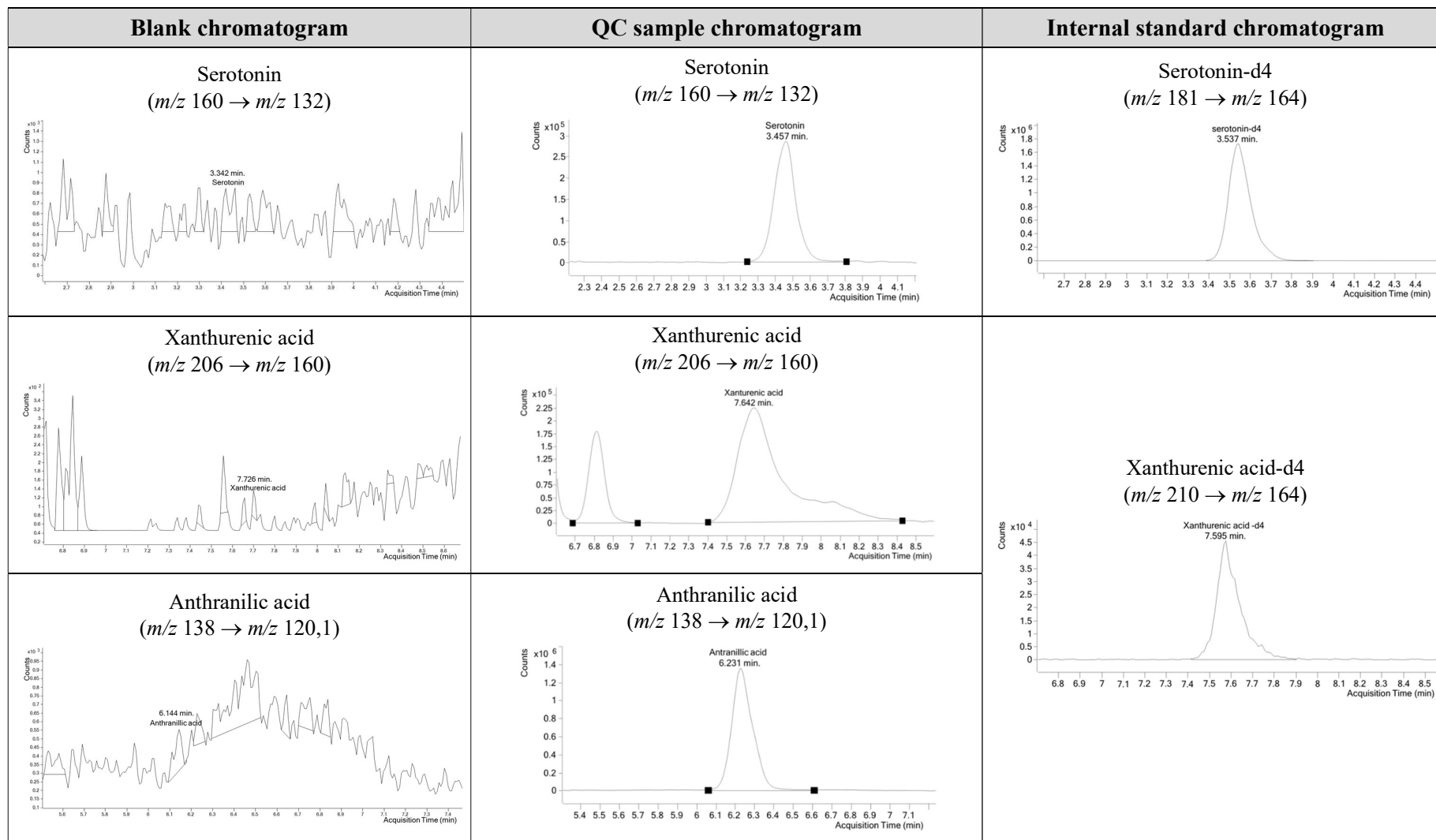


Figure 8 – Mass-chromatograms of the blank samples, QC samples, and internal standards (cont.)



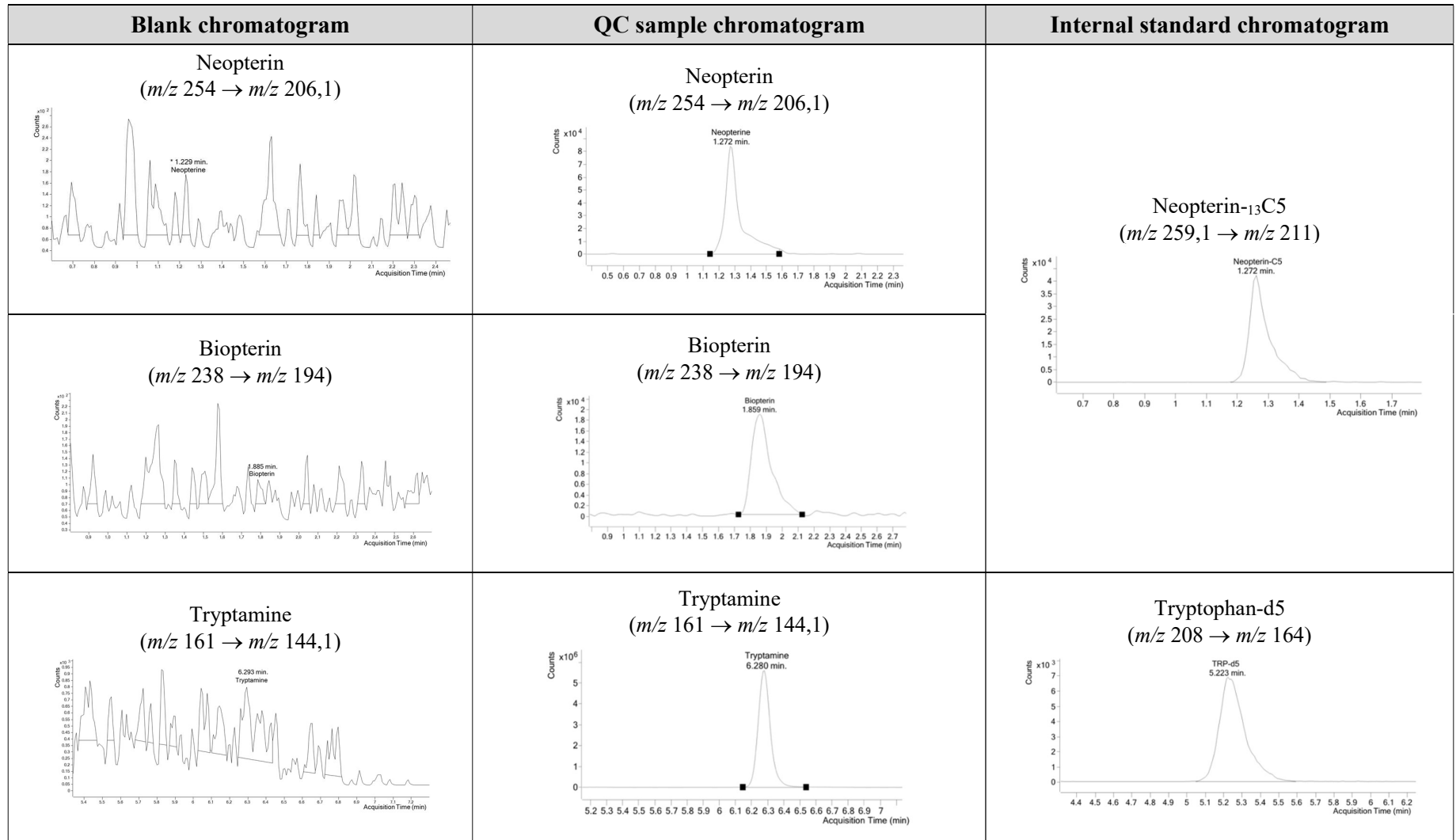


Figure 8 – Mass-chromatograms of the blank samples, QC samples, and internal standards (cont.)

### 3.2.2. Calibration curve and lowest limit of quantification

To investigate the dependence between the concentrations of the metabolites in the samples, calibration curves were made. The calibrators were made using blank samples that were previously spiked with the known concentrations of the analytes.

Calibration curves were made using six calibration levels, and each was analyzed in three replicates. Weighted linear regression models were used for the building of the calibration curves. The slope, intercept, and determination coefficient (R<sup>2</sup>) were calculated for each analyte. The calibration curve acceptance criterion was: R<sup>2</sup> coefficient was >0.97.

Also, LLOQ was quantified in this assessment. LLOQ was defined as the concentration of the analyte that can be determined with high accuracy and precision; the analyte's signal in the assessment was more than five times higher than this in the blank sample. The calibration curve parameters are represented in Table 6.

Table 6 – Calibration curve characteristics for endogenous metabolites

Metabolite	Linear range	Slope	Intercept	Determination coefficient (r <sup>2</sup> )
Tryptophan	10-1000 ug/ml	0,8531	-2,3589	0,9961
Kynurenine	10-50000 ng/ml	0,4001	-0,1024	0,9998
Choline	1-100 ug/ml	0,5206	0,1729	0,9936
Serotonin	1-25000 ng/ml	0,0990	-0,0052	0,9998
Quinolinic acid	1-1000 ng/ml	0,054	-0,0033	0,9999
Indole-3-propionic acid	1-1000 ng/ml	0,068	-0,0020	0,9996
Indole-3-lactic acid	10-10000 ng/ml	0,2631	-0,027	0,9954
Indole-3-acetic acid	10-1000 ng/ml	0,1058	0,0039	0,9991
Xanthurenic acid	0,2-2000 ng/ml	10,415	-0,1453	0,9995
Tryptamine	0,02-200 ng/ml	2,118	0,0105	0,9980
Biopterin	0,2-200 ng/ml	0,0073	-0,0002	0,9953
Kynurenic acid	0,2-200 ng/ml	1,632	-0,010	0,9968
Indole-3-carboxaldehyde	0,2-200 ng/ml	1,257	0,028	0,9981
Indole-3-butyric acid	0,2-200 ng/ml	1,216	0,011	0,9918
Indole-3-acrylic acid	0,2-200 ng/ml	4,097	0,040	0,9967
5-hydroxyindole acetic acid	0,2-200 ng/ml	1,077	0,045	0,9852
Dopamine	0,2-200 ng/ml	0,8632	-0,014	0,9987
Neopterin	0,2-200 ng/ml	0,0030	0,00002	0,9918
Anthranilic acid	0,2-200 ng/ml	2,118	0,671	0,9993
GABA	1-500 ng/ml	0,0543	-0,0002	0,9995
5-hydroxytryptophan	1-1000 ng/ml	1,936	-0,054	0,9970

Metabolite	Linear range	Slope	Intercept	Determination coefficient (r <sup>2</sup> )
Acetylcholine	0,1-100 ng/ml	12,940	7,490	0,9981
Asparagine	1-1000 ng/ml	0,070	0,029	0,9868
Aspartic acid	1-1000 ng/ml	0,097	0,139	0,9733
Citrulline	50-5000 ng/ml	4,190	3,367	0,9970
Cortisol	0,1-1000 ng/ml	0,103	-0,0041	0,9936
Epinephrine	1-500 ng/ml	13,597	3,995	0,9820
Glutamic acid	10-5000 ng/ml	0,396	0,113	0,9970
Glutamine	10-5000 ng/ml	0,225	0,111	0,9923
L-DOPA	1-1000 ng/ml	0,417	0,042	0,9996
Metanephrine	10-5000 ng/ml	7,423	1,025	0,9762
Norepinephrine	1-1000 ng/ml	12,988	-0,427	0,9839
Normetanephrine	1-500 ng/ml	24,801	-0,098	0,9896
Phenylalanine	1-100 ug/ml	1,821	0,762	0,9993
Picolinic acid	1-1000 ng/ml	3,876	1,249	0,9993
Tyrosine	1-100 ug/ml	0,484	0,308	0,9992

### 3.2.3. Carryover

The carryover of the analytes was assessed through the injection of the blank sample right after the injection of the calibration sample with the highest concentration. The carryover was taken as acceptable if the analyte signal in the blank sample was less than 20% of the LLOQ.

### 3.2.4. Precision and accuracy

Precision and accuracy assessment of the developed method was performed using QC samples. The precision and accuracy were quantified for within-runs and between-runs. Within-run precision and accuracy were assessed by measuring QC samples at four concentration levels during one analytical cycle. Every QC sample was analyzed six times. Between-run precision and accuracy were evaluated by measuring QC samples at four concentration levels during three analytical cycles. The measured concentrations were assessed using calibration curves. Precision and accuracy were considered acceptable if:

1. Mean concentrations of the analytes were in the limit of  $\pm 20\%$  of the nominal values;

2. Within- and between-runs coefficients of variation were in the limit of  $\pm 20\%$ .

The results are shown in Table 7.

Table 7 – Accuracy and precision of the method

Metabolite	Percent from the nominal concentration of QC, % (RSD, %)				
		LLOQ QC	LQC	MQC	HQC
Tryptophan	1 cycle	91,9 (7,9)	100,4 (5,8)	98,8 (7,9)	102,3 (5,0)
	2 cycle	101,8 (6,3)	102,7 (5,9)	100,3 (5,1)	103,0 (5,4)
	3 cycle	105,9 (8,0)	112,8 (5,3)	92,4 (6,6)	105,3 (6,6)
	<b>Between cycles</b>	<b>102,3 (9,8)</b>	<b>105,5 (8,7)</b>	<b>97,1 (9,6)</b>	<b>103,6 (10,9)</b>
Kynurenine	1 cycle	80,3 (6,5)	104,3 (5,2)	95,0 (5,3)	99,6 (5,7)
	2 cycle	119,1 (6,9)	87,2 (6,2)	93,9 (6,4)	100,9 (5,5)
	3 cycle	87,5 (7,7)	106,8 (6,4)	91,6 (6,9)	100,6 (8,0)
	<b>Between cycles</b>	<b>95,6 (11,5)</b>	<b>99,4 (8,7)</b>	<b>93,5 (9,7)</b>	<b>100,3 (9,2)</b>
Choline	1 cycle	91,9 (7,3)	84,0 (7,2)	103,9 (5,1)	87,4 (5,7)
	2 cycle	109,5 (7,3)	98,0 (7,0)	106,8 (5,1)	86,5 (7,0)
	3 cycle	108,0 (5,2)	114,4 (5,6)	101,1 (7,6)	93,4 (5,4)
	<b>Between cycles</b>	<b>103,1 (12,5)</b>	<b>98,8 (10,2)</b>	<b>104,0 (12,3)</b>	<b>89,1 (11,9)</b>
Serotonin	1 cycle	112,1 (7,8)	118,4 (6,2)	100,0 (6,5)	105,1 (7,7)
	2 cycle	115,9 (5,7)	113,4 (7,7)	103,5 (6,6)	107,8 (6,1)
	3 cycle	106,3 (6,4)	111,9 (7,8)	102,6 (5,3)	103,3 (6,2)
	<b>Between cycles</b>	<b>111,4 (10,9)</b>	<b>114,6 (11,5)</b>	<b>100,7 (10,5)</b>	<b>105,3 (8,7)</b>
Quinolinic acid	1 cycle	93,8 (6,8)	106,9 (6,5)	112,1 (7,6)	111,3 (5,1)
	2 cycle	113,7 (7,8)	99,7 (5,4)	108,0 (7,6)	110,1 (6,1)
	3 cycle	97,4 (5,1)	111,4 (5,1)	111,1 (7,4)	109,8 (7,4)
	<b>Between cycles</b>	<b>101,6 (11,1)</b>	<b>106,0 (9,8)</b>	<b>110,4 (12,4)</b>	<b>110,4 (8,9)</b>
Indole-3-propionic acid	1 cycle	96,0 (7,5)	111,6 (5,8)	99,4 (5,5)	96,7 (6,1)
	2 cycle	114,7 (5,3)	110,1 (5,6)	103,0 (5,4)	97,2 (6,0)
	3 cycle	93,1 (6,4)	109,0 (5,1)	100,6 (7,6)	96,5 (5,2)
	<b>Between cycles</b>	<b>101,2 (8,3)</b>	<b>110,2 (9,9)</b>	<b>101,0 (10,4)</b>	<b>96,8 (11,6)</b>
Indole-3-lactic acid	1 cycle	99,8 (7,2)	115,9 (5,4)	100,8 (5,3)	105,2 (6,1)
	2 cycle	90,6 (7,6)	103,0 (6,6)	103,5 (6,8)	107,8 (5,0)
	3 cycle	107,9 (7,6)	107,5 (6,3)	102,6 (6,6)	103,3 (6,4)
	<b>Between cycles</b>	<b>99,5 (8,3)</b>	<b>108,8 (9,9)</b>	<b>100,8 (10,4)</b>	<b>105,2 (11,6)</b>
Indole-3-acetic acid	1 cycle	108,4 (7,3)	117,5 (6,3)	106,6 (8,0)	96,8 (6,1)

Metabolite	Percent from the nominal concentration of QC, % (RSD, %)				
		LLOQ QC	LQC	MQC	HQC
	2 cycle	81,7 (7,4)	113,0 (7,3)	102,0 (6,7)	100,9 (8,0)
	3 cycle	119,2 (6,8)	84,0 (6,0)	106,4 (5,9)	100,4 (7,1)
	<b>Between cycles</b>	<b>103,1 (12,4)</b>	<b>104,9 (10,1)</b>	<b>105,0 (8,8)</b>	<b>99,3 (9,3)</b>
Xanthurenic acid	1 cycle	104,6 (5,7)	105,3 (7,9)	99,6 (5,0)	96,8 (5,9)
	2 cycle	113,5 (7,3)	92,5 (5,2)	100,8 (7,0)	98,9 (7,7)
	3 cycle	86,0 (5,1)	99,9 (6,0)	100,8 (5,9)	99,0 (5,0)
	<b>Between cycles</b>	<b>101,3 (8,4)</b>	<b>99,2 (9,8)</b>	<b>100,4 (10,3)</b>	<b>98,3 (9,8)</b>
Tryptamine	1 cycle	97,1 (6,5)	92,0 (5,6)	106,6 (5,4)	111,3 (6,1)
	2 cycle	119,1 (7,7)	116,1 (5,1)	102,0 (7,0)	110,1 (7,3)
	3 cycle	109,5 (5,5)	106,2 (6,4)	106,4 (6,3)	109,8 (6,2)
	<b>Between cycles</b>	<b>94,4 (11,2)</b>	<b>104,7 (8,0)</b>	<b>105,0 (9,1)</b>	<b>110,4 (9,4)</b>
Biopterin	1 cycle	101,6 (6,3)	91,8 (5,5)	108,9 (7,7)	96,8 (8,0)
	2 cycle	99,0 (7,2)	109,4 (7,3)	111,3 (7,6)	98,9 (7,7)
	3 cycle	116,1 (7,5)	92,0 (5,6)	109,0 (5,3)	99,0 (6,0)
	<b>Between cycles</b>	<b>117,4 (9,9)</b>	<b>97,7 (10,5)</b>	<b>109,8 (9,5)</b>	<b>98,3 (9,7)</b>
Kynurenic acid	1 cycle	116,7 (5,8)	106,0 (7,2)	100,8 (7,0)	105,2 (6,7)
	2 cycle	93,1 (6,9)	94,9 (6,6)	103,5 (7,4)	107,8 (7,6)
	3 cycle	97,1 (6,8)	100,0 (6,6)	102,6 (5,8)	103,3 (7,1)
	<b>Between cycles</b>	<b>93,5 (8,3)</b>	<b>100,3 (9,1)</b>	<b>100,8 (8,1)</b>	<b>105,2 (8,4)</b>
Indole-3-carboxaldehyde	1 cycle	87,7 (7,9)	101,7 (6,6)	112,1 (5,3)	110,2 (6,6)
	2 cycle	109,5 (7,4)	99,1 (6,9)	108,0 (7,2)	112,0 (6,8)
	3 cycle	87,6 (6,5)	80,7 (7,8)	111,1 (5,6)	105,6 (7,3)
	<b>Between cycles</b>	<b>82,3 (8,6)</b>	<b>93,8 (9,5)</b>	<b>110,4 (12,8)</b>	<b>109,3 (11,2)</b>
Indole-3-butyric acid	1 cycle	116,2 (5,8)	106,2 (6,8)	101,0 (5,7)	101,6 (7,8)
	2 cycle	118,9 (5,5)	111,2 (7,6)	102,8 (5,3)	104,6 (5,2)
	3 cycle	84,3 (5,7)	85,5 (6,4)	100,4 (5,6)	100,9 (5,5)
	<b>Between cycles</b>	<b>111,8 (11,6)</b>	<b>100,9 (11,5)</b>	<b>101,4 (9,9)</b>	<b>102,8 (9,0)</b>
Indole-3-acrylic acid	1 cycle	103,7 (6,8)	88,1 (6,4)	104,1 (6,4)	96,7 (6,1)
	2 cycle	110,7 (6,5)	100,4 (5,3)	104,8 (7,9)	97,2 (5,8)
	3 cycle	93,9 (5,2)	112,0 (6,4)	106,6 (6,7)	96,5 (6,8)

Metabolite	Percent from the nominal concentration of QC, % (RSD, %)				
		LLOQ QC	LQC	MQC	HQC
	<b>Between cycles</b>	<b>100,3 (11,0)</b>	<b>100,2 (9,5)</b>	<b>105,1 (10,4)</b>	<b>96,8 (8,5)</b>
5-hydroxyindole acetic acid	1 cycle	91,8 (7,2)	89,7 (7,4)	100,8 (7,5)	96,8 (7,4)
	2 cycle	118,4 (6,1)	80,7 (7,1)	103,5 (5,8)	98,9 (6,4)
	3 cycle	115,6 (7,5)	112,8 (5,9)	102,6 (5,7)	99,0 (7,6)
	<b>Between cycles</b>	<b>81,9 (10,0)</b>	<b>94,4 (10,5)</b>	<b>100,8 (11,6)</b>	<b>98,3 (12,1)</b>
Dopamine	1 cycle	84,7 (6,6)	106,4 (6,8)	100,6 (6,3)	106,8 (5,8)
	2 cycle	80,3 (7,6)	106,9 (6,2)	105,4 (5,4)	107,6 (6,7)
	3 cycle	99,3 (6,0)	103,9 (6,3)	103,6 (5,9)	102,1 (7,0)
	<b>Between cycles</b>	<b>111,4 (12,1)</b>	<b>105,7 (9,3)</b>	<b>103,3 (10,2)</b>	<b>105,4 (8,6)</b>
Neopterin	1 cycle	114,5 (6,1)	83,2 (6,0)	106,6 (5,2)	106,8 (5,4)
	2 cycle	86,2 (5,5)	112,3 (6,1)	102,0 (7,1)	107,6 (6,1)
	3 cycle	117,7 (8,0)	114,3 (6,6)	106,4 (6,7)	102,1 (7,4)
	<b>Between cycles</b>	<b>112,7 (9,4)</b>	<b>103,2 (10,5)</b>	<b>105,0 (9,3)</b>	<b>105,4 (10,4)</b>
Anthranilic acid	1 cycle	88,8 (6,3)	103,5 (5,2)	96,4 (5,4)	103,9 (5,1)
	2 cycle	88,4 (5,9)	86,6 (6,4)	98,4 (6,0)	105,8 (7,3)
	3 cycle	117,5 (6,7)	106,7 (8,0)	96,5 (5,9)	99,3 (7,2)
	<b>Between cycles</b>	<b>81,4 (11,6)</b>	<b>98,9 (12,4)</b>	<b>97,3 (10,0)</b>	<b>103,0 (9,4)</b>
GABA	1 cycle	111,0 (5,5)	97,8 (5,3)	105,8 (6,3)	99,6 (5,1)
	2 cycle	104,4 (5,5)	98,5 (7,8)	93,4 (7,8)	101,1 (5,9)
	3 cycle	84,8 (5,8)	110,3 (6,7)	94,1 (6,1)	99,0 (6,7)
	<b>Between cycles</b>	<b>100,1 (9,4)</b>	<b>102,2 (11,4)</b>	<b>97,8 (12,5)</b>	<b>100,0 (8,3)</b>
5-hydroxytryptophan	1 cycle	92,2 (5,3)	98,5 (7,3)	99,7 (5,7)	98,0 (5,7)
	2 cycle	86,1 (6,7)	95,6 (7,9)	96,0 (6,8)	96,2 (7,9)
	3 cycle	109,4 (7,1)	100,2 (6,2)	98,8 (6,9)	95,6 (6,7)
	<b>Between cycles</b>	<b>95,9 (9,2)</b>	<b>98,1 (10,1)</b>	<b>98,1 (8,9)</b>	<b>96,6 (11,5)</b>
Acetylcholine	1 cycle	81,8 (6,4)	109,3 (6,7)	96,8 (5,3)	104,9 (7,2)
	2 cycle	80,4 (5,7)	110,3 (7,1)	98,9 (6,5)	108,3 (5,5)
	3 cycle	113,0 (5,5)	100,8 (5,7)	96,9 (7,0)	108,4 (5,5)
	<b>Between cycles</b>	<b>85,6 (9,4)</b>	<b>106,8 (8,1)</b>	<b>97,6 (9,6)</b>	<b>107,2 (12,5)</b>
Asparagine	1 cycle	81,6 (6,0)	105,3 (6,5)	98,8 (6,7)	105,6 (7,5)

Metabolite	Percent from the nominal concentration of QC, % (RSD, %)				
		LLOQ QC	LQC	MQC	HQC
	2 cycle	101,7 (6,3)	84,8 (5,1)	100,1 (6,0)	105,8 (6,3)
	3 cycle	94,3 (7,5)	107,5 (5,8)	100,1 (6,3)	105,8 (6,3)
	<b>Between cycles</b>	<b>104,4 (9,1)</b>	<b>99,2 (8,2)</b>	<b>100,0 (8,6)</b>	<b>105,7 (12,2)</b>
Aspartic acid	1 cycle	115,8 (7,9)	115,3 (7,2)	112,1 (6,6)	108,0 (6,7)
	2 cycle	109,5 (5,3)	81,7 (6,7)	108,0 (8,0)	106,2 (6,3)
	3 cycle	90,9 (6,5)	118,0 (6,0)	111,1 (5,5)	105,6 (5,2)
	<b>Between cycles</b>	<b>105,4 (10,4)</b>	<b>105,0 (12,7)</b>	<b>110,4 (12,4)</b>	<b>106,6 (9,8)</b>
Citrulline	1 cycle	116,9 (5,3)	100,3 (6,4)	95,0 (5,7)	99,6 (5,5)
	2 cycle	92,1 (6,3)	91,9 (6,6)	93,9 (6,2)	100,9 (5,7)
	3 cycle	83,2 (7,0)	81,9 (6,7)	91,6 (7,8)	100,5 (7,0)
	<b>Between cycles</b>	<b>97,4 (12,4)</b>	<b>91,4 (9,7)</b>	<b>93,5 (10,1)</b>	<b>100,3 (9,0)</b>
Cortisol	1 cycle	92,9 (6,0)	97,8 (6,1)	104,2 (5,6)	105,5 (7,2)
	2 cycle	111,5 (5,4)	86,0 (5,3)	109,2 (7,3)	105,6 (6,4)
	3 cycle	85,2 (6,0)	111,4 (6,3)	103,0 (6,9)	105,4 (7,9)
	<b>Between cycles</b>	<b>116,2 (10,0)</b>	<b>98,4 (12,7)</b>	<b>101,8 (9,5)</b>	<b>105,5 (10,4)</b>
Epinephrine	1 cycle	92,0 (5,9)	112,8 (6,1)	100,7 (6,6)	91,3 (5,7)
	2 cycle	106,4 (7,4)	84,6 (5,1)	92,4 (7,4)	102,3 (5,3)
	3 cycle	118,8 (6,8)	100,8 (7,7)	100,2 (6,9)	101,2 (6,1)
	<b>Between cycles</b>	<b>105,8 (11,1)</b>	<b>99,4 (8,3)</b>	<b>97,8 (8,2)</b>	<b>98,0 (10,8)</b>
Glutamic acid	1 cycle	95,3 (5,9)	114,1 (7,2)	103,9 (5,6)	97,9 (6,7)
	2 cycle	113,4 (5,4)	87,2 (5,7)	106,9 (6,2)	95,2 (5,6)
	3 cycle	107,2 (6,1)	96,0 (6,2)	101,1 (6,0)	94,7 (5,3)
	<b>Between cycles</b>	<b>105,3 (8,4)</b>	<b>99,1 (8,3)</b>	<b>104,0 (12,0)</b>	<b>99,3 (9,3)</b>
Glutamine	1 cycle	83,2 (6,2)	86,6 (5,6)	95,0 (6,4)	99,7 (5,6)
	2 cycle	115,6 (5,4)	87,5 (5,1)	93,9 (7,2)	100,7 (7,2)
	3 cycle	87,6 (5,8)	111,6 (6,4)	91,6 (5,3)	100,4 (7,8)
	<b>Between cycles</b>	<b>95,5 (10,0)</b>	<b>95,2 (10,5)</b>	<b>93,5 (12,8)</b>	<b>100,2 (10,9)</b>
L-DOPA	1 cycle	106,6 (6,1)	91,6 (6,4)	100,8 (7,6)	108,3 (7,9)
	2 cycle	102,3 (6,2)	113,7 (5,8)	103,5 (7,7)	102,5 (6,4)
	3 cycle	105,5 (5,7)	101,7 (6,5)	102,6 (6,4)	105,3 (5,7)



Metabolite	Percent from the nominal concentration of QC, % (RSD, %)				
		LLOQ QC	LQC	MQC	HQC
	<b>Between cycles</b>	<b>104,8 (12,6)</b>	<b>102,3 (12,3)</b>	<b>100,8 (8,8)</b>	<b>108,3 (8,5)</b>
Metanephrine	1 cycle	86,6 (6,8)	112,3 (7,1)	95,0 (5,5)	119,7 (5,6)
	2 cycle	103,1 (6,0)	116,3 (6,9)	93,9 (6,7)	100,7 (7,9)
	3 cycle	89,9 (6,2)	95,7 (7,5)	91,6 (6,7)	100,4 (7,4)
	<b>Between cycles</b>	<b>93,2 (8,2)</b>	<b>108,1 (8,7)</b>	<b>93,5 (12,1)</b>	<b>100,2 (10,7)</b>
Norepinephrine	1 cycle	110,6 (7,8)	109,9 (7,6)	112,1 (5,3)	108,0 (5,2)
	2 cycle	105,7 (7,6)	115,0 (7,9)	108,0 (5,1)	106,2 (7,2)
	3 cycle	104,7 (7,2)	85,6 (7,9)	111,1 (5,8)	105,6 (5,4)
	<b>Between cycles</b>	<b>107,0 (9,2)</b>	<b>103,5 (12,3)</b>	<b>110,4 (12,7)</b>	<b>106,6 (9,8)</b>
Normetanephrine	1 cycle	108,0 (6,9)	89,6 (7,7)	106,6 (7,6)	109,6 (7,0)
	2 cycle	100,0 (7,0)	82,4 (5,8)	102,0 (5,0)	102,8 (6,4)
	3 cycle	106,0 (5,6)	93,2 (5,5)	106,4 (6,8)	101,4 (7,5)
	<b>Between cycles</b>	<b>104,7 (11,0)</b>	<b>88,4 (11,6)</b>	<b>105,0 (8,9)</b>	<b>117,6 (12,2)</b>
Phenylalanine	1 cycle	105,0 (6,1)	100,0 (5,4)	98,8 (6,6)	100,9 (5,9)
	2 cycle	105,1 (6,7)	100,3 (7,3)	100,3 (7,5)	101,2 (7,5)
	3 cycle	105,3 (6,7)	112,7 (6,3)	92,4 (7,7)	102,1 (5,9)
	<b>Between cycles</b>	<b>105,1 (9,0)</b>	<b>105,3 (10,1)</b>	<b>97,1 (12,8)</b>	<b>101,4 (12,2)</b>
Picolinic acid	1 cycle	99,1 (5,6)	111,4 (7,3)	100,8 (6,3)	108,3 (7,4)
	2 cycle	98,3 (6,5)	116,6 (6,2)	103,5 (6,7)	102,5 (7,9)
	3 cycle	113,3 (5,5)	93,7 (6,0)	102,6 (5,2)	105,3 (5,9)
	<b>Between cycles</b>	<b>103,5 (11,1)</b>	<b>107,3 (10,2)</b>	<b>100,8 (10,5)</b>	<b>108,3 (8,3)</b>
Tyrosine	1 cycle	100,5 (6,7)	93,3 (5,2)	103,9 (7,4)	100,9 (6,9)
	2 cycle	102,5 (7,7)	100,6 (6,3)	106,8 (7,9)	100,8 (6,5)
	3 cycle	104,5 (6,5)	101,6 (6,6)	101,1 (7,4)	100,7 (5,4)
	<b>Between cycles</b>	<b>103,8 (8,2)</b>	<b>102,3 (9,4)</b>	<b>104,0 (10,7)</b>	<b>101,0 (12,6)</b>

### 3.2.5. Matrix effect

Matrix effect assessment was made using six series of blank samples. Matrix effects were quantified for LQC and HQC levels. The level of matrix effect was applicable if the RSD was in the limits of  $\pm 15\%$ . The results are shown in Table 8.

Table 8 – Matrix effect for the measured metabolites

Metabolite	LQC		HQC	
	% from the nominal concentration	RSD, %	% from the nominal concentration	RSD, %
Tryptophan	96,1	7,9	101,1	6,8
Kynurenine	111,4	3,4	102,1	4,5
Choline	100,1	3,2	110,2	7,9
Serotonin	92,1	6,8	103,1	4,5
Quinolinic acid	95,7	2,3	96,1	6,8
Indole-3-propionic acid	97,1	3,4	93,3	3,4
Indole-3-lactic acid	103,1	1,1	100,1	4,5
Indole-3-acetic acid	98,1	3,4	95,9	1,1
Xanthurenic acid	96,1	2,3	106,2	6,8
Tryptamine	110,2	5,7	111,8	4,5
Biopterin	112,7	5,9	109,2	6,7
Kynurenic acid	99,1	7,9	100,1	6,0
Indole-3-carboxaldehyde	101,1	1,1	93,0	6,1
Indole-3-butyric acid	91,8	1,8	93,0	7,9
Indole-3-acrylic acid	99,1	4,5	109,2	4,5
5-hydroxyindole acetic acid	100,1	6,8	111,4	1,1
Dopamine	107,2	9,1	94,3	3,4
Neopterin	102,1	1,1	95,7	2,3
Anthranilic acid	91,4	6,8	92,7	7,9
GABA	111,2	5,7	104,1	7,9
5-hydroxytryptophan	110,2	3,4	99,1	3,4
Acetylcholine	106,2	9,1	104,1	4,5
Asparagine	95,5	7,9	91,0	4,5
Aspartic acid	98,1	5,7	105,2	7,9
Citrulline	103,1	4,5	111,2	2,3
Cortisol	96,1	7,9	92,0	2,3
Epinephrine	107,2	6,8	97,1	3,4
Glutamic acid	104,4	6,8	107,2	5,7
Glutamine	95,0	2,3	105,2	6,8
L-DOPA	96,1	7,9	104,1	5,7
Metanephrine	99,1	3,4	95,0	4,5
Norepinephrine	109,2	5,7	102,1	7,9
Normetanephrine	94,0	7,8	106,2	3,4
Phenylalanine	107,6	7,0	100,1	4,5
Picolinic acid	100,1	7,1	98,1	2,3
Tyrosine	93,0	6,8	106,2	1,1

### 3.2.6. Extraction coefficient

The extraction coefficient is calculated as a comparison of the peak areas of the analytes in the samples spiked with the calibration solutions before and after the extraction process. The assessment was made using LQC and HQC samples. The extraction coefficient was applicable if the RSD was in the limits of  $\pm 15\%$ . The results are shown in Table 9.

Table 9 – Extraction coefficient for the measured metabolites

Соединение	LQC		HQC	
	% from the nominal concentration	RSD, %	% from the nominal concentration	RSD, %
Tryptophan	91,0	2,3	97,1	3,4
Kynurenine	108,2	5,7	108,2	6,9
Choline	93,3	1,1	97,1	7,9
Serotonin	91,7	9,1	105,1	4,5
Quinolinic acid	95,0	5,7	98,1	7,1
Indole-3-propionic acid	99,1	9,1	104,2	5,7
Indole-3-lactic acid	91,9	6,8	95,0	9,1
Indole-3-acetic acid	92,5	2,3	98,1	3,4
Xanthurenic acid	104,1	1,1	105,2	5,7
Tryptamine	94,4	3,1	108,9	6,8
Biopterin	104,1	5,3	92,0	3,4
Kynurenic acid	93,7	1,1	97,1	6,8
Indole-3-carboxaldehyde	108,2	3,4	98,1	7,9
Indole-3-butyric acid	102,1	6,8	95,0	5,7
Indole-3-acrylic acid	93,1	2,3	106,2	9,1
5-hydroxyindole acetic acid	103,1	5,7	93,0	5,7
Dopamine	102,1	7,9	111,2	1,1
Neopterin	95,0	6,8	101,1	7,9
Anthranilic acid	109,2	2,3	106,2	7,8
GABA	101,1	7,9	92,0	7,7
5-hydroxytryptophan	95,0	1,1	100,1	3,4
Acetylcholine	103,1	3,4	91,0	1,1
Asparagine	97,1	7,9	107,2	2,3
Aspartic acid	107,2	3,4	100,1	3,4
Citrulline	104,1	5,7	98,1	9,1
Cortisol	100,1	4,5	97,1	5,7
Epinephrine	107,2	6,8	95,0	1,1
Glutamic acid	107,2	1,1	109,2	3,4
Glutamine	108,2	4,5	110,2	3,4
L-DOPA	111,2	9,1	91,0	2,3
Metanephrine	93,0	4,5	99,1	3,4
Norepinephrine	106,2	9,1	96,3	3,4
Normetanephrine	92,0	6,8	91,0	5,7

Phenylalanine	103,1	5,7	94,0	1,1
Picolinic acid	105,2	7,9	108,2	9,1
Tyrosine	109,2	1,1	103,1	9,1

### 3.2.7. Stability

The stability of the analytes was assessed using LQC, and HQC samples were analyzed right after the sample preparation and after designed storage conditions.

The stability was assessed for:

1. The working solutions of the analytes after 6 h storage at room temperature ( $21 \pm 3^{\circ}\text{C}$ );
2. Biological samples, stored for 24 h in the autosampler at the temperature of  $10 \pm 0,5^{\circ}\text{C}$ ;
3. Biological samples that underwent three freeze/thaw cycles;
4. Biological samples stored in the freezer with a temperature of  $\text{minus } 35 \pm 1^{\circ}\text{C}$  for 30 days.

The stability was acceptable if the RSD of the measured concentrations were in the limit of  $\pm 15\%$  of their nominal values. The results of the assessment are shown in Table 10.

Table 10 – Stability results for the measured metabolites

Metabolite	LQC				HQC			
	6 h, room temp (standard)	24 h, autosampler	30 days in -35±1°C	After three freeze-thaw cycles	6 h, room temp (standard)	24 h, autosampler	30 days in -35±1°C	After three freeze-thaw cycles
Tryptophan	100,9	103.3	98.8	112,2	102.6	90,7	102.6	108,1
Kynurenine	111.7	105.0	95.9	110,2	99.3	95.9	99.3	101,1
Choline	99.9	97.5	101.6	100,1	98.1	100,9	102.9	109,2
Serotonin	97.5	103.3	97.2	111,8	100,9	99.2	104.4	103,1
Quinolinic acid	99.2	105.0	98.8	107,2	101.5	97.0	102.3	108,8
Indole-3-propionic acid	97.0	101.6	95.9	101,1	97.7	96.0	102.6	108,2
Indole-3-lactic acid	96.0	97.5	101.6	110,2	105.4	102.6	99.3	97,1
Indole-3-acetic acid	102.6	101.1	97.2	92,0	97.7	106.4	102.9	100,1
Xanthurenic acid	106.4	100,9	100,9	111,2	98.1	103.1	104.4	105,2
Tryptamine	103.1	111.7	99.2	98,1	100,9	98.0	102.3	94,0
Biopterin	99.2	99.9	97.0	93,0	101.5	95.3	102.6	99,1
Kynurenic acid	97.0	103.3	96.0	97,1	97.7	100,0	101.6	95,0
Indole-3-carboxaldehyde	99.5	105.0	102.6	110,2	102.9	90,7	98.7	109,2
Indole-3-butyric acid	96.4	97.5	106.4	110,2	104.4	95.9	95.8	100,8
Indole-3-acrylic acid	98.7	103.3	100,9	100,1	102.3	100,9	96.8	92,0
5-hydroxyindole acetic acid	99.4	105.0	99.2	102,1	103.2	99.2	99.7	97,1
Dopamine	104.3	101.6	97.0	92,7	102.9	97.0	94.6	92,7
Neopterin	102.0	97.5	96.0	96,1	104.4	96.0	98.7	109,2
Anthranilic acid	96.3	106.4	104.3	103,1	102.3	101.1	105.4	101,9
GABA	101.6	98.0	106.4	97,1	100,9	99.2	101.6	99,1
5-hydroxytryptophan	97.5	95.3	103.1	111,2	99.2	97.0	97.5	102,3
Acetylcholine	101.1	100,0	98.0	92,0	97.0	96.0	101.1	98,1

Metabolite	LQC				HQC			
	6 h, room temp (standard)	24 h, autosampler	30 days in -35±1°C	After three freeze-thaw cycles	6 h, room temp (standard)	24 h, autosampler	30 days in -35±1°C	After three freeze-thaw cycles
Asparagine	100,9	90,7	95,3	102,1	96,0	102,6	100,9	101,1
Aspartic acid	111,7	95,9	100,0	105,8	102,6	106,4	111,7	102,8
Citrulline	99,9	100,9	90,7	105,0	106,4	103,1	99,9	108,2
Cortisol	103,3	99,2	95,9	107,2	100,9	99,2	103,3	103,1
Epinephrine	105,0	97,0	100,9	94,4	99,2	97,0	105,0	107,4
Glutamic acid	97,5	96,0	99,2	96,1	97,0	99,5	97,5	91,0
Glutamine	103,3	101,1	111,7	105,2	96,0	96,4	103,3	94,5
L-DOPA	97,0	102,3	99,9	108,2	104,3	98,7	102,3	109,2
Metanephrine	96,0	103,2	103,3	99,1	102,6	99,2	103,2	99,1
Norepinephrine	104,3	102,9	105,0	106,2	97,1	97,0	102,9	111,2
Normetanephrine	102,6	104,4	97,5	99,1	110,2	96,0	104,4	104,1
Phenylalanine	94,2	102,3	103,3	108,2	110,2	101,1	102,3	92,3
Picolinic acid	96,3	97,2	93,5	100,1	100,1	97,5	97,2	109,2
Tyrosine	101,2	98,7	92,6	96,1	102,1	99,7	102,4	95,4

### **3.3. Neurotransmitters metabolomics after short- and long-term exposure of diazepam in zebrafish larvae**

To investigate the possibility of the usage of the zebrafish as a model organism in the assessment of the pharmacological action of the neurotropic drugs using the pharmacometabolomic approach, the concentrations of the metabolites of GABAergic, serotonergic, dopaminergic/adrenergic, cholinergic neurotransmitter systems, aspartic acid system, kynurenine, and indole pathway metabolites, and other related metabolites after the exposure of diazepam at the doses of 0.8, 1.6, 16, 160 ug/L for short- (2.5 h) and long-term (96 h). Diazepam is a pharmacological compound with clearly described properties and mechanism of action on the central nervous system. Diazepam is used as a reference compound in investigating potential anxiolytic drugs [5, 29].

The list of the measured compounds is represented in Table 1. The method of quantification of these compounds was developed and validated. The validation results of the method are presented in chapter 3, section 2.

The main statistical differences in the concentrations of endogenous metabolites after short-term diazepam exposure are presented in Table 11. The main statistical differences in the concentrations of endogenous metabolites after long-term diazepam exposure are shown in Table 12.

Table 11 – Detailed information on the statistical differences across experimental groups after short-term diazepam exposure

Metabolite	Contr. vs 1	Contr. vs 2	Contr. vs 3	Contr. vs 4	1 vs 2	1 vs 3	1 vs 4	2 vs 3	2 vs 4	3 vs 4
GABA	-	-	-	-	-	-	-	<0,05 ↓	<0,05 ↓	-
Glutamic acid	-	-	-	-	-	-	<0,01 ↑	-	-	-
Glutamine	-	-	-	-	-	-	-	-	-	-
Tryptophan	-	-	-	<0,05 ↑	-	<0,01 ↑	<0,001 ↑	-	-	-
5-hydroxytryptophan	<0,05 ↓	-	-	-	-	-	<0,001 ↑	-	-	-
Serotonin	-	-	<0,001 ↑	<0,001 ↑	-	<0,05 ↑	<0,05 ↑	-	-	-
5-hydroxyindole acetic acid	-	<0,001 ↓	-	-	-	-	-	-	<0,001 ↑	-
Tryptamine	-	-	-	-	-	-	-	-	-	-
Phenylalanine	-	-	-	-	-	-	<0,01 ↑	-	<0,01 ↑	-
Tyrosine	<0,05 ↓	-	-	-	-	-	<0,001 ↑	-	<0,01 ↑	-
L-DOPA	-	-	-	-	-	<0,05 ↓	<0,01 ↓	-	-	-
Dopamine	-	-	-	<0,05 ↓	<0,05 ↓	-	<0,001 ↓	-	-	-
Norepinephrine	<0,05 ↑	-	-	-	<0,001 ↓	-	-	-	-	-
Normetanephrine	-	<0,05 ↓	-	-	<0,001 ↓	<0,01 ↓	-	-	-	-
Epinephrine	-	-	-	-	<0,001 ↓	<0,05 ↓	<0,01 ↓	-	-	-
Metanephrine	<0,05 ↓	<0,05 ↓	-	<0,05 ↓	-	-	-	-	-	-
Aspartic acid	-	-	-	<0,05 ↑	-	<0,05 ↑	<0,001 ↑	-	-	-
Asparagine	-	-	-	-	-	-	-	-	-	-
Acetylcholine	-	-	-	-	-	-	-	<0,05 ↓	-	-





Table 12 – Detailed information on the statistical differences across experimental groups after long-term diazepam exposure

Metabolite	Contr. vs 1	Contr. vs 2	Contr. vs 3	Contr. vs 4	1 vs 2	1 vs 3	1 vs 4	2 vs 3	2 vs 4	3 vs 4
GABA	-	-	-	-	-	-	-	-	-	-
Glutamic acid	-	-	-	-	-	-	-	-	-	-
Glutamine	-	-	-	-	-	-	-	-	-	-
Tryptophan	<0,001 ↓	-	<0,05 ↓	<0,05 ↓	<0,01 ↑	-	-	-	-	-
5-hydroxytryptophan	<0,001 ↓	-	<0,01 ↓	<0,05 ↓	-	-	-	-	-	-
Serotonin	-	0,01 ↑	-	<0,05 ↑	<0,001 ↑	-	<0,01 ↑	-	-	-
5-hydroxyindole acetic acid	<0,01 ↓	-	-	<0,001 ↓	-	-	-	-	<0,01 ↓	-
Tryptamine	-	-	-	-	-	-	-	-	-	-
Phenylalanine	<0,05 ↑	-	<0,05 ↑	<0,001 ↑	-	-	-	-	-	-
Tyrosine	-	-	<0,01 ↓	<0,001 ↓	-	-	-	-	<0,01 ↓	-
L-DOPA	-	-	-	-	-	-	-	-	-	-
Dopamine	-	-	-	<0,05 ↓	-	-	-	-	<0,01 ↓	-
Norepinephrine	-	-	-	<0,05 ↑	-	-	<0,05 ↑	-	-	-
Normetanephrine	-	-	-	-	<0,05 ↑	-	-	-	-	-
Epinephrine	-	<0,001 ↑	-	-	-	-	-	-	<0,01 ↓	-
Metanephrine	-	-	<0,01 ↑	<0,05 ↑	-	-	-	-	-	-
Aspartic acid	-	-	<0,05 ↑	<0,001 ↑	-	-	-	-	-	-
Asparagine	-	-	-	-	-	-	-	-	-	-
Acetylcholine	<0,05 ↓	-	-	<0,001 ↓	-	-	-	-	<0,01 ↓	<0,05 ↓



### 3.3.1. Morphological characteristics

Morphologically, the zebrafish larvae did not present any significant alterations for the short or medium-term exposures. In particular, there were no disturbances in the body formation, tail formation, hyperpigmentation found; the fins, somites, and notochords were formed correctly; there were no disturbances in the internal organs' formation found (Figure 9).



Figure 9 – Zebrafish larvae after the exposure to diazepam at a concentration of 160 ug/L for a long-term.

### 3.3.2. GABAergic system and aspartic acid system

This section presents the results of the short- and long-term exposure of diazepam on the levels of endogenous metabolites of the GABAergic and aspartic

acid systems. Figure 10 shows the scheme of aspartic and glutamic acid and GABA metabolism.

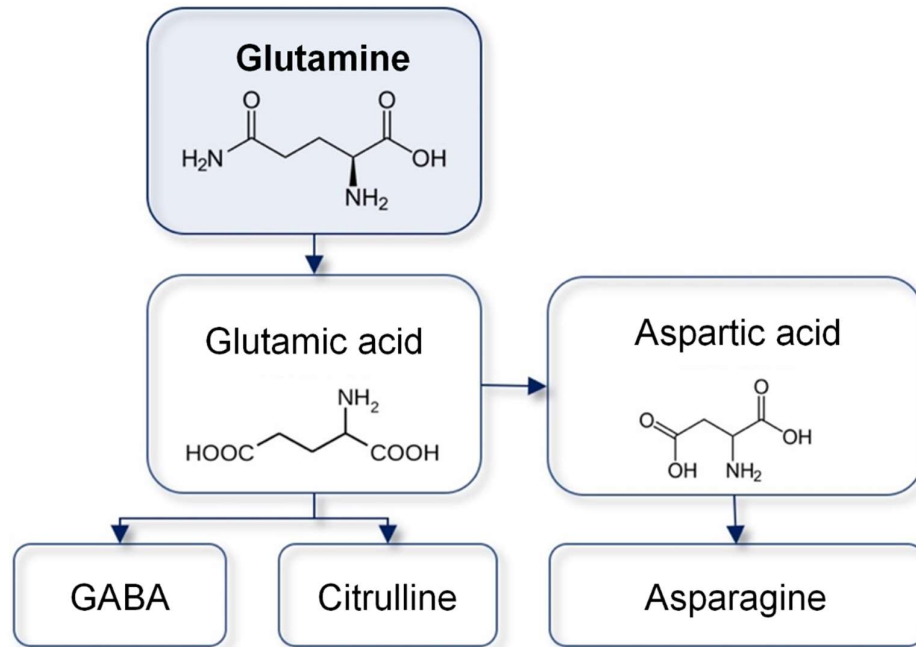


Figure 10 – GABAergic, aspartic acid, and glutamic acid system biochemical pathway.

### ***GABAergic system***

In short-term exposure, no dose-dependent trends in increasing or decreasing concentrations of GABA were found. The only group which presented higher ( $p < 0.05$ ) concentrations of GABA was the group that was exposed to 1.6  $\mu\text{g/L}$  versus the groups exposed to 16 and 160  $\mu\text{g/L}$  (Figure 11A). Also, in 96 h exposure, none of the groups showed significant changes in GABA concentrations (Figure 11A). Concerning glutamic acid, the only group which showed a significant increase of concentrations ( $p < 0.01$ ) was the group exposed to the highest dose (160  $\mu\text{g/L}$ ), versus the group receiving 0.8  $\mu\text{g/L}$  of diazepam (Figure 11B). In long-term exposure, none of the groups were significantly different (Figure 11B). Glutamine concentrations did not change in any group in 2.5 h and 96 h exposures (Figure 11C).

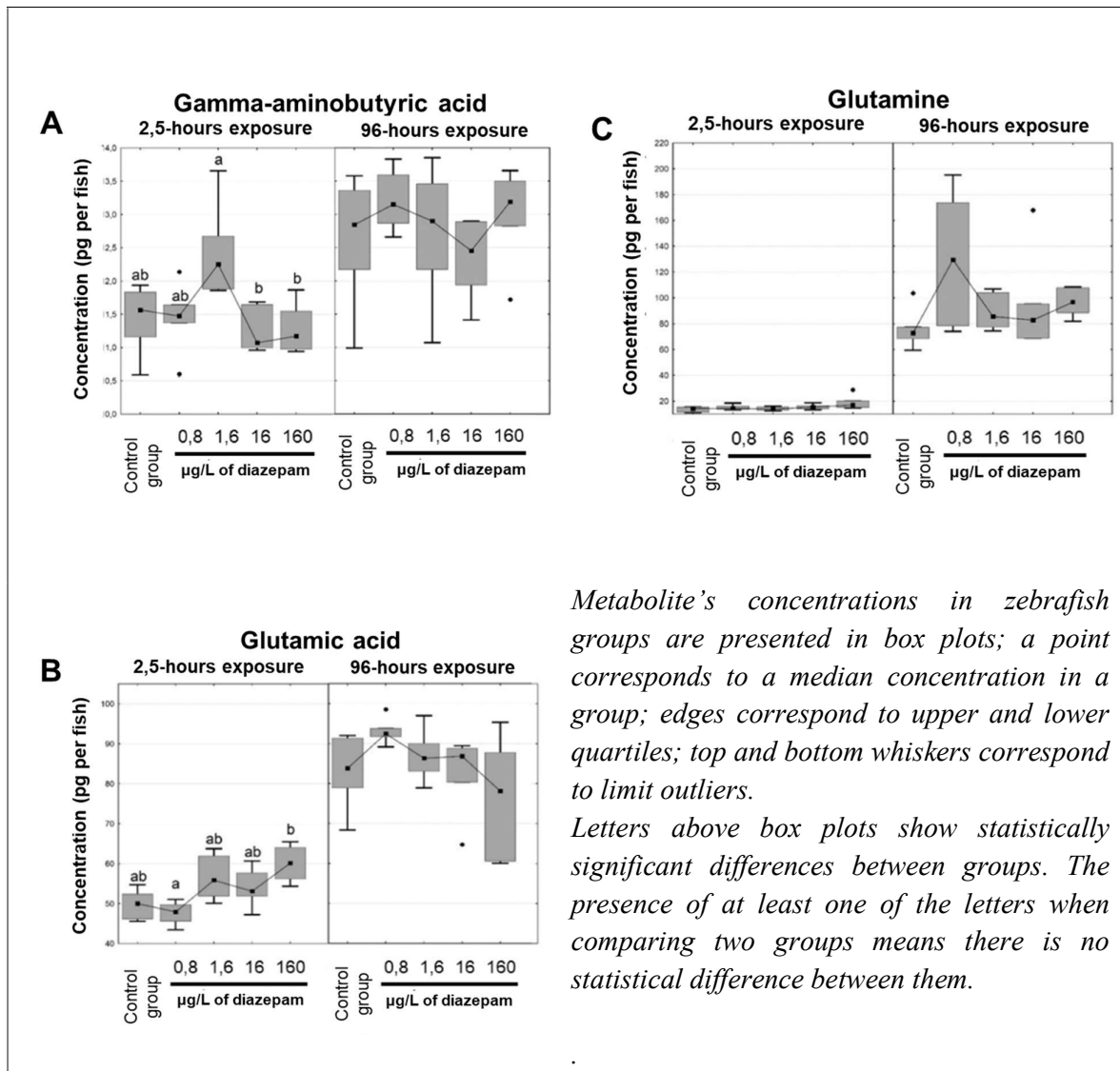


Figure 11 – Metabolites related to GABAergic and glutaminergic system.

### *Aspartic acid system*

In 2.5 h exposure, aspartic acid concentrations presented higher concentrations at higher doses. The group that received 160 µg/L of diazepam showed higher concentrations than the vehicle control group and compared to the group that received 0.8 µg/L ( $p < 0.05$ , and  $p < 0.001$ , respectively). The group treated with 16 µg/L showed significantly higher aspartic acid concentrations than those exposed to 0.8 µg/L (Figure 12A). After 96 h exposure, aspartic acid concentrations were higher in the groups exposed to 16 and 160 µg/L of diazepam compared to the vehicle control ( $p < 0.05$ , and  $p < 0.001$ , respectively) (Figure 12A).

The metabolite asparagine, known to be a precursor of aspartic acid, did not show any significant difference or trend for short- or medium-term exposures (Figure 12B).

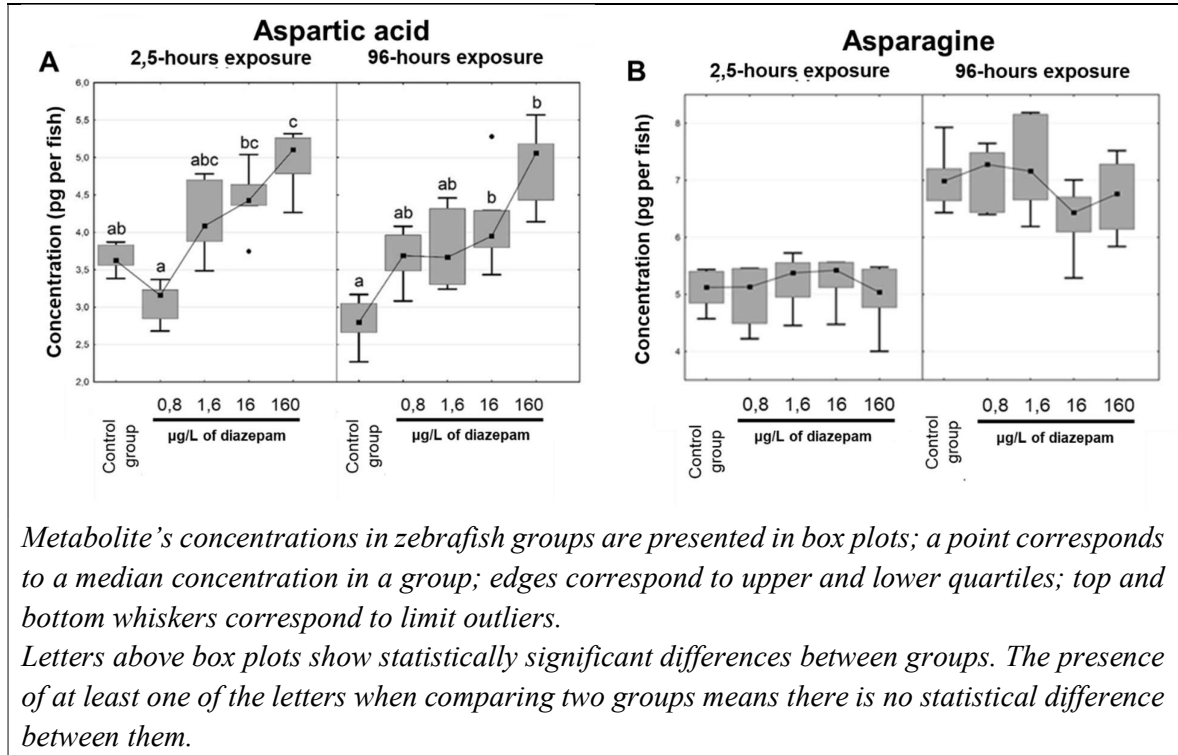


Figure 12 – Metabolites related to aspartic acid system.

### 3.3.3. Serotonergic system and kynurenine pathway

This section presents the results of the short- and long-term exposures of diazepam on the levels of endogenous metabolites of the serotonergic system and kynurenine pathway. Figure 13 shows the scheme of the tryptophan metabolism through serotonin, kynurenine, and indole pathways.

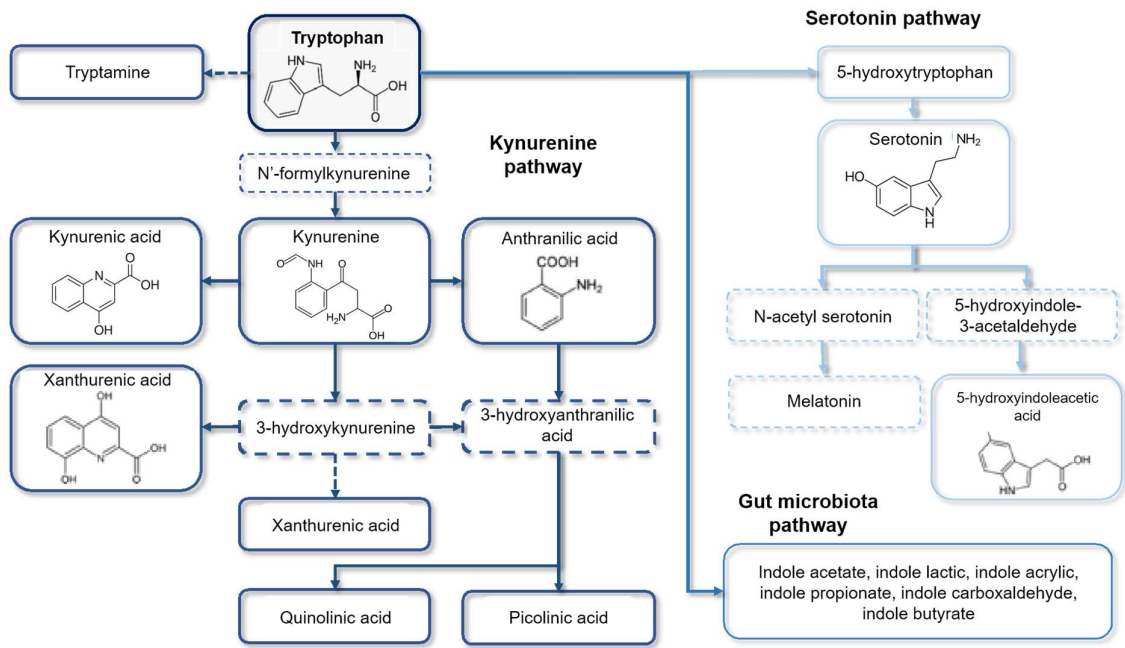


Figure 13 – The scheme of tryptophan metabolism.

### *Serotonergic system*

In short-term exposure, tryptophan presented higher concentrations at higher doses. The group treated with 160  $\mu\text{g/L}$  of diazepam presented higher ( $p < 0.05$ ) concentrations than the vehicle control group. Also, the groups that received 16  $\mu\text{g/L}$  and 160  $\mu\text{g/L}$  presented higher ( $p < 0.01$  and  $p < 0.001$ , respectively) concentrations of tryptophan than the group that received 0.8  $\mu\text{g/L}$  of diazepam (Figure 14A). In contrast, tryptophan presented decreased concentration in the long-term treatments at higher doses of exposure. Indeed, the groups that received 0.8, 16 and 160  $\mu\text{g/L}$  showed lower ( $p < 0.001$ ,  $p < 0.05$ , and  $p < 0.05$ , respectively) concentrations than the vehicle control group (Figure 14A). In the case of serotonin, under 2.5 h treatment, this metabolite presented a trend of increasing concentrations at higher doses of exposure. The groups that received 16 and 160  $\mu\text{g/L}$  presented higher ( $p < 0.001$ ) concentrations than the control group and also higher ( $p < 0.05$ ) than the group that received 0.8  $\mu\text{g/L}$  (Figure 14B). Overall, in the 96 h treatments, there was also a trend of increasing serotonin concentrations at higher doses of exposure. The groups that received 1.6 and 160  $\mu\text{g/L}$  diazepam showed higher ( $p < 0.05$  and  $p <$



0.01, respectively) concentrations than the vehicle control group, and also higher than the group that received 0.8 µg/L of diazepam ( $p < 0.01$ , and  $p < 0.001$ , respectively) (Figure 14B). Other metabolites such as 5-hydroxytryptophan, 5-hydroxyindole acetic acid, and tryptamine involved in the serotonergic system-serotonin pathway were also measured; however, these metabolites presented inconsistent responses (Figures 14C-E).

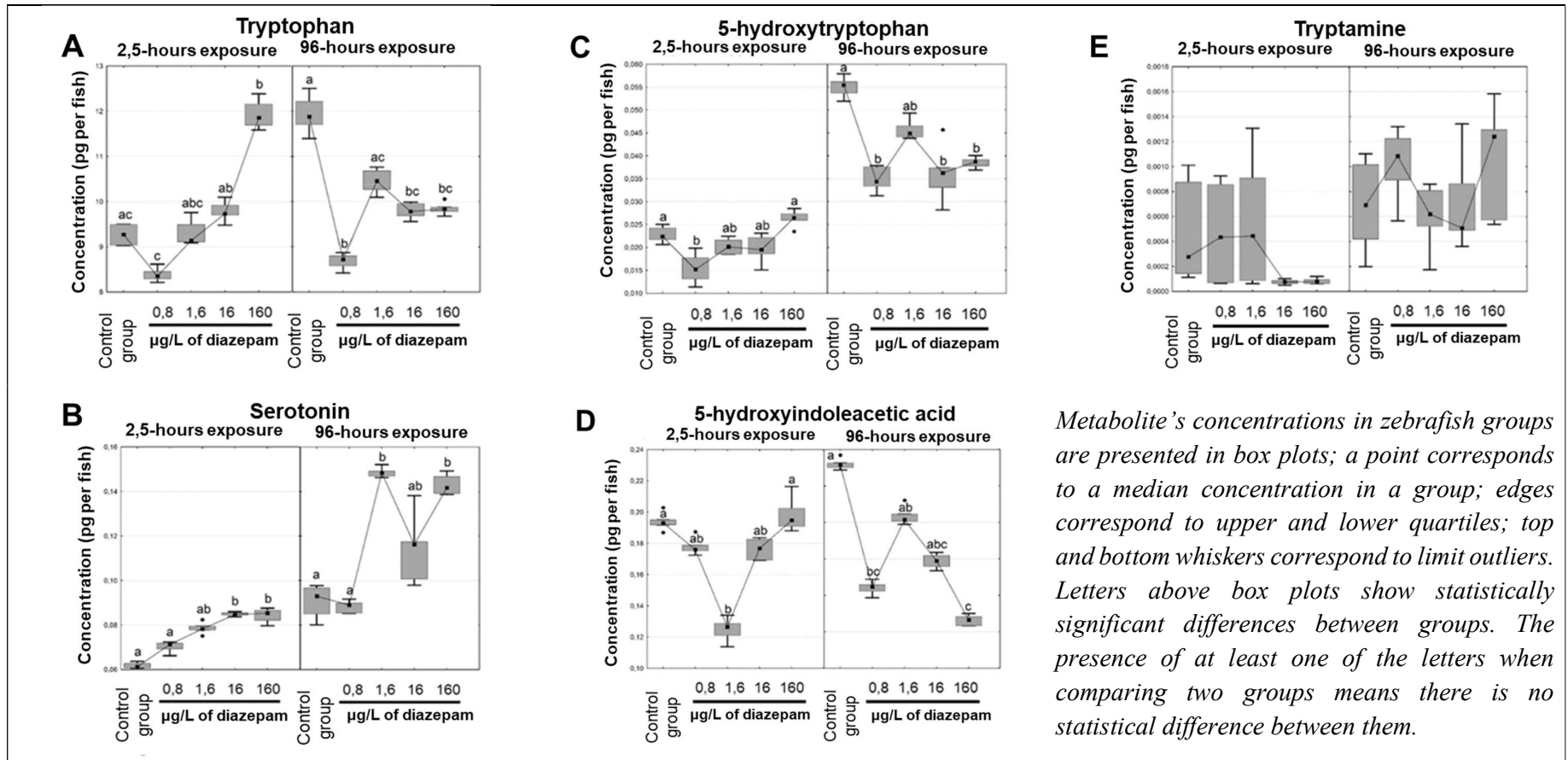


Figure 14 – Metabolites related to serotonergic system.

### *Kynurenine pathway*

The kynurenine and picolinic acid concentrations changed after both short- and long-term exposures to diazepam. Short-term exposure led to the decrease in the levels of kynurenine in the group exposed to 16  $\mu\text{g/L}$  compared to the 160  $\mu\text{g/L}$  and vehicle control groups (Figure 15A). Long-term diazepam exposure led to the decrease of the kynurenine concentrations in the group exposed to 1.6  $\mu\text{g/L}$  compared to the control group, but also in the group exposed to 160  $\mu\text{g/L}$  of diazepam compared to the 16  $\mu\text{g/L}$  and vehicle control groups (Figure 15A). Short-term diazepam exposure led to increased concentrations of the picolinic acid in the groups exposed to 0.8 and 160  $\mu\text{g/L}$  compared to the vehicle control group. Long-term diazepam exposure led to the increase in the levels of picolinic acid in the group exposed to 160  $\mu\text{g/L}$  compared to 1.6  $\mu\text{g/L}$  and the vehicle control group (Figure 15B).

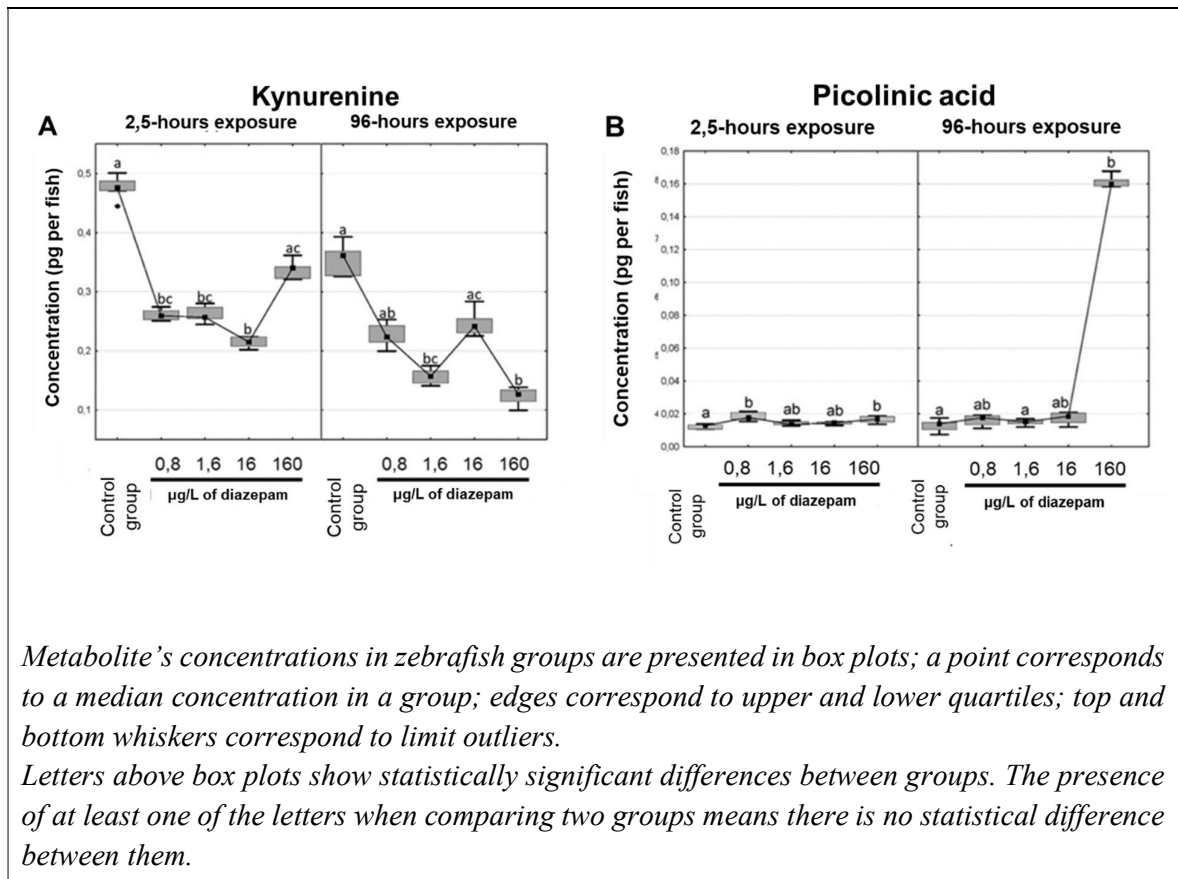


Figure 15 – Metabolites related to kynurenine pathway.

### 3.3.4. Dopaminergic system

This section presents the results of the short- and long-term exposures of diazepam on the levels of endogenous metabolites of the dopaminergic/adrenergic system. Figure 16 shows the scheme of the dopaminergic/adrenergic system metabolism.

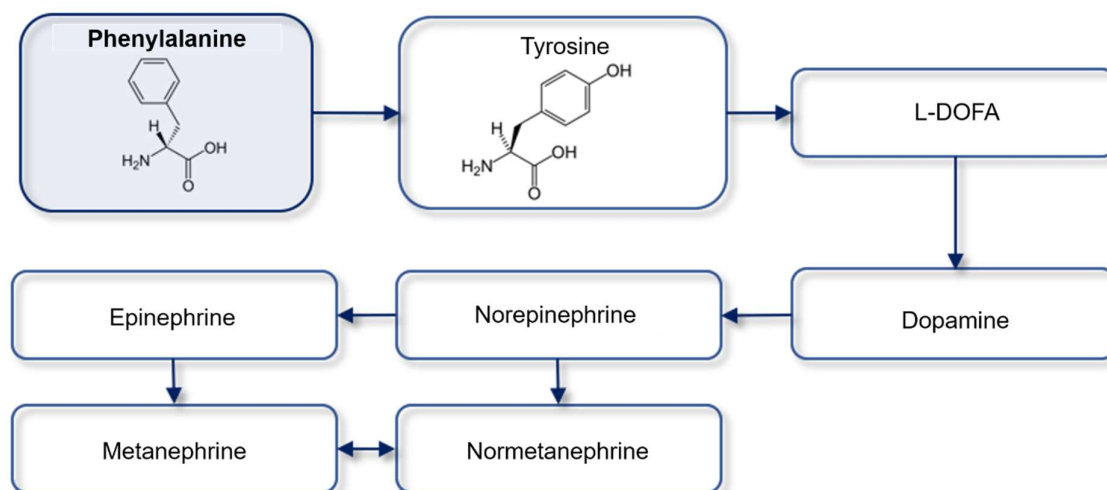


Figure 16 – The scheme of dopaminergic/adrenergic system metabolism.

In short-term exposure, phenylalanine presented significantly higher concentrations in the groups receiving higher doses of diazepam. The group that received 160  $\mu\text{g/L}$  of diazepam showed higher ( $p < 0.01$ ) concentrations than the groups that received 0.8 and 1.6  $\mu\text{g/L}$  (Figure 17A). Under long-term exposure, phenylalanine concentrations in the group that received 160  $\mu\text{g/L}$  of diazepam presented increased concentrations versus the vehicle control ( $p < 0.001$ ). Also, the groups that received 0.8 and 16  $\mu\text{g/L}$  of diazepam presented higher concentrations of phenylalanine compared to the vehicle control ( $p < 0.05$ ) (Figure 17A). After 2.5 h exposure, tyrosine concentrations were significantly higher in the group that received 160  $\mu\text{g/L}$  of diazepam compared to the groups that received 0.8 and 1.6  $\mu\text{g/L}$  of diazepam ( $p < 0.001$ , and  $p < 0.01$ , respectively). In addition, the concentrations of tyrosine in the group exposed to 0.8  $\mu\text{g/L}$  of diazepam were lower than those in the vehicle control group (Figure 17B). In contrast, tyrosine

concentrations after 96 h were lower in the group exposed to 16 and 160  $\mu\text{g/L}$  of diazepam than the vehicle control ( $p < 0.01$ , and  $p < 0.001$ , respectively). Further, the group treated with 160  $\mu\text{g/L}$  of diazepam presented lower concentrations of diazepam compared to the group exposed to 1.6  $\mu\text{g/L}$  of diazepam ( $p < 0.01$ ) (Figure 17B). The other metabolites of the dopaminergic/adrenergic system, including L-DOPA, dopamine, norepinephrine, epinephrine, normetanephrine, and metanephrine, presented occasional statistical differences in their concentrations in both short- and long-term exposures. However, the only systematic trend observed was an increased concentration at 0.8  $\mu\text{g/L}$  doses in short-term exposure for most of these metabolites, but without a clear consistency with the diazepam concentrations (Figures 17C-E and 18A-C).

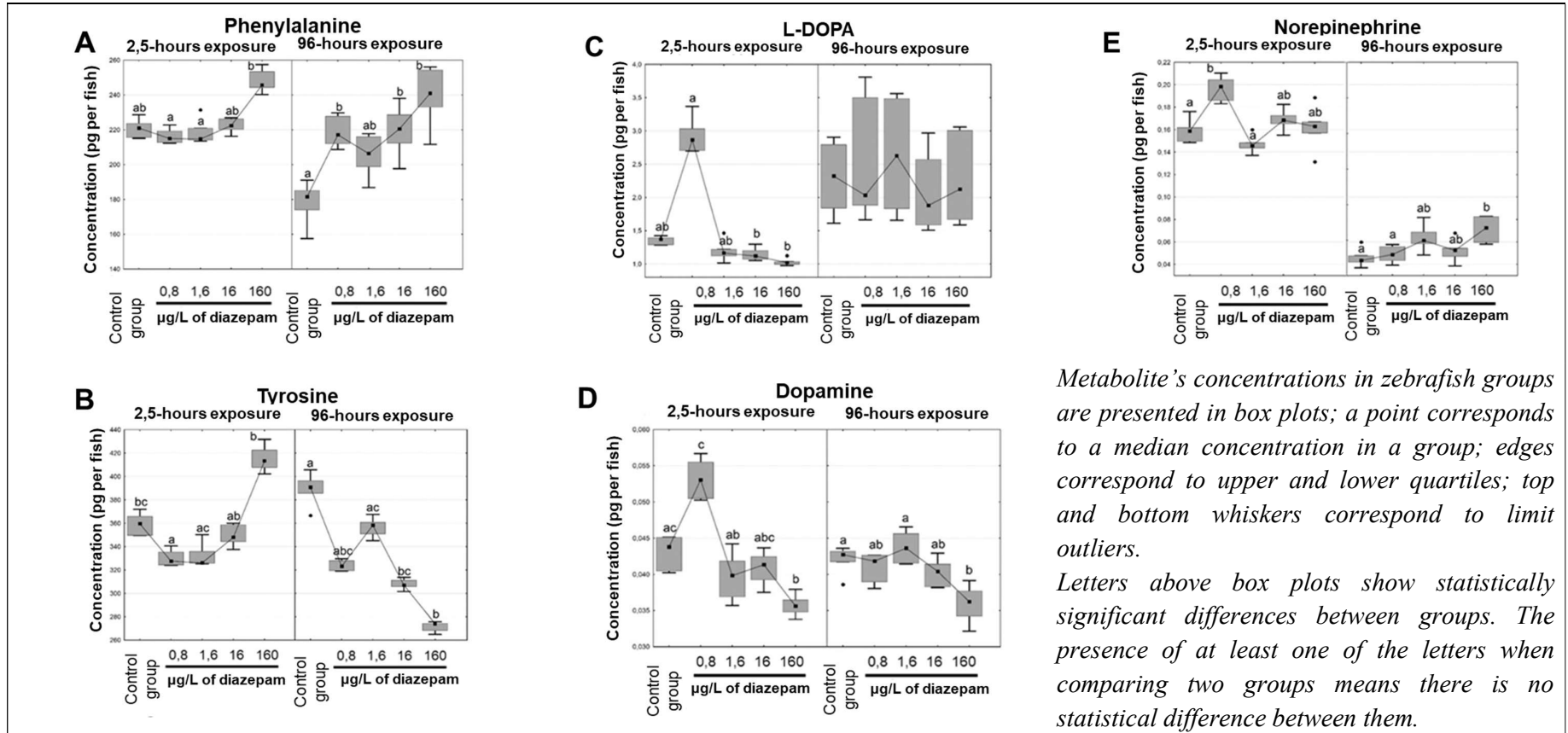


Figure 17 – Metabolites related to dopaminergic/adrenergic system (part 1).

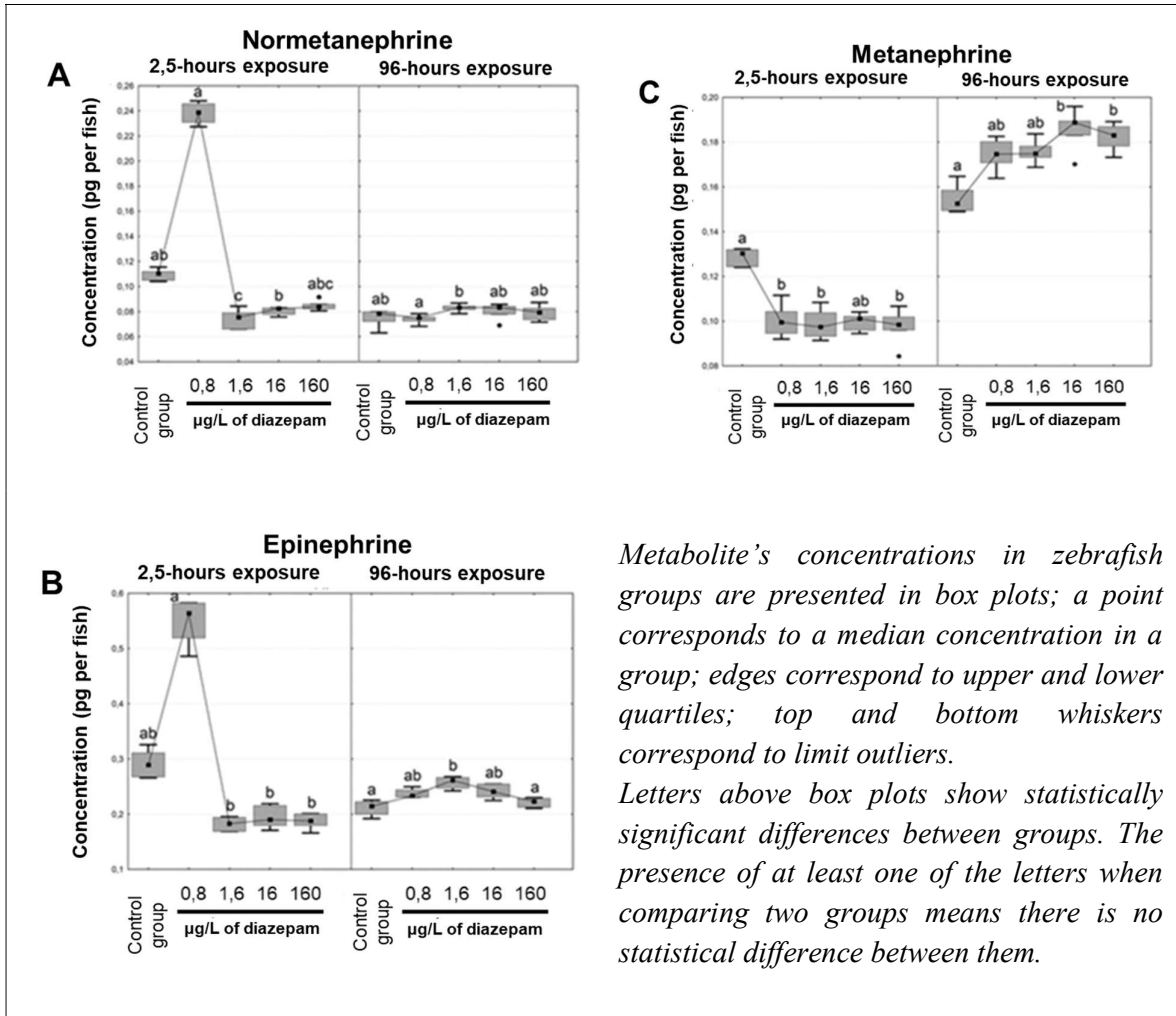


Figure 18 – Metabolites related to dopaminergic/adrenergic system (part 2).

### 3.3.5. Cholinergic system

This section presents the results of the short- and long-term exposures of diazepam on the levels of endogenous metabolites of the cholinergic system.

Choline and acetylcholine concentrations changed both after short- and long-term exposures. In particular, the concentrations of acetylcholine in the group exposed to 16 µg/L of diazepam for a short period were lower than those exposed to 1.6 µg/L. Long-term exposure led to the decrease in acetylcholine concentrations in the groups exposed to 0.8 and 160 µg/L of diazepam compared to vehicle control (Figure 19A). Choline concentrations were higher in the group exposed to 160 µg/L

of diazepam for a short period compared to other exposure groups. Long-term exposure led to the increase of the choline concentrations in the group exposed to 1.6  $\mu\text{g/L}$  of diazepam compared to the group exposed to 0.8  $\mu\text{g/L}$  and vehicle control group (Figure 19B).

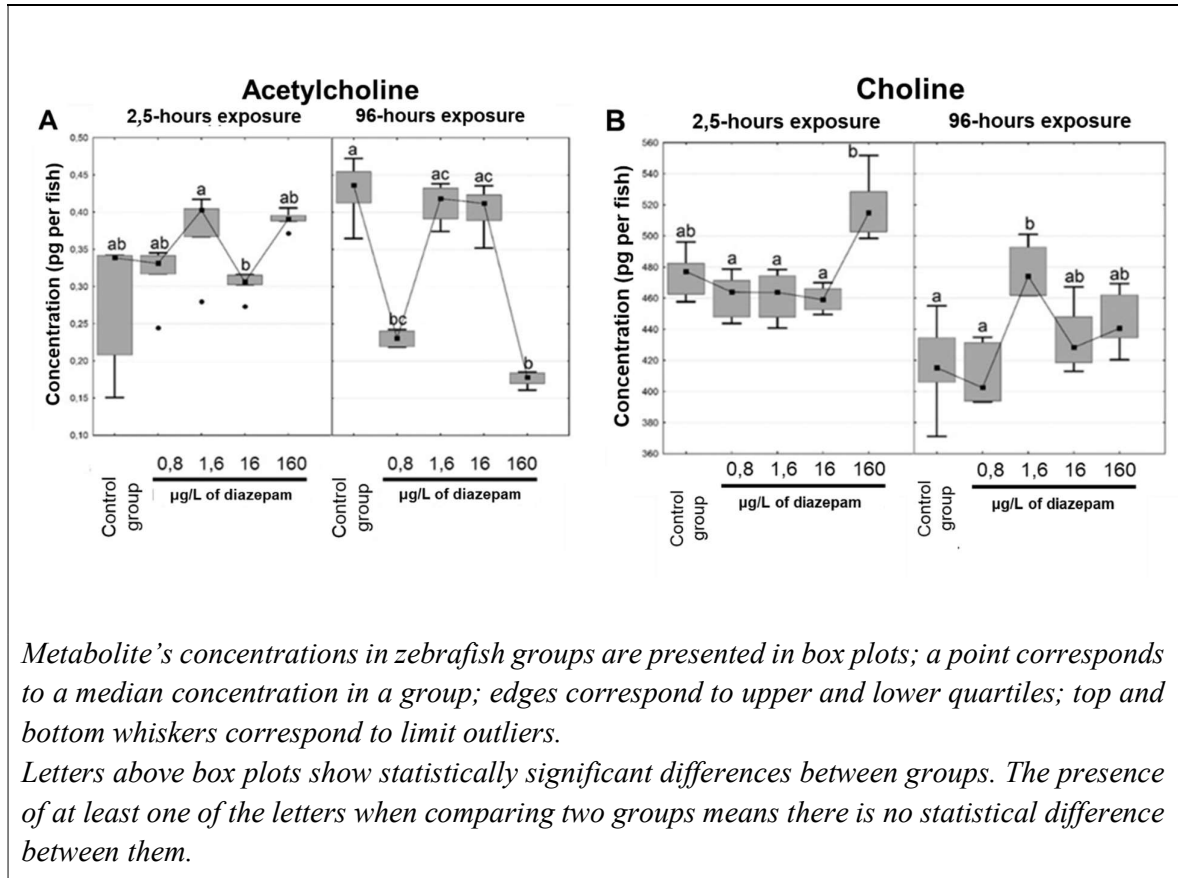


Figure 19 – Metabolites related to cholinergic system.

### 3.3.6. Other metabolites related to neurotransmission

This section presents the results of the short- and long-term exposures of diazepam on the levels of endogenous metabolites of the neurotransmission-related pathways.

Microbial tryptophan catabolism metabolites (indole-3-carboxaldehyde, indole-3-acetic acid, indole-3-butyric acid, indole-3-lactic acid, indole-3-acrylic acid, and indole-3-propionic acid) and other biological compounds (cortisol, citrulline, biopterin, and neopterin) involved in neurotransmission displayed inconsistent



changes and were hard to interpret across different diazepam concentrations for both the 2.5 h and 96 h experiments.

### 3.4. Determination of the half-lethal concentration of 5F-APINAC

To determine the concentrations of the working solutions of 5F-APINAC, half-lethal concentration (LC<sub>50</sub>) of 5F-APINAC was determined. The results of the assessment are presented in Table 13 and Figure 20.

Table 13 – Survival rates of zebrafish larvae in the LC<sub>50</sub> assessment

Experimental group	Nº of embryos in the group	Nº of dead embryos	Survival rate (%)
10 uM 5F-APINAC	20	0	100
20 uM 5F-APINAC	20	2	90
40 uM 5F-APINAC	20	5	75
80 uM 5F-APINAC	20	13	35
100 uM 5F-APINAC	20	18	10
Positive control (4 ug/l 3,4-dichloroaniline in 1% solution of DMSO in E3 medium)	20	15	25
Negative control (E3 medium)	20	1	95
Carrier solvent control (1% DMSO in E3 medium)	20	0	100

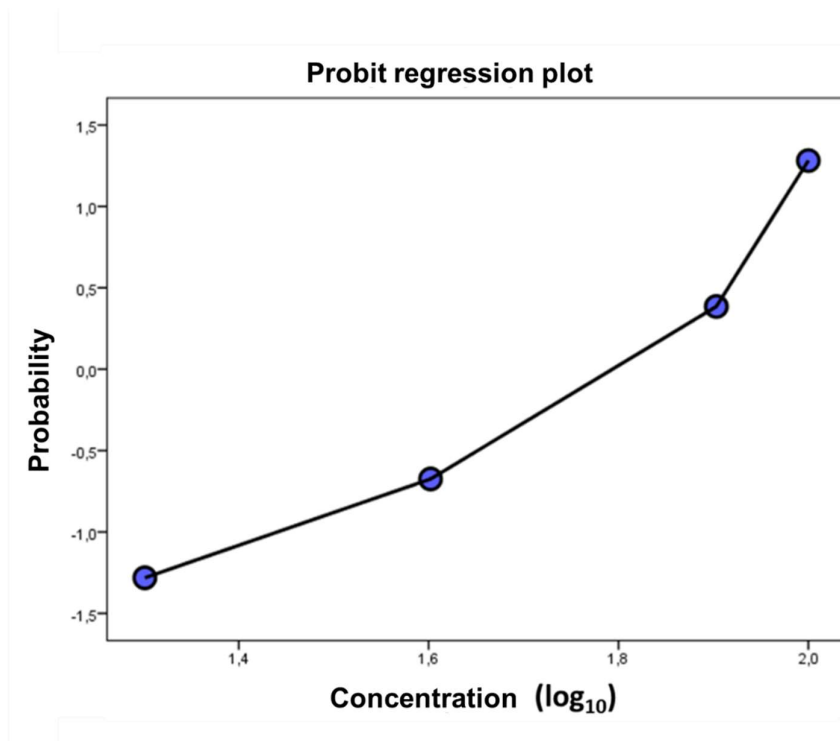


Figure 20 – Probit-regression analysis of half-lethal concentration assessment of 5F-APINAC.

Probit-regression analysis had shown that LC<sub>50</sub> for 5F-APINAC was 55.0 uM (95% CI: 44.3-68.7 uM). The survival rate of the embryos in the negative control – 95%, in the vehicle control – 100%; lethality in the positive control was 75%. This data is within the acceptance criteria for the test (survival rate in the negative control and vehicle control > 90%, lethality in the positive control > 30%).

5F-APINAC has demonstrated that it has levels of toxicity compared to other cannabinoids. Thus, for zebrafish larvae, the lethality of  $\Delta^9$ -THC and synthetic cannabinoids CP 55,940 and WIN 55,212-2 are 10, 50, and 3 uM, respectively [45].

Based on the obtained results and the results about the toxicity of the defluorinated analog of 5F-APINAC – APINAC [210] – 10 uM concentration of 5F-APINAC was used as the highest.

### **3.5. Neurotransmitters metabolomics after short- and long-term exposure of 5F-APINAC in zebrafish larvae**

In order to investigate the possibility of the usage of the zebrafish as a model organism in the assessment of the pharmacological action of the neurotropic drugs of cannabimimetic action using the pharmacometabolomic approach, the concentrations of the metabolites of GABAergic, serotonergic, dopaminergic/adrenergic, cholinergic neurotransmitter systems, aspartic acid system, kynurenine, and indole pathway metabolites, and other related metabolites after the exposure of 5F-APINAC at the doses of 0.001, 0.01, 0.1, 1.0, and 10  $\mu\text{M}$  for short- (4 h) and long-term (96 h). 5F-APINAC is a pharmacological compound with cannabimimetic properties. There were no complex investigations made in the field of the action of cannabimimetics action on the CNS.

. The list of the measured compounds is represented in Table 1. The method of quantification of these compounds was developed and validated. The validation results of the method are presented in chapter 3, section 2.

The main statistical differences in the concentrations of endogenous metabolites after short-term 5F-APINAC exposure are presented in Table 14. The main statistical differences in the concentrations of endogenous metabolites after long-term 5F-APINAC exposure are shown in Table 15.

Table 14 – Detailed information on the statistical differences across experimental groups after short-term 5F-APINAC exposure

Metabolite	Contr. vs 1	Contr. vs 2	Contr. vs 3	Contr. vs 4	Contr. vs 5	1 vs 2	1 vs 3	1 vs 4	1 vs 5	2 vs 3	2 vs 4	2 vs 5	3 vs 4	3 vs 5	4 vs 5
GABA	-	-	-	-	<0,01 ↓	-	<0,01 ↓	-	<0,001 ↓	-	-	<0,01 ↓	-	-	<0,01 ↓
Glutamic acid	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Glutamine	-	-	-	-	<0,001 ↓	-	-	-	<0,001 ↓	-	-	<0,01 ↓	-	<0,05 ↓	<0,05 ↓
Tryptophan	-	-	-	-	-	-	-	-	<0,05 ↓	-	-	-	-	-	-
5-hydroxytryptophan	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Serotonin	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
5-hydroxyindole acetic acid	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Tryptamine	-	-	-	<0,05 ↓	<0,001 ↓	-	-	-	<0,001 ↓	-	-	<0,001 ↓	-	<0,001 ↓	<0,01 ↓
Phenylalanine	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Tyrosine	-	-	-	-	<0,05 ↓	-	-	-	<0,01 ↓	-	-	-	-	-	<0,05 ↓
L-DOPA	-	-	<0,05 ↑	-	-	-	-	-	-	-	-	-	-	-	-
Dopamine	<0,01 ↑	-	<0,001 ↑	<0,05 ↑	<0,05 ↑	-	-	-	-	<0,01 ↑	-	-	-	-	-
Norepinephrine	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Normetanephrine	-	-	-	-	<0,01 ↓	-	-	-	<0,001 ↓	-	-	<0,05 ↓	-	-	<0,001 ↓
Epinephrine	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Metanephrine	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Aspartic acid	-	-	<0,01 ↓	-	<0,01 ↓	-	<0,001 ↓	-	<0,001 ↓	<0,01 ↓	-	<0,05 ↓	-	-	-
Asparagine	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Acetylcholine	<0,01 ↑	<0,001 ↑	<0,001 ↑	<0,001 ↑	<0,001 ↑	-	<0,001 ↑	-	-	<0,001 ↑	-	-	<0,001 ↓	<0,001 ↓	-



Table 15 – Detailed information on the statistical differences across experimental groups after short-term 5F-APINAC exposure

Metabolite	Contr. vs 1	Contr. vs 2	Contr. vs 3	Contr. vs 4	Contr. vs 5	1 vs 2	1 vs 3	1 vs 4	1 vs 5	2 vs 3	2 vs 4	2 vs 5	3 vs 4	3 vs 5	4 vs 5
GABA	-	-	-	-	<0,001 ↓	-	<0,05 ↑	<0,001 ↑	<0,001 ↓	-	<0,05 ↑	<0,001 ↓	-	<0,001 ↓	<0,001 ↓
Glutamic acid	-	-	-	<0,05 ↑	-	-	-	<0,001 ↑	-	-	<0,01 ↑	-	<0,01 ↑	-	<0,05 ↑
Glutamine	-	-	-	-	<0,05 ↑	-	-	<0,05 ↑	<0,01 ↑	-	-	-	-	<0,05 ↑	-
Tryptophan	-	-	<0,05 ↓	<0,05 ↓	<0,001 ↑	-	-	-	<0,001 ↑	-	-	<0,001 ↑	-	<0,001 ↑	<0,001 ↑
5-hydroxytryptophan	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Serotonin	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
5-hydroxyindole acetic acid	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Tryptamine	-	-	<0,01 ↓	-	-	-	-	-	<0,05 ↑	-	-	-	-	<0,001 ↑	<0,05 ↑
Phenylalanine	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Tyrosine	-	-	<0,01 ↓	-	-	<0,05 ↓	-	-	-	<0,001 ↓	-	-	-	<0,05 ↑	-
L-DOPA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Dopamine	<0,05 ↑	<0,05 ↑	<0,001 ↑	-	-	-	-	<0,001 ↓	<0,001 ↓	-	<0,001 ↓	<0,001 ↓	<0,001 ↓	<0,001 ↓	-
Norepinephrine	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Normetanephrine	-	-	-	-	-	-	<0,05 ↑	-	-	-	-	-	-	-	-
Epinephrine	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Metanephrine	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Aspartic acid	-	-	-	-	-	-	-	-	<0,01 ↑	-	-	-	-	<0,05 ↑	-
Asparagine	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Acetylcholine	-	-	<0,001 ↑	<0,001 ↓	<0,001 ↓	-	<0,001 ↑	<0,001 ↓	<0,001 ↓	<0,05 ↑	<0,001 ↓	<0,001 ↓	<0,001 ↓	<0,001 ↓	-



### 3.5.1. Morphological characteristics

In acute exposure, there were no visible malformations in any group. In chronic exposure, the groups of larvae exposed to 5F-APINAC at the highest concentration (10  $\mu$ M) presented multiple morphological and developmental alterations. Approximately 60% of the larvae were unhatched, 20% had a curved tail related to spinal cord malformations, and all of them presented hyperpigmentation (Figure 21). The groups of larvae exposed to all other concentrations of 5F-APINAC and the vehicle control groups in chronic exposure did not present alterations in morphology or development.



Figure 21 – Zebrafish larvae after the exposure to 5F-APINAC at a concentration of 10  $\mu$ M for a long-term.



### 3.5.2. GABAergic system

This section presents the results of the short- and long-term exposure of 5F-APINAC on the levels of endogenous metabolites of the GABAergic and aspartic acid systems.

GABA presented the lowest concentration at the highest dose of exposure (10  $\mu\text{M}$  5F-APINAC) in the acute ( $p < 0.01$ ) and chronic ( $p < 0.001$ ) experiments compared to the vehicle control group (Figure 22A). In acute exposure, there was a descending trend of glutamine concentrations, being the group that received 10  $\mu\text{M}$  5F-APINAC the one that had the lowest value ( $p < 0.001$ ) compared to the vehicle control (Figure 22B). In contrast, in chronic exposure, glutamine concentrations presented an overall ascending trend being higher at the highest doses of exposure ( $p < 0.05$ ) (Figure 22B). Glutamic acid concentrations demonstrated several individual significant differences in acute and chronic exposures but without clear dose-dependent trends.

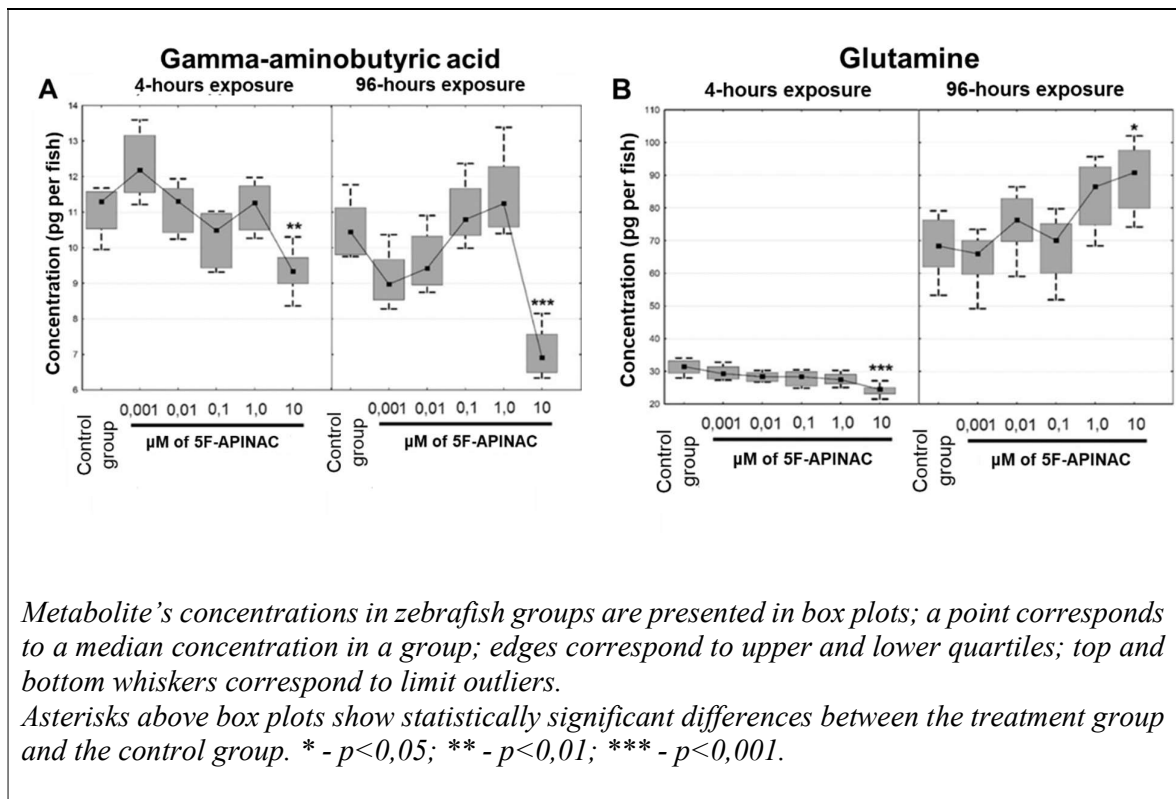


Figure 22 – Metabolites related to GABAergic and glutaminergic system.

### 3.5.3. Serotonergic system and kynurenine pathway

This section presents the results of the short- and long-term exposures of 5F-APINAC on the levels of endogenous metabolites of the serotonergic system and kynurenine pathway.

#### *Serotonergic system*

Tryptophan concentrations in acute exposure did not have significant differences among groups. In chronic exposure, tryptophan concentrations presented an overall descending trend with a statistically neat increase of concentration at 10  $\mu$ M 5F-APINAC ( $p < 0.001$ ) as compared to the vehicle control group (Figure 23A). Tryptamine concentrations in acute exposure presented lower ( $p < 0.05$ ) concentrations in the intervention groups at higher doses versus the vehicle control. This was especially clear in the group receiving 10  $\mu$ M 5F-APINAC ( $p < 0.001$ ) (Figure 23B). The concentrations in the chronic exposure experiment were characterized by very low values in all groups (below 0.005 pg/fish) (Figure 23B). 5-Hydroxytryptophan, serotonin, and 5-hydroxyindole acetic acids did not present any statistical differences among groups.

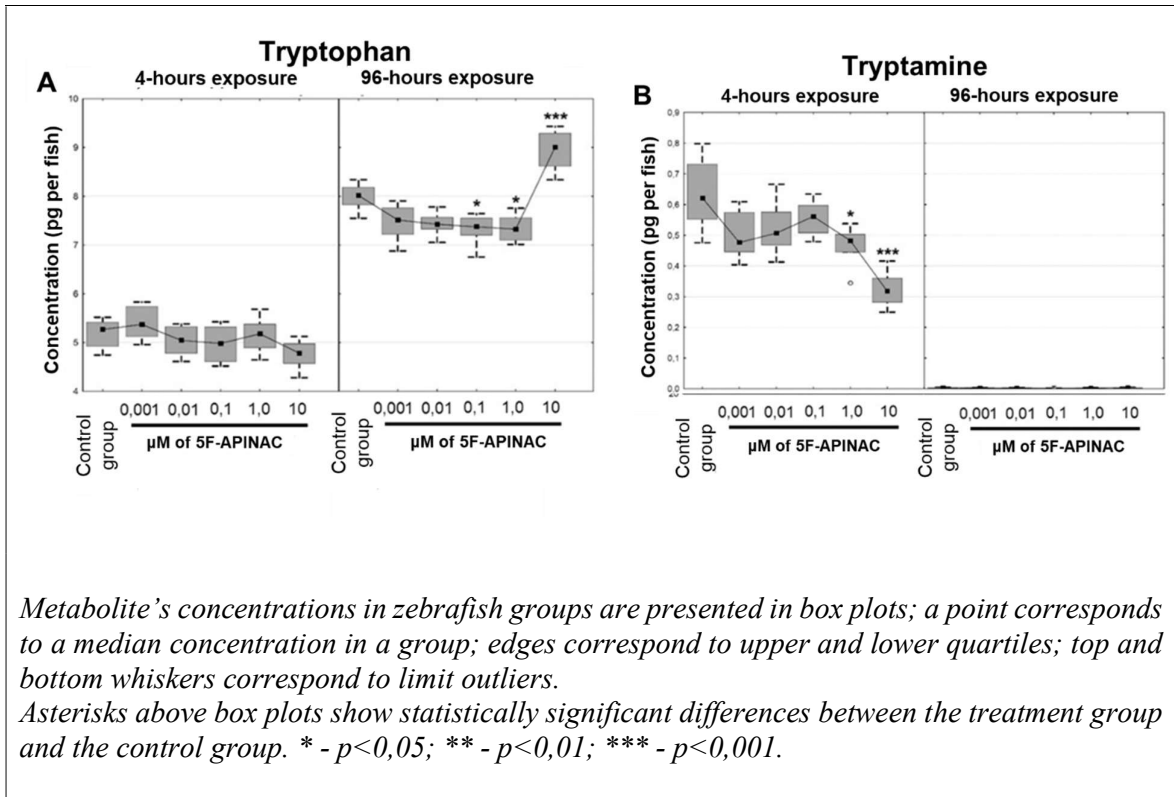


Figure 23 – Metabolites related to serotonergic system.

### ***Kynurenine pathway***

Xanthurenic acid and picolinic acid were the only metabolites that presented clear trajectories in this pathway. Xanthurenic acid concentrations were not different among groups in acute exposure (Figure 24A), but in chronic exposure, there was a descending trend with an apparent increase in the group that received 10  $\mu\text{M}$  5F-APINAC ( $p < 0.05$  compared to control) (Figure 24A). Picolinic acid concentrations were not affected during acute exposure (Figure 24B), but in chronic exposure, the groups receiving the highest doses (1.0 and 10  $\mu\text{M}$  5F-APINAC) had drastic increases ( $p < 0.001$ ) (Figure 24B). Other metabolites involved in the kynurenine pathway (kynurenine, kynurenic acid, anthranilic acid, and quinolinic acid) did not have clear trends (Figure 24 C-E).

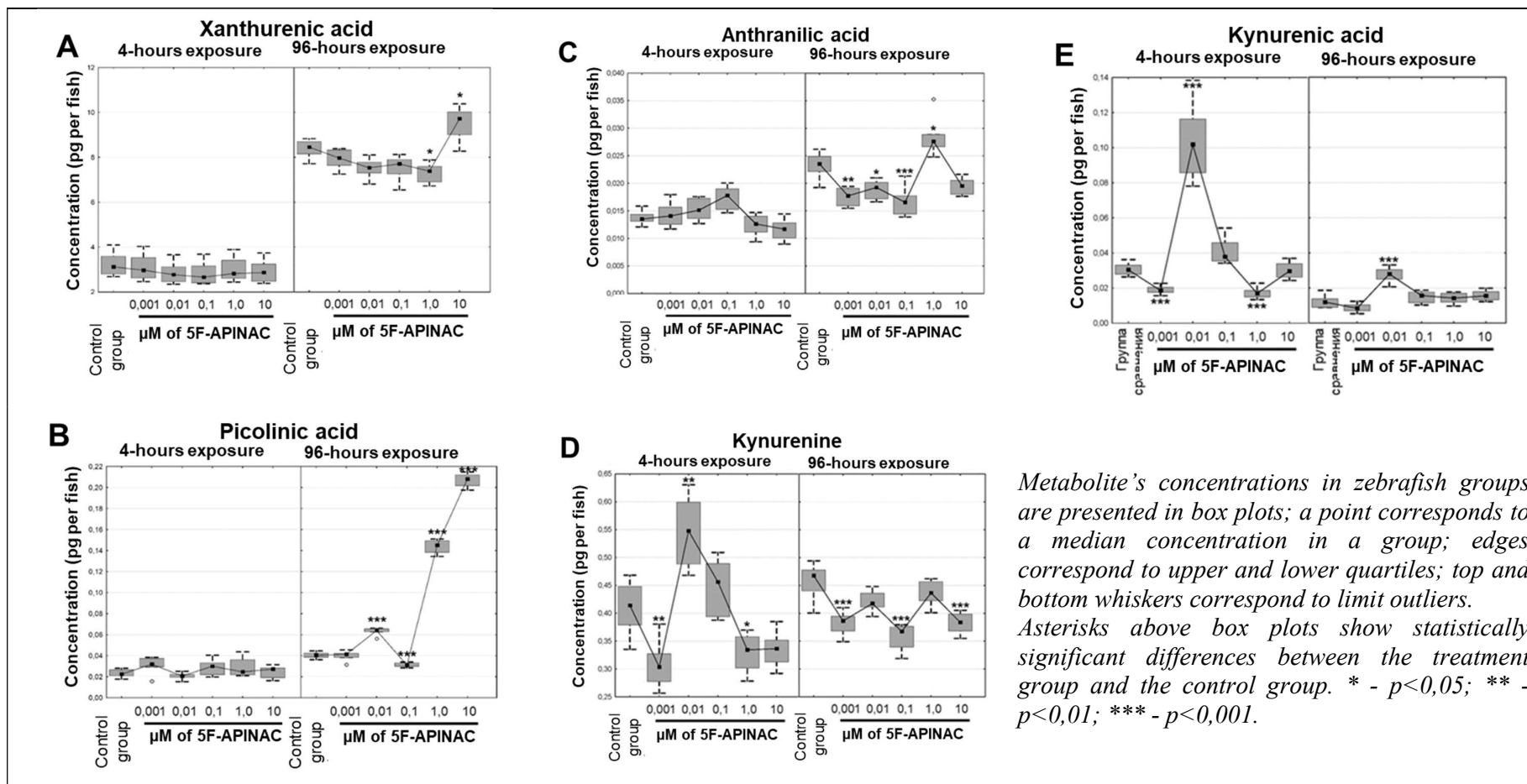


Figure 24 – Metabolites related to kynurenine pathway.

### 3.5.4. Dopaminergic system

This section presents the results of the short- and long-term exposures of 5F-APINAC on the levels of endogenous metabolites of the dopaminergic/adrenergic system.

The only metabolite in this neurotransmitter system that presented consistent trajectories was dopamine. In acute exposure, most of the intervention groups had higher ( $p < 0.05$ ) concentrations than the vehicle control (Figure 25). In chronic exposure, there was also a similar trend of increases in the concentrations at higher doses; however, the groups receiving the highest doses (1.0  $\mu\text{M}$  and 10  $\mu\text{M}$ ) presented a concentration drop (Figure 25). Phenylalanine, tyrosine, L-DOPA, norepinephrine, normetanephrine, epinephrine, and metanephrine did not have clear trends among groups.

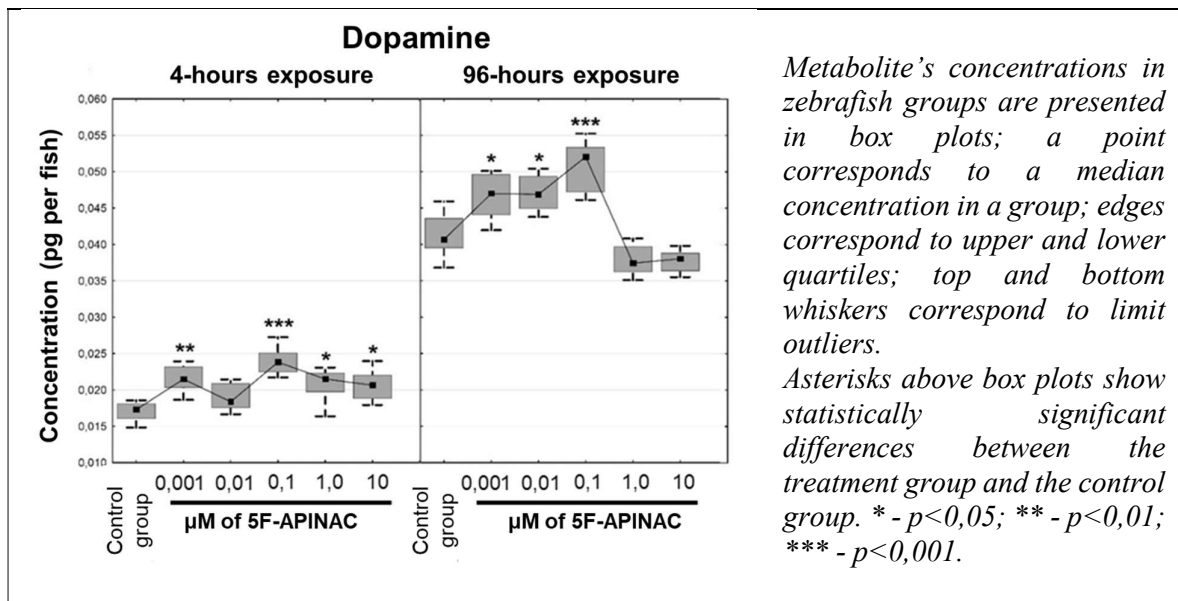


Figure 25 – Metabolites related to dopaminergic system.

### 3.5.5. Cholinergic system

This section presents the results of the short- and long-term exposures of 5F-APINAC on the levels of endogenous metabolites of the cholinergic system.

In acute exposure, the neurotransmitter acetylcholine had significantly higher concentrations in all intervention groups compared to the vehicle control ( $p < 0.01$ ) (Figure 26). There was a similar ascending trend in chronic exposure, but there was a significant drop in the groups exposed to 1.0 and 10  $\mu\text{M}$  5F-APINAC compared to the vehicle control ( $p < 0.001$ ). (Figure 26). Choline, a precursor of acetylcholine, presented no trend among groups.

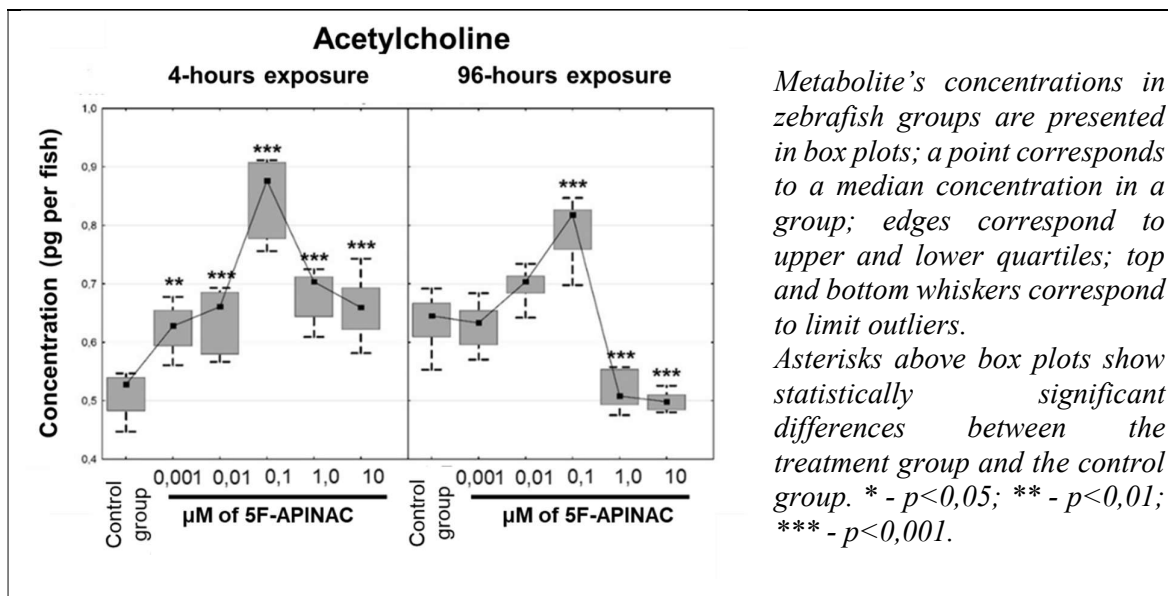


Figure 26 – Metabolites related to cholinergic system.

### 3.5.6. Other metabolites related to neurotransmission

This section presents the results of the short- and long-term exposures of 5F-APINAC on the levels of endogenous metabolites of the neurotransmission-related pathways.

Concentrations of aspartic acid were lower in the groups exposed to 0.1 and 10  $\mu\text{M}$  of 5F-APINAC for the short-term compared to the vehicle control group.

None of the microbial tryptophan catabolism metabolites (indole-3-carboxaldehyde, indole-3-acetic acid, indole-3-butyric acid, indole-3-lactic acid, indole-3-acrylic acid, and indole-3-propionic acid) were significantly altered in acute or chronic experiments.

Citrulline was the only metabolite that presented interpretable results from the extra available metabolites related to neurotransmission, which, however, were not classified in any pathway or system. During acute exposure, citrulline concentrations presented a descending trend within all the intervention groups versus the vehicle control ( $p < 0.05$ ) (Figure 27). In chronic exposure, the group that was exposed to the highest dose (10  $\mu\text{M}$  5F-APINAC) had a dramatically higher concentration compared to the control group ( $p < 0.001$ ) (Figure 27). Cortisol, biopterin, and neopterin were not informative.

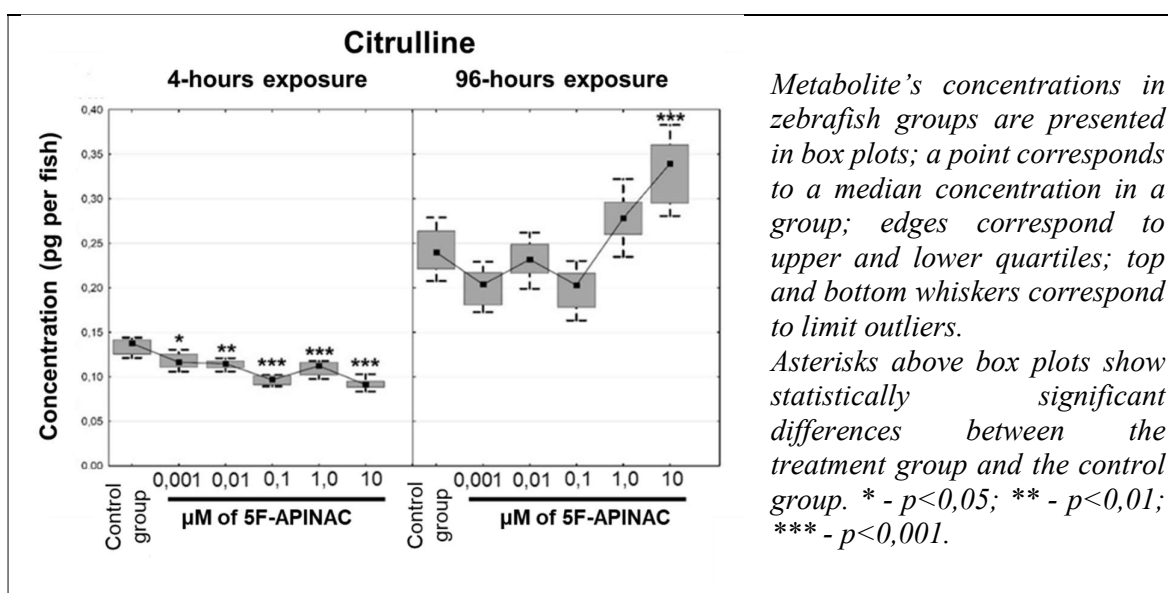


Figure 27 – The concentration graph of citrulline.

### 3.6. Behavioral study of 5F-APINAC exposure in zebrafish larvae

To confirm the effects of 5F-APINAC of the CNS and to investigate the correlations between behavioral effects and metabolomics changes induced by 5F-APINAC, behavioral studies were conducted.

Short-term 5F-APINAC exposure resulted in the dose-dependent decrease of the total distance traveled by zebrafish larvae (Table 16 and Figures 28 and 30) [23, 25, 40]. Long-term 5F-APINAC exposure was also connected to lowering the total distance traveled by zebrafish (Table 16 and Figures 29 and 30) [23, 199]. The

exposure of the highest dose of 5F-APINAC resulted in a dramatic decrease of locomotor activity, which lasted until the end of the exposure on the second day of the experiment (Figures 28 and 29) [45, 224].

Table 16 – The values of total distance traveled by zebrafish larvae exposed to different concentrations of 5F-APINAC for short and long periods

<b>Total distance travelled</b>		
<b>Groups</b>	<b>Mean ± SD (mm)</b>	<b><i>p</i>-value compared to vehicle control</b>
<b>4 h exposure</b>		
Vehicle control	9957,3 ± 885,5	—
Experimental group №1 (0,001 uM)	8140,2±882,7	NS*
Experimental group №2 (0,01 uM)	7969,8±530,4	NS*
Experimental group №3 (0,1 uM)	7518,0±533,5	>0,01
Experimental group №4 (1,0 uM)	5496,1±461,3	>0,001
Experimental group №5 (10 uM)	3608,4±285,8	>0,001
<b>48 h exposure</b>		
Vehicle control	51718,4±3018,6	—
Experimental group №1 (0,001 uM)	47797,4±2271,9	NS*
Experimental group №2 (0,01 uM)	45747,2±2515,5	>0,01
Experimental group №3 (0,1 uM)	46283,6±2156,1	>0,05
Experimental group №4 (1,0 uM)	43150,3±2098,0	>0,001
Experimental group №5 (10 uM)	29406,8±1783,8	>0,001

\* - not significant ( $p > 0,05$ ).



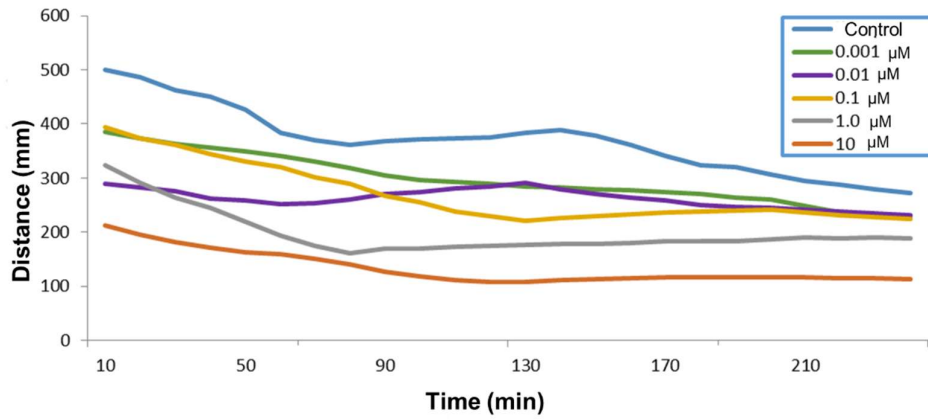


Figure 28 – Total distance traveled by zebrafish larvae in 4 h exposure to 5F-APINAC.

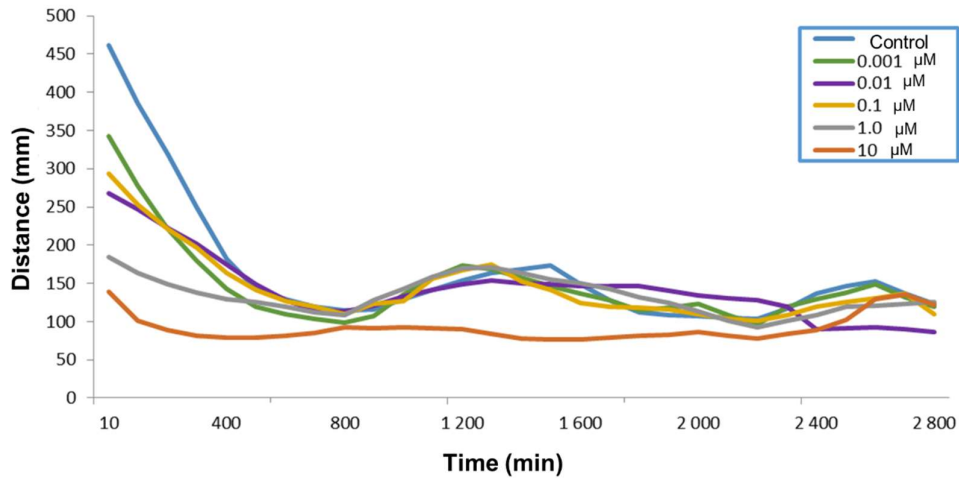


Figure 29 – Total distance traveled by zebrafish larvae in 48 h exposure to 5F-APINAC.

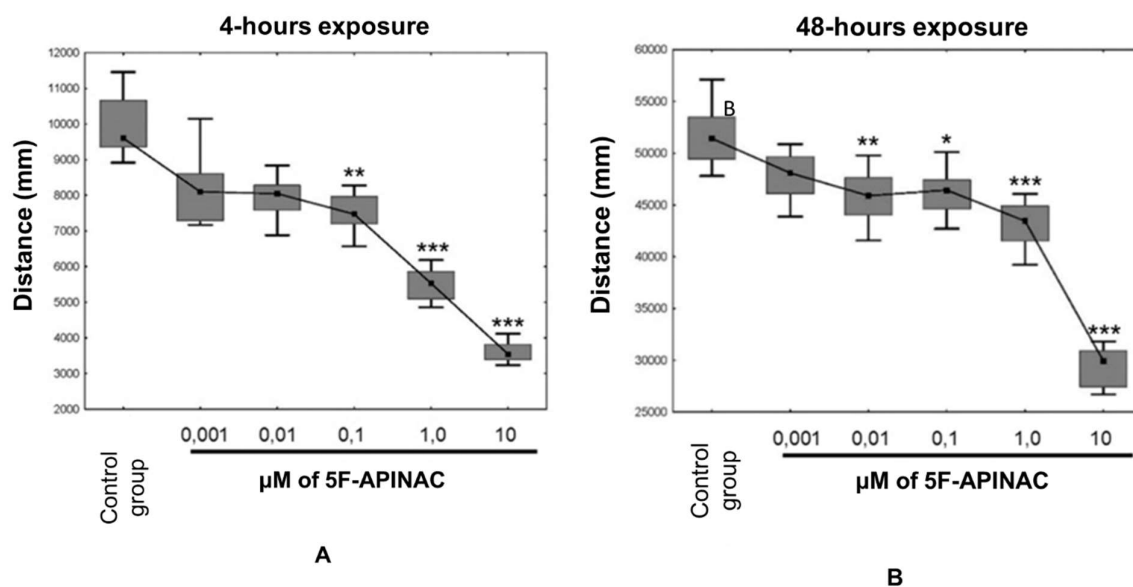


Figure 30 – Total distance traveled by zebrafish larvae in 4 and 48 h exposures to 5F-APINAC.

Several neurotransmitters have been shown to have statistically significant correlations with the total distance traveled. The results of the correlation analysis are presented in Table 17 and Figures 31-37.

Table 17 – Correlations between the concentrations of endogenous metabolites and total distance traveled after 4 h exposure to 5F-APINAC

Metabolite	Spearman's rank correlation coefficient <i>r</i>	<i>p</i> -value
GABA	0,58	<0,001
Glutamic acid	0,22	—
Glutamine	0,81	<0,001
Tryptophan	0,47	<0,01
5-hydroxytryptophan	0,06	—
Serotonin	0,11	—
5-hydroxyindole acetic acid	0,13	—
Tryptamine	0,82	<0,001
Phenylalanine	0,52	<0,01
Tyrosine	0,57	<0,001
L-DOPA	-0,08	—
Dopamine	-0,18	—
Norepinephrine	0,21	—

<b>Metabolite</b>	<b>Spearman's rank correlation coefficient r</b>	<b>p-value</b>
Normetanephrine	0,50	<0,01
Epinephrine	0,05	—
Metanephrine	0,16	—
Aspartic acid	0,62	<0,001
Asparagine	0,33	<0,05
Acetylcholine	-0,25	—
Choline	0,53	<0,001
Kynurenine	0,42	<0,05
Kynurenic acid	0,23	—
Anthranilic acid	0,51	<0,01
Xanthurenic acid	0,27	—
Quinolinic acid	0,45	<0,01
Picolinic acid	0,04	—
Indole-3-carboxaldehyde	0,55	<0,001
Indole-3-acetic acid	0,06	—
Indole-3-butyric acid	0,22	—
Indole-3-lactic acid	0,29	—
Indole-3-acrylic acid	0,35	<0,05
Indole-3-propionic acid	0,39	<0,05
Cortisol	0,25	—
Citrulline	0,77	<0,001
Biopterin	0,06	—
Neopterin	0,25	—

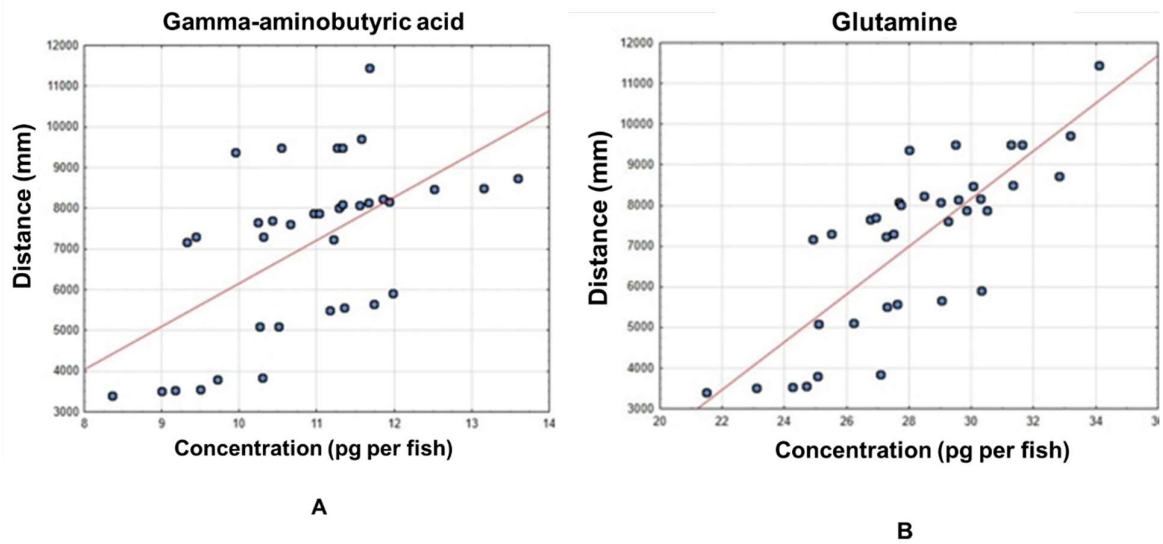


Figure 31 – Correlation between metabolites related to neurotransmission and total distance traveled by zebrafish larvae after 4 h exposure to 5F-APINAC (part 1).

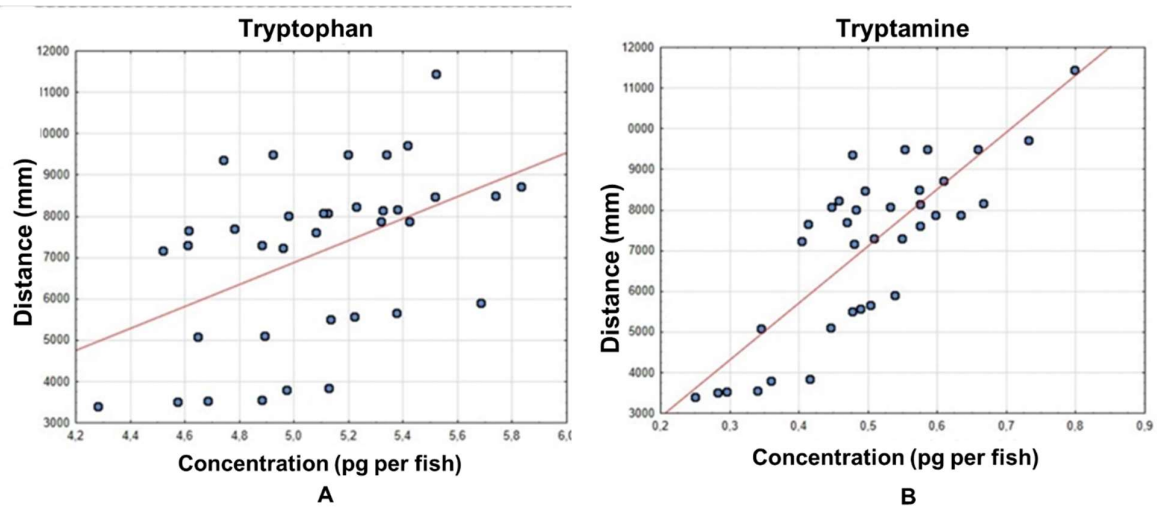


Figure 32 – Correlation between metabolites related to neurotransmission and total distance traveled by zebrafish larvae after 4 h exposure to 5F-APINAC (part 2).

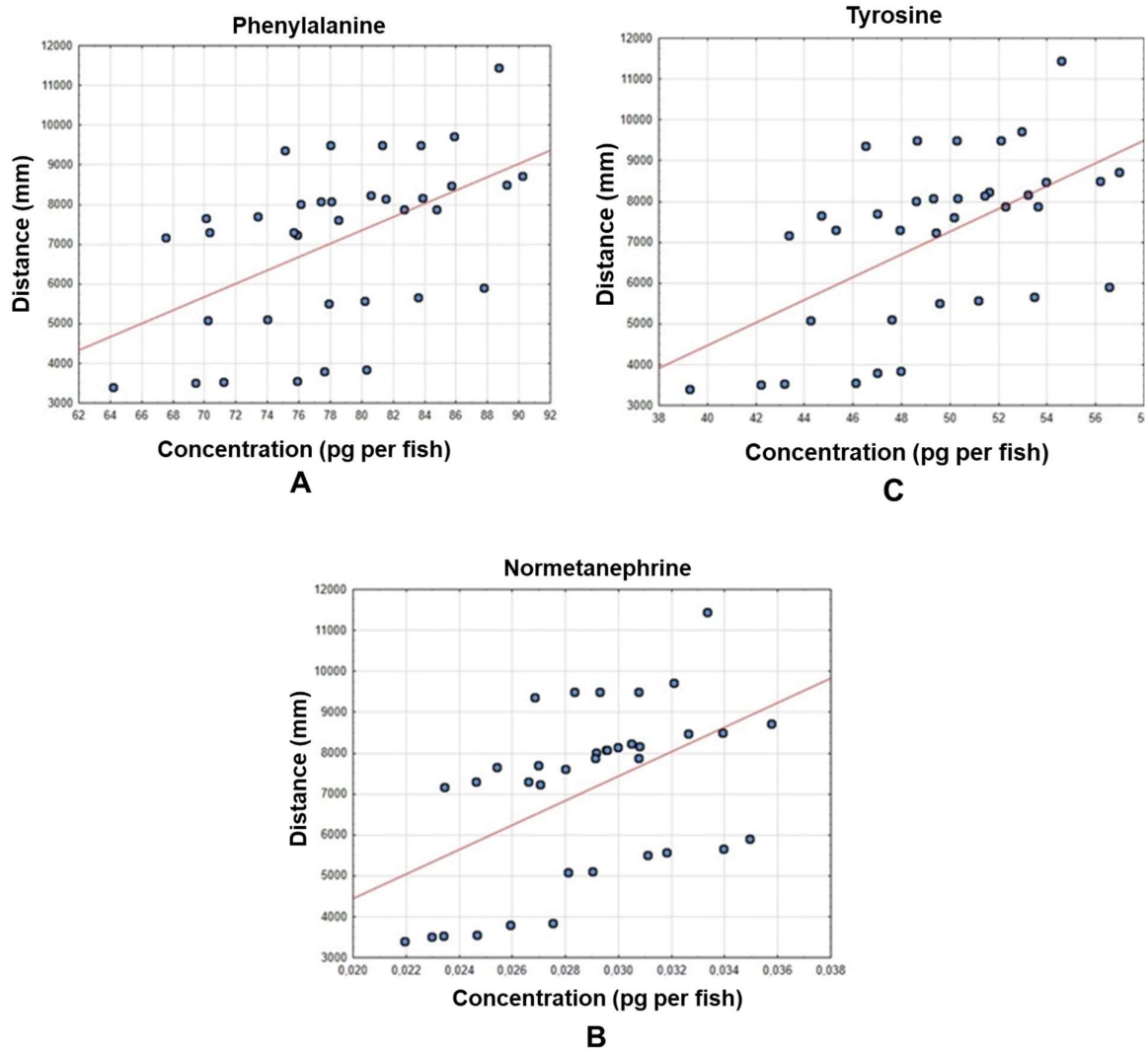


Figure 33 – Correlation between metabolites related to neurotransmission and total distance traveled by zebrafish larvae after 4 h exposure to 5F-APINAC (part 3).

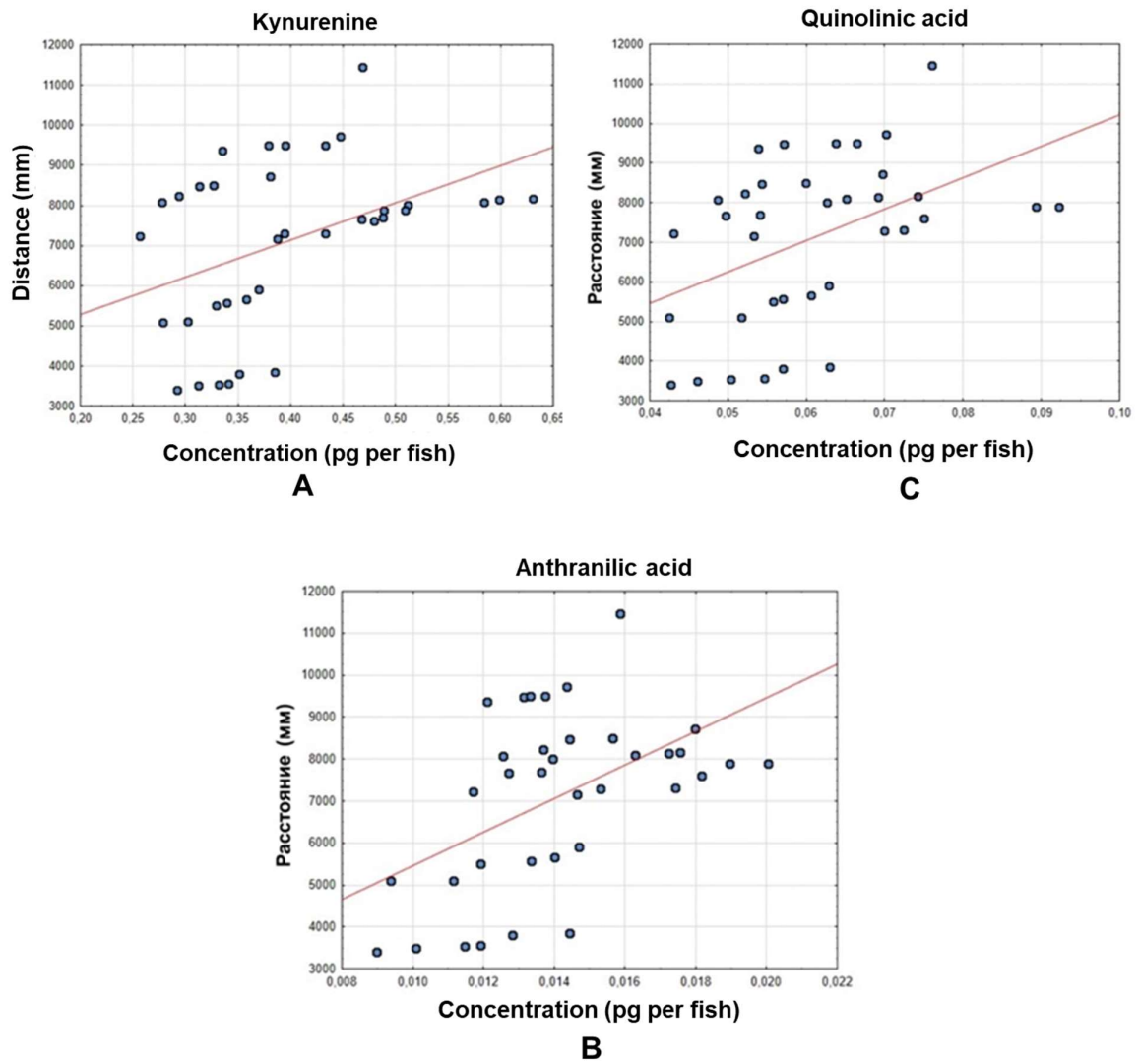


Figure 34 – Correlation between metabolites related to neurotransmission and total distance traveled by zebrafish larvae after 4 h exposure to 5F-APINAC (part 4).

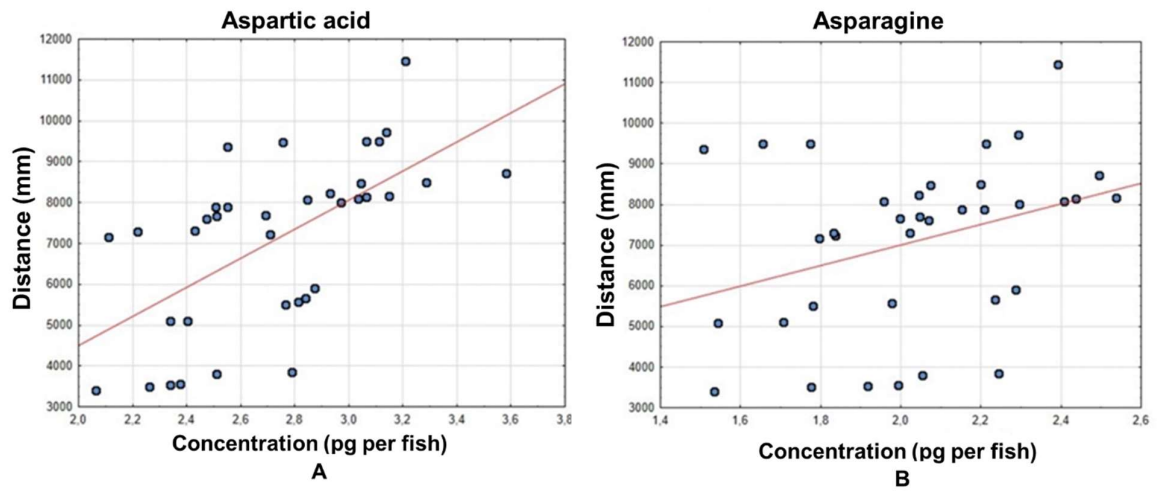


Figure 35 – Correlation between metabolites related to neurotransmission and total distance traveled by zebrafish larvae after 4 h exposure to 5F-APINAC (part 5).

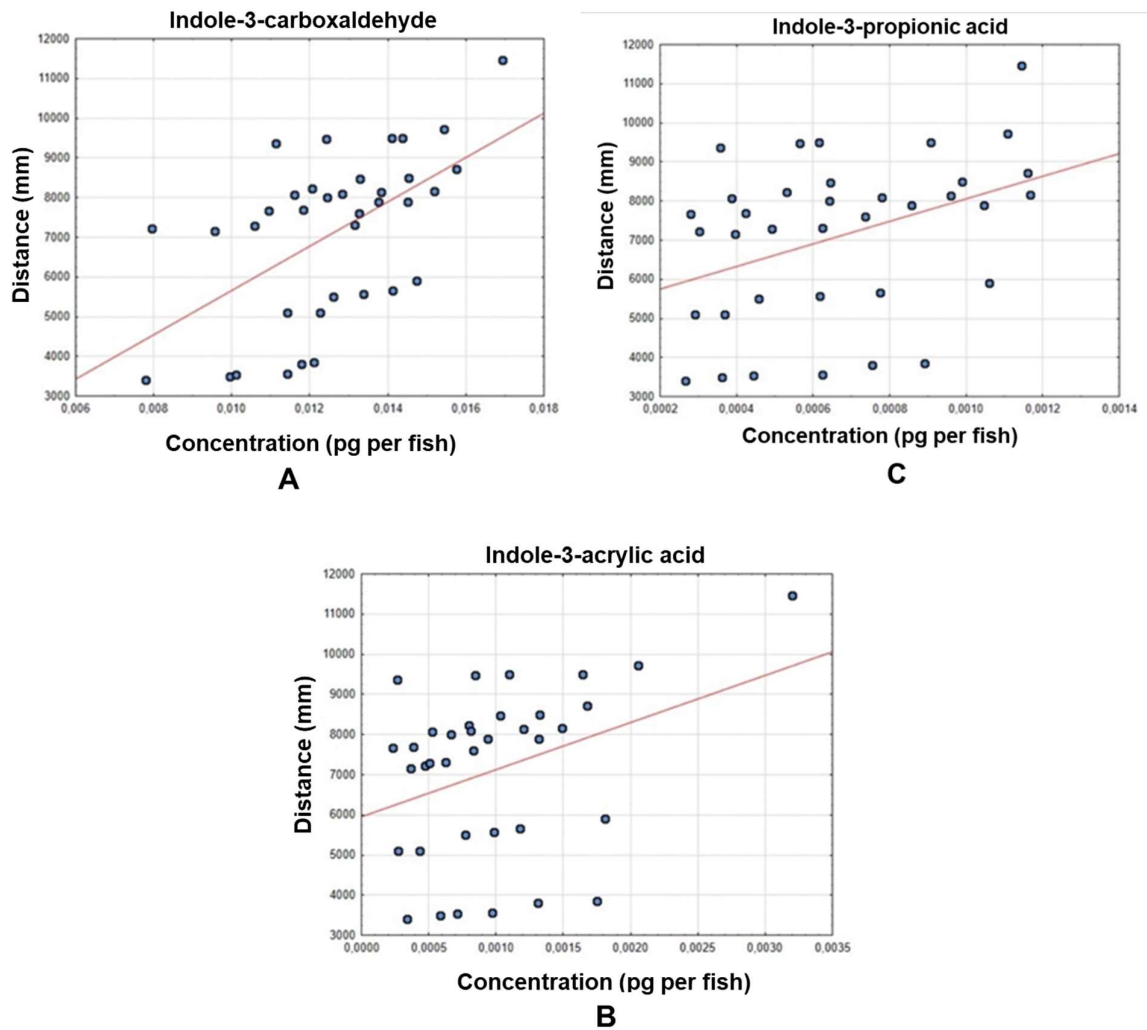


Figure 36 – Correlation between metabolites related to neurotransmission and total distance traveled by zebrafish larvae after 4 h exposure to 5F-APINAC (part 6).



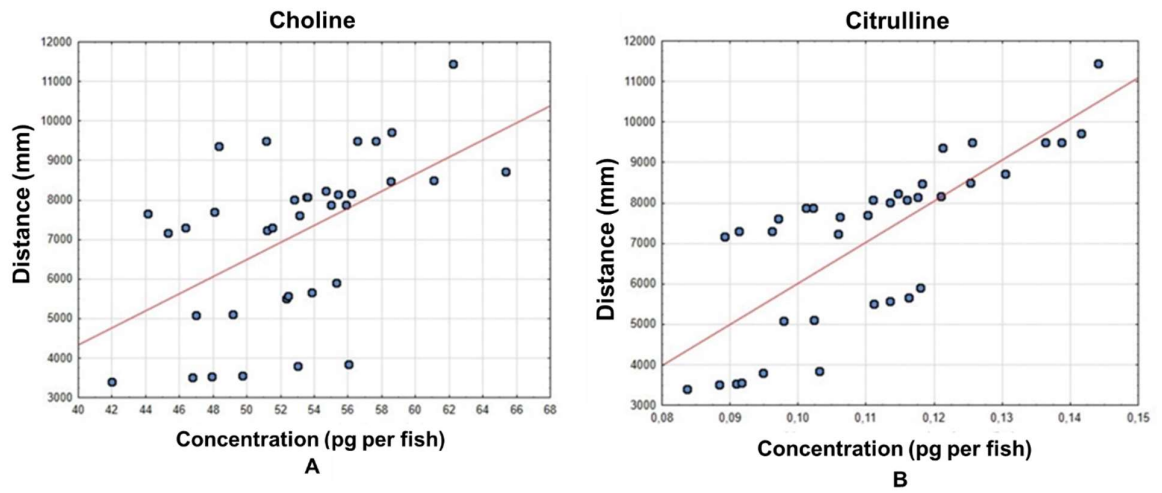


Figure 37 – Correlation between metabolites related to neurotransmission and total distance traveled by zebrafish larvae after 4 h exposure to 5F-APINAC (part 7).

#### 4. Discussion

The use of novel approaches in search of new pharmacological substances and potential drugs of abuse and the extensive search of new animal models is an integral part of the modernization of experimental pharmacology. The studies that were carried out made it possible to develop the main methodological approaches for studying pharmacological effects of physiologically active substances using *Danio rerio* as a model organism in the pharmacometabolomics investigations.

At the first step, it is crucial to establish the most significant metabolic pathways that may provide information about the mode of action of the studied substances. When studying the effects of potentially neurotropic drugs using an untargeted metabolomics approach, it is necessary to pay special attention to the endogenous compounds potentially associated with neuronal transmission. Examples of such compounds would be amino acids – precursors for neurotransmitters synthesis (e.g., phenylalanine, tyrosine, tryptophan), organic acids, steroids, etc. The untargeted pharmacometabolomics approach had shown that diazepam caused alterations in the concentrations of endogenous metabolites related to neurotransmission, which made it possible to hypothesize that diazepam affects multiple metabolomics pathways related to neurotransmitters synthesis; also, this assessment has proven the ability to use zebrafish larvae as a model organism for studying the pharmacological effects of neurotropic drugs using pharmacometabolomics approach.

After establishing the metabolic pathways of interest through untargeted metabolomics, it is necessary to develop and validate the methods of targeted metabolomics approach to determine the concentrations of endogenous metabolites involved in the metabolic pathways. In the case of studying the pharmacological effects of neurotropic drugs, it is necessary to develop a method for the quantitative determination of endogenous compounds involved in various neurotransmitter systems. When the targeted metabolomics approach is conducted on a large number of metabolites, it is possible to assess a wide range of potential effects of the drug on the CNS.

To assess the effects of the pharmacological substances on targeted metabolic pathways, it is necessary to select a reference pharmacologically active substance with a well-described impact on the organism; besides, it has to affect the metabolic pathways studied. Thus, diazepam was chosen to study the pharmacometabolomics effects of the neurotropic substances using *Danio rerio* as a model animal. Diazepam is a pharmacological substance with well-described effects and the mechanism of action on the central nervous system. It is frequently used as a reference drug in the assessments of searching for new anxiolytic drugs [5, 6, 15].

There were no dose-dependent changes in the levels of neurotransmitters of the GABAergic system found in the experiments of diazepam exposure. The obtained results may be explained by the fact that diazepam's primary mode of action is binding to the GABA<sub>A</sub>-receptors, thus allosterically enhancing their responsiveness to GABA [47]. It is known that diazepam can modulate GABA<sub>A</sub>-receptors when combined with low GABA concentrations [236]. Therefore, these results suggest that the drug's effectiveness relies far more on its impact on GABA receptors rather than the amount of the synthesis of GABA.

Glutamic acid in its' ionized form (glutamate) is one of the most abundant amino acids found in the CNS and is also one of the primary excitatory neurotransmitters [333]. Also, glutamic acid is a precursor of GABA. The reaction of glutamate conversion into GABA is regulated with the glutamate decarboxylase enzyme [110]. Several of the authors found that glutamate plays a pivotal role in forming benzodiazepine dependence; moreover, the injection of glutamate antagonists led to a much rapid formation of dependence [280]. There was a tendency to increase glutamic acid concentrations in the zebrafish groups exposed to diazepam for a short period. The increase in glutamic acid levels after short-term exposure to diazepam may indicate the lowering of GABA synthesis due to an increase in GABAergic innervation.

The concentrations of aspartic acid were increased after both short-term and long-term exposure to diazepam. Aspartic acid is an alpha-amino acid that plays an important role in the biosynthesis of proteins, urea cycle, and gluconeogenesis, and

also is an agonist of N-methyl-D-aspartate (NMDA) and alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionic acid (AMPA) receptors. The obtained results are consistent with the previous studies, which report increasing aspartate levels in the rodent's brain [45]. The activation of NMDA- and AMPA-receptors leads to the formation of excitotoxic effects; in fact, aspartic acid effects are opposite to those from GABA. It was found that the elevated levels of aspartic acid are connected to the excitotoxic effects [251]. It was also reported that the increased NMDA receptors stimulation takes place in diazepam dependence [250]. Therefore, it is conceivable that diazepam-induced elevated aspartic acid levels may contribute to its debilitating withdrawal signs such as anxiety, muscle rigidity, and seizures.

Diazepam had an influence on serotonergic system metabolites concentrations. Interestingly, tryptophan presented increased concentrations at higher doses of diazepam in short-term exposure but lower concentrations in long-term exposure. Consistent with our findings observed in the short-term exposure, studies performed in mice have shown that the acute administration of diazepam may cause an elevation of tryptophan concentrations in the brain [192]. Furthermore, long-term studies have observed reduced tryptophan concentrations in the brains of rats exposed to diazepam for a long period [62, 243]. Tryptophan is an alpha-amino acid that is a precursor of the neurotransmitter serotonin and several other derivatives. Tryptophan is an essential amino acid, so its concentrations in zebrafish larvae are related only to the nutrients in the yolk sac. Increased concentrations of tryptophan in the groups exposed to the highest dose of diazepam for a short term may be explained by the lower conversion rate of this amino acid into its' metabolites, which may be connected with the lowering of tryptophan hydroxylase activity. Decreasing tryptophan concentrations after long-term exposure may be interpreted as an enhancement of tryptophan catabolism into serotonin as a consequence of increasing tolerance to diazepam. This may be supported by the increased serotonin levels after 96 h exposure and decreased levels of its precursor, 5-hydroxytryptophan.

It is worth noting that serotonin is involved in an important neurotransmitter system regulating multiple physiological processes, including mood, reducing depression and anxiety [281]. Several researchers reported that diazepam's anxiolytic action involves the serotonergic system, specifically serotonin and its precursor [99, 234]. Other data indicate that diazepam exposure reduces the release of serotonin in neuronal cells [236, 241]. The lowering of serotonin release and the increase of its synthesis may be connected to the alterations in the levels of this metabolite.

Long-term diazepam exposure decreased the levels of 5-hydroxyindole acetic acid. The studies in this field present controversial data. Pratt et al. and Rastogi et al. postulate that the exposure of several benzodiazepines (clonazepam, diazepam, chlordiazepoxide, clobazam) led to the increase in the levels of 5-hydroxyindole acetic acid in rats' brains [236, 241]. In contrast, Boix et al. reported that intraperitoneal injection of diazepam did not cause the effect on the levels of 5-hydroxyindole acetic acid [62]. In the experiment on zebrafish larvae, 5-hydroxyindole acetic acid concentrations were lower in the groups exposed to diazepam for 96 h, indicating the lowering of the serotonin biotransformation rate. However, because the data about this metabolite is controversial, the results should be proven by using different animal models.

The concentrations of the metabolites of the kynurenine pathway were affected by diazepam exposure. The kynurenine concentrations were lower in the groups of zebrafish exposed to diazepam, while picolinic acid concentrations were higher in the groups of zebrafish exposed to the highest dose of diazepam for a long period.

Both kynurenine and picolinic acid are potential antagonists of NMDA-receptors. The lowering of the kynurenine concentrations may indicate that the increase of serotonergic system metabolites anabolism and kynurenine synthesis took place. These metabolites had shown to exhibit neuroprotective action [92]. In the meantime, the increase of the picolinic acid concentrations may postulate

compensatory reactions forwarded to decrease the excitotoxic effects of aspartic acid.

Phenylalanine and tyrosine concentrations similarly increased after 2.5 h exposure but had differential changes after 96 h exposure. Phenylalanine and tyrosine are amino acids that are precursors of the synthesis of the monoamines of the dopamine family. The information on the behavior of these metabolites during diazepam exposure is scarce, but some investigations have suggested that the expression of tyrosine hydroxylase (the enzyme that catalyzes the conversion of tyrosine into L-DOPA) is increased after diazepam administration [273]. Also, long-term exposure of diazepam to pregnant Long-Evans rats led to the decrease of the tyrosine levels in the brains of offspring [124]. The conversion of tyrosine into L-DOPA and subsequent metabolites and the lowering of tyrosine hydroxylase expression may explain the decrease in the tyrosine levels after long-term diazepam exposure. The increase in phenylalanine levels may be explained by the drop in the conversion rate of this metabolite into tyrosine through the inhibition of phenylalanine hydroxylase. The increase of phenylalanine and tyrosine levels after short-term exposure may be connected to the decrease in the conversion rate of these metabolites. This theory is proven by the general lowering trend of the dopamine family metabolites.

It is worth noting that the concentrations of L-DOPA, dopamine, normetanephrine and epinephrine were increased in the experimental group №1, followed by a subsequent decreasing trend relative to the increasing concentrations of diazepam after short-term exposure. Some authors report that diazepam elevates locomotor activity in mice, showing a “biphasic” response with increased activity at low doses and reduced activity at higher doses [101, 217, 330]. In addition, there is evidence that administration of a catecholamine synthesis inhibitor and dopamine receptor antagonists inhibit the diazepam-related increase in locomotor activity [279]. In this context, the results further support the hypothesis of diazepam's influence on dopamine levels linked to locomotor activity through the dopaminergic system. There is an acute biphasic response for most dopaminergic/adrenergic

metabolites at low diazepam concentration. Also, a similar trend of the concentrations of the dopaminergic/adrenergic metabolites may indicate that the biphasic behavioral response may be connected to dopamine and other metabolites of this system. The long-term diazepam exposure led to a decrease in dopamine levels in zebrafish larvae. The lowering of the concentrations of this metabolite may be connected to the depletion of dopaminergic synapses due to the formation of diazepam dependence.

The information about the influence of benzodiazepines on the levels of epinephrine and norepinephrine is scarce at this moment. Thus, Stein et al. found that alprazolam exposure led to the reduction of epinephrine turnover in the rats CNS [277]. At the same time, Rastogi et al. postulate that the chronic exposure of diazepam and bromazepam caused an increase in the levels of norepinephrine in several brain regions of rats [241]. So, the assumption can be made that the increase in the levels of norepinephrine after a long-term exposure may be connected to the lowering of its' catabolism; also, the increase of the epinephrine and norepinephrine concentrations may be interpreted as a lowering of dopamine catabolism. The abovementioned conclusions are in agreement with the trending of metanephrine, which was the decrease after short-term and the increase after long-term exposures to diazepam.

Acetylcholine is one of the main neurotransmitters in the CNS. There is a lack of information about the influence of diazepam on the cholinergic system. Lundgren et al. had shown that diazepam exposure led to the increase in the levels of acetylcholine, wherein did not cause the disruption in the levels of choline and did not alter the activity of choline transferase and acetylcholine transferase in the experiments on mice [93]. The elevated levels of acetylcholine may be connected to a slight anticholinergic activity of diazepam that develops due to the lowering of the release of acetylcholine from the preganglionic nerve cells, which leads to the decrease of its cleavage [93, 231]. To further investigate the true causes of the obtained results, more targeted investigations are needed.

There is no information about the effect of diazepam on the levels of microbiota tryptophan conversion pathway metabolites. However, there are data about the possibility of these metabolites binding to the benzodiazepines' site with the subsequent allosteric modification of GABA receptors [289]. Thus, changes in the levels of these metabolites may bring information about yet unknown action on the CNS.

When investigating the pharmacometabolomics effects of the poorly studied drugs, one should consider the information about the effects of the drugs of the same pharmacological group. Thus, when interpreting the results obtained after 5F-APINAC exposure, the data were compared with those received after exposure to other synthetic cannabinoids.

Besides the metabolomics changes, the exposure group №5 that received 10 uM solution of 5F-APINAC for a long period presented multiple morphological and developmental alterations. Approximately 60% of the larvae were unhatched, 20% had a curved tail related to spinal cord malformations, and all of them presented hyperpigmentation. Similar alterations were found in the experiments with different cannabimimetics. For example, the exposure of  $\Delta^9$ -THC and synthetic cannabinoids CP 55940 and WIN 55,212-2 caused spinal curvatures, yolk sac edema, and pericardial edema [125]. Also, adverse effects of the cannabimimetics on embryo development were found using different animal models. For example, it was found that the fetus death rate was higher in the pregnant rabbits that were exposed to the  $\Delta^9$ -THC in concentrations of 0.7 and 1.4 mg/kg [267]. Further investigations had shown that exposure to  $\Delta^9$ -THC and marijuana increased levels of miscarriage, the rates of skeletal and soft tissues development (e.g., hydronephrosis, hydrocephalus, orofacial cleft, etc.) in rodents [214]. The exposure of the chick embryos to synthetic cannabinoid HU 210 led not only to the increase in death rates but also to the decrease in the mass and length of the body and the mass of the brain of embryos [89]. In humans, consumption of  $\Delta^9$ -THC is reported to be connected with the number of miscarriages, fetal alcohol syndrome, and lower memory and studying skills in children [210]. According to WHO reports, case-control studies indicate



that using cannabinoids during pregnancy is connected to negative consequences for an embryo, e.g., lower weight and length of the body, sleep quality, verbal activity, and the memory of a child [150]. In the experiments of 5F-APINAC exposure, it was found that this cannabimimetic presents teratogenic activity; nevertheless, there was no increase in the death rates found. These data are in agreement with ones about a non-fluorinated analog of 5F-APINAC – APINAC [60, 270]. Though it should be noted that the assessment of the stability of this drug in the E3 medium was not studied, additional investigations are needed to address the question about the consistency of 5F-APINAC concentrations in the solutions.

GABA presented the lowest concentrations at the highest dose of exposure (10  $\mu$ M 5F-APINAC) in the acute and chronic experiments compared to the vehicle control group. Cannabinoids have been found to inhibit the release of several neurotransmitters, including GABA, and inhibit the GABAergic innervation system [98]. Synthetic cannabinoids have been postulated to depress locomotor activity by inhibiting GABA uptake. Also, it is known that the endocannabinoid system modulates GABA receptors. It has been postulated that endocannabinoids can potentiate the stimulation of GABA<sub>A</sub> receptors at lower doses of GABA [79]. Also, evidence shows that prolonged treatment with cannabimimetics causes hyperexcitability and an increase in GABA release [54, 137]. Decreased levels of GABA in the groups treated with the highest dose of 5F-APINAC may indicate that cannabimimetics can increase GABAergic activity, which potentially leads to the lowering of GABA synthesis. Also, lower levels of GABA may be connected to the increased levels of its cleavage in the synaptic cleft due to its higher release.

Glutamine concentrations were also found to be altered, being lower at higher doses in acute exposure. In the chronic exposure experiment, glutamine concentrations were higher at higher exposure doses. Glutamine is a precursor of the neurotransmitters glutamate and GABA. Previous research did show that  $\Delta^9$ -THC administration increased the total levels of glutamate + glutamine in humans [107, 152]. Also, it has been suggested that cannabinoid receptors agonists inhibit glutamine release [209]. Despite the lacking information about glutamine levels in

the CNS, it may be postulated that 5F-APINAC short-term exposure caused the decrease of glutamine release from neuronal cells, lowering its synthesis, while long-term exposure led to the increase of the synthesis, possibly through the rise of the GABA catabolism.

Several significant changes in the tryptophan and tryptamine levels attributable to 5F-APINAC exposure were observed in the study. The serotonergic system is key to regulating multiple neurophysiological processes, particularly mood, perception, anger, aggression, attention, and anxiety [226]. There is research suggesting that the endocannabinoids system is involved in the regulation of mood and depression via the serotonergic system [206]. It was found that  $\Delta^9$ -THC and a synthetic cannabinoid WIN 55,212-2 inhibited the synthesis of 5-hydroxytryptophan and serotonin through the effect on tryptophan hydroxylase activity in different brain regions of rats [285]. In our study, elevated concentrations of tryptophan after long-term exposure may be explained by the inhibition of tryptophan hydroxylase, leading to the lowering of tryptophan conversion.

Nowadays, tryptamine is referred to as a group of "trace amines", compounds that are structurally and metabolically related to classical monoamines and that have agonist action to the trace amine-associated receptor 1 (TAAR1) [60]. Trace amines play a role in the regulation of the number of monoamines in the synaptic cleft, particularly stimulating TAAR1 receptors, which cause the release of neurotransmitters and prevent their reuptake [209]. There is a dearth of reliable information about tryptamine levels or their synthesis after exposure to cannabimimetics. Although, works report that tryptamine is readily metabolized by the brain monoamine oxidases, so it has a very short half-life period [79]. Overuse of this trace amine due to the increase of the effects of monoamines in the brain may explain its lowering levels in acute exposure, and very low levels after chronic exposure to 5F-APINAC may have resulted in nearly undetectable concentrations.

Several statistical differences on concentration levels of the kynurenine pathway were also found. These metabolites are connected to the kynurenine pathway, the main metabolic pathway of tryptophan conversion. Most of the

metabolites of the kynurenine pathway are connected to NMDA receptors transmission. Excessive levels of NMDA receptors agonists have been found to be connected with excitotoxicity in the brain [122]. Cannabinoids have been shown to reduce NMDA activity through NMDA receptors antagonism, thus decreasing excitotoxicity. Opposite to these findings, other studies have shown that exposure to synthetic cannabinoid WIN 55,212-2 and endocannabinoid anandamide enhance the effects of NMDA [49, 196, 197, 210, 264]. Kynurenic acid presents an antagonism to the NMDA receptors, thus performing neuroprotective and neuroinhibitory actions [92]. Xanthurenic acid is believed to have neuromodulator action by increasing neurotransmission rate [326]. It is also known that anthranilic and picolinic acids decrease excitotoxic effects by increasing the polarization of neuronal cells membranes [284]. Despite these facts, in our study, we found that the metabolites of the kynurenine pathway that are reported to be connected with neuroprotective effect were significantly increased after 5F-APINAC exposure. It may be interpreted and a realization of neuroprotective action as a response to the exposure to toxic agent – 5F-APINAC.

In the present study, higher dopamine levels after acute exposure and lower levels after chronic exposure at the highest doses of 5F-APINAC were observed. Dopamine, one of the main neurotransmitters, plays a significant role in reward-motivated behavior, and many addictive abuse substances increase dopamine release or block its reuptake into neurons. It is known that dopamine receptors are modulated by the endocannabinoid system and that acute  $\Delta^9$ -THC exposure is associated with increased dopaminergic cell firing, increased dopamine synthesis, and increased dopamine release [298]. Also, acute  $\Delta^9$ -THC and WIN 55,212-2 treatments have been shown to increase dopamine and noradrenaline synthesis in different regions of the brains of rats [302]. Repeated administration of synthetic cannabinoids increased the expression of tyrosine hydroxylase, the enzyme that catalyzes the reaction of tyrosine conversion into the metabolites of the dopamine family, in the brain of animals [118]. The increase of dopamine levels after a short-term 5F-APINAC exposure may be connected to the increase of its' synthesis. In the long-

term exposure, the increase of dopamine levels in the experimental groups №1-3 may also be linked to its' synthesis increase. In contrast, the decrease of dopamine in the experimental groups №4-5 may be potentially explained by the exhaustion of its' reserves in the cells during the formation of dependence.

Acetylcholine presented higher concentrations after acute exposure and lower concentrations after chronic exposure. It has been observed that the administration of  $\Delta^9$ -THC can cause significant elevations in acetylcholine and choline levels in multiple brain regions in mice [100]. Administration of WIN 55,212–2 at a low dose induced stimulation of hippocampal acetylcholine efflux, while a higher dose exposure resulted in prolonged inhibition of efflux [101, 217]. Acetylcholine release in hippocampal synaptosomes was inhibited by the synthetic cannabinoid WIN 55,212-2 [108, 258]. Also, classic studies in this field have shown that acetylcholine levels were strongly reduced, especially in the hippocampus [205]. Despite the contradictory results obtained in the earlier studies, it may be postulated that short-term exposure of 5F-APINAC caused an increase of acetylcholine synthesis, while long-term exposure decreased its' efflux into the synaptic cleft.

Citrulline concentrations were lower in the groups of zebrafish exposed to 5F-APINAC for a short-term, while long-term exposure increased concentrations in the experimental group №5 compared to control. Citrulline is a substrate for the synthesis of the metabolites of the GABAergic innervation system [327]. Currently, there are no data describing the changes of citrulline concentrations after cannabimimetics exposure. The disturbance of citrulline concentrations may be connected to both the alterations of the GABAergic pathway metabolites catabolism and the difference in the balance of other biochemical pathways (e.g., urea cycle).

To confirm the action of 5F-APINAC on the CNS and investigate the connections between metabolomics data and the effect of 5F-APINAC, the behavioral assessment using zebrafish larvae was done.

A dose-dependent decrease of total locomotor activity was observed in the behavioral study. The activity was decreasing as the concentrations of 5F-APINAC were increasing. According to the available literature data, the locomotor activity of

zebrafish is changed in the form of a biphasic response, i.e., the increase of the activity at the lower doses of cannabimimetics, followed by the decrease at higher doses [102]. This type of response was found when exposing *Danio rerio* to such agonists of cannabinoid receptors as anandamide [223, 224],  $\Delta^9$ -THC [73], WIN 55,212-2 [74], JWH-018 [247], AKB48, 5F-AKB48 [247], 5F-ADBINAACA, AB-FUBINAACA and STS-135 [261], and presupposes that the biphasic activity response is typical not just for a specific cannabinoid, but for all of the potential agonists of cannabinoid receptors [23, 211, 224]. Movement alterations up to akinesia are the most common side effects observed in cannabinoids intake [23, 24, 211]. The alterations in locomotor activity caused by cannabimimetics may be connected to their ability to increase the dopamine release in the nucleus accumbens [153, 280]. 5F-APINAC exposure, however, did not cause a biphasic response. This discrepancy may be connected to the concentrations tested in this study.

The exposure to 5F-APINAC caused a dose-dependent decrease of a total distance traveled both at 4 h exposure and 48 h exposure. These results are in agreement with ones obtained for  $\Delta^9$ -THC in zebrafish [152, 288, 306]. The inhibiting effect of cannabinoid receptor agonists on locomotor activity is traditionally considered as a development of anxiety-like behavior. In contrast, recent studies have shown that cannabimimetics induce synaptic activity in the neuromuscular junctions, decreased heart rate, and the strength of the reaction on acute stress [113, 275]. These results show that the lowering of the zebrafish activity during cannabimimetics exposure may be interpreted not only as a building of anxiety.

Several investigations show that the lowering of the levels of GABA [90, 193], glutamine [132], tryptophan [187], choline [59], among others, is connected to anxiety behavior. Since the lowering of traveled distance is postulated as an indicator of stress [151, 152], the obtained results are in agreement with the literature data

## Conclusions

The main stages of studying the pharmacological effects of biologically active substances through the pharmacometabolomics approach using *Danio rerio* as an animal model were developed. The applicability of the developed methodology was proven by studying the effects caused by the compounds with neurotropic action.

The analytical method for determining the metabolomic panel of endogenous metabolites related to neurotransmission was developed and validated. The developed method allows one to determine many of the essential endogenous compounds and makes it possible to assess the type and the strength of action of biologically active substances on the CNS.

The assessment of the diazepam action on the concentrations of neurotransmitters was made to investigate the possibility of *Danio rerio* usage in the investigations of pharmacodynamics of neurotropic drugs through the pharmacometabolomics approach. Diazepam exposure caused alterations in the levels of metabolites of different neurotransmitter systems. It is interesting to note that GABA concentrations did not change (or did not show a dose-dependent response) across all of the experimental groups, which suggests that the mechanism of action of diazepam is only realized through the modulation of GABA<sub>A</sub> receptors, wherein not changing the rate of synthesis of GABA.

The exposure of a novel synthetic cannabinoid 5F-APINAC caused alterations in the levels of neurotransmitters and related metabolites. The most notable changes were found in GABA, dopamine, tryptamine, and acetylcholine levels. The obtained results are in agreement with the effects of other cannabinoid receptor agonists, proving the effects of cannabimimetics on the turnover of neurotransmitters. The exposure of 5F-APINAC for 96 h led to the formation of morphological alterations in zebrafish embryos, proving the embryotoxic effect of this drug.

5F-APINAC exposure caused a dose-dependent decrease of locomotor activity of zebrafish larvae; besides that, 10  $\mu$ M concentration of 5F-APINAC led to the dramatic decrease of activity, which indicates that this dose is toxic. The

correlations between traveled distance and the concentrations of neurotransmitters were found. This data is in agreement with the anxiogenic effect of cannabinoids.

The perspective of the further investigations on this topic may be connected to the evaluation of pharmacometabolomics effects of different neurotropic drugs to accumulate the data to predict the effects of unknown chemicals with a potential neurotropic mode of action. It is also needed to conduct additional behavioral studies to establish the type of neurotropic action. In addition, it is possible to develop other analytical methods for studying the effects of different drugs on the other organ systems (cardiovascular, digestive, etc.). Also, further studies in the field of "omics" approaches may be conducted to make complex investigations of the drugs of interest on the organism.

### **List of abbreviations**

ED<sub>50</sub> – half-effective dose

LD<sub>50</sub> – half-lethal dose

LC<sub>50</sub> – half-lethal concentration

RNA – ribonucleic acid

mRNA – matrix ribonucleic acid

DNA – desoxyribonucleic acid

GC – gas chromatography

GC-MS – gas chromatography coupled to mass-spectrometry

NMR – nuclear magnetic resonance

MS – mass-spectrometry

HPLC – high-performance liquid chromatography

HPLC-MS – high-performance liquid chromatography coupled with mass-spectrometry

HPLC-MS/MS – high-performance liquid chromatography coupled with tandem mass-spectrometry

PET – positron emission tomography

MALDI – matrix-assisted laser desorption/ionization

DM – diabetes mellitus

IEMs – inborn errors of metabolism

5F-APINAC – adamantan-1-yl-1-(5-fluoropentyl)-1H-indazole-3-carboxylate

E3 – zebrafish embryo medium

dpf – days post fertilization

MRM – multiple reaction monitoring

CNS – central nervous system

GABA – gamma-aminobutyric acid

L-DOPA – L-dioxyphenylalanine

NMDA-receptor – receptor of N-methyl-D-aspartate

AMPA-receptor – receptor of alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionic acid

GABA<sub>A</sub>-receptor – type A GABA receptor

$\Delta^9$ -THC – tetrahydrocannabinol

WHO – World Health Organization

TAAR1 – trace amine associated receptors, type 1



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