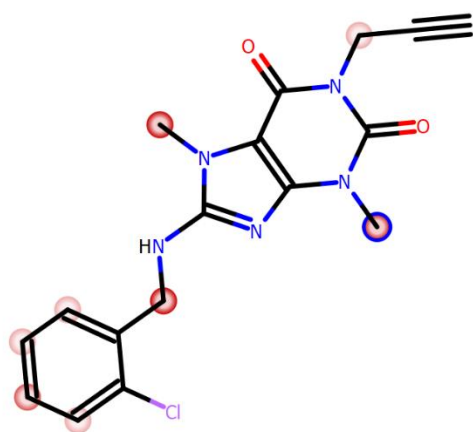
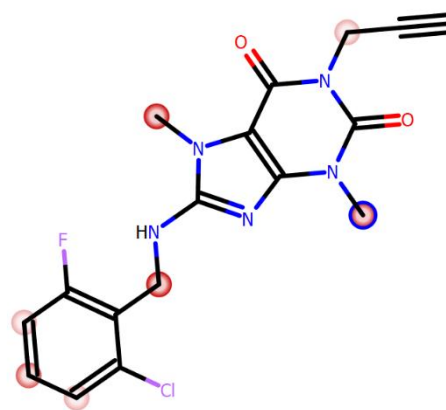


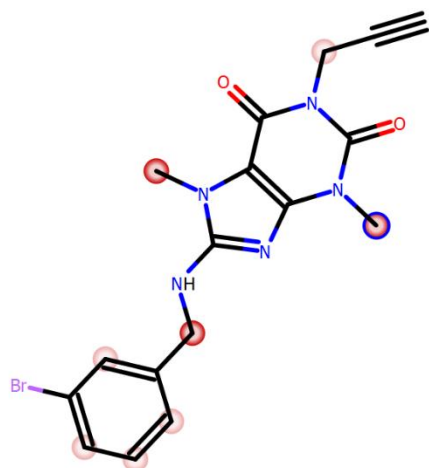
## Metabolic stability studies of selected compounds



MZ1483 (compound 19)



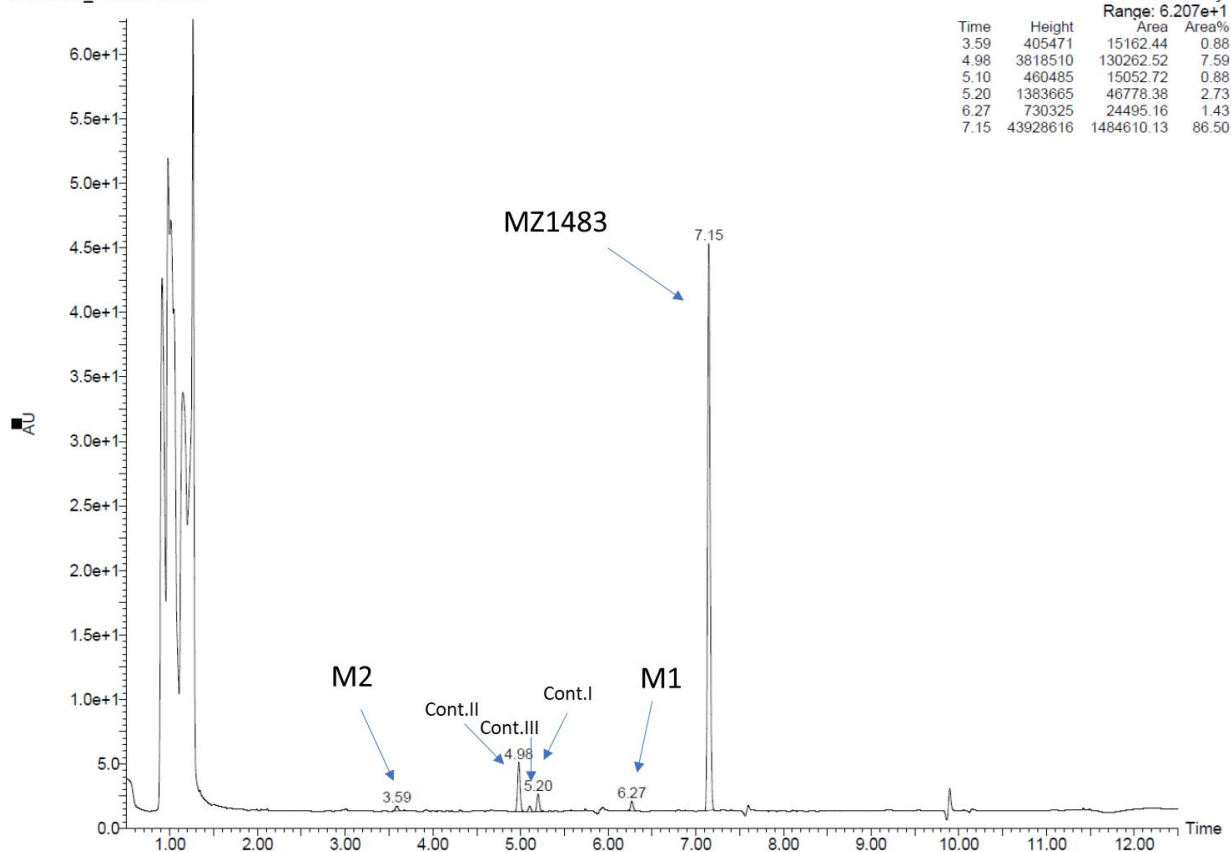
MZ1490 (compound 22)



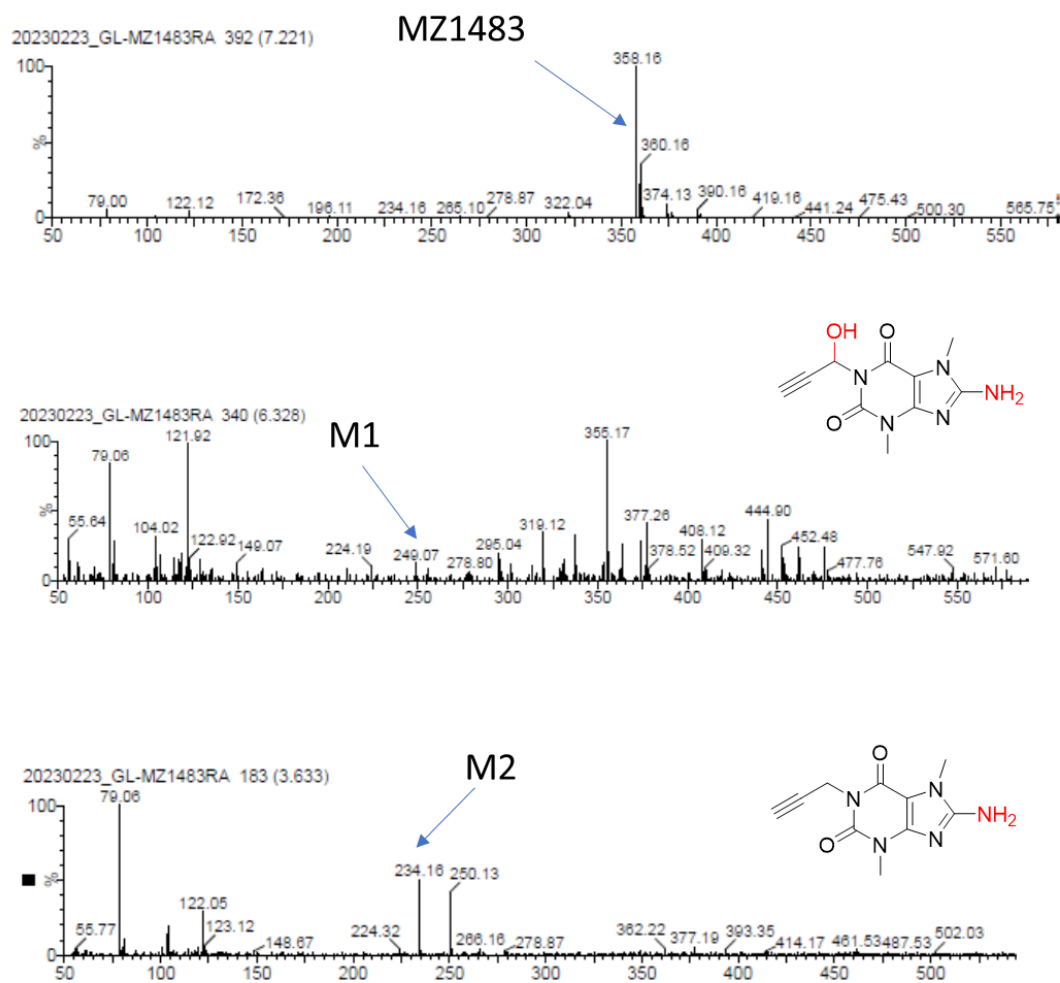
MZ1495 (compound 24)

**Figure S5.** The MetaSite 6.0.1. software prediction of the most probable sites of metabolism. The darker red color - the higher probability to be involved in the metabolism pathway. The blue circle marked the site of compound with the highest probability of metabolic bioconversion.

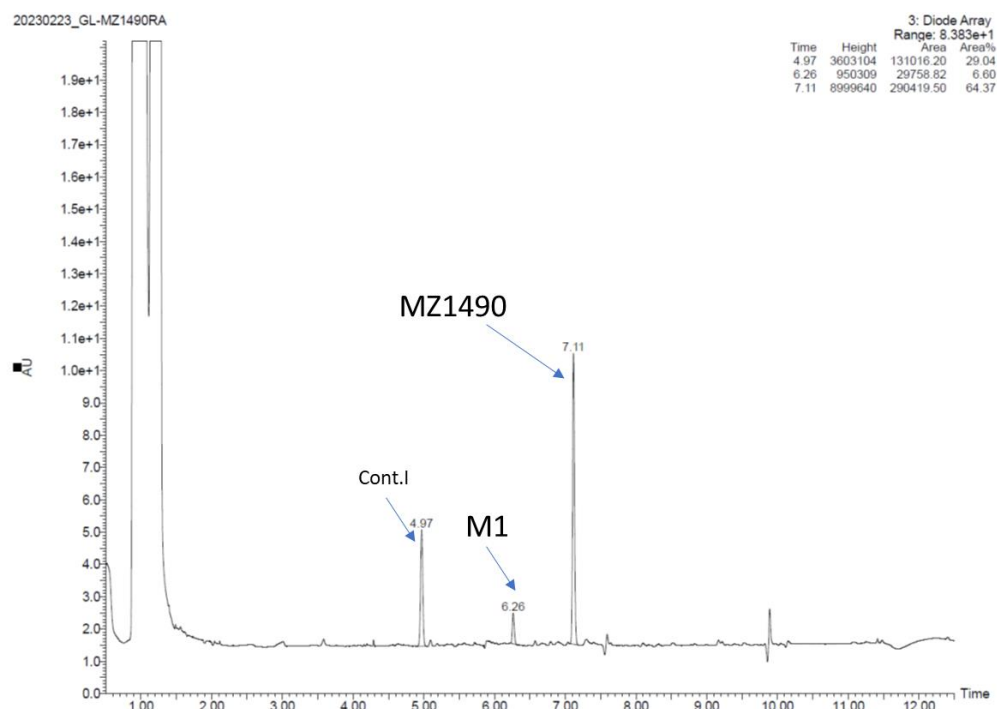
20230223\_GL-MZ1483RA



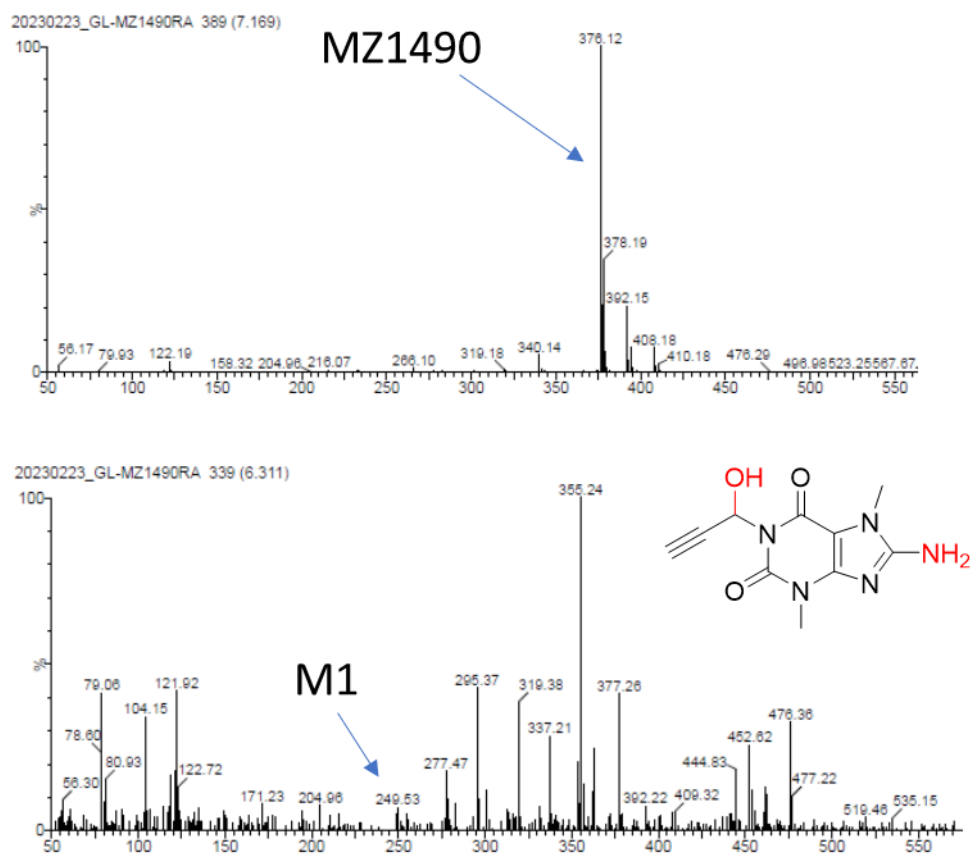
**Figure S6.** UPLC spectra after 120 min incubation of compound **MZ1483** with human liver microsomes (HLMs) in TRIS buffer pH=7.4 at 37°C. Two metabolites were found. Three contaminations were identified.



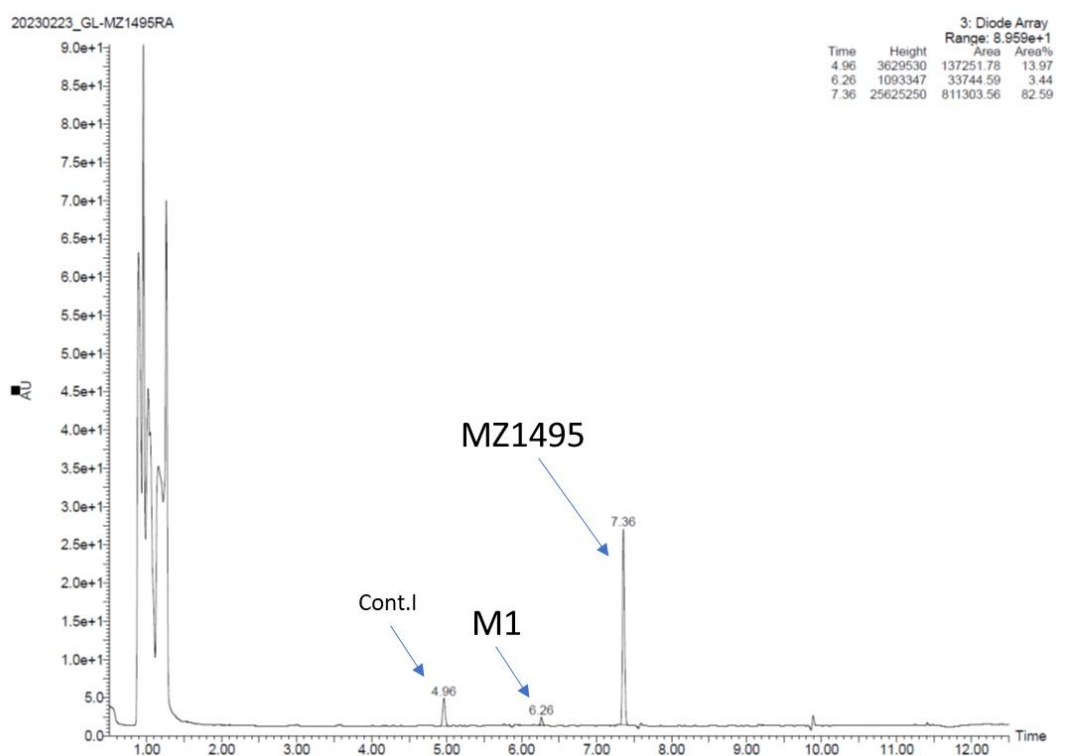
**Figure S7.** MS analyses of **MZ1483** and its metabolites M1 and M2. The most probable structures of metabolites were proposed based on MS analyses and the data obtained *in silico* (**Figure S5**).



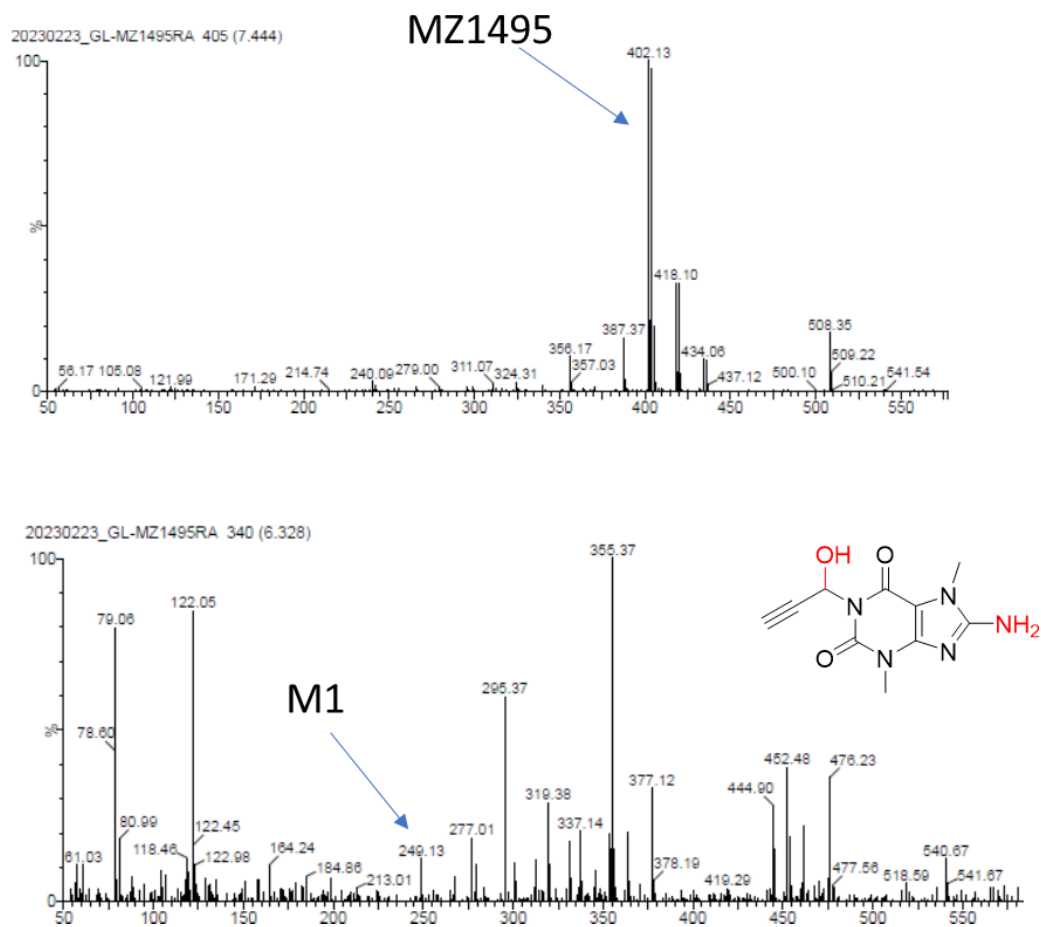
**Figure S8.** UPLC spectra after 120 min incubation of compound **MZ1490** with human liver microsomes (HLMs) in TRIS buffer pH = 7.4 at 37 °C. One metabolite was found. One contamination was identified.



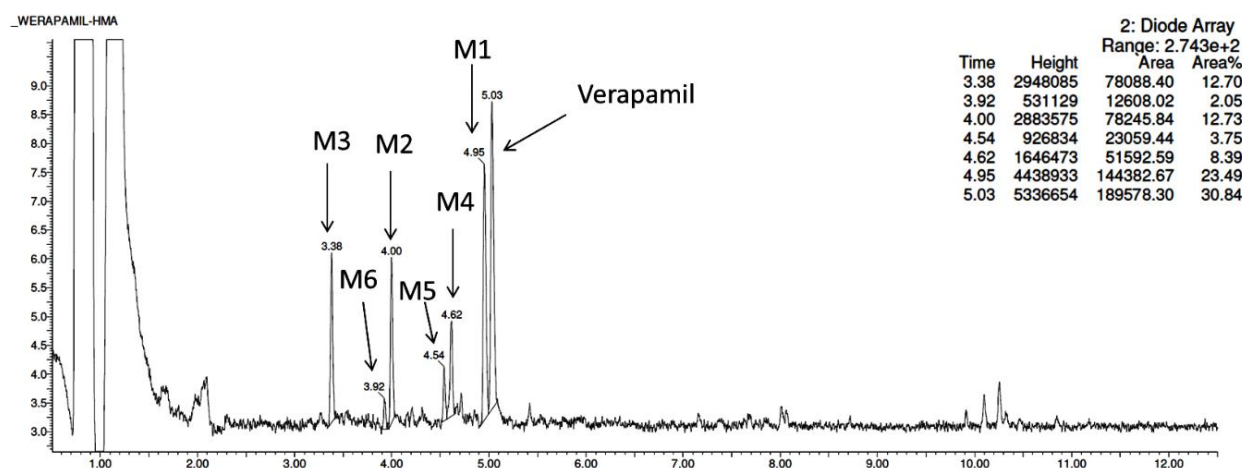
**Figure S9.** MS analyses of **MZ1490** and its metabolite **M1**. The most probable structure of metabolite was proposed based on MS analyses and the data obtained *in silico* (**Figure S5**).



**Figure S10.** UPLC spectra after 120 min incubation of compound **MZ1495** with human liver microsomes (HLMs) in TRIS buffer pH = 7.4 at 37 °C. One metabolite was found. One contamination was identified.



**Figure S11.** MS analyses of **MZ1495** and its metabolite M1. The most probable structure of metabolite was proposed based on MS analyses and the data obtained *in silico* (Figure S5).



**Figure S12.** UPLC spectra after 120 min incubation of reference unstable drug **Verapamil** with human liver microsomes (HLMs) in TRIS buffer pH = 7.4 at 37 °C.