One of the main reasons for the treatment failure of infections caused by pathogenic microorganisms is the overexpressing of efflux membrane proteins, which actively remove drugs from cells, leading to a phenomenon called multidrug resistance MDR. In this work, we focused on the functional characterization of the MDR pump Pdr5p in the yeast *Saccharomyces cerevisiae*. We have verified that diS-$C_3(3)$ fluorescence method can be used to determine the binding sites where the substrates bind in the binding pocket of the pump *Sc*Pdr5p. We focused on the study of the *Sc*Pdr5p binding pocket using triazole derivatives: ravuconazole, voriconazole and fluconazole. Using disc diffusion assay, we showed that all three studied triazoles are substrates of the pump *Sc*Pdr5p. We have found that these structural analogs have a significantly different effect on the inhibition of the potentiometric fluorescent probe diS-$C_3(3)$ transport by the pump *Sc*Pdr5p, and also that ravuconazole and voriconazole compete with each other for transport by the pump *Sc*Pdr5p. We have used a fluorescent approach to study the binding of azoles to the binding pocket of pump *Sc*Pdr5p using benchmark substrates, that bind selectively to only one binding site in the binding pocket of the pump *Sc*Pdr5p, and we have supported the hypothesis that ravuconazole and voriconazole bind to more than one binding site.