The provided text discusses the challenges posed by intra-tumour heterogeneity (ITH) in devising effective treatment strategies in clinical practice. Single-cell RNA sequencing (scRNA-seq) is acknowledged as a powerful tool for exploring ITH at the transcriptional level, offering a unique opportunity for therapeutic intervention. The results section introduces the emerging field of research focused on drug response prediction at the single-cell level, aiming to enhance the efficacy and precision of cancer treatments. The text then introduces a computational method named DREEP (Drug Response Estimation from single-cell Expression Profiles). DREEP utilizes publicly available pharmacogenomic screens from GDSC2, CTRP2, and PRISM, along with functional enrichment analysis, to predict single-cell drug sensitivity from transcriptomic data. Extensive in vitro validation of DREEP is conducted using multiple independent single-cell datasets comprising over 200 cancer cell lines, demonstrating the method's accuracy and robustness. Furthermore, DREEP is applied to molecularly barcoded breast cancer cells, leading to the identification of drugs capable of selectively targeting specific cell populations. In the conclusion, DREEP is highlighted as an in silico framework providing a means to prioritize drugs based on single-cell transcriptional profiles of tumors. The tool is positioned as valuable for designing personalized treatment strategies and expediting drug repurposing studies. The availability of DREEP is mentioned, with a link to its GitHub repository. Keywords such as "Drug prediction," "Single-cell transcriptomics," "Precision oncology," and "Cancer" summarize the key aspects covered in the text.