

We used the abstracts and their elaborated version on ChatGPT from the following articles for the testing phase

- [1] Failli, M., Demir, S., Del Río-Álvarez, Á., Carrillo-Reixach, J., Royo, L., Domingo-Sàbat, M., Childs, M., Maibach, R., Alaggio, R., Czauderna, P., Morland, B., Branchereau, S., Cairo, S., Kappler, R., Armengol, C., & di Bernardo, D. (2023). Computational drug prediction in hepatoblastoma by integrating pan-cancer transcriptomics with pharmacological response. *Hepatology* (Baltimore, Md.), 10.1097/HEP.0000000000000601. Advance online publication. <https://doi.org/10.1097/HEP.0000000000000601>
- [2] Chen, J., Wang, X., Ma, A., Wang, Q. E., Liu, B., Li, L., Xu, D., & Ma, Q. (2022). Deep transfer learning of cancer drug responses by integrating bulk and single-cell RNA-seq data. *Nature communications*, 13(1), 6494. <https://doi.org/10.1038/s41467-022-34277-7>
- [3] Pellicchia, S., Viscido, G., Franchini, M., & Gambardella, G. (2023). Predicting drug response from single-cell expression profiles of tumours. *BMC medicine*, 21(1), 476. <https://doi.org/10.1186/s12916-023-03182-1>
- [4] Gambardella, G., Viscido, G., Tumaini, B., Isacchi, A., Bosotti, R., & di Bernardo, D. (2022). A single-cell analysis of breast cancer cell lines to study tumour heterogeneity and drug response. *Nature communications*, 13(1), 1714. <https://doi.org/10.1038/s41467-022-29358-6>
- [5] Hsieh, C. Y., Wen, J. H., Lin, S. M., Tseng, T. Y., Huang, J. H., Huang, H. C., & Juan, H. F. (2022). scDrug: From single-cell RNA-seq to drug response prediction. *Computational and structural biotechnology journal*, 21, 150–157. <https://doi.org/10.1016/j.csbj.2022.11.055>
- [6] Xia, F., Allen, J., Balaprakash, P., Brettin, T., Garcia-Cardona, C., Clyde, A., Cohn, J., Doroshow, J., Duan, X., Dubinkina, V., Evrard, Y., Fan, Y. J., Gans, J., He, S., Lu, P., Maslov, S., Partin, A., Shukla, M., Stahlberg, E., Wozniak, J. M., ... Stevens, R. (2022). A cross-study analysis of drug response prediction in cancer cell lines. *Briefings in bioinformatics*, 23(1), bbab356. <https://doi.org/10.1093/bib/bbab356>
- [7] Majumdar, A., Liu, Y., Lu, Y., Wu, S., & Cheng, L. (2021). kESVR: An Ensemble Model for Drug Response Prediction in Precision Medicine Using Cancer Cell Lines Gene Expression. *Genes*, 12(6), 844. <https://doi.org/10.3390/genes12060844>
- [8] Franchini, M., Pellicchia, S., Viscido, G., & Gambardella, G. (2023). Single-cell gene set enrichment analysis and transfer learning for functional annotation of scRNA-seq data. *NAR genomics and bioinformatics*, 5(1), lqad024. <https://doi.org/10.1093/nargab/lqad024>
- [9] De Carluccio, G., Fusco, V., di Bernardo, D. (2023) The CASwitch: a synthetic biology solution for high-performance inducible gene expression systems in biotechnology. *bioRxiv* 2023.09.20.558637. <https://doi.org/10.1101/2023.09.20.558637>
- [10] Aufiero, M. A., Shlezinger, N., Gjonbalaj, M., Mills, K. A. M., Ballabio, A., & Hohl, T. M. (2023). Dectin-1/CARD9 induction of the TFEB and TFE3 gene network is dispensable for phagocyte anti-*Aspergillus* activity in the lung. *Infection and immunity*, 91(11), e0021723. <https://doi.org/10.1128/iai.00217-23>
- [11] Pasquier, A., Pastore, N., D'Orsi, L., Colonna, R., Esposito, A., Maffia, V., De Cegli, R., Mutarelli, M., Ambrosio, S., Tufano, G., Grimaldi, A., Cesana, M., Cacchiarelli, D., Delalleau, N., Napolitano, G., & Ballabio, A. (2023). TFEB and TFE3 control glucose homeostasis by regulating insulin gene expression. *The EMBO journal*, 42(21), e113928. <https://doi.org/10.15252/embj.2023113928>
- [12] Di Malta, C., Zampelli, A., Granieri, L., Vilardo, C., De Cegli, R., Cinque, L., Nusco, E., Pece, S., Tosoni, D., Sanguedolce, F., Sorrentino, N. C., Merino, M. J., Nielsen, D., Srinivasan, R., Ball, M. W., Ricketts, C. J., Vocke, C. D., Lang, M., Karim, B., Lanfrancone, L., ... Ballabio, A. (2023). TFEB and TFE3 drive kidney cystogenesis and tumorigenesis. *EMBO molecular medicine*, 15(5), e16877. <https://doi.org/10.15252/emmm.202216877>

- [13] Cesana, M., Tufano, G., Panariello, F., Zampelli, N., Ambrosio, S., De Cegli, R., Mutarelli, M., Vaccaro, L., Ziller, M. J., Cacchiarelli, D., Medina, D. L., & Ballabio, A. (2023). EGR1 drives cell proliferation by directly stimulating TFEB transcription in response to starvation. *PLoS biology*, 21(3), e3002034. <https://doi.org/10.1371/journal.pbio.3002034>
- [14] Nakamura, J., Yamamoto, T., Takabatake, Y., Namba-Hamano, T., Minami, S., Takahashi, A., Matsuda, J., Sakai, S., Yonishi, H., Maeda, S., Matsui, S., Matsui, I., Hamano, T., Takahashi, M., Goto, M., Izumi, Y., Bamba, T., Sasai, M., Yamamoto, M., Matsusaka, T., ... Isaka, Y. (2023). TFEB-mediated lysosomal exocytosis alleviates high-fat diet-induced lipotoxicity in the kidney. *JCI insight*, 8(4), e162498. <https://doi.org/10.1172/jci.insight.162498>
- [15] Astanina, E., Doronzo, G., Corà, D., Neri, F., Oliviero, S., Genova, T., Mussano, F., Middonti, E., Vallariello, E., Cencioni, C., Valdembrì, D., Serini, G., Limana, F., Foglio, E., Ballabio, A., & Bussolino, F. (2022). The TFEB-TGIF1 axis regulates EMT in mouse epicardial cells. *Nature communications*, 13(1), 5191. <https://doi.org/10.1038/s41467-022-32855-3>
- [16] Schuster, E. M., Eppler, M. W., Glaser, K. M., Mhlan, M., Lucht, K., Zimmermann, J. A., Bremser, A., Polyzou, A., Obier, N., Cabezas-Wallscheid, N., Trompouki, E., Ballabio, A., Vogel, J., Buescher, J. M., Westermann, A. J., & Rambold, A. S. (2022). TFEB induces mitochondrial itaconate synthesis to suppress bacterial growth in macrophages. *Nature metabolism*, 4(7), 856–866. <https://doi.org/10.1038/s42255-022-00605-w>
- [17] Sass, F., Schlein, C., Jaekstein, M. Y., Pertzborn, P., Schweizer, M., Schinke, T., Ballabio, A., Scheja, L., Heeren, J., & Fischer, A. W. (2021). TFEB deficiency attenuates mitochondrial degradation upon brown adipose tissue whitening at thermoneutrality. *Molecular metabolism*, 47, 101173. <https://doi.org/10.1016/j.molmet.2021.101173>
- [18] Onuchic, L., Padovano, V., Schena, G., Rajendran, V., Dong, K., Shi, X., Pandya, R., Rai, V., Gresko, N. P., Ahmed, O., Lam, T. T., Wang, W., Shen, H., Somlo, S., & Caplan, M. J. (2023). The C-terminal tail of polycystin-1 suppresses cystic disease in a mitochondrial enzyme-dependent fashion. *Nature communications*, 14(1), 1790. <https://doi.org/10.1038/s41467-023-37449-1>
- [19] Luo, L., Roy, S., Li, L., & Ma, M. (2023). Polycystic kidney disease: novel insights into polycystin function. *Trends in molecular medicine*, 29(4), 268–281. <https://doi.org/10.1016/j.molmed.2023.01.005>
- [20] Wu, M., Chen, M., Jing, Y., Gu, J., Mei, S., Yao, Q., Zhou, J., Yang, M., Sun, L., Wang, W., Hu, H., Wüthrich, R. P., & Mei, C. (2016). The C-terminal tail of polycystin-1 regulates complement factor B expression by signal transducer and activator of transcription 1. *American journal of physiology. Renal physiology*, 310(11), F1284–F1294. <https://doi.org/10.1152/ajprenal.00428.2015>
- [21] Ma, M. (2021). Cilia and polycystic kidney disease. *Seminars in cell & developmental biology*, 110, 139–148. <https://doi.org/10.1016/j.semcdb.2020.05.003>
- [22] Talbot, J. J., Shillingford, J. M., Vasanth, S., Doerr, N., Mukherjee, S., Kinter, M. T., Watnick, T., & Weimbs, T. (2011). Polycystin-1 regulates STAT activity by a dual mechanism. *Proceedings of the National Academy of Sciences of the United States of America*, 108(19), 7985–7990. <https://doi.org/10.1073/pnas.1103816108>
- [23] Pepe, G., Guarracino, A., Ballesio, F., Parca, L., Ausiello, G., & Helmer-Citterich, M. (2022). Evaluation of potential miRNA sponge effects of SARS genomes in human. *Non-coding RNA research*, 7(1), 48–53. <https://doi.org/10.1016/j.ncrna.2022.01.003>
- [24] Guarracino, A., Pepe, G., Ballesio, F., Adinolfi, M., Pietrosanto, M., Sangiovanni, E., Vitale, I., Ausiello, G., & Helmer-Citterich, M. (2021). BRIO: a web server for RNA sequence and structure motif scan. *Nucleic acids research*, 49(W1), W67–W71. <https://doi.org/10.1093/nar/gkab400>
- [25] Failli, M., Paananen, J., & Fortino, V. (2020). ThETA: transcriptome-driven efficacy estimates for gene-based Target discovery. *Bioinformatics (Oxford, England)*, 36(14), 4214–4216. <https://doi.org/10.1093/bioinformatics/btaa518>

- [26] Zappa, F., Wilson, C., Di Tullio, G., Santoro, M., Pucci, P., Monti, M., D'Amico, D., Pisonero-Vaquero, S., De Cegli, R., Romano, A., Saleem, M. A., Polishchuk, E., Failli, M., Giaquinto, L., & De Matteis, M. A. (2019). The TRAPP complex mediates secretion arrest induced by stress granule assembly. *The EMBO journal*, 38(19), e101704. <https://doi.org/10.15252/embj.2019101704>
- [27] Failli, M., Paananen, J., & Fortino, V. (2019). Prioritizing target-disease associations with novel safety and efficacy scoring methods. *Scientific reports*, 9(1), 9852. <https://doi.org/10.1038/s41598-019-46293-7>
- [28] Zappa, F., Failli, M., & De Matteis, M. A. (2018). The Golgi complex in disease and therapy. *Current opinion in cell biology*, 50, 102–116. <https://doi.org/10.1016/j.ceb.2018.03.005>
- [29] de Hoffer, A., Vatani, S., Cot, C., Cacciapaglia, G., Chiusano, M. L., Cimorelli, A., Conventi, F., Giannini, A., Hohenegger, S., & Sannino, F. (2022). Variant-driven early warning via unsupervised machine learning analysis of spike protein mutations for COVID-19. *Scientific reports*, 12(1), 9275. <https://doi.org/10.1038/s41598-022-12442-8>