

5 - 67 Identification of SLC2A1, a Prognostic Marker for Lung Adenocarcinoma and a Simulation of Corresponding Drug Ligands

Li Yang^{1,2,4}, Gao Feifei^{1,2,4}, Liu Jiawei³, Yuan Lingyan^{1,4}, Yang Qiong¹, Yang Lei¹ and Bing Zhitong^{1,4*}

¹Institute of modern physics, Chinese Academy of Sciences, Lanzhou 730000, China;

²Life Sciences, University of Chinese Academy of Sciences, Beijing 100000, China;

³Lanzhou University, Lanzhou 730000, China;

⁴Advanced Energy Science and Technology Guangdong Laboratory, Huizhou 516000, Guangdong, China)

Using mRNA expression profile data, we screened out differential genes related to survival in lung adenocarcinoma (LUAD) patients and established a LUAD prognosis prediction model using the machine learning method-Lasso-Cox. We evaluated its predictive performance and found that the model can accurately distinguish between high and low-risk LUAD patients and reflect patients' one-year, three-year, and five-year survival rates. As shown in Fig. 1, a lead compound (BAY-588) for the possible treatment of LUAD was screened from the ChEMBL database using a high-throughput screening method based on the target in the model (SLC2A1).

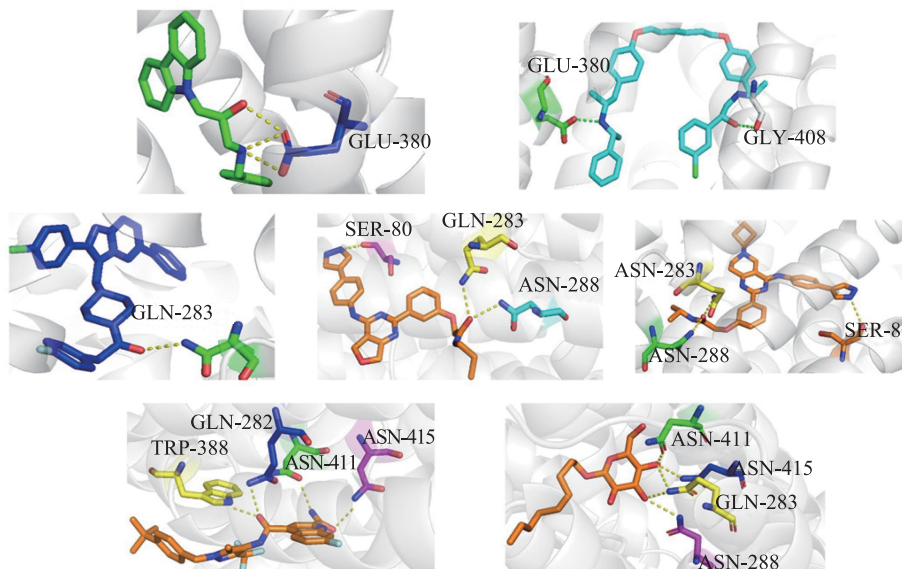


Fig. 1 (color online) High-throughput screening of the target molecule BNG-588.