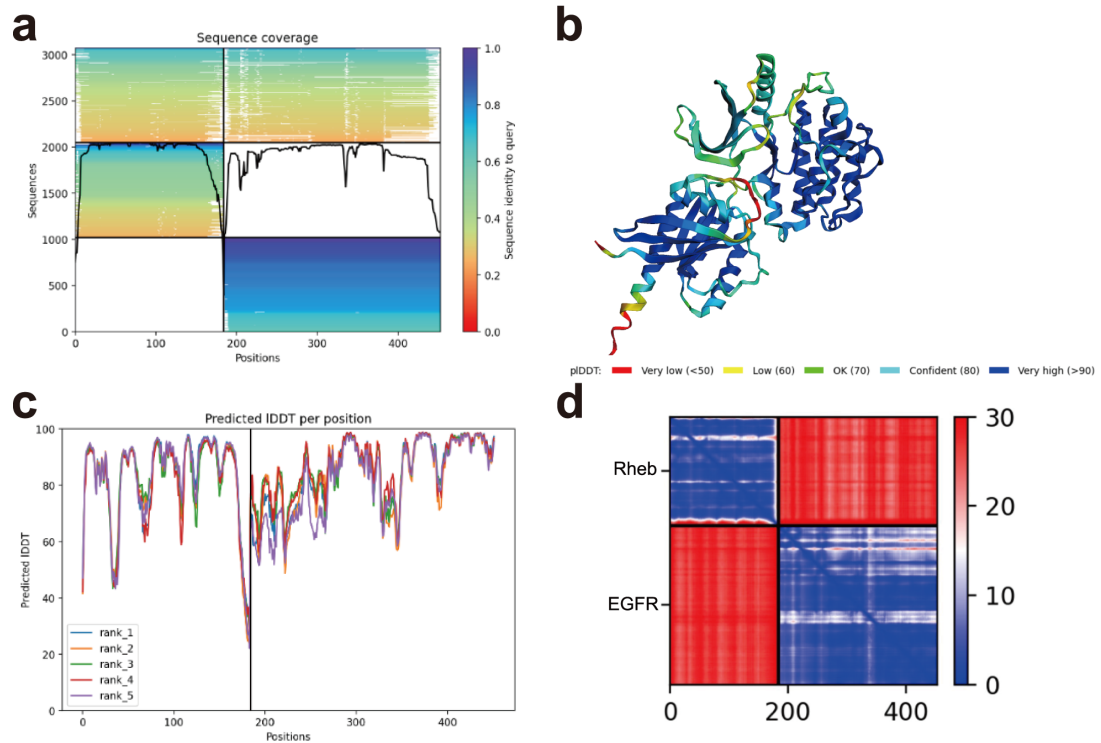


Supplementary Figure 8



Supplementary Figure 8 The quality of predicted EGFR-Rheb complex by AlphaFold2-Multimer.

(a) and (b) The structure shown in **Fig. 4a** is colored by pLDDT value, a measure of the confidence that an amino acid is positioned correctly relative to neighboring residues. (c) pLDDT values for the EGFR-Rheb complex displayed as a graph. pLDDT values for each model are shown as differently colored lines. The values for rank_1 to rank_5 are 83.8, 83.8, 84.4, 84.2, and 82.2, respectively. The highest value of rank_3 was used in the main figure. (d) Predicted alignment error plot for the EGFR-TKD and Rheb interaction.