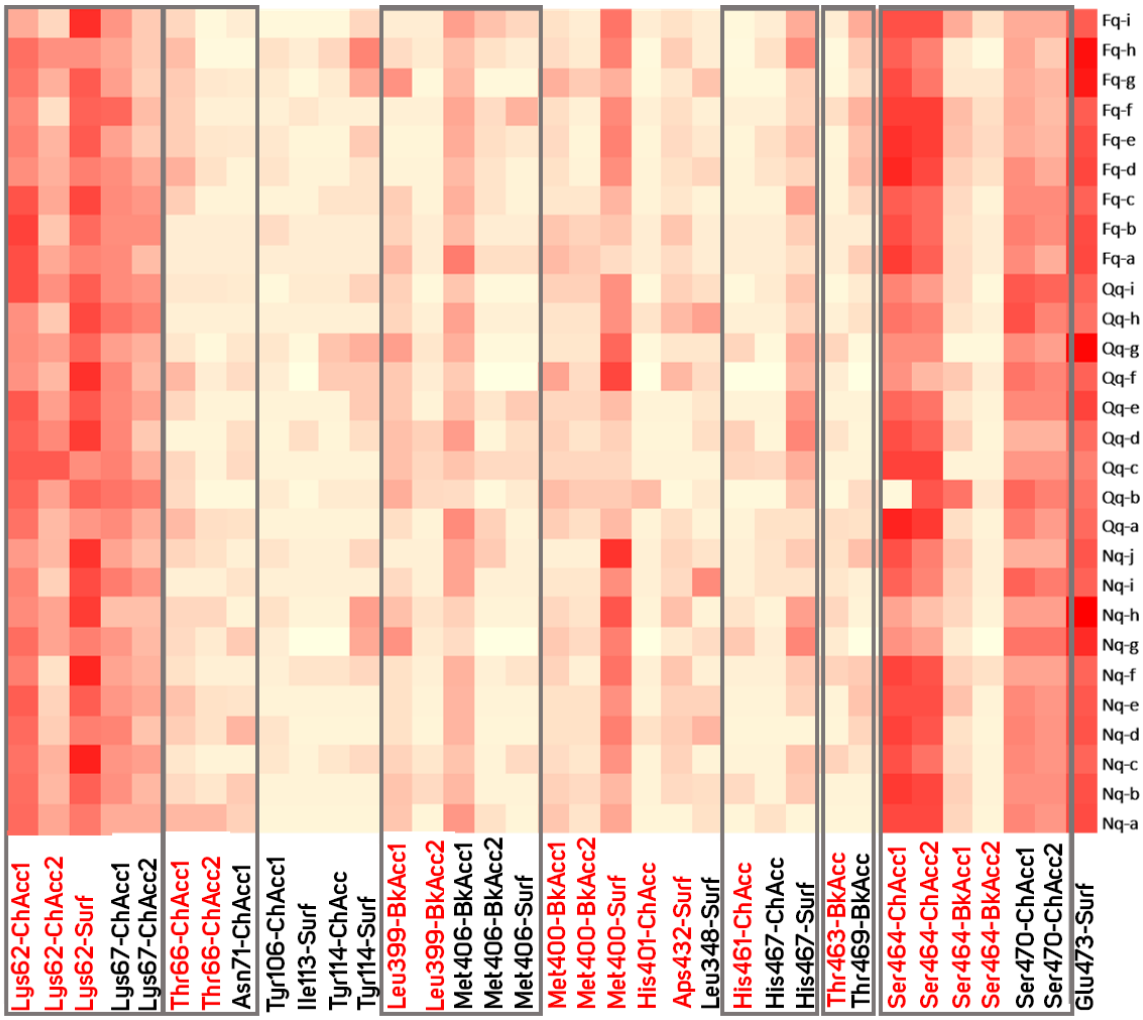SUPPLEMENTARY MATERIAL TABLE B. PLIF-HeatMap representing the amount (percentage) of conformers of a quinone making a contact with a given amino acid in TR or GR detected by PLIF. X-axis: aminoacid and contact codes. Y-axis: aryloxy-quinones set. Contact codes are: Side chain H-donor and acceptor (ChDon), Backbone H-donor and acceptor (BkDon), and Surface contact (Surf). Blocks are colored along a gradient from white (low percentage of contact) to dark red (high percentage of contact). Dark red blocks indicate a highly frequent contact. Black frames were used to groupe similar residues in TR/GR. The amount of conformers here represented are despicted in the TABLE 5.