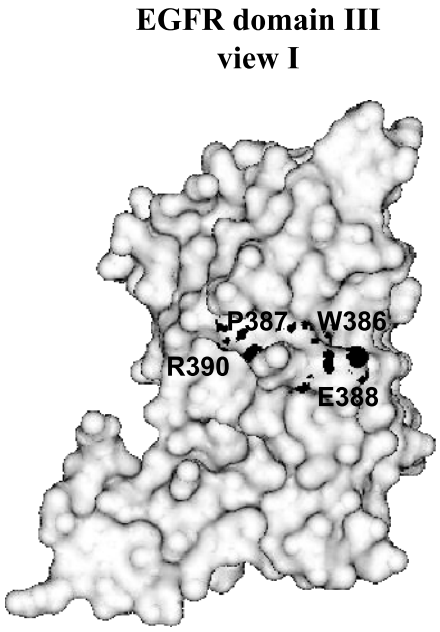

Figure W1. Computational modeling of potential panitumumab epitope using phage-displayed peptides. The P(X)WD(XX)R motif was mapped back to the three-dimensional EGFR structure using the MIMOX algorithm. The presumed panitumumab epitope is shown in black.

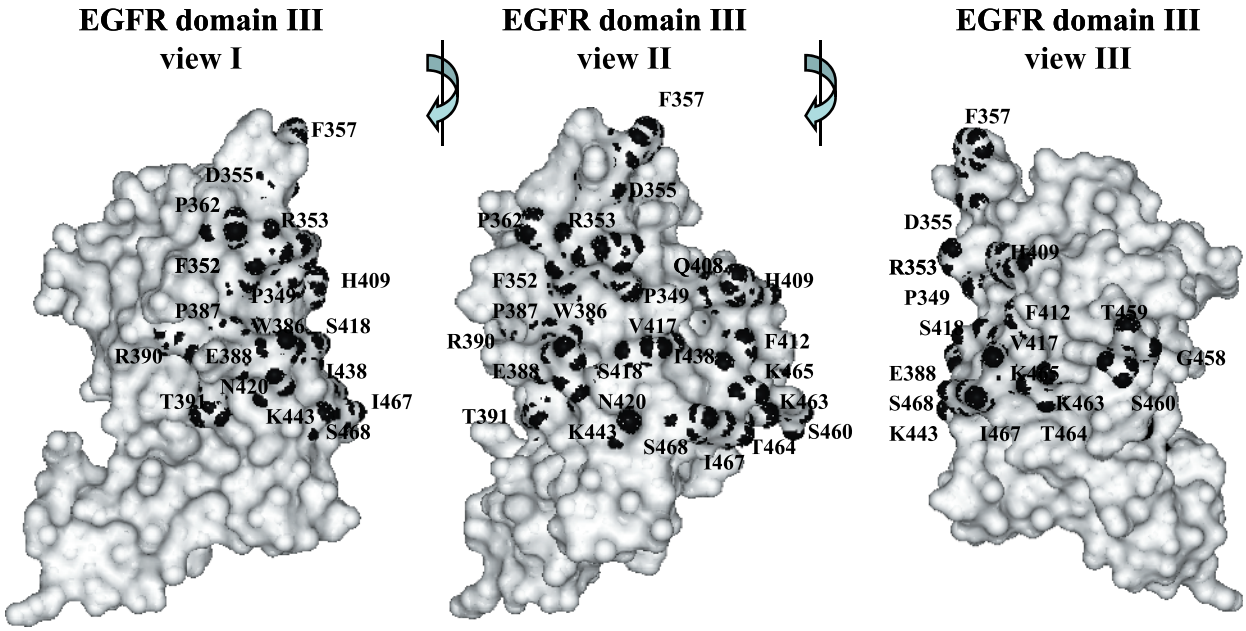

Figure W2. Generation of EGFR mutants. Localization of mutated amino acid positions on three-dimensional model of EGFR domain III. Left, middle, and right panels show different views on EGFR domain III.

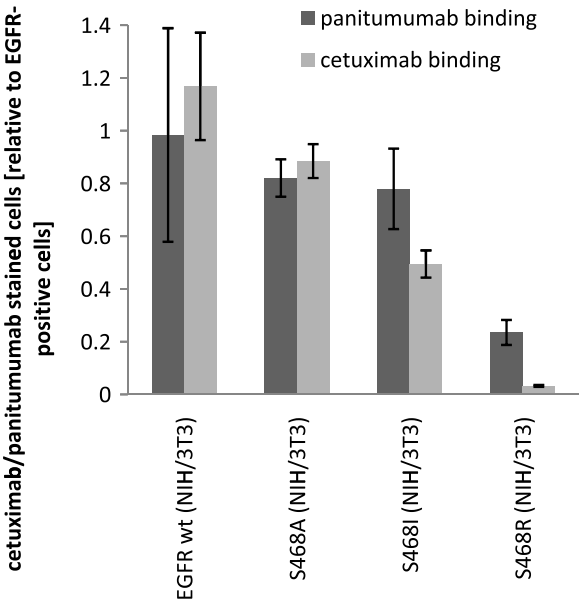

Figure W3. Mutational analysis of position S468. Position **S**468 was mutated to alanine, isoleucine, and arginine. After transfection into NIH 3T3 cells, binding of panitumumab and cetuximab as well as polyclonal EGFR antibody was studied by flow cytometry. Data are shown as relative values compared to EGFR-positive cells (percentage of EGFR-positive cells set to 1) and means of triplicate experiments ± SEM.