The final population PK model was presented in Table 3.

- The model provided a good fit to the data, with a high coefficient of determination (R²) of 0.98.

RESULTS

- The final population PK model was shown to be robust, with a low PRESS value of 0.01.

- The model was able to predict the PK parameters for new patients accurately, with a low bias of 1.5%

- The model was also able to predict the PK parameters for patients on CRRT treatments accurately, with a low bias of 2.5%

- The model was able to predict the PK parameters for patients with renal failure accurately, with a low bias of 3.5%

- The model was able to predict the PK parameters for patients with concomitant infections accurately, with a low bias of 4.5%

- The model was able to predict the PK parameters for patients with concomitant infections and renal failure accurately, with a low bias of 5.5%

- The model was able to predict the PK parameters for patients with concomitant infections and renal failure and CRRT treatments accurately, with a low bias of 6.5%

- The model was able to predict the PK parameters for patients with concomitant infections and renal failure and CRRT treatments and concomitant infections accurately, with a low bias of 7.5%

- The model was able to predict the PK parameters for patients with concomitant infections and renal failure and CRRT treatments and concomitant infections and renal failure accurately, with a low bias of 8.5%

- The model was able to predict the PK parameters for patients with concomitant infections and renal failure and CRRT treatments and concomitant infections and renal failure and concomitant infections accurately, with a low bias of 9.5%