Details of statistical analysis

Table 3. In the analysis of the impact of individual side effects of treatment with tyrosine kinase inhibitors in patients with chronic myelogenous leukaemia on the level of depressive symptoms measured by the GHQ, the regression algorithm reached its final solution in step 3. The model was well fitted to the data – $F_{(3.87)} = 9.16$; $p < 0.001$ and explained 21% of the variance of the dependent variable ($R^2_{adj} = 0.21$).

Table 4. In the analysis of the impact of individual side effects on the level of depressive symptoms measured by the 4DSQ, the regression model reached the final solution in step 1 and was well fitted to the data – $F_{(1.89)} = 10.97$; $p < 0.001$. This model allowed to explain 10% of the variance.

Table 6. The results showed that in the case of women surveyed with the GHQ, the regression algorithm achieved the final solution in step 2. The model turned out to be well fitted to the data – $F_{(2.50)} = 16.72$; $p = 0.004$ and allowed to explain 16% of the variance of the dependent variable ($R^2_{adj} = 0.16$).

Table 7. In women examined with the 4DSQ, the regression algorithm reached the final solution in step 1. The model turned out to be well fitted to the data – $F_{(1.51)} = 4.45$; $p < 0.013$ and allowed to explain 10% of the variance of the dependent variable ($R^2_{adj} = 0.10$).

Table 8. In men tested with the GHQ, the regression algorithm reached the final solution in step 3. The model was well fitted to the data – $F_{(3.34)} = 6.03$; $p = 0.001$ and allowed to explain 31% of the variance in the occurrence of depressive symptoms measured by the GHQ ($R^2_{adj} = 0.31$).

Table 9. In men tested with the 4DSQ, the regression algorithm reached the final solution in step 1. The model turned out to be well fitted to the data – $F_{(1.36)} = 0.77$; $p = 0.002$ and allowed to explain 21% of the variance of the dependent variable ($R^2_{adj} = 0.21$).