Three modelling systems (MultiCase (R), LeadScope (R) and MDL (R) QSAR) were used for construction of androgenic receptor antagonist models. There were 923-942 chemicals in the training sets. The models were cross-validated (leave-groups-out) with concordances of 77-81%, specificity of 78-91% and sensitivity of 51-76%. The specificity was highest in the MultiCase (R) model and the sensitivity was highest in the MDL (R) QSAR model. A complementary use of the models may be a valuable tool when optimizing the prediction of chemicals for androgenic receptor antagonism. When evaluating the fitness of the model for a particular application, balance of training sets, domain definition, and cut-offs for prediction interpretation should also be taken into account. Different descriptors in the modelling systems are illustrated with hydroxyflutamide and dexamethasone as examples (a non-steroid and a steroid anti-androgen, respectively). More research concerning the mechanism of anti-androgens would increase the possibility for further optimization of the QSAR models. Further expansion of the basis for the models is in progress, including the addition of more drugs.