Abstract: <strong><span style="line-height: 115%; font-family: 'times new roman', serif; font-size: 12pt; ">
Introduction: HIV integrase is a good candidate for developing new inhibitors against AIDS because it hasn't any human homologue. QSAR is very useful method for designing drugs according to the rational drug design. The mathematical models which reflect the structural information of drugs by series of descriptors could be constructed in the QSAR modeling.</span></strong><br />

**Method:** Dragon5.4 and ACD Labs software used for calculation the descriptors of 67 derivatives of 1,3,4-oxadiazole naphthyridine as HIV-1 integrase inhibitors. The suitable descriptors analyzed and selected by the help of SPSS and MATLAB software according to stepwise and GAPLS algorithms. Based on MLR procedure, two models constructed then improved to Stepwise-MLR (consensus) and GAPLS-MLR (consensus) models by using some of the already developed model descriptors. Both of the models were validated via different statistical approaches. Both of the consensus models are high efficiency in prediction of the biological activity for test set compounds. The descriptors expressed the presence of amide, alcohol and acid groups that essential for the activities of compounds. The robust of consensus models is depend on the different training set in our study with previous one. Our finding could be help to design new and effective drugs for AIDS therapy.