



Sensorgrams obtained for binding of 100, 200 and 500 nM of the selected pool (round 9) of sequences to immobilised RNase H1,

Sensorgrams were fitted simultaneously to association and dissociation phases accordingly to an heterogenous model (parallel binding to heterogenous ligand due to non oriented immobilisation of the RNase H via its amine groups) with Biaevaluation 3.1 software.

Global fitting ($\chi^2 = 1.31$) determines dissociation constants $Kd_1 = 20$ nM and $Kd_2 = 61$ nM

Individual fittings ($\chi^2 < 0.2$) of the curves indicate dissociation constants ranging from 10 to 80 nM