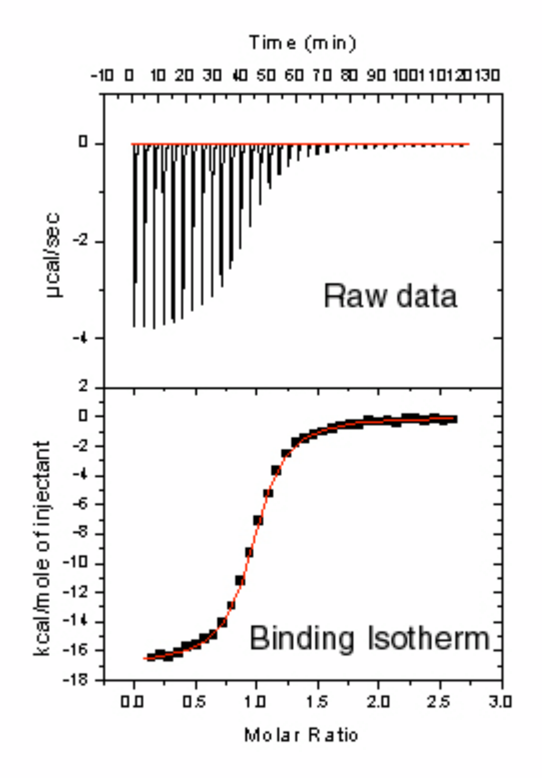
Titration of RNase with 2'-CMP

High protein concentration

Cell:	**RNase**	**64 uM**
Syringe:	**2'-CMP**	**2.19 mM**

2 uL injections



The area underneath each injection peak (top panel) is equal to the total heat released for that injection. When this is plotted against the molar ratio of ligand added to macromolecule in the cell, a complete binding isotherm for the interaction is obtained (bottom panel).

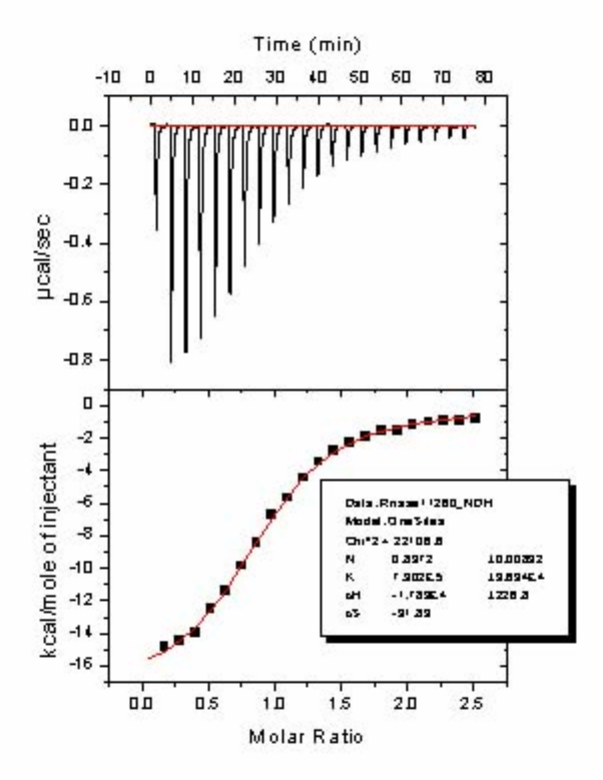
The fitted isotherm provides the following binding parameters:

Data: RNAseEwa11_NDH
Model: OneSites
Chi^2 = 9521.08

N = 0.9617 ± 0.001882 (Stoichiometry; mass ratio)
K = 7.566 ± 0.1958 E5 (Binding constant)
delta H = -1.692 E4 ± 48.84 (Enthalpy of binding reaction)
delta S = -28.90 (Entropy of binding reaction)

Low protein concentration

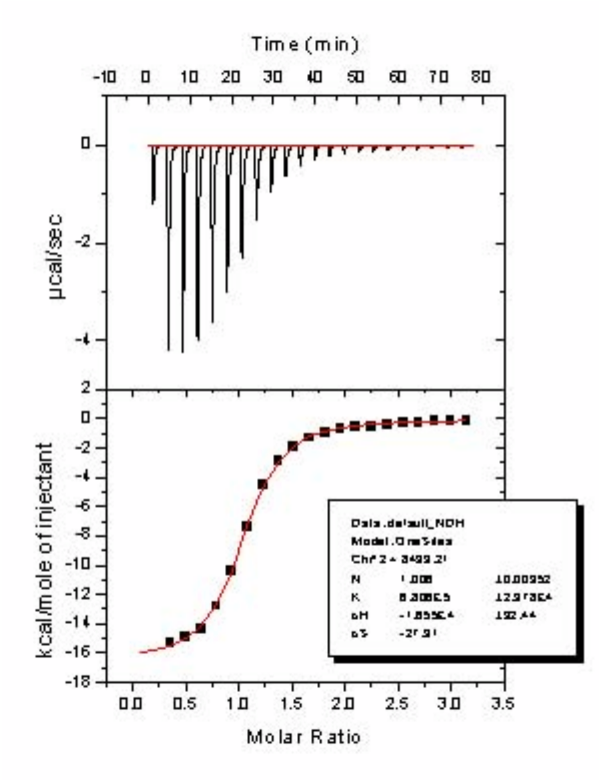
RNase 11.4 uM
2'-CMP 0.544 mM



Data: RNAseEwa112602_NDH
Model: OneSites
Chi^2 = 22106.6

N = 0.8972 ± 0.00832
K = 7.902 ± 0.369 E5
delta H = -1.783 E4 ± 226.8
delta S = -31.83

RNase 40 uM
2'-CMP 2.72 mM



Data: RNAseEwa112502_NDH
Model: OneSites
Chi^2 = 8499.21

N = 1.006 ± 0.00352
K = 6.806 ± 0.2378 E5
delta H = -1.655 E4 ± 92.44
delta S = -27.91