

**Table 1:** Characteristics of mRNA oligomer hybridization

Sequence	Binding energy (k.cal/mol)	$k_{\text{translation}}$ (input rate) (/sec)	Force (pN)
No oligomer	----	0.12	
TTTTTTTTTTTTTTTTTTTTTTTTTTTT (nonspecific 30 mer)		0.099	
ACCGCTGGAGAGCAACTGCATAAGGCTATG (specific 30 mer)	38.8	0.053	~26.2
ACCGCTGGAGAGCAACTGCATAAGGCTATG AAGAGATACGCCCTG (specific 45 mer)	61.4	0.004	~27.15
ACCGCTGGAGAGGAAC TG CATAAGGCTATG (specific 30 mer with one base mutation)	39.43*	0.051	
ACCGCTGGAGAGATGTACTGCATAAGGCTATG (specific 30 mer with three base mutation)	40.42*	0.009	
ACCGCTGGAGTATGGACTGCATAAGGCTATG (specific 30 mer with five base mutation)	39.8*	0.025	

\* Value Predicted from our model, taking ribosomal force to be 26.7pN.

**Table 2:** Sensitive parameters in simulation

Parameter (P)	V <sub>0</sub> (P)	V <sub>0</sub> (P×0.1)	V <sub>0</sub> (P×10)
Non-sensitive parameters	5.7	5.34	5.76
Concentration of nucleotides	5.7	1.14	8.23
Initiation of transcription forward rate	5.7	1.14	8.23
Luciferase K <sub>4</sub>	5.7	0.615	46.5
Luciferase K <sub>6</sub>	5.7	6.31	3.1
A_subunit - RNA binding complex forward rate	5.7	0.65	29.3
A_subunit - RNA binding complex backward rate	5.7	29.27	0.65
A_subunit decay rate	5.7	37.5	0.00034
B-subunit of ribosome binding to A_mRNA, forward rate	5.7	0.5	57
B-subunit of ribosome binding to A_mRNA, backward rate	5.7	40.6	0.594

P: value of the parameter used in simulation.

V<sub>0</sub> (P): velocity of reaction at P.