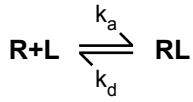
A

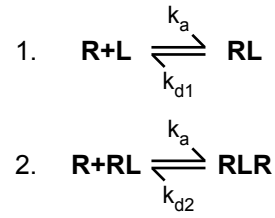
Single-step binding model



	dsRNA length (bp)	k_a $(M*s)^{-1}$ $x10^{-2}$	k_d $(s)^{-1}$ $x10^4$
pH 5.5	39	2150 (30)	156 (2)
	48	2860 (20)	38.9 (0.5)
	139	4070 (40)	37.4 (0.5)
	540	3730 (20)	17.3 (0.3)
pH 6.0	39	1780 (40)	907 (20)
	48	1490 (30)	232 (5)
	139	1870 (20)	59.2 (0.6)
	540	1660 (20)	46.8 (0.9)
pH 6.5	39	189 (3)	425 (6)
	48	297 (5)	776 (11)
	139	394 (5)	192 (2)
	540	293 (3)	229 (2)

B

Cooperative binding model



	dsRNA length (bp)	k_a $(M*s)^{-1}$ $x10^{-3}$	k_{d1} $(s)^{-1}$ $x10^3$	k_{d2} $(s)^{-1}$ $x10^5$
pH 5.5	39	2250 (60)	1890 (90)	1360 (10)
	48	3070 (100)	1580 (110)	286 (3)
	139	1710 (110)	314 (42)	292 (5)
	540	2990 (150)	1020 (110)	121 (2)
pH 6.0	39	625 (20)	820 (45)	8950 (120)
	48	2740 (30)	7360 (160)	1860 (14)
	139	746 (36)	213 (21)	482 (7)
	540	907 (28)	345 (22)	343 (4)
pH 6.5	39	82.8 (3.2)	329 (22)	3770 (50)
	48	133 (5)	615 (39)	6050 (80)
	139	270 (5)	595 (21)	1580 (10)
	540	146 (4)	377 (19)	2010 (10)

Table 2 Rate constants for TLR3-dsRNA binding. Kinetic data from surface plasmon resonance experiments were fit to either a simple single-step model (A) or a cooperative binding model (B) using BIAevaluation 4.1 software (BIAcore/ GE Healthcare) to calculate association (k_a) and dissociation (k_d) constants. Each model is described diagrammatically above (R = TLR3, L = dsRNA). In the cooperative model, the association rate constants for both reactions are equivalent (k_a), but the dissociation rate constants are independent of one another. The standard error associated with each calculation is indicated in parentheses.