Correction to "In silico simulation of inhibitor drug effects on nuclear factor-κB pathway dynamics"

In the above article [Sung M-H and Simon R (2004) *Mol Pharmacol* **66:**70–75], an error was introduced into Table 1 during the proofreading process. The corrected version of the table appears below.

We regret this error and apologize for any confusion or inconvenience it may have caused.

TABLE 1
AUIC comparison of various therapeutic situations

Inhibitor Type	Maximum Concentration or Activity (% Inhibition)	Binding Affinity	AUIC
		nM	%
A	50 (nM)	6.8[a]	40.3
	150 (nM)	6.8	73.8
	50 (nM)	0.68	67.6
B	50 (nM)	1[a]	20.1
	150 (nM)	1	44.7
	50 (nM)	0.1	48.2
	60 (%)	N/A	19.6
Bortezomib	100 (%)	N/A	39.9

[a] These values are from the original assumption about binding affinities of inhibitor A and B.