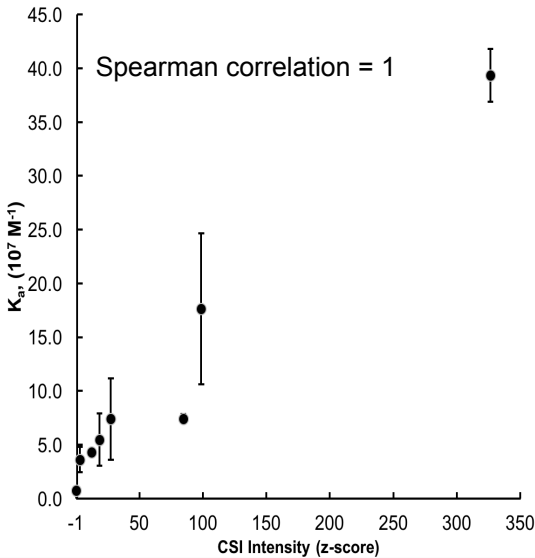


A

	Sequence	K _a , 10 ⁷ M ⁻¹
a	gagtccaGATGACGTCATCtccgtag	39.4 ± 3
b	gagtccaGATTACGTCATCtccgtag	17.6 ± 7
c	gagtcccCATGACGTCATGgccgtag	7.4 ± 0.1
d	gagtcccCATTACGTCATGgccgtag	7.4 ± 2
e	gagtccaGATGACGTCAAAaccgtag	5.5 ± 0.4
f	gagtccaGACGACGTCATCtccgtag	4.3 ± 2
g	gagtcccCACGACGTCATGgccgtag	3.6 ± 1
h	gagtcctTTTGACGTCAAAaccgtag	0.7 ± 0.1

B



C

