

**Table S4.**  $K_d$  values for interactions with the PSD-95 PDZ domains determined by surface plasmon resonance.

Competitor	Species	Family	$K_d$ ( $\mu\text{M}$ ) <sup>a,b</sup>		
			PDZ1	PDZ2	PDZ3
<b>Reference proteins</b>					
CRIP1	Human	CRIP1	ND	ND	1.5 ± 0.055
GluN2B	Human	Glutamate gated ion channel	ND	1.4 ± 0.12	ND
KIF1B $\alpha$	Human	Kinesin-like	2.2 ± 0.28	1.1 ± 0.16	ND
<b>G protein-coupled receptors</b>					
5-HTR <sub>2A</sub>	Human	5-Hydroxytryptamine receptors	630 ± 12	110 ± 4.3	ND
5-HTR <sub>2C</sub>	Human	5-Hydroxytryptamine receptors	160 ± 12	62 ± 1.6	780 ± 31
$\beta_1$ AR	Human	Adrenergic receptors	ND	180 ± 9.4	400 ± 27
$\beta_2$ AR	Human	Adrenergic receptors	ND	2086 ± 230	ND
BAI1	Human	Class B Orphans	120 ± 3.8	74 ± 3.6	2400 ± 630
Ghrelin	Human	Ghrelin receptor	NA	NA	NA
SSTR1	Human	Somatostatin receptors	84 ± 3.4	76 ± 1.5	ND
SSTR1	Mouse	Somatostatin receptors	270 ± 9.1	ND	ND
SSTR3	Human	Somatostatin receptors	ND	ND	240 ± 7.1

<sup>a</sup>The shown data are  $K_d \pm$  fitting error.

<sup>b</sup>NA, no affinity. ND, not determined.