

TABLE I
Total Receptors: Distribution and Turnover

Location/time	(AChR sites/ μm^2) $\times 10^{-3}$		
	Zero time*	2 d [†]	$t_{1/2\text{tot}}$ [§]
Thick pjm	13.0 \pm 1.3	11.1 \pm 2.4	8.5
Nonthick bottom fold	1.2 \pm 0.3	0.98 \pm 0.3	6.7
Ratio of site densities	10.7 \pm 2.9	11.0 \pm 4	—

* Total receptors at zero time are all receptors at junction seen after labeling with ^{125}I -BTX. Data are pooled from two animals and more than 100 grains per animal. Site density was calculated as described in text. Error ranges are derived from χ^2 minimization (36).

[†] Residual receptors 2 d after labeling were derived by subtracting new receptors 2 d after cold BTX (y-intercept Fig. 2) from total receptors immediately after labeling with hot BTX (zero time). Error ranges are relatively larger than for zero time since they are the combined error from the y-intercept and the zero-time value.

[§] The $t_{1/2\text{tot}}$ is half-life for total receptors derived as described in text.

^{||} Ratio is of site densities at thickened pjm to that at bottom fold.