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**Supporting Material**

**Linking the acetylcholine receptor-channel agonist binding sites with the gate**

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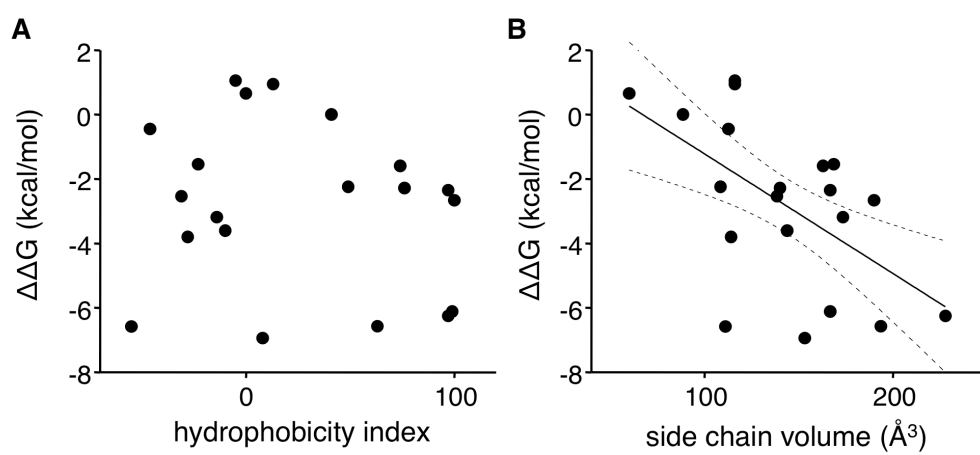


Figure S1

**Figure S1:  $\Delta\Delta G$  measurements of  $\alpha$ A96 mutations correlate with side chain volume but not hydrophobicity.**

A.  $\Delta\Delta G$  plotted as a function of side chain hydrophobicity, for all 20 natural amino acid side chains. There is no correlation of this parameter with the equilibrium constant.

B.  $\Delta\Delta G$  plotted as a function of side chain volume, for all 20 natural amino acid side chains. There is a tendency for  $E_o$  to increase with increasing side chain volume. The slope of the line is  $-0.037 \text{ kcal mol}^{-1} (\text{\AA}^3)^{-1} \pm 0.012 \text{ (SE)}$ ,  $R^2=0.29$ . Dotted lines are  $\pm 90\%$  confidence limits.

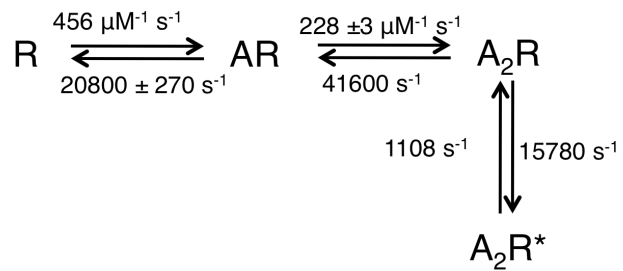
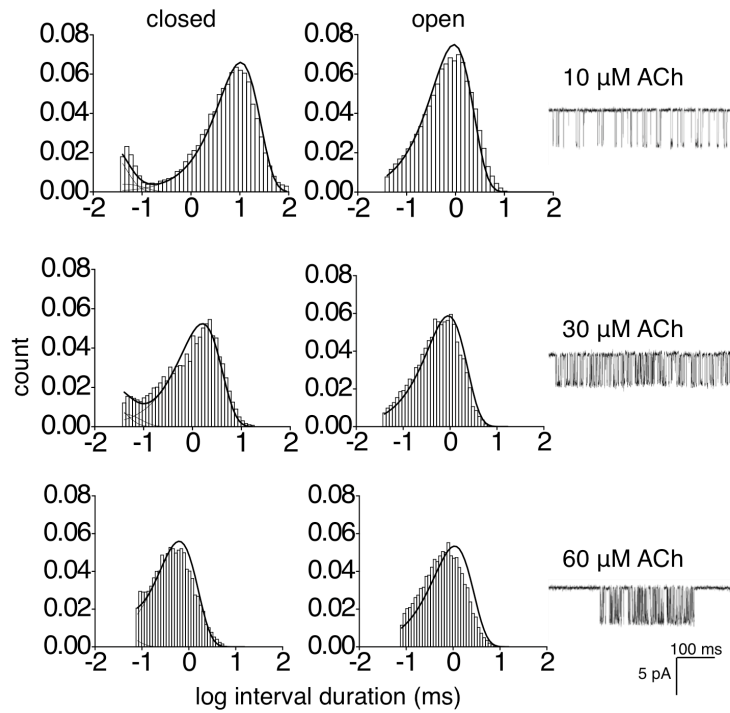
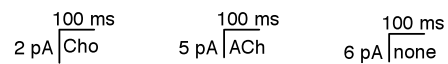
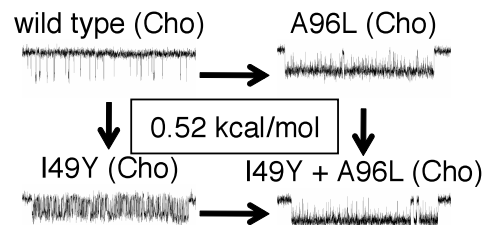
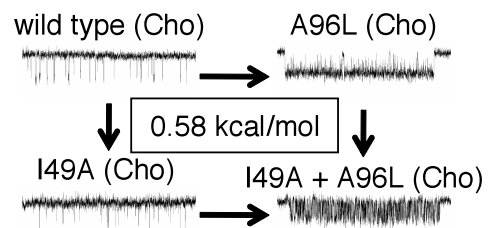
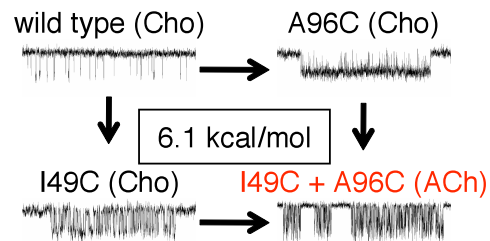
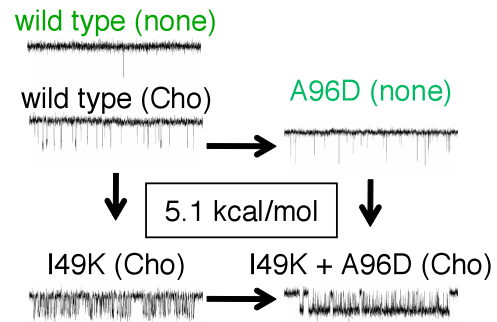
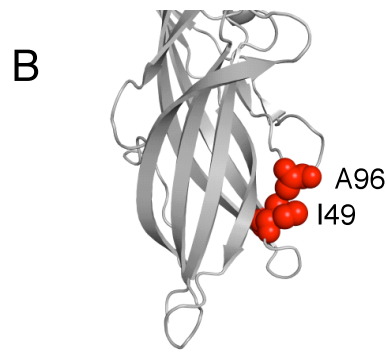
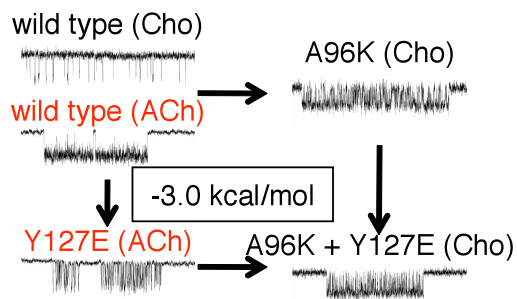
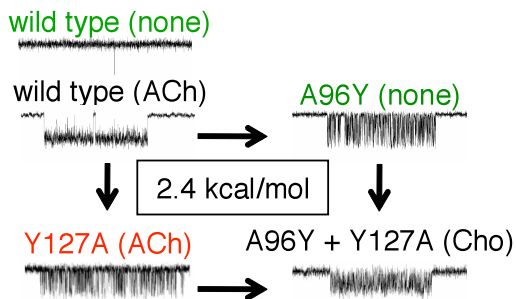
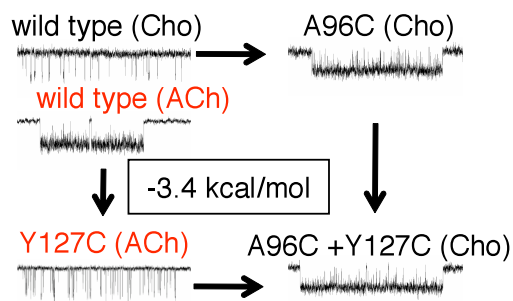
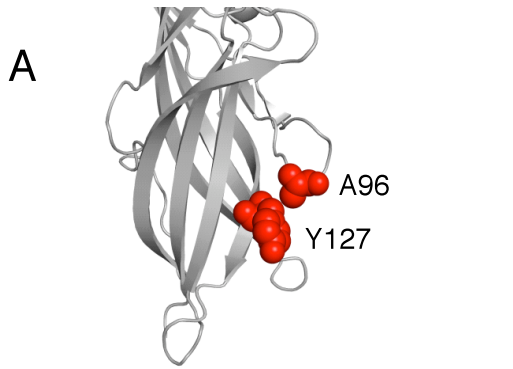


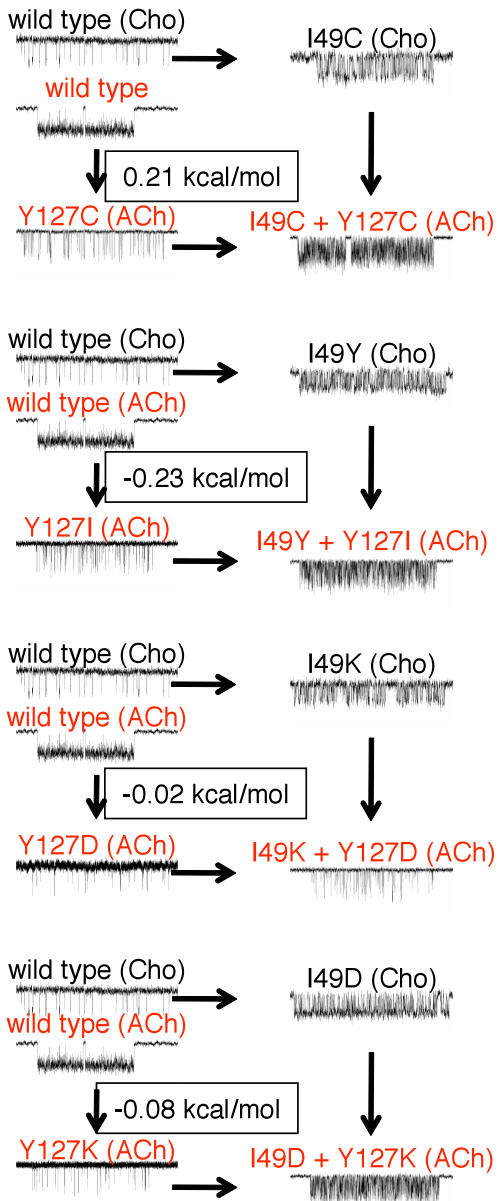
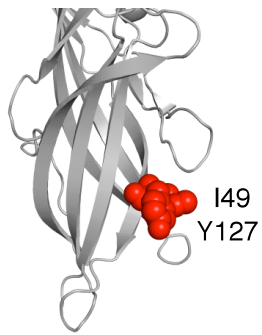
Figure S2

## Figure S2: The mutation $\alpha$ A96G has little effect on ACh binding

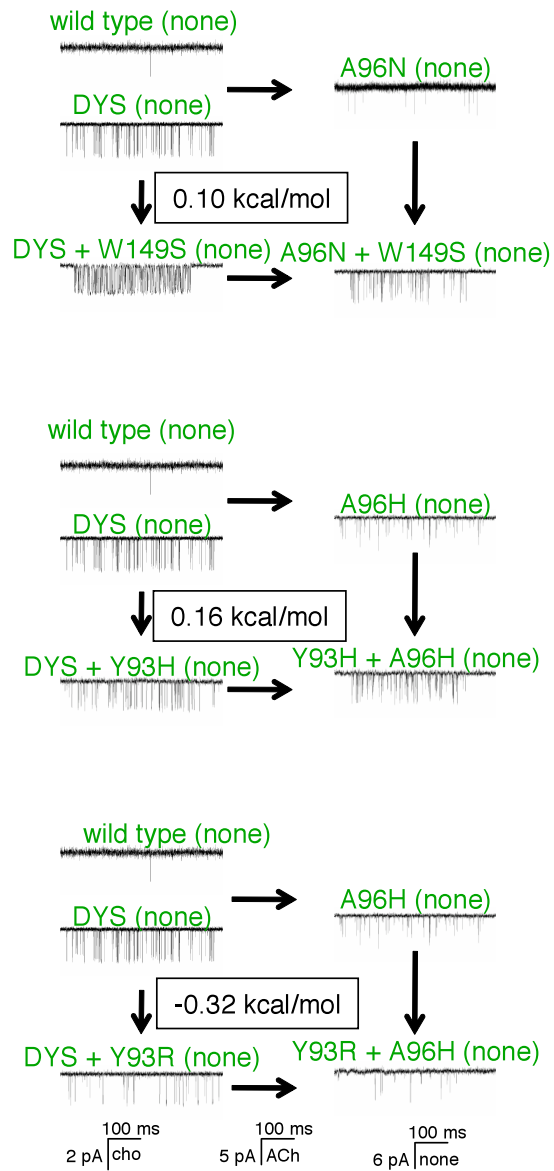
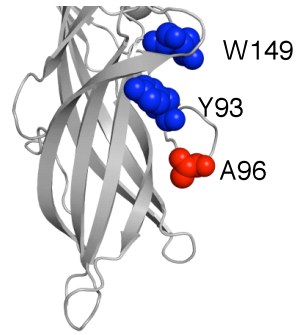
Intracluster interval durations were fitted globally using a linear binding-gating kinetic scheme (below) at three different concentrations of ACh. The models assumed two equal and independent binding steps followed by a single isomerization step. Left, observed interval duration histograms (bars) and probability density functions (solid lines) calculated from the globally-fitted rate constant estimates. Right, example clusters. The optimal binding rate constants were: association,  $k_+ = 228 \pm 3 \mu\text{M}^{-1}\text{s}^{-1}$ ; dissociation,  $k_- = 20,800 \pm 270 \text{ s}^{-1}$ .  $K_d = k_-/k_+ = 91 \mu\text{M}$ . These values are similar to the wt values:  $k_+=140 \mu\text{M}^{-1}\text{s}^{-1}$ ,  $k_- = 20,000 \text{ s}^{-1}$ .  $K_d = 140 \mu\text{M}$ .



C



D



### Figure S3: Mutant cycle analysis

Coupling energies (boxed; Table 2) were calculated for each pair of side chain substitution:  $(\text{kcal/mol}) = -0.59 \ln[(E^{\text{double mutant}})(E^{\text{wild type}})/(E^{\text{mutant 1}})(E^{\text{mutant 2}})]$ . An example cluster for each construct is shown. For each cycle, upper left is wild type and lower right is double mutant. Red letters, ACh-activated; black letters, choline-activated; green letters, spontaneously active. A.  $\alpha\text{A96}-\alpha\text{Y127}$  show a coupling energy that ranges between -3.4 kcal/mol (Cys-Cys) to +2.4 kcal/mol (Tyr-Ala). B.  $\alpha\text{A96}-\alpha\text{I49}$  show a coupling energy that ranges between +0.5 kcal/mol (Tyr-Leu) to +5.1 kcal/mol (Lys-Asp). C.  $\alpha\text{I49}-\alpha\text{Y127}$  show little interaction, as the coupling energy ranges between -0.2 kcal/mol (Tyr-Ile) to +2 kcal/mol (Cys-Cys). D.  $\alpha\text{IA96}$  is not coupled significantly to either  $\alpha\text{W149}$  or  $\alpha\text{Y93}$ .