Review
1 Exploring cells with targeted biosensors. Diana Pendin, Elisa Greotti, Konstantinos Lefkimmiatis, and Tullio Pozzan

Viewpoint
37 Progress in ciliary ion channel physiology. Juan Lorenzo Pablo, Paul G. DeCaen, and David E. Clapham

Commentary
49 Trojan triplets: RNA-based pathomechanisms for muscle dysfunction in Huntington’s disease. Martin Skov and Robert T. Dirksen

Research Articles
55 Progressive Cl⁻ channel defects reveal disrupted skeletal muscle maturation in R6/2 Huntington’s mice. Daniel R. Miranda, Monica Wong, Shannon H. Romer, Cynthia McKee, Gabriela Garza-Vasquez, Alyssa C. Medina, Volker Bahn, Andrew D. Steele, Robert J. Talmadge, and Andrew A. Voss
75 Diabetes induced by gain-of-function mutations in the Kir6.1 subunit of the K<sub>ATP</sub> channel. Maria S. Remedi, Jonathan B. Friedman, and Colin G. Nichols
85 A mechanism for acetylcholine receptor gating based on structure, coupling, phi, and flip. Shaweta Gupta, Srirupa Chakraborty, Ridhima Vij, and Anthony Auerbach
105 Structural identifiability of equilibrium ligand-binding parameters. Thomas R. Middendorf and Richard W. Aldrich
121 The structure of binding curves and practical identifiability of equilibrium ligand-binding parameters. Thomas R. Middendorf and Richard W. Aldrich

Methods and Approaches

Cover picture: The universe of all possible binding curve line shapes for proteins containing four ligand-binding sites can be represented by the values of three shape parameters (a, b, and c). The points in the region of the (a, b, c) space enclosed by the blue, red, and black sheets correspond to binding curves for which accurate estimates of binding parameters are possible (see Research Article by Middendorf and Aldrich, 121–147).