

EDITORIAL

e202012597

First steps

David Eisner

RESEARCH NEWS

e202012600

The pre-M1 helix controls NMDA receptor gating

Ben Short

COMMENTARY

e202012588

Move quickly to detach: Strain rate-dependent myosin detachment and cardiac relaxation

Charles S. Chung

RESEARCH ARTICLES

e201912484

Enhancing diastolic function by strain-dependent detachment of cardiac myosin crossbridges

Bradley M. Palmer, Douglas M. Swank, Mark S. Miller, Bertrand C.W. Tanner, Markus Meyer, and Martin M. LeWinter

e201912462

The mechanisms shaping CA2 pyramidal neurons action potential bursting induced by muscarinic acetylcholine receptor activation

Vincent Robert, Ludivine Therreau, M. Felicia Davatolhagh, F. Javier Bernardo-Garcia, Katie N. Clements, Vivien Chevaleyre, and Rebecca A. Piskorowski

e201912362

NMDA receptor channel gating control by the pre-M1 helix

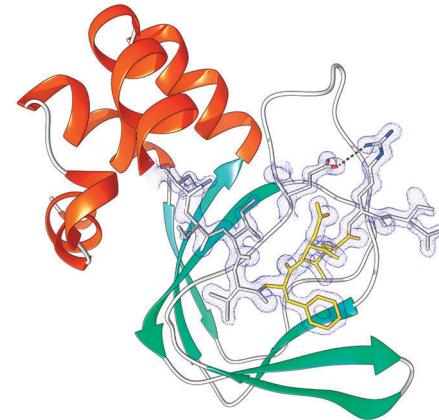
Miranda J. McDaniel, Kevin K. Ogden, Steven A. Kell, Pieter B. Burger, Dennis C. Liotta, and Stephen F. Traynelis

COMMUNICATION

e201912505

Structure of KCNH2 cyclic nucleotide-binding homology domain reveals a functionally vital salt-bridge

Ariel Ben-Bassat, Moshe Giladi, and Yoni Haitin

**ON THE COVER**

The crystal structure of the human KCNH2 channel (hKCNH2) cyclic nucleotide-binding homology domain (CNBHD), resolved at 1.5 Å resolution (blue mesh).

The structure highlights a newly identified E807-R863 salt-bridge (dashed line) as a vital component of hKCNH2 channel function.

Indeed, by its proximity to the canonical KCNH intrinsic ligand motif, consisting of the ⁸⁶⁰FNL⁸⁶² tripeptide (yellow sticks), this salt-bridge may serve as a strategically positioned linchpin, supporting both the spatial organization of the intrinsic ligand and the intracellular complex interface.

Image © Ben-Bassat et al., 2020. See <http://doi.org/10.1085/jgp.201912505>