The research in Dr. Bernhard Flucher’s laboratory focuses on the organization of voltage-activated calcium channels in cellular signaling machines. Calcium channels play a central role in important bodily functions such as the control of muscle contraction or the transmission and modulation of signals in the nervous system. In order to accomplish these diverse functions, different types of calcium channels need to be incorporated into complex molecular signaling machines located in distinct compartments of muscle and nerve cells. However, the mechanisms underlying the correct targeting of the channels into specific subcellular compartments and their protein-protein interactions with associated scaffolding and signaling proteins are still poorly understood. To address these problems, our laboratory utilizes cell cultures from calcium channel null-mutant mice reconstituted with normal and mutated recombinant channels. Thus, effects on the incorporation into the signaling complex and on cell function of molecular alterations of a channel protein—like chimeras of channels with distinct properties or mutations causing human disease—can be analyzed in the native environment of the muscle and nerve cells. In recent years, this approach has allowed us to determine sequences within the calcium channel $\alpha_1$ subunit that are involved in the subcellular targeting and in functional interactions with other constituents of the macromolecular signaling complexes (http://physiologieuibk.ac.at/flucher/).

Efficient genotype tests are necessary for the generation of genetically modified mouse models, such as the Immortomouse™, and for the characterization of derivative cell lines. To this end, genome walking was employed to identify the genomic sequences flanking the $H2K^b$-tsA58 transgene. This not only provided the necessary information to develop the first PCR-based genotype assay for this commonly used mouse model, but it also showed that no other known gene had been disrupted by the random insertion of the transgene into the mouse genome. Moreover, genome walking proved to be a convenient strategy for the localization of transgenes, for most of which the insertion sites have never been determined. With the availability of this simple method for the identification of flanking sequences and with the sequencing of the mouse genome near to completion, the genomic localization of transgenes and the demonstration that its insertion did not disrupt other important genes may soon become state of the art in the characterization of newly developed transgenic mouse models.