

Legends for Supplemental Table and Figures

Supplemental Table S1. Proteins (A) and peptides (B, C) identified in olfactory ciliary membrane-enriched fractions by gel-based and gel-free LC/MS analyses. MS data were processed with MaxQuant/Andromeda (version 1.2.0.18). Proteins listed in (A) were identified with a false discovery rate of < 1% on peptide and protein level and a minimum of two peptides, one of which unique, in at least two out of three replicates for either the gel-based or the gel-free dataset. IBAQ values calculated by MaxQuant indicate the relative abundance of a protein in the respective dataset. Information about the subcellular localization of individual proteins were derived from UniProt and the Gene Ontology (GO) database. The set of proteins identified in this study was compared with transcriptome data of mature, ciliated OSNs (24) as well as previous proteomics studies (11, 16). MW, molecular weight; PEP, posterior error probability; TM, transmembrane; *m/z*, mass-to-charge; GOBP, GOMF, GOCC, GO terms for biological process, molecular function, and cellular compartment.

Supplemental Figure S1. Enrichment of ciliary membrane proteins by Na₂CO₃-treatment.

A ciliary extract obtained from olfactory epithelia of mice employing the Ca²⁺/K⁺-shock method (16) was centrifuged at 26,000 x g and the resulting cilia-containing pellet (P26K) was washed with 100 mM Na₂CO₃ (pH 11.2). Centrifugation at 100,000 x g resulted in a fraction enriched in ciliary membrane proteins (P100K). Equal fractions of the ciliary extract and the supernatants and pellets obtained after the centrifugation steps were subjected to Western Blot analyses using specific antibodies against marker proteins of the ciliary membrane (adenylyl cyclase III, AC III), microvilli (ezrin), the ciliary axoneme (acetylated alpha-tubulin, Ac-tubulin) and the mitochondrial membrane (COX IV). S26K and S100K, supernatants after centrifugation at 26,000 and 100,000 x g.

Supplemental Figure S2. Peptide intensity profile of olfactory receptor proteins identified from ciliary membranes by SDS-PAGE and LC/MS. Based on total peptide intensities, olfactory receptor proteins were detected in the range of approx. 37, 80 and 160 kDa indicating their electrophoretic separation as monomers, dimers and tetramers under denaturing conditions.

Supplemental Figure S3. GO terms enriched in the set of 308 olfactory cilia-specific proteins. Shown are GO terms enriched in the categories "Biological process", "Cellular compartment" and "Molecular function". The analysis was performed using the Cytoscape plugin BiNGO 2.44 and the whole mouse genome as background. The significances for the enrichment of individual GO terms are indicated by a color gradient ranging from yellow to dark orange representing decreasing p-values. The circle size reflects the number of proteins in the respective categories.