IFT88 maintains sensory function by localising signalling proteins along Drosophila cilia

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Ciliary defects cause several ciliopathies, some of which have late onset, suggesting cilia are actively maintained. Still, we have a poor understanding of the mechanisms underlying their maintenance. Here, we show Drosophila melanogaster IFT88 (DmIFT88/nompB) continues to move along fully formed sensory cilia. We further identify Inactive, a TRPV channel subunit involved in Drosophila hearing and negative-gravitaxis behaviour, and a yet uncharacterised Drosophila Guanylyl Cyclase 2d (DmGucy2d/CG34357) as DmIFT88 cargoes. We also show DmIFT88 binding to the cyclase’s intracellular part, which is evolutionarily conserved and mutated in several degenerative retinal diseases, is important for the ciliary localisation of DmGucy2d. Finally, acute knockdown of both DmIFT88 and DmGucy2d in ciliated neurons of adult flies caused defects in the maintenance of cilium function, impairing hearing and negative-gravitaxis behaviour, but did not significantly affect ciliary ultrastructure. We conclude that the sensory ciliary function underlying hearing in the adult fly requires an active maintenance program which involves DmIFT88 and at least two of its signalling transmembrane cargoes, DmGucy2d and Inactive.

DOI 10.26508/lsa.202302289 | Received 25 July 2023 | Revised 7 February 2024 | Accepted 8 February 2024 | Published online 19 February 2024

Introduction

Cilia are microtubule (MT)-based organelles that emanate from the surface of eukaryotic cells and are vital for several functions, including motility and sensing (reviewed in Reiter & Leroux [2017]; Breslow & Holland [2019]; Sreekumar & Norris [2019]). Cilia biogenesis is a multistep process that is evolutionarily conserved and regulated during cell differentiation. A cilium consists of two regions: a ciliary base and a ciliary protrusion or shaft. The latter grows from the ciliary base and is composed of an MT-based skeleton (the axoneme) and a ciliary membrane. Ciliary proteins are produced in the cell body and then move either by diffusion or by active transport through the ciliary base, containing a diffusion barrier, into the ciliary shaft. A large proportion of these active transports is manifested by a process called intraflagellar transport (IFT), which depends on molecular motors moving from the ciliary base to the axoneme tip (anterograde) and in reverse (retrograde) direction (reviewed in Breslow & Holland [2019]).

Defects in cilium structure and function cause several human disorders, called ciliopathies, causing, for example, alterations in body symmetry, obesity, retinal degeneration, and cystic kidneys (reviewed in Bettencourt-Dias et al [2011]; Brown & Witman [2014]; Braun & Hildebrandt [2017]; Wang & Dynlacht [2018]; Anvarian et al [2019]). Whereas defects in cilia assembly can lead to numerous diseases, they do not account for all symptoms of many cilia-related disorders, such as retinitis pigmentosa, nephropthysis, and Alström syndrome, which show progressive tissue degeneration or late pathological onset in the patients (reviewed in Reiter & Leroux [2017]; Sreekumar & Norris [2019]). Given that many ciliated cells such as photoreceptors, ciliated sensory neurons, and epithelial cells are long-lived, it is possible that the breakdown of ciliary maintenance is causal of those diseases. IFT has been implicated in regulating ciliary structural and functional properties such as flagella length and the ciliary localisation of signalling receptors, such as osins, transient receptor potential vanilloid (TRPV) channels, somatostatin receptors (SSTR3), and guanylyl cyclases (GC), in various organisms (Marshall et al, 2005; Qin et al, 2005; Bhowmick et al, 2009; Ye et al, 2013; Eguether et al, 2014; Jiang et al, 2015; van der Burght et al, 2020). Interestingly, in the unicellular parasite Trypanosoma, IFT88 depletion does not affect the structure of fully formed flagella but impairs their beating, pointing to a deregulation/mislocalisation of flagella components (e.g.,
PKAR, kinesin 9, FAM8) that are implicated in flagellar beating (Fort et al, 2016). Furthermore, entry of several receptors, such as smoothened (SMO) and olfactory receptor coreceptor (Orco) into the cilia is IFT-independent (Milenkovic et al, 2009; Williams et al, 2014; Jana et al, 2021). Altogether, the existing evidence suggests that the maintenance of ciliary structure and sensory function may be regulated in a cell- and organism-specific manner by mechanisms that are hardly understood.

Here we study the underpinnings of ciliary maintenance in a genetically tractable organism, Drosophila melanogaster. In particular, we focus on adult auditory ciliated (Type-I) sensory neurons, as they rarely get replenished (Fernandez-Hernandez et al, 2021) and are involved in different sensory functions with straightforward experimental readouts, including hearing and negative-gravitaxis (Han et al, 2003; Jana et al, 2018). Given the importance of IFT in cilium assembly and maintenance in Chlamydomonas (Pazour et al, 2002; Marshall et al, 2005), we chose to investigate the function of the key IFT-B1 protein, IFT88, in the maintenance of ciliary structure and function. IFT88 gene is also known as nompB (no mechanoreceptor potential B) in D. melanogaster (Han et al, 2003), and we henceforth refer to it as DmIFT88. We first found that DmIFT88-containing trains move within fully grown chordotal cilia (Figs 1 and 2A), suggesting IFT might play an active role in Drosophila cilia maintenance. We next observed that acute depletion of DmIFT88 in adult ciliated sensory neurons subtly alters cilium bending at the ciliary base without affecting ultrastructures of the axoneme and impairs sensory cilium function, causing defects in hearing and negative-gravitaxis behaviour (Figs 2, S2, S3, and S4). In the search for distinct DmIFT88 cargoes, we discovered that DmIFT88 binds and contributes to the ciliary localisation of the TRPV channel subunit Inactive (Iav) (Fig 3) and the fly homologue of an evolutionarily conserved particulate Guanylyl Cyclase (Gucy2d) (Figs 4, 5, S5, S6, S7, S8, and S9) that is involved in human ciliopathies. Altogether, our research shows that IFT88 is dispensable for ciliary structure retention (Fig S4a) but critical for the maintenance of sensory cilium function in adult Drosophila, partly through the binding and localisation of different signalling proteins, including Inactive and DmGucy2d.

Results

IFT88 protein sequences show high conservation of structural domains

D. melanogaster homologues of IFT proteins (i.e., A-complex, B-complex, and BBSome) have been identified through bioinformatics analysis (for a summary, see our compilation of all information in Fig S1A, and Table S1). Several of these proteins were shown to be expressed in ciliated neurons or in the fly head (Avidor-Reiss et al, 2004; Chintapalli et al, 2007; Lee et al, 2008, 2018; Mourao et al, 2016), yet only a small number have been investigated mechanistically, such as DmIFT88 and DmIFT40 (Han et al, 2003; Lee et al, 2008). Studies in other model organisms suggest that only a few evolutionarily conserved IFT proteins are critical for cilia formation (Pazour et al, 2002; Fan et al, 2010; Eguether et al, 2014; Fort et al, 2016). Among them is IFT88, and thus, we investigated whether it is active after the cilia assembly is complete and might also have an important role in transporting components needed for cilium maintenance.

In D. melanogaster, two isoforms of DmIFT88 have been described with similar amino acid compositions (Fig 1Aii) (Han et al, 2003). Both isoforms are predicted to bear 10 tetra-tricopeptide repeat (TPR) domains (Karpenahalli et al, 2007) (Fig 1Aii), which often act as interfaces for protein-protein interactions (Allan & Ratajczak, 2011; Taschner et al, 2012), and, accordingly, seem good candidates for transporting cargoes into the cilium. In fact, all IFT88 homologues (in insects and vertebrates) are predicted to comprise 10–15 TPRs (Fig 1Aii; for a detailed list of protein accession numbers, see Tables S2 and S3), pointing to conserved roles in mediating protein interactions, either within the IFT-B core complex or between IFT and various cargoes (Taschner et al, 2012). We thus investigated whether DmIFT88 transports cargoes and continues to do so after cilium assembly, contributing to cilia maintenance.

DmIFT88 trains are visible in fully assembled cilia

To assess the localisation of DmIFT88 protein in fully assembled cilia, we first tested a transgenic fly line expressing GFP-tagged DmIFT88 protein (GFP::DmIFT88) under its endogenous promoter (Han et al, 2003). Yet, the weak signal resulting from GFP-tagged DmIFT88’s expression did not allow for live imaging. We thus generated transgenic lines carrying a UAS-eGFP::DmIFT88 (isoform-RD) construct, as this isoform suffices to rescue IFT88 function in nompB (a DmIFT88 functional null mutant) flies in which all isoforms are affected (Han et al, 2003). To test whether DmIFT88 is part of IFT trains in assembled cilia, the transgene was expressed using a chordotal neuron-specific driver (Gal4i404) (Fig 1Bi–iii) (Gong et al, 2004). We were able to track DmIFT88 particles in the proximal compartment of the cilium of lateral chordotal organ (ichs) neurons in wandering L3 larvae, a developmental stage at which larval ciliogenesis is considered to be concluded. Quantification of the velocity of the eGFP::DmIFT88 signal (Fig 1Ci and Video 1) revealed that the particles move about five times faster in the retrograde direction (1.2 μm/s) than in the anterograde direction (0.22 μm/s). A recent study on the chordotal neurons in developing Drosophila pupae found different anterograde (~0.44 μm/s) and retrograde velocities varied (~0.12 and ~0.7 μm/s) in proximal and distal compartments, respectively for IFT88 (Lee et al, 2018). These observations suggest that DmIFT88 velocities vary between developmental stages and ciliary compartments. This large variability was also shown before for different cell types in single species (Besschletnova et al, 2010; Williams et al, 2014; an overview of different IFT velocities is provided in Table S4).

We also noticed that the signal intensities of the anterograde trains of eGFP::DmIFT88 appear stronger than the retrograde train intensities, similar to features observed in other organisms, including Chlamydomonas and Trypanosoma (Fort et al, 2016; Wingfield et al, 2021). Measurements of DmIFT88 train lengths (Fig 1Ci), although limited by the resolution of the confocal microscope, suggest that anterograde trains have an average length of 358 nm (ranging from 152–650 nm as minimum and maximum length). This would correspond to trains with ~58 IFT-B particles, based on a recent report in Chlamydomonas (van den Hoek et al, 2022). We found that retrograde
trains are significantly shorter, with an average of 237 nm (ranging from 115–433 nm as minimum and maximum length), corresponding to ~38 IFT-B particles (Fig 1Cii). Although IFT trains in the fly have not been studied in detail by electron microscopy (EM), these numbers are very close to those found in other species by EM or cryo-ET, supporting previous indications that, compared to retrograde trains, anterograde trains contain more IFT complexes and move in a tighter conformation (Pigino et al, 2009; Buisson et al, 2013; Fort et al, 2016; Chien et al, 2017; Jordan et al, 2018).

In Chlamydomonas flagella, a microtubule doublet is considered a double track for IFTs, with retrograde trains moving along A-microtubules and anterograde trains moving on B-microtubules (Stepanek & Pigino, 2016). Whereas IFT movement has not been as well detailed in Drosophila, our analysis of DmIFT88 train movements revealed interesting features. We observed that anterograde trains move slowly and remain unperturbed by any encounter with retrograde trains. In contrast, retrograde train movements are irregular (Fig 1Biii), half of them stalling their trip at least once along the length of the proximal ciliary region.

Figure 1. DmIFT88 is evolutionarily conserved and its trains are visible in Drosophila sensory cilia. (A) Drosophila IFT88 shows structural-domain conservation despite low amino acid sequence conservation. (i) Schematic representation of the two annotated DmIFT88 isoforms (RNA and proteins) in the fly. The grey boxes represent coding sequences. (ii) Left: Maximum-likelihood phylogenetic tree for IFT88 from various vertebrate and insect species, displaying bootstrap branch “support values” in percentages (%). The accession numbers of the proteins used in this analysis and a list of abbreviations are provided in Table S2. NA: the “support value” could not be calculated because of the method used to generate the sequence alignment. The amino acid identity of each sequence compared to Drosophila melanogaster is shown in percentages (%), and the number of predicted tetratricopeptide repeat domains in each species is displayed. Right: Multiple sequence alignment of IFT88 from 11 species represented as a heat map generated using JProfiloGrid2. Each position in the alignment is shown as a box, colour-coded according to the similarity score. The relative positions of the 10 tetratricopeptide repeats of Drosophila melanogaster are indicated by black boxes. (B) GFP::DmIFT88 trains are visible in wandering L3 larvae. (i) Schematic representation of a L3 larva showing the segmentally arranged groups of chordotonal neurons (a group of five neurons is called lch5). Membrane-bound GFP (UAS-mCD8::GFP) is expressed using Gal4 to visualise the morphology, including cilia (arrowhead), of one such group (lch5) of neurons. (ii) A video still showing ectopically expressed GFP::DmIFT88 in the dendrite tip and cilia in lch5 neurons using Gal4. Empty and filled arrowheads mark ciliary dilation and IFT particles along the proximal cilium, respectively. (iii) A scheme of a cilium showing the IFT particles moving in anterograde (magenta) and retrograde (green) directions. Below are two examples of merged kymographs with both types of DmIFT88 particle trains colour-coded depending on their direction. On the right of each merged kymograph example, separated grey anterograde (first) and retrograde (second) kymographs are shown. The train-tracks were extracted using the Kymograph Clear macro toolset from ImageJ. Magenta arrowheads, green arrowheads and arrows indicate the anterograde, retrograde and stalled trains, respectively. (C) (i) Left: Quantifications of the speed of the DmIFT88 particles, extracted from videos from 5 larvae from three different experiments. (ii) Quantifications of the lengths of DmIFT88 particles in the proximal part of lch5 cilia. (iii) Percentages of visualised trains that pass or pause when encountering an opposite train along the proximal region of the cilium. In (C), P-values are calculated using Mann-Whitney test (***(P-value ≤ 0.0001) on Prism. Source data are available for this figure.
Proteins with the ability to switch protofilaments of the chondrotonal cilium, often when encountering anterograde or retrograde particles (76%) temporarily paused before resuming their trip without delay and no change in velocity, whereas most of the retrograde particles (24%) are the ones that switch protofilaments/MT tracks within a doublet. A further detailed analysis of the IFT features in Drosophila would be required to uncover underlying mechanisms of these intriguing IFT features.

Given that DmIFT88 moves along fully formed chordotonal cilia of larvae, we wondered whether it might also be present in chordotonal cilia of adult flies, using Gal4 and mCherry drivers. We detected both DmIFT88 isoforms (Fig S2B) in mRNA isolated from the adult antennae after analysis of RNA hairpins.

Electrophysiology data (right): All-range box plots of antennal fluctuation powers (Energi) and maximum sensitivity gain to mechanical amplification (Maximum Mechanical Gain) of the hearing nerve responses (median ± min and maximum) the flies with genotypes stated in the graphs legend. In (D, E), P-values are calculated using Mann-Whitney test (ns - P-value > 0.05, *P-value ≤ 0.05 and **P-value ≤ 0.01) in Prism. Source data are available for this figure.

**Figure 2. Acute removal of DmIFT88 in adult flies leads to impaired sensory functions.**

(A) DmIFT88 protein is found in fully formed cilia in the adult. Top: Representation of the transgene (from Han et al [2003]), expressing GFP-DmIFT88 near endogenous level, used to observe the DmIFT88 localisation in fly cilia. Left: A scheme of the chondrotonal neuron architecture in the second antennal segment of adult flies showing the expected localisation of Drosophila Pericentrin-like protein and glutamylated tubulin (GT335) in the basal bodies and the axoneme, respectively. Right: representative image of the localisation of endogenous GFP-DmIFT88 with respect to the two aforementioned markers in the adult chordotonal cilia. Note that GFP-DmIFT88 signals were enhanced with an anti-GFP antibody. Arrowheads mark GFP-DmIFT88 puncta at the ciliary dilation and along the axoneme (inset). (B) Scheme of the approach and timeline of the conditional knockdown (DmIFT88 and mCherry RNAi) experiments. DmIFT88 and mCherry genes are knocked-down in cholinergic neurons, including chordotonal neurons, using Gal4 drivers, and flies are reared at 18°C to repress the expression of the hairpin during development through the co-expression of a temperature-sensitive version of GaIn ubiquitously (TubGal80ts). After flies come of pupae, adult flies are shifted to 29°C (non-permissive temperature for GaIn) to activate the expression of RNA hairpins. (C) Schematic representation of the climbing (negative-gravitaxis) behavioural assay. The effect on sensory cilia function is approximated by quantifying climbing behaviour (number of flies reaching a certain height in a specific time) on a controlled setup of the adult flies on specific days (arrows) after temperature shift. (D) Time-dependent changes in climbing behaviour at 29°C in control (mCherry) and DmIFT88 RNAi flies under Gal4Chord90 and Gal4m drivers (left and right, respectively). Each box-plot corresponds to a total of 60 flies measured in sets of 10 animals each. The data are fitted using linear regression, where the area around the curve represents the 95% confidence interval. The two lines are significantly different at 29°C. (E) Scheme of the set-up of the electrophysiology experiments performed in the 9 d old flies’ antennae after analysis of the hearing nerve function (left). The strong signals near
the ciliary base and the dilation may represent an immobile fraction of the DmIFT88 pool (Fig 1Bii and Video 1). Additional smaller and weaker GFP puncta, similar to the ones observed in the larvae (Fig 1Bii, filled arrowhead), were detected along the axoneme, likely representing IFT trains (inset on Fig 2A). Together, our observations on larvae and adult flies (Figs 1Biii and 2A) suggest that IFT88 features observed in the fly are to some extent evolutionarily conserved and that DmIFT88 is actively transported along the chordotonal cilia beyond ciliogenesis.

Conditional knockdown of DmIFT88 in adult cilia impairs hearing and gravitaxis behaviour

We next investigated whether DmIFT88 has any significant role in the maintenance of cilia. Because this protein is essential for ciliogenesis in sensory neurons (Han et al., 2003), we could not take advantage of the available mutant, as it does not assemble cilia. We thus aimed at knocking down DmIFT88 expression in a certain subset of sensory neurons using RNAi (Table S5), which was only active after the cilia had formed.

We first tested for the efficacy of the RNAi line (with a hairpin that targets an exon common to both DmIFT88 isoforms and without any predicted off-targets) using a ubiquitously active promoter (Gal4Tubulin). We found that the mRNA levels of both isoforms are strongly reduced (~75–80%) in the antennae of flies expressing the DmIFT88 hairpin (UAS-DmIFT88-IR), as compared to negative controls (UAS-mCherry-IR, as mCherry is not encoded in the fly genome; Fig S2A–C). Importantly, sound stimulation-evoked compound action potentials recorded from JO chordotonal neurons were significantly reduced in DmIFT88 knockdown flies compared to

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**Figure 3.** Inactive, a ciliary TRPV channel, binds DmIFT88 and requires it for its localisation.

(A) Co-immunoprecipitation (co-IP) assay performed upon co-overexpression of 3xHA:DmIFT88 and Inactive::GFP (or GFP as negative control) in Drosophila Dmel cells. DmIFT88 co-immunoprecipitates with Inactive::GFP but not with GFP alone (N = 3 repeats). The green asterisk marks the expected band of the transfected Inactive::GFP plasmid. The rest of bands seen with the GFP antibody were found in all the three independent experiments and most likely are because of possible phosphorylation or to unwanted degradation (for details on the antibodies used, see Table S7).

(B) Left: Representative immunofluorescence images of adult chordotonal cilia with Inactive (lav) and NOMPC, in the proximal and distal zone of the cilia, in red and blue, respectively. Upper two examples are from control flies (mCherry RNAi); below two examples are from DmIFT88 RNAi flies. For details on the antibodies used, see Table S7. Scale bar: 1 μm. Right: All-range box plots of the normalised average lav signal (per antennae) along the proximal part of the axoneme in flies with the aforementioned genotypes. **P-value is calculated using Mann-Whitney test (**P-value ≤ 0.01).

Source data are available for this figure.
controls (Fig S2D), consistent with the hearing defects reported in DmIFT88/nompB null mutants (Han et al., 2003). Interestingly, we found that whereas flies with the ubiquitous DmIFT88 knockdown do not assemble cilia, they can still build the transition zone (Fig S2E–H), similar to the phenotype observed in IFT88 and kinesin-2 mutants in various model organisms (Pazour et al., 2002; Sarpal et al., 2003).

To test for defects in cilium maintenance, we used a temperature-sensitive (ts) system that allows us to control gene expression in a cell- and time-specific manner (Gal4-UAS-Gal80Ts) (Fig 2B; see the “Material and Methods” section) (McGuire et al., 2003). We used the Gal4(Cha19D) driver, which expresses in the peripheral and central nervous system, including JO neurons during development (Salvaterra & Kitamoto, 2001). In antennal tissue, this driver expresses at the pupal stages, long after neurogenesis begins, and a few hours after ciliogenesis begins. It continues to be expressed in the adult nervous system, including JO neurons during development (Jana et al., 2021) at different ages, for up to 9 d after induced RNAi expression (reducing ~30% DmIFT88 mRNA levels compared to control flies; Fig S3C) because the climbing behaviour of the flies older than 9 d (at 29°C) could be affected by natural ageing in the adults (Figs 2B and C, 3E, and 5D; Kamikouchi et al., 2009). Importantly, DmIFT88 RNAi flies developed negative gravitaxis defects in 3 d old flies (reared at 29°C) that, with time, became more pronounced (Fig 2D). When flies were reared at 18°C (Gal4 inhibited), there was no significant negative-
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https://doi.org/10.26508/lsa.202302289

Figure 5. DmGucy2d is localised in the cilium via DmIFT88, and it is important for the maintenance of behavioural sensory functions.

(A) Representation of the drivers’ expression in the experimental settings used in the following sections of the figure as mentioned in the scheme. (B) Immunofluorescence images show that the ectopically expressed GFP-tagged T1-truncation of DmGucy2d (using Gal4Flp) accumulates in chordotonal neuron cell body, dendrite and ciliary dilation. Insets highlight that the GFP signal is also seen in the cilium axoneme. Proximal and distal cilia zones are marked with lav (red) and NOMPC (blue) antibodies, respectively. (C) Scheme summarises the experimental strategy in which T1-DmGucy2d:GFP is expressed in the chordotonal neurons (using Gal4Flp) with or without RNAi against DmIFT88. The resulting adult flies were analysed 6 d after they came of pupae. (B, D) Representative immunofluorescence images of the adult chordotonal cilium from flies with different genotypes (described in (B)). Insets show T1-GFP localisation along the proximal zone of the cilium (marked with dashed grey lines based on the anti-lav antibody signal). Scale bars: 1 μm. (E, F, G) Graphs are all-range box plots of: the percentage of cilia with GFP signal at the ciliary dilation (D), the average GFP signal along the proximal zone of the cilium (E), and normalised signal intensities of GFP at the ciliary base (F). Here, P-values are calculated using Welch corrected (One-tailed) unpaired t test (ns - P-value ≥ 0.05, *P-value < 0.05, **P-value < 0.01). (H) Negative gravitaxis behaviours of flies during time at 29°C carrying the corresponding control (mCherry RNAi) and DmGucy2d RNAi, under the expression of the Gal4Flp driver. Each box plot corresponds to a total of 60 flies measured in sets of 10 animals each. The data are fitted using linear regression on the left panel, where the area around the curve represents the 95% confidence interval. The two lines are significantly different at 29°C. (I) Scheme of the set-up of the electrophysiology experiments performed on the 9 d old flies’ antennae to analyse hearing nerve function (left). Electrophysiology data (right): All-range box plots of: the percentage of cilia with GFP signal along the proximal zone of the cilium (E), and normalised signal intensities of GFP at the ciliary base (F). Here, P-values are calculated using Welch corrected (One-tailed) unpaired t test (ns - P-value ≥ 0.05, *P-value < 0.05, **P-value < 0.01). Source data are available for this figure.

Gravitaxis behaviour impairment at any time point tested, compared to control flies (Fig S3B). To assess whether this behavioural phenotype is because of the loss of DmIFT88 in chordotonal organs only in adults, the conditional knockdown experiment was repeated using a temperature-sensitive system with a more restricted promotor for Gal4 expression, Gal4Flp. This driver is expressed only in chordotonal neurons, but it is also weaker, which forced us to extend the study up to 14 d. The analysis of this condition also showed that upon knockdown of DmIFT88, there is a significant impairment on climbing behaviour (Fig S3E).

In addition to impairing negative-gravitaxis, acute DmIFT88 knockdown in cholinergic neurons (Fig 2E) negatively affected the function of the cholinergic chordotonal neurons of the fly’s JO on hearing. These neurons transduce antennal vibrations into electrical signals and, in addition, actively amplify these vibrations on a cycle-by-cycle basis through ciliary motility (Gopfert & Robert, 2003; Nadrowski et al, 2008; Karak et al, 2015). This motility was strongly reduced by DmIFT88 knockdown (after 9 d), as witnessed by a drop of the mechanical sensitivity gain and a reduced power of the antenna’s mechanical free fluctuations (Fig 2E). Altogether, these results document the importance of DmIFT88 for maintaining sensory function after ciliogenesis is completed.

To investigate whether sensory function loss in the acute DmIFT88 knockdown flies is because of defects in the ciliary/...
axoneme structure, we studied the ultrastructure of chordotonal neuron cilia in JO. Strikingly, cilia were always present, but in 9- and 15-d post-knockdown flies, the curvature of the base of cilia mildly increased compared to controls (Fig S3D). Although in larval chordotonal neurons, ciliary dysfunction has been associated with a bending of the cilia (Zanini et al, 2018), the significance of this morphological phenotype in sensory function in adults is still unclear.

To further check to what extent IFT88 is required for the maintenance of the ciliary structure, we knocked down DmIFT88 under the Gal4\textsuperscript{Chor1\textsubscript{1}} driver, but without the use of the TubGal80\textsuperscript{ts} system (Fig S4A). In this condition, we expected to further increase the depletion of the DmIFT88 gene in a ciliary maintenance context. Indeed, we found similar levels of mRNA knockdown to those previously observed with the constitutive driver Gal4\textsuperscript{Tubulin}, which avoided entire ciliary axoneme formation (Fig S2C) (66 ± 20% RNA knockdown for Gal4\textsuperscript{Chor1\textsubscript{1}} versus 71 ± 12% RNA knockdown for Gal4\textsuperscript{Tubulin}) (Fig S4C). Despite Gal4\textsuperscript{Chor1\textsubscript{1}} DmIFT88 RNAi flies displaying a strong gravitaxis behaviour phenotype (Fig S4B), the number of cilia per scolopale, gross ciliary features (such as transition zone and axoneme), and ultrastructural properties (e.g., the number of doublets and inner and outer dynein arms) remained largely unaffected in these Gal4\textsuperscript{Chor1\textsubscript{1}} DmIFT88 knockdown flies (even after 15 d of knockdown) when compared to controls (Fig S4D–F). These results further confirm DmIFT88’s important role in cilia function maintenance without a key implication on cilia ultrastructure maintenance.

Inactive, a TRPV calcium channel subunit, is a DmIFT88 cargo

Loss of chordotonal cilia function in conditional knockdown of DmIFT88 suggests that DmIFT88-dependent cargo transport is continuing even after ciliogenesis is complete. Given the acute knockdown of DmIFT88 did not affect the axonemal ultrastructure, including the number of MT doublets and dynein arms (Fig S4D–F), we hypothesised that the deterioration of the ciliary function of chordotonal neurons might reflect an impaired transport of signalling proteins along the cilia. Only a few signalling proteins have been characterised in the chordotonal cilia of the fly. One interesting signalling protein is the TRPV channel subunit Inactive (lav). TRPVs belong to the conserved TRP superfamily of cation-selective channels. They are cation transporter channels, highly calcium selective, and have multiple functions as sensory mediators in various tissue types and species (reviewed in Baylie & Brayden [2011]; Liu et al [2022]). In particular, lav (Drosophila orthologous to human TRPV1-6) resides in the proximal ciliary region of fully formed chordotonal cilia and is required for locomotion and hearing (Gong et al, 2004; Sun et al, 2009; Zhang et al, 2013; Kwon et al, 2020). Moreover, IFT is implicated in the localisations of several TRP channels along the ciliary shaft in Chlamydomonas and Caenorhabditis elegans (Qin et al, 2005; Huang et al, 2007). In particular, loss of other IFT components (e.g., rempA/IFT140) or retrograde IFT motors (btv/cytospliac dynein heavy chain) during cilia assembly in Drosophila leads to defects in lav localisation (Lee et al, 2008; Kwon et al, 2020), proposing that lav could be an IFT-dependent ciliary cargo.

Therefore, to test this hypothesis, we first explored whether DmIFT88 interacts with lav. We used D. melanogaster (Dmel) cultured cells, which normally express neither of these proteins nor most of the IFT proteins (Hu et al, 2017), including DmIFT88, making them an appropriate system to test for protein-protein interactions. We performed co-IP experiments using Dmel cells that ectopically and transiently expressed both pUAS-3xHA::DmIFT88 (this study) and p-UAS-lav::GFP (kindly provided by Yun Duo Chung [Gong et al, 2004]) or p-UAS-GFP under an ubiquitous Gal4\textsuperscript{Act5C} driver. 3xHA: DmIFT88 specifically bound to lav::GFP but not to cytoplasmic GFP control (Fig 3A), strongly suggesting lav is an interactor of DmIFT88.

To further test whether lav is a cargo of DmIFT88, we acutely knocked down DmIFT88 in chordotonal neurons of the antennal JO and assessed lav localisation using an anti-lav antibody (Gong et al, 2004). In the DmIFT88 knockdown flies, although lav continued to localise in the proximal compartment of the chordotonal ciliary, the channel’s concentration was mildly but significantly reduced (by ~9%, median) compared to the control (Fig 3B). Altogether, these data strongly suggest Drosophila lav is a cargo of DmIFT88 at least in adult hearing ciliated neurons.

The small reduction of lav along the proximal region of the cilia upon DmIFT88 RNAi knockdown seems unlikely to account for the strong negative-gravitaxis and hearing defects seen in the DmIFT88 RNAi flies. Moreover, lav knockout increases ciliary motility and, thus, the mechanical amplification provided by JO neurons (Gopfert et al, 2006), whereas in DmIFT88 RNAi knockdown flies, this amplification was reduced. Therefore, we hypothesise that the sensory defects caused by DmIFT88 knockdown, rather than being caused by the mislocalisation of one cargo alone, may reflect the combined phenotype of the mislocalisation of several DmIFT88 indirect and direct cargoes, with lav being one of them.

CG34357, an orthologue of mouse Gucy2e, localises to chordotonal cilia and binds to DmIFT88 by its intracellular domain

In mouse photoreceptors, a hypomorphic mutation in IFT88 exhibited retinal degeneration (Pazour et al, 2002), and in humans, heterozygous mutations in IFT88 give rise to inherited retinal degeneration (Chekuri et al, 2018). This suggests that mutations in some of its cargos might cause similar phenotypes. Indeed, several TRP channels are expressed in retinal cells, and their dysfunction is also implicated in retinal degenerative pathologies (reviewed in Thebault [2021]). In addition, vertebrate Gucy2d/e, a membrane-bound (particulate) cGMP-generating enzyme, alternatively known as Guanylyl Cyclase (GC), is required for photoreceptor function. Gucy2e mutations are in fact implicated in human retina-specific ciliopathies that can be related to the development/maintenance of ciliary function, such as Leber congenital amaurosis (LCA) and retinitis pigmentosa (Zagel & Koch, 2014). Importantly, in IMCD3 cells, IFT88 was shown to transport ectopically expressed mouse Gucy2e to primary cilia (Bhowmick et al, 2009). The synthesised cGMP is a second messenger of signal transduction essential for several sensory functions such as olfaction and vision. Components of this primordial signalling pathway, which include GCs, phosphodiesterases (PDE), and protein kinase G (PKG), are known to regulate a wide range of sensory functions, such as nociception.
olfaction, and phototransduction, in various animals (reviewed in Johnson & Leroux [2010]; Wen et al [2014]; Maruyama [2016]). Not surprisingly, cGMP signalling components are found in vertebrate and invertebrate organisms located within cilia (Morton, 2004; Johnson & Leroux, 2010), although this signalling has not been yet associated with the function of Drosophila cilia. Therefore, we investigated the evolutionary conservation of the mouse Gucy2e (Table S3) and searched for its D. melanogaster homologue.

The Drosophila genome encodes several particulate membrane GCs (Morton, 2004), but none of them has so far been associated with gravitaxis behaviour or sensory cilium function. Using the protein sequence of the mouse Gucy2e (an orthologue of human Gucy2d) in PSI-BLAST search (Altschul et al, 1997) against the D. melanogaster protein database, we identified several putative particulate GCs (Fig S5A). Because cGMP signalling components are important for sensory behaviour in several organisms and cell types (Johnson & Leroux, 2010), we reasoned that knockdown of a GC in chordotonal organs might impair cGMP generation in neurons, thus the negative-gravitaxis behaviour. Fly stocks bearing RNAi constructs for six putative GCs (four particulate and two soluble) were available, and we used them to knockdown the respective genes using Gal4_chart19b (for expression pattern of this driver, see Fig S4A) and to perform climbing assays for each of them. Our results showed that the knockdown of three of the four particulate transmembrane candidates caused behavioural defects (Fig S5A), whereas the predicted soluble GCs did not.

The closest Drosophila homologue of mouse Gucy2e, the protein product of which was reported to be transported by IFT88, is the uncharactierised gene CG34357, and knockdown of this gene leads to negative-gravitaxis behaviour defect in adult flies (Fig S5A, B, and D). Thus, for follow-up studies, we focused on it. According to the human gene nomenclature, we renamed CG34357 as DmGucy2d.

To further pursue our analysis of DmGucy2d, we first investigated the expression profile of this gene. The information publicly available suggests that DmGucy2d gene is expressed in the PNS and in CNS (Graveley et al, 2011; Brown et al, 2014), and we tested its endogenous expression in chordotonal neurons. For that purpose, we used an enhancer Gal4-trap line (NP02701) to express a membrane-bound GFP reporter (UAS-mCD8::GFP) (Fig S6A and B). We observed that the enhancer is expressed in the chordotonal neurons in both L3 larvae (Fig S6C) and the adult second antennal segment (Fig 4A). We detected GFP signal only in a subset of adult chordotonal neurons, suggesting that the enhancer trap line might not fully recapitulate the endogenous gene expression or that only a subset of chordotonal neurons express DmGucy2d. Notably, we also observed expression of DmGucy2d in Type-III dendritic neurons. Therefore, for further studies, we expressed or perturbed this gene only using specific drivers expressed only in a subset of sensory neurons (e.g., Gal4_chart19b and Gal4_scrib express in cholinergic and chordotonal ciliated neurons, respectively), without compromising DmGucy2d expression and protein localisation in other cell-types. To further assess DmGucy2d’s subcellular protein localisation, we cloned the coding sequence of its longer isoform (RD/RC) and generated transgenic flies. The protein was tagged with GFP at the C-terminus to avoid cleavage of the tag because of a predicted N-terminal signal peptide (Figs 4D and SSB and C). When UAS-DmGucy2d::GFP was expressed using a chordotonal neuron-specific driver (Gal4_scrib), GFP fluorescence was observed in the dendrites and along their cilia (Figs 4B and S6D).

To test whether DmGucy2d might be a DmIFT88 cargo, we examined if DmGucy2d binds to DmIFT88 using Drosophila cultured cells (Dmel), as previously done to study interactions between DmIFT88 and lav (see Fig 3A). Note that both DmGucy2d or DmIFT88 do not express in these Dmel cells (Hu et al, 2017). We co-expressed either DmGucy2d::GFP (this study) or cytoplasmic GFP alone, together with HA-tagged DmIFT88. Unlike the GFP control, DmGucy2d::GFP (full length, FL) binds to HA::DmIFT88 (Fig 4C).

A typical particulate GC has several protein domains (Figs 4D and SSB and C): (i) a signal peptide at the extracellular domain; (ii) a short transmembrane domain; (iii) a kinase homology domain important for the interaction with other intracellular proteins, such as the GC-E activator (the membrane-anchored activating protein, activated by Ca2+); (iv) a homodimerisation domain important for the activation of the catalytic domain; and (v) a cyclase catalytic domain, which synthesises the cGMP that can in turn activate ion channels or be used by PKG or PDE. The predicted protein product of DmGucy2d has all these features (Fig S9B). To narrow down the DmIFT88 binding region of DmGucy2d, we generated truncated constructs of the cyclase (Fig 4D). The T1 fragment (T1-DmGucy2d::GFP, Fig 4D) exclusively comprises the entire intracellular part of the protein. The other four fragments (T2–T5) all contain the extracellular and transmembrane domains that might be necessary for membrane localisation and various truncations of the intracellular domain. Each of these (T2–T5) fragments is successively longer towards the intracellular C-terminus (Fig 4D). Our co-immunoprecipitation experiments revealed that T1, T4, and T5 co-immunoprecipitate DmIFT88 (Fig 4E; three or more experimental repeats per construct were plotted in the graph and statistically analysed), suggesting that the interaction requires the intracellular portion encountered mainly between the kinase domain and the cyclase/dimerisation domains. Because neither lav nor DmGucy2d nor most of the IFT proteins, including DmIFT88, are expressed in Dmel cells (Hu et al, 2017), our results suggest that DmGucy2d::DmIFT88 and lav-DmIFT88 interactions are direct. Still, we cannot entirely rule out an intermediate player in assembling these complexes.

Our data also strongly suggest that the intracellular domain of DmGucy2d plays a key role in DmGucy2d localisation, presumably through its transport by DmIFT88. To test whether this is true, we investigated: (i) whether GFP-tagged full-length and T1 (entire intracellular domain) fragment of the cyclase move along the cilia in similar manner as DmIFT88; and (ii) the effect of knockdown of DmIFT88 on the localisation of GFP-tagged T1-DmGucy2d along the cilia. We extensively attempted to live-image DmGucy2d::GFP and T1-DmGucy2d::GFP in the Ich5 neurons of L3 larvae. Both DmGucy2d::GFP and T1-DmGucy2d::GFP, when overexpressed (using Gal4_scrib) in a WT background, were highly enriched in the dendrites and the base of the cilia with a membranous and particle-like appearance, albeit show fainter localisation along the proximal segment and at ciliary dilation of the chordotonal cilia (Fig S6D). These results suggest this cyclase is transported up the cilia dilation and accumulated there. However, despite of extensive trials, we failed to observe
particulate movement along the ciliary shaft for either GFP-tagged DmGucy2d or T1-DmGucy2d (each live-imaging was of at least for 3 min, n = 28 Ich5 organs from 8 larvae analysed on five experimental days; n = 20 Ich5, from 6 larvae analysed on four experimental days, respectively), suggesting unlike DmIFT88 the DmGucy2d does not move into and along the cilia continuously, at least during our imaging period (Figs 5B and S6D empty arrowheads). Furthermore, these results prevented us from investigating the role of DmIFT88 in live transport of DmGucy2d along the cilia and limited our experiments to fixed adult tissues (Figs 4B and 5B). In DmIFT88 knockdown adult flies (Fig 5A and C), the percentage of cilia with T1-DmGucy2d::GFP signal at the ciliary dilation was strongly reduced (by ~40%, median) compared to controls (Fig 5D and E). In addition, the mean intensity of T1-DmGucy2d::GFP was significantly reduced (by ~38%, median) at the proximal region of the cilium (Fig 5D and F). At the ciliary base, however, GFP fluorescence remained unaltered (Fig 5D and G), suggesting that DmIFT88 specifically regulates T1-DmGucy2d localisation in the ciliary shaft but not its localisation at the dendrite tip/ciliary pocket.

We next tested whether DmGucy2d is important for maintaining ciliary function in chordotonal neurons. We used the conditional inducible promoter system Gal4 (UAS- TubaGal80) to express the hairpin RNA against DmGucy2d in adult ciliated chordotonal neurons (see Fig S8A and B for RNAi knocking-down efficiency). DmGucy2d RNAi knockdown slightly reduced negative-gravitaxis at 18°C (Fig 5A and B), possibly reflecting leaky expression of the construct. Importantly, after the temperature shift to 29°C, compared to control flies, those with DmGucy2d knockdown developed mild, albeit significant climbing defects (Fig 5H). Similar mild climb defects were found with the use of the more restricted driver, Gal4lav (Fig S7A and C), and with the use of another RNAi (KK110863, VDRC) line under the same acute Gal4 Chat199 conditions (Fig S7D and Table S5). This finding further documents that DmGucy2d in adult chordotonal neurons is needed for the maintenance of the proper sensory input and thus maintains the normal negative gravitaxis behaviour. In addition to affecting gravity sensing, 9-d acute RNAi of DmIFT88 resulted in reduced maximum sensitivity gain and energy of the antenna’s mechanical free fluctuations (Fig S1). Hence, like DmIFT88, DmGucy2d is required for maintaining normal hearing in adult flies.

Finally, we further characterised the relationship between DmIFT88 and the two cargoes identified in this work. With that purpose, we first studied the ciliary bending in acute DmGucy2d knockdown flies. Unlike DmIFT88, DmGucy2d conditional knockdown did not alter the angle of the chordotonal cilia at their bases (Fig S8C), suggesting this DmIFT88 knockdown phenotype is not linked to DmGucy2d. Moreover, the acute knockdown of DmGucy2d in adults did not change lav mean intensity along the proximal region of the cilia in the chordotonal organ at 9 and 15 d after the adult flies emerge (Fig S8D), suggesting ciliary localisation of lav is independent of DmGucy2d. These results further support the idea that DmIFT88 transports several cargoes, whose localisation and functions at the cilium may or may not be dependent on one another, and that are together involved in the maintenance of ciliary function.

**Discussion**

Cilia biogenesis depends on the activity of an exclusive transport system called IFT (Pazour et al, 2002; Egeyer et al, 2014; Jiang et al, 2015), yet whether IFT also has a role in maintaining metazoan cilium has been little explored (Marshall et al, 2005; Hao et al, 2011; Fort et al, 2016). Here we show that DmIFT88, an evolutionarily conserved core IFT-B1 complex component (Fig S1), is present in chordotonal neurons and is continuously mobile along the length of mature sensory cilia (Fig 1). Acute depletion of DmIFT88 after ciliogenesis in ciliated neurons leads to impaired sensory function and behavioural defects without severely affecting axoneme ultrastructure, suggesting an involvement of IFT in sensory cilium function beyond its known pivotal role in ciliary axoneme assembly (Figs 2, S2, S3, and S4). We hypothesised that impairment of the localisation of cargoes, directly or indirectly transported by DmIFT88, would explain the observed function defects upon the IFT88’s conditional knockdown. A few ciliary transmembrane signalling molecules were considered IFT-cargoes in various eukaryotes (reviewed in Lechtreck (2015)), but no DmIFT88-dependent direct cargoes in the fruit fly were known. Here, we identify two Drosophila IFT88-dependent cargoes: lav, a TRPV Ca2+ channel subunit involved in sound and gravity sensing (Fig 3); and the transmembrane protein DmGucy2d (CG34357), which we characterise in this study and whose homologues serve multiple signalling roles in eukaryotes. We further demonstrate that DmIFT88 binds to the intracellular domain of DmGucy2d (Fig 4). Mutations in this region of the cyclase are implicated in human diseases (Figs S5 and S9). Finally, we show that depletion of this cyclase in mature sensory neurons impairs negative-gravitaxis behaviour and hearing, substantiating its role in Drosophila auditory ciliary function maintenance (Figs 5, S6, S7, and S8).

**DmIFT88 plays differential roles in cilia assembly and maintenance**

Multiple mechanisms have been implicated in the regulation of cilium homeostasis in diverse model organisms (Marshall et al, 2005; Hao et al, 2011; Jiang et al, 2015; Fort et al, 2016). Ciliary structure and composition have to be maintained, and they are likely to be dynamic and altered in response to external stimuli, as was shown for C. elegans sensory cilia (DiTirro et al, 2019). Studies in Chlamydomonas, worms, and mice suggest that continuous tubulin turnover at the ciliary tip is required to maintain flagellum/cilium length (Marshall et al, 2005; Hao et al, 2011; Jiang et al, 2015). In contrast, in fruit flies, even though DmIFT88 is pivotal for axoneme assembly (Han et al, 2003), Fig S2E–H as in other organisms (Pazour et al, 2002; Kohl et al, 2003), we show that it has no major role in maintaining axoneme ultrastructure and only a minor influence on maintaining ciliary gross morphological features (Figs S3 and S4). We found here that DmIFT88 knockdown in adults, after ciliogenesis is complete, leads to a decrease in sound-evoked action potentials and impaired negative-gravitaxis, which suggests that sensory cilia function (i.e., auditory and gravity-sensing-related transductions) during adulthood may require a maintenance program. These results show that DmIFT88, a core evolutionarily conserved
component of the IFT-B1 complex, plays distinct roles at different developmental times within even the same cell type. Note that our result is similar to what was reported in *Trypanosoma*, suggesting that although IFT88’s role in ciliary skeleton homeostasis is not conserved among different ciliated species and tissues, this protein plays an evolutionarily conserved role in the maintenance of ciliary sensory function (Fort et al, 2016). Further, studies in the future, are required to investigate whether other evolutionarily conserved IFT proteins are involved in ciliary structure homeostasis.

Both DmIFT88 cargoes, lav and DmGucy2d, are involved in sound and gravity sensing in the adult flies

Chordotonal ciliated neurons are important to sense external mechanical stimuli (i.e., wind, sound, and gravity) during adulthood for the fly to escape, mating and foraging (Hehlert et al, 2021). Chordotonal JO’s neurons are exquisitely sensitive, amplifying sound-induced mechanical vibrations, even if they hardly exceed Brownian motion, to facilitate their detection (Nadowski et al, 2008). Although several transmembrane and signalling proteins have been implicated previously to be IFT-associated cargoes in other organisms (Qin et al, 2005; Huang et al, 2007; Williams et al, 2014), neither homologues of those molecules were shown to be essential for fly sensory cilia functions nor the signalling molecules implicated in *Drosophila* JO neurons functions were associated to IFT. Our data suggest that the transport of various ciliary transmembrane signalling novel cargoes by DmIFT88, including lav and DmGucy2d, in fully formed sensory cilia is critical for the homeostasis of the ciliated chordotonal neurons’ functions (Figs 3–5).

Mechanotransduction in *Drosophila* chordotonal organs involves TRP channels (Hehlert et al, 2021), probably because of the role of the cations exchanged to transduce external stimuli to the cell (Li et al, 2021). In particular, several subfamilies of Ca²⁺ TRPV transporters are found in the cilia of sensory neurons, being essential for several sensory functions, including chemosensation, proprioception, and hearing in a variety of species (Gong et al, 2004; Bargmann, 2006). In *Drosophila*, the TRPV subunit Iav, an essential pore subunit for auditory transduction, is expressed in chordotonal organs and localises to the proximal region of the cillum (Gong et al, 2004; Li et al, 2021). Mutants for Iav are deaf (Gong et al, 2004) and show defective negative-gravitaxis (Sun et al, 2009). The low (9%) Iav protein intensity decrease found upon DmIFT88 knockdown during adulthood (~30% DmIFT88 RNA decrease) (Figs 3 and S3) might be because of either a slow Iav turnover along the auditory cilia or a DmIFT88-independent process that is also involved in maintaining some fraction of axonemal Iav at the adult stage. These hypotheses remain to be further investigated.

DmGucy2d, a particulate GC, could contribute to the signal amplification of auditory transduction in multiple ways. On the one hand, the cGMP that it synthesises might be used by the ciliary machinery (i.e., cGMP is directly used by ion channels, PKGs, or PDEs) after being activated by low-level external stimulation, as it happens in mouse photoreceptor cells where Ca²⁺ regulates the activity of Gucy2d (Johnson & Leroux, 2010; Wen et al, 2014; Maruyama, 2016). On the other hand, it might also be involved in modifying the mechanical properties of the cillum in response to stimulation, by adjusting the activities of dynein arms present at the proximal region of the auditory cillum that are critical for ciliary motility and sound sensitivity (Karak et al, 2015; Li et al, 2021).

Recently, IFT88 was described to interact with the leucine-rich repeat containing 56 protein (LRRC56) when both were ectopically co-expressed in HEK293 mammalian cells (Bonnefoy et al, 2018). Similarly, we found both lav and DmGucy2d independently bind to DmIFT88 in Dmel cells, an in vitro system where none of these three proteins express in a physiological condition. To fully appreciate the potential of IFT in regulating various ciliary properties, such as structural maintenance, plasticity, composition, and function, it will be important in the future to identify additional cargoes transported by IFT88 and other IFT proteins. Moreover, to fully understand how cilia are maintained, it will be interesting to uncover whether and how IFT-independent transport could play a role in that process.

Evolutionarily conservation of Gucy2d structure and function and its possible implications in human retinal diseases

Several mutations spread along the entire sequence of the guanylyl cyclase Gucy2d are implicated in retinal disorders, including LCA (Fig S9C). LCA is a family of congenital retinal dystrophies that results in severe vision loss due, in some cases, to the inability of the phototransduction cascade to take place in the patients’ eyes (reviewed in den Hollander et al [2008]; Tsin et al [2018]). Little is known about the mechanisms by which those mutations cause the disease. Mutations affecting either the cyclase activity (Jacobson et al, 2013), protein stability, or transport into the cilia can potentially be harmful. Although several results indicate that Gucy2d gene therapy replacement could be a good treatment for this family of diseases, to date, there is no cure or treatment for these patients (reviewed in Chacon-Camacho & Zenteno [2015]).

Our research uncovered that the intracellular domain of the cyclase, which we found to be essential for its localisation in the *Drosophila* sensory cillum, is evolutionarily conserved (Fig S9A and B). Furthermore, we discovered that several of the human Gucy2d residues found to be modified in some LCA patients in the intracellular region are conserved in *Drosophila* Gucy2d (Fig S9C and Table S6) (Tucker et al, 2004; Li et al, 2011; Jacobson et al, 2013; de Castro-Miro et al, 2014; Zigel & Koch, 2014; Feng et al, 2020; Liu et al, 2020; Salehi Chaleshtori et al, 2020). Our work suggests a novel role of the evolutionarily conserved intracellular domain of DmGucy2d, which is to bind to DmIFT88 for the cyclase to be appropriately localised/transported along the cilia. We hypothesise that the possible defective transport of Gucy2d along human photoreceptor cilia is one of the causes of LCA disease not contemplated before.

Materials and Methods

Materials

Find lists of accession numbers for IFT88 proteins from different organisms, accession numbers of GC proteins from various
species, antibodies (primary and secondary) and their dilutions, primers, and the genotypes of the flies used in this study in Tables S2, S3, S5, S7, and S8, respectively.

**Methods**

**Bioinformatics analysis**

For IFT88, the gene model for DmIFT88 was extracted from the Ensembl Genome Browser (Yates et al, 2016). The number of TPR domains was predicted using the TPRpred tool (Karpenahalli et al, 2007). For phylogenetic analysis, IFT88 protein sequences of 11 metazoan species were used (see Table S2). Whenever several IFT88 isoforms were reported for one species, the largest one was chosen for analysis. The MegAlign program (Lasergene suite, Version 8.1.3, DNASTAR) was used to generate a phylogenetic tree summarising sequence similarities as a function of the number of amino acid substitutions between sequences. Sequences were aligned using the ClustalW algorithm with default settings. Bootstrapping analysis was performed with default values to calculate the "support value" of each branching point in the tree (Fig 1Ai left). Multiple sequence alignments are presented as a heatmap. An alignment file in the FASTA format using the web browser-based MUSCLE tool was created (Edgar, 2004) to extract sequence identities. Subsequently, the ProfiIgrid tool (Roca et al, 2008) was used with default settings to assign a similarity score to each position in the alignment, with the score assuming values between 0 and 1. The results are presented as a heatmap, which was visualised with RStudio (RStudio) and the ggplot2 package (Wickham, 2016) (Fig 1Ai right).

For guanylyl cyclases, including DmGucy2d/CG34357: Sequence analysis for guanylyl cyclases (Fig S5A) was performed as described above. For the accession number of guanylyl cyclase protein sequences used in this analysis, see Table S3. The gene model for CG34357 was taken from the Ensembl Genome Browser (Yates et al, 2016).

**Cryo-sectioning, immunolabeling, and image analysis**

Histological sections of the adult antenna were prepared as described before (Mishra, 2015; Jana et al, 2016). If not stated otherwise, preparation steps were carried out at room temperature. Flies were anaesthetised using CO2 and decapitated. The heads were collected in pre-cooled fixation buffer (4% PFA, 75 mM PIPES buffer [pH 7.6], 0.05% Triton-X, picric acid) and incubated for 40 min. Good fixation requires the heads to sink to the bottom of the reaction tube. The heads were washed three times in PBST (PBS with 0.05% Triton-X) and then incubated on a rotator in PBST with 10% sucrose, first for 1 h at room temperature and then, overnight, in 25% at 4°C. The heads were embedded and oriented appropriately in OCT (optimal cutting temperature formulation; Tissue-Tek; Sakura Finetek), and the OCT was frozen on dry ice. Head samples were sectioned at 12 μm thickness in a Leica Cryostat CM 3050 S (Leica). The sections were collected on poly-L-lysine-coated slides (Sigma-Aldrich).

Sections were washed with PBST (PBS with 0.05% Triton-X) three times for 10 min each, followed by incubation in blocking buffer (10% BSA in PBST) for 1 h and subsequent incubation with the primary antibody diluted in blocking buffer overnight at 4°C. Samples were washed three times in blocking buffer and incubated for 1 h with secondary antibody in blocking buffer. Finally, after three additional washing steps using PBS for 5 min each, samples were embedded in Vectashield supplemented with DAPI (Vector Laboratories). 12-bit images were acquired on a TCS SP5 upright confocal microscope (Leica) using an PL APO CS 63.0 × 1.4 OIL objective with a pinhole at 1 Airy unit and a pixel size of 80–200 nm (lateral) and 400 nm (axial). For details of the antibodies used, see Table S7.

To quantify in the DmIFT88 knockdown experiments the signal intensities of inactive (iav, a marker for the proximal cilium) antibody staining and the GFP signal of the T1-DmGucy2d::GFP at the proximal cilium (Fig 3B, 9-d old flies; and Fig 5D, 6-d old flies), image stacks were analysed with the Imaris software v.9.2.1 (Bitplane). For analysis and generation of Fig 3B: the Iav channel was used to generate segmented volume surfaces, and the Iav intensity values were retrieved from Imaris, averaged per antennae in Excel (Microsoft Office), and normalised to the negative control of each repeated experiment. For graphs in Fig 5E–G: the channel was used to generate segmented volume surfaces. Next, mean intensity values of Iav antibody staining and T1-DmGucy2d::GFP at the segmented Iav surfaces were retrieved from Imaris, averaged per antennae in Excel (Microsoft Office), and statistically analysed (non-parametric Mann–Whitney t test or Welch Two Sample t test) in Prism (GraphPad). Data were represented on box plots (median ± full range, each dot representing individual averaged values) using Prism 5.2.

To quantify the T1-DmGucy2d::GFP intensity at the end of the dendrites in the adult chordotonal neurons (Fig 5E), the image stacks were deconvoluted using the Huygens Deconvolution v17.4 software (Scientific Volume Imaging) with an CMLE algorithm followed by image analysis in Imaris (as mentioned above). This deconvolution step facilitated the segmentation of the crowded dendrite population in the adult antennae by increasing the signal-to-noise ratio (SNR) (N > 10 antenna in all conditions).

**mRNA isolation from adult antenna and reverse transcription analysis**

Between 100 and 200 flies were decapitated per genotype. Heads were collected in Protein LoBind tubes (Eppendorf) on dry ice. 10–20 heads were collected at a time to avoid compromising the tissue because of long exposure to room temperature. Tubes were snap-frozen in liquid nitrogen. Antennae were dissociated from heads through mechanical force using a vortex mixer (three times for 10 s, cooled in between again on dry ice). To separate antennae from heads, tubes were opened and inverted. Heads will fall out, whereas most of the antennae will adhere to the walls of the tubes. Total mRNA was isolated from antennae using the PureLink RNA Mini Kit (Ambion Life Technologies). Antennae were lysed in 250 μl of lysis buffer. The protocol was carried out as described in the accompanying manual of the kit. No DNase treatment was performed. The mRNA was always converted to cDNA immediately. For cloning, 1 μg of total mRNA was reverse transcribed. The reverse transcription reaction was performed with the Transcriptor First Strand cDNA Synthesis Kit (Roche). For quantifying mRNA levels,
50–70 heads were used. For cloning DmIFT88, cDNA was generated using poly-dT primers included in the kit. The cDNA samples were stored at −20°C until further use.

Cloning and generation of transgenic flies

For DmIFT88, the cDNA for cloning DmIFT88 was obtained from mRNA isolated from antennae of w1118 flies. DmIFT88 (isoform-RD) was amplified using the KOD polymerase kit (EMD Millipore) in 50-μl reaction volume (for PCR primers, see Table S8). PCR was set up as outlined for the kit. The reaction mix was supplemented with DMSO. The PCR product was purified using the DNA Clean & Concentrator kit (Zymo Research) and adenylated at the 5′ ends through incubation with DreamTaq (Thermo Fisher Scientific) using the appropriate buffer and dNTPs at 70°C for 1 h. Subsequently, the PCR product was ligated into pGEM-T Easy (Promega) following the manufacturer’s instructions, and plasmids were confirmed through sequencing (for sequencing primers, see Table S8). Using the Gateway system, the coding sequence was first cloned into pDONR 221 in a BP-reaction (Invitrogen), following the instructions for the kit, and subsequently transferred to pTHW and pTGW in an LR-reaction (Invitrogen) to fuse the resulting protein with three HA-tags or one GFP-tag on the N-terminus, respectively (for details on pTHW and pTGW, see Drosophila Genomic Resource Centre). DmIFT88 was tagged at the N-terminus because the GFP:: DmIFT88 fusion protein was previously shown to rescue the DmIFT88/nompB mutant phenotype and can hence be considered fully functional (Han et al, 2003).

For DmGucy2d/CG34357 full length (FL) and truncated T1- DmGucy2d GFP constructs, the CG34357 coding sequence was cloned from mRNA isolated from antennae of w1118 flies, as described above. DmGucy2d could only be amplified from cDNA produced with random hexamer primers (included in the Transcriptor First Strand cDNA Synthesis Kit; Roche). For primer sequences, see Table S8. To enhance the chance to amplify the desired target (coding sequence of CG34357-RD, Fig S4B) even further, the mRNA was reverse-transcribed using a primer on the 3′-untranslated region of DmGucy2d (CG34357_3UTR_rev 2 μM in a 20 μl reaction volume, 1 μg of total mRNA were used as template). Two rounds of PCRs were performed to obtain the DmGucy2d with the appropriate overhangs for Gateway cloning (Invitrogen). In the first round, the DmGucy2d coding sequence was amplified using primers located on each of the untranslated regions. For the second PCR, 2 μl of unpurified PCR product of the first PCR was used as a template. Primers containing appropriate sequences for gateway cloning were used for the second PCR. The coding sequence was cloned without the stop codon to allow for gene fusion at the C-terminus. Tagging at the N-terminus was not considered because the protein is predicted to undergo cleavage of the signal peptide (30 amino acids, Fig S5B, black arrowhead). The coding sequence was confirmed through sequencing and sub-cloned into pTWG (Drosophila Genomic Resource Centre) for C-terminal fusion with GFP.

Plasmid DNA was amplified in E. coli DH5α and purified using ZR Plasmid MiniprepTM-Classic (Zymo research). ZymoPURE Midiprep Kit (Zymo research) was used for large-scale DNA purification that is required (DmIFT88, DmGucy2d, or T1-DmGucy2d in pTWG) for transfection experiments and fly transgenesis. Injections into Drosophila embryos and selection of positive transformants were outsourced (BestGene or IGC transgenics facility) (see Table S5 for detailed genotypes of flies used).

Detection of DmGucy2d gene expression: to detect expression of DmGucy2d in different developmental stages, an enhancer Gal4 trap line (CG34357[NP0270]) was obtained (Brand & Perrimon, 1993). Flies carrying the enhancer trap insertion were crossed with flies encoding 40xUAS-IVS-mCD8::GFP (see Table S5 for detailed genotypes of flies). The mCD8::GFP fusion protein is targeted to the membrane of the cells and was used to visualise the morphology of cells. 40 UAS tandem insertions were chosen to increase the signal intensity (see Fig 4B).

For imaging adult antenna, the cuticle of the heads was cleared, as further explained below, and the second antenna segment was imaged entirely on an SP5 Live Upright microscope (Leica). Confocal Z-stack images were deconvolved using the Huygens v17.4 software (SVI) and 3D reconstructed using the Imaris v6.4 software (Bitplane), which was also used to prepare the video (Video 2). Wandering L3 larvae were mounted and imaged as described for the live-imaging of L3 larvae below.

Live imaging of chordotonal cilia in L3 larvae and measurement of IFT88 train lengths

GFP:: DmIFT88 was expressed in chordotonal neurons using Gal4lox (Gong et al, 2004; see Table S5 for detailed genotypes of flies). Flies were reared at 25°C to the third larval stage, and all experiments were performed with wandering L3 larvae. Larvae were collected and briefly washed in PBS. For imaging, larvae were immobilised between a coverslip and a slide in a drop of PBS (Zhang et al, 2013). The cover slip was held in place using transparent double-sticky tape. Imaging was performed using a Roper spinning disc microscope (Nikon). Samples were kept at 25°C through the imaging process. To prevent artefacts from cell death, larvae were always imaged immediately after immobilisation and for a maximum duration of 2 min. Images were acquired every 120 ms with 100 ms exposure time (Figs 1B and S6). Images were analysed using the Fiji software (Schindelin et al, 2012), and kymographs were generated using the Kymograph-Clear plugin (Mangeol et al, 2016).

To obtain the IFT train lengths, we used these kymographs (examples shown in Fig 1Bii) showing separately DmIFT88 anterograde and retrograde trains. To measure the approximate lengths of the trains, we used the Straight Line and Measure Tools from Fiji to draw and measure the thickness, and thus the length, of the trains (a total of 30 trains in both directions were measured). Data plot and statistical analysis were done using Prism (GraphPad).

Quantification of DmIFT88 expression levels from adult antennae

For measuring DmIFT88 expression levels, the total mRNA was isolated from the antennae of adult flies with specific genotypes
up to 4 d after adult flies emerged from pupae using real-time PCR (qRT-PCR) (see Table S5 for detailed genotypes of flies). The web browser-based Primer-BLAST tool (Ye et al., 2012) was used to design primers specific for a given transcript. At least one primer in a pair was designed to span an exon-exon junction to avoid amplification of genomic DNA that might contaminate the samples. All primers (see Table S8) used in this study were tested to only yield a single product and not amplify genomic DNA. The DmIFT88, DmGucy2d, and several housekeeping genes (e.g., elf1A, Sul(Tpl), TBP) primers were confirmed to only amplify the respective isoform using cDNA (data not shown). 150 ng of total mRNA were reverse transcribed to cDNA in a reaction volume of 20 μl. The cDNA mix was diluted 1:10, and 4 μl of the dilutions were used in each reaction. iTaq Universal SYBR Green Supermix (Bio-Rad) or THERMO Maxima SYBR Green qRT-PCR Master Mix was used to detect amplification of the PCR products. The reactions were set-up up according to the manufacturer’s protocols and run on the CFX384 Touch (Bio-Rad) or Applied Biosystem QuantStudio (Flex 6) Real-Time PCR Detection System (Bio-Rad) (Figs S3C, S4C, and S8B). The total mRNA was isolated three times per genotype, and each sample was measured in triplicates. Results were analysed using RStudio (Rstudio) or Prism (GraphPad).

Measurements of sound evoked neuronal responses and antennal mechanics

Flies of the respective genotype and age (mentioned on the respective figures and their legends) were immobilised and glued (with a 50/50 mixture bee-wax:paraffin) to a holder. All measurements were recorded from head-fixed flies. The head and non-measured antenna were affixed to the thorax using UV-hardening dental glue, and the reference electrode was positioned in the thorax (for details, see Gopfert et al. [2005]).

For maximum compound action potential (μV) (Fig S2D) recording, a tungsten needle was inserted into the antenna’s base (i.e., between the head and antenna). The other antenna was immobilised, and the reference electrode was positioned in the thorax.

For maximum mechanical gain and antennal fluctuation powers (kBT) (Figs 2E and 5I), displacements of the free antenna were measured in non-loading condition near the tip of the antennal arista with a scanning laser Doppler vibrometer (Polytec PSV-400, Polytec; Waidbronn) equipped with a DD-500 displacement decoder, with or without external sound stimulation.

To calculate the fluctuation energy of the antennal sound receiver, the mechanical free fluctuations of the receiver were measured in the absence of sound stimulation. Velocity amplitudes were Fourier-transformed to generate a frequency spectrum for the antenna’s vibration velocity \( \langle \dot{X}(\omega) \rangle \) in the range of 100–1,500 Hz. Velocity amplitudes were subsequently converted into displacement amplitudes \( \langle X(\omega) \rangle = \langle \dot{X}(\omega) \rangle / \omega \) with \( \omega = 2\pi f \) and squared, yielding the power spectral density (PSD) \( \langle X^2(\omega) \rangle \) of the antennal displacement. To describe the fluctuations, the PSD was fitted with the function of a simple harmonic oscillator model, \( \langle X^2(\omega) \rangle = \frac{F_0^2}{\omega^2 + (\omega_0^2/\gamma^2)}. \)

where \( F_0 \) is the external force, \( m \) is the mass (50 ng [Albert et al., 2007]), and \( \omega_0 \) is the natural angular frequency \( \langle \dot{X}(\omega) \rangle = \sqrt{K_s/m} \) where \( K_s \) is the spring constant, and \( Q \) is the quality factor (\( Q = m\omega_0 / \gamma \), where \( \gamma \) is the damping factor). When in equilibrium with its surrounding, antenna fluctuates in response to the thermal noise, described as:

\[
\frac{1}{2}K(\omega^2) = \frac{1}{2}h_b T = K_s, \quad K_s \text{ the spring constant, } h_b \text{ the Boltzmann constant } (1.38 \times 10^{-23} \text{ J/K}), \quad T \text{ is absolute temperature in Kelvin. To calculate the total energy (power) of the oscillator, we can describe the system as: } E = \frac{1}{2} K (b_k T), \text{ where } K \text{ is derived from the fit.}
\]

To measure the mechanical sensitivity gain flies were stimulated with pure tones at the mechanical eigen-frequency (\( f_{eigen} \)) for the antenna measured, generated by a loudspeaker close to the animal. Sound particle velocities (SPVs) were recorded by a closely placed pressure-gradient microphone (Emkay NR 3158), as described (Gopfert & Robert, 2002). Flies were stimulated with pure tones covering an intensity-range of 96 dB, in steps of 6 dB. The displacement amplitudes of the antenna at the stimulus frequency were read out from the displacement spectrum. Mechanical sensitivity was determined by normalising the displacement amplitude to the tone particle velocity. To determine the amplification gain provided by motile responses of Johnston’s organ neurons, the sensitivity the antenna reached at low tone particle velocities was normalised to that observed at high particle velocities, and calculated via:

\[
\text{gain} = \frac{\text{Displacement(m)}}{\omega/\text{SPV(m/s)}} \quad \text{with } \omega = 2f_{eigen}. \quad \text{Mechanical sensitivity is then } \text{gain}_{\text{max}} / \text{gain}_{\text{min}} \text{ for the respective fly. Data were analysed and graphs were generated using RStudio (Rstudio) or Prism (GraphPad).}
\]

Sample preparation and image acquisition in transmission electron microscope

The samples for electron microscopy were processed and sectioned as previously described (Jana et al., 2016). Antennae were dissected from the heads and incubated in fixative (2% formaldehyde, 2.5% glutaraldehyde in 0.1 M sodium biphosphate buffer pH 7.2–7.4) overnight. Samples were washed several times in PBS and then incubated for 1.5 h in 1% osmium tetroxide for post-fixation. Samples were washed several times in deionised water before incubating them in 2% uranyl acetate for 20 min on a rotator for en bloc staining. After this step, samples were dehydrated in a graded sequence of alcohol dilutions (from 50% to a 100%). Ethanol was removed through two incubation steps with propylene oxide for 30 min. Samples were embedded in resin overnight and transferred to a fresh batch of resin for 1 h. Under a dissection microscope, the second segment of the antenna was separated from the third. The second segment was placed in the desired orientation into a mould with resin and polymerised. Samples were sectioned ~70 nm thick, collected on formvar-coated copper slot grids and stained with 2% uranyl acetate followed by lead citrate staining. Finally, samples were air-dried and investigated and photographed at 100 keV or 120 keV using the Hitachi H-7650 or FEI Tecnai T12 transmission electron microscope (Figs S1B, S2E–H, and S4D–F).
Conditional knockdown in the flies

The Gal4\textsuperscript{chot19b} driver is active in cholinergic neurons, including chordotonal and olfactory neurons, in all developmental stages of the fly (Salvaterra & Kitamoto, 2001; Jana et al., 2011). Thus, to avoid confounding effects from the ciliogenesis defects and be able to spatiotemporally knockdown our gene of interest in the adults, we adopted a Gal4\textsuperscript{chot19b} (or Gal4\textsuperscript{Avy}) TubGal80\textsuperscript{ts}-UAS-RNAi-based system. The Gal4 activity was repressed through co-expression of a temperature sensitive version of Gal80 under Tubulin promoter (denoted as TubGal80\textsuperscript{ts}). At the permissive temperature (18°C) TubGal80ts is functional, acting as a negative regulator by binding to Gal4 and preventing it from attracting polymerase to a UAS element in the fly genome (McGuire et al., 2003). Thus, a candidate (i.e., DmIFT88, DmGucy2d) mRNA will only be reduced through RNAi if flies are kept at the restrictive temperature (29°C). Flies were reared at 18°C, shifted to the restrictive temperature after they emerged from pupae (when ciliogenesis is finished) and then submitted to the climbing (negative-gravitaxis) assay for up to 15 d (also see, Fig 2B).

Climbing (or negative-gravitaxis) assay

To quantify climbing behaviour, a behavioural readout of sensory function, flies were collected in 24-h time windows and kept in groups of the same age. The animals were transferred to vials with fresh food every 3 d. Before the behaviour experiments, flies were separated according to sex into groups of 10 animals that would be tested jointly. Flies were briefly anaesthetised using CO\textsubscript{2} for sorting. The flies were kept in the room where the behavioural experiments were conducted for about 1 h before the actual experiment. This time period was given to allow the animals to acclimatise to potentially different light and temperature regimes. Experiments were conducted in measuring cylinders made of glass. Animals were placed in cylinders a couple of minutes before the assay was started. Cylinders were sealed on top with perforated para- toms. The climbing (negative-gravitaxis) assay used in Jana et al. [2021]. Data and statistical analysis, and generation of graphs were done using R Studio (RStudio) or Prism (GraphPad).

Cell culture and immunoprecipitation experiments

For co-immunoprecipitation of ectopically expressed proteins (Figs 3A and 4C and E), D. melanogaster (Dmel) cultured cells were co-transfected with the corresponding constructs (GFP-tagged at the C-terminus of either DmGucy2d full-length or fragments [T1–T5]; eGFP-tagged at the C-terminus end of the lav protein) with 3xHA::DmIFT88. The co-overexpression of GFP alone with 3xHA::DmIFT88 serves as a negative control in these experiments. Cells were seeded at a density of 3 × 10\textsuperscript{6} cells/well in six-well plates (Orange Scientific). 1 h later, they were transfected using Effectene Transfection Reagent (Qiagen) according to the manufacturer (see Table S8 for primer information). Cells were harvested 3 d after transfection. Cells were resuspended, the suspension was collected and centrifuged and pellets were stored at −80°C, if not processed immediately. Ectopically expressed DmGucy2d::GFP or lav::GFP were immunoprecipitated at 4°C for 2 h from Dmel cell lysates (three wells in total for each condition per experiment) using polyclonal anti-GFP antibodies and protein A or G magnetic Dynabeads (Thermo Fisher Scientific). 2 μg anti-GFP antibodies were added to protein-A or -G magnetic beads and incubated for 30 min at room temperature. Cells were homogenised in lysis buffer: 50 mM Tris–HCl pH 8, 250 mM NaCl, 1 mM DTT, 2% NP-40, 0.5% of SDS, 0.5% sodium deoxycholate, 1+ protease inhibitor, 5 μg/ml leupeptin and 15 μg/ml aprotinin, 0.1% digitonin at 4°C for 30 min. Then, benzonase was added to the lysate (final concentration 0.25 U/μl) and incubated for another 15 min. After centrifugation at 13,500 g for 20 min at 4°C, the pre-cleared supernatants were incubated with the coupled beads with antibodies. After several washes with lysis buffer, bead pellets were boiled in SDS sample buffer, separated by 4–15% gradient SDS–PAGE and transferred onto LI-COR nitrocellulose membranes for Odyssey. GFP, DmGucy2d::GFP, Iav::GFP constructs, and HA:: DmIFT88 were visualised with anti-GFP or anti-HA antibodies. Secondary Li-COR antibodies IRDye 680RD and IRDye 800 (Li-COR) were used as a second step (see Table S7 for details on the antibodies used).

Cuticle clearing and imaging of antennae whole-mounts

The cuticle of the adult flies is opaque and autofluorescent, which makes this organ generally unsuitable for imaging. A clearing method that made the cuticle transparent without affecting the morphology of the cells/tissues was developed to image the cytoplasmic GFP expressed in the chordotonal neurons in adult flies with different genotypes. It allowed imaging of the whole antenna without mechanical manipulation. The whole heads were fixed in 4% of PFA in PBS (supplemented with 0.05% Triton-X) for 40 min on ice (Kolesova et al., 2016). Heads were then transferred to a reaction tube containing FocusClear (CelExplorer) and incubated overnight. For imaging, heads were mounted on a slide in MountClear (CelExplorer). Several layers of clear tape were used as spacers between the slide and the coverslip. Images were acquired on a SP5 Upright microscope (Leica). The size of the image stack was chosen to contain the whole antenna segment. Images were then analysed using ImageJ or Imaris v6.4 software (Bitplane).

Statistical analysis

All statistical analyses were performed using either RStudio (RStudio) or Prism (GraphPad). The details of the software and statistical method used to analyse a given set of experiments are...
mentioned in the relevant figure legends. In all figures and source data files, $P \leq 0.05$ is indicated by "ns" (not significant), and $P \leq 0.01$, $\leq 0.001$, and $\leq 0.0001$ are represented by *, **, ***, and **** symbols, respectively.

**Supplementary Information**

Supplementary Information is available at https://doi.org/10.26508/lsa.202302289.

**Acknowledgements**

We thank Daniel F. Eberl, Li E. Cheng, Changsoo Kim, Yun Doo Chung, and Élio Sucena for reagents, and Tejaswini M. and Chaithra D. for help in some experiments. We thank M Bettencourt-Dias and SC Jana Lab members for reviewing the manuscript and providing helpful discussions on the manuscript. We thank the IGC Advanced Imaging unit (and its head, Gabriel G Martins), IGC Electron Microscopy unit (and its Head, Erin Tranfield), NCBS Central Imaging & FACS Facility, and NCBS Electron Microscopy Facility for helping us with image acquisition, and the IGC and NCBS fly facilities for assisting us with fly husbandry. S Werner (SFRH/BD/52176/2013), P Okeneve-Ramos (PTDC/BIA-BID/32225/2017), P Priya (20161014058), and SC Jana (SFRH/BPD/87479/2013) are supported by the FCT (Fundação Portuguesa para a Ciência e Tecnologia, Portugal), CSIR (Council of Scientific & Industrial Research, India), and NCBS-Tata Institute for Fundamental Research (TIFR) Fellowships/Grants/Contracts. SC Jana and M Bettencourt-Dias acknowledge FCT (PTDC/BIA-CEL/32631/2017 to SC Jana), TIFR-DAE (Intramural Project Grant to SC Jana), and the European Research Council Consolidator Grant (CoG683528 to M Bettencourt-Dias) for their support through research grants.

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SC Jana: conceptualization, resources, data curation, formal analysis, supervision, funding acquisition, validation, visualization, methodology, project administration, and writing—original draft, review, and editing.

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**Conflict of Interest Statement**

The authors declare that they have no conflict of interest.

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