On the inscrutable role of Inscuteable: structural basis and functional implications for the competitive binding of NuMA and Inscuteable to LGN

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1. Summary
Alignment of the mitotic spindle to the cellular polarity axis is a prerequisite for asymmetric cell divisions. The protein network coordinating the spindle position with cortical polarity includes the molecular machinery pulling on astral microtubules, which is assembled on conserved NuMA:LGN:Gaia complexes, the polarity proteins Par3:Par6:aPKC and an adaptor molecule known as Inscuteable (Insc). To date, all these components were assumed to enter a macromolecular complex localized at polarity sites in mitosis. However, recent structural studies revealed the Insc and NuMA are mutually exclusive interactors of LGN, implying that the molecular mechanism of spindle coupling to polarity is more sophisticated than has been believed to date.

2. Introduction
The asymmetric outcome of a cell division relies on the tight coordination between cortical polarity and the orientation of the mitotic spindle. During asymmetric mitoses, membrane-associated proteins distribute in discrete cortical domains, establishing a cellular polarity axis. In this configuration, the position of the mitotic spindle, and hence of the cytokinesis plane, determines whether the two daughter cells will (i) inherit the same set of cellular components, (ii) retain analogous contacts to the external tissue and (iii) have the same size (figure 1a).

Our understanding of the basic mechanisms underlying spindle coupling to cortical polarity in asymmetric divisions greatly benefited from genetic studies conducted in the late 1980s in model systems such as Drosophila neuroblasts (the stem cells of the central nervous system in flies) and Caenorhabditis elegans zygotes [1]. In particular, fly neuroblasts undergo self-renewing asymmetric divisions, generating one neuroblast and one ganglion mother cell destined for differentiation. After delamination from the neuroepithelium, mitotic neuroblasts organize an apical cortical domain where the polarity proteins Bazooka(Par3):Par6:aPKC are clustered, and a basal cortical crescent where the fate determinants Numb and Prospero are confined (figure 1b). Par complexes recruit at the apical site macromolecular machines known as force...
Figure 1. (a) Schematic definition of symmetric and asymmetric cell divisions. A prerequisite for asymmetric cell divisions is the establishment of a cellular polarity axis (black arrow), which entails the recruitment and maintenance at restricted cortical sites of defined sets of membrane-associated proteins (blue and pink crescent). Polarity establishment can be either a self-autonomous process occurring in early mitosis, as is the case for Drosophila neuroblasts and Caenorhabditis elegans zygotes, or it can be instructed from the tissue in which the cell is embedded. As mitosis proceeds, the proteins organized in distinct cortical domains (including the conserved Par3, Par6 and aPKC polarity proteins) coordinate the asymmetric distribution of fate determinants (i.e., components able to impart differential fate to daughter cells such as transcription factors and mRNAs—brown dots). In this configuration, if the mitotic spindle (in green) aligns parallel to the polarity axis, sibling cells will inherit a differential set of components (top panel). Furthermore, if one of the mother cell’s cortical domains is in contact with a specific microenvironment (generally referred to as a niche), only one of the daughters will retain a similar contact. In addition, if the spindle is not central to the cell but displaced towards one side, the cytokinesis furrow will not ingress at the equatorial section, and upon cytokinesis daughters with different sizes will be generated (top panel). Conversely, if the spindle orients perpendicularly to the polarity axis, the division will be symmetrical, giving rise to two identical siblings (bottom panel). (b) Distribution of polarity proteins (Par3:Par6:aPKC), spindle orientation machinery (dynein-bound Mud:Pins:Gαi complexes) and of the bridging molecule mInsc in fruitfly neuroblasts at metaphase. Before division, neuroblasts delaminate from a neuroepithelium (top cell layer), to which they remain attached with a membrane region organizing the apical domain. Par proteins restrict the localization of fate determinants such as Prospero and Numb at the basal site. Despite the known force-generating complexes localizing apically, in neuroblasts the spindle is displaced towards the basal site in such a way that the cleavage plane (purple dotted line) parts the cytoplasm unequally. (c) During epidermal development, progenitors organized in a monolayered epithelium divide vertically to stratify the skin. mInsc mediates the recruitment of NuMA:LGN:Gαi at the apical site in order to properly orient the mitotic spindle. (d) Vertebrate neural stem cells, known as radial glial cells, undergo planar symmetric divisions (left) and semiplanar asymmetric divisions (right), with a proportion that is finely regulated throughout neurogenesis. Planar divisions occur with the spindle axis parallel to the ventricular surface, and the cleavage plane bisecting both the apical end-foot and the basal process. A minor tilt in the spindle axis is sufficient for the asymmetric segregation of the basal process and the apical end-foot between daughters. In radial glial cells, NuMA:LGN:Gαi complexes localize in an equatorial belt, away from Par proteins, which are found in the apical end-foot. Although mInsc regulates the balance between planar and semiplanar divisions of radial glia, its compartmentalization in mitosis is not yet clear.
generators, able to capture astral microtubules emanating from the spindle poles and to establish pulling forces. Genetic screens combined with imaging studies in developing fly embryos and larval brains revealed that force generators are assembled on Mud:Pins:Go4 complexes brought at sites of polarization by a adaptor named InsCuteable (hereafter referred to as dInsc, where ‘d’ stands for Drosophila) that directly interacts with Bazooka (the fly Par3) [2–5]. The traction force exerted on microtubules is generated by the minus-end-directed movement of Dynamin/Dynactin that directly interacts with Mud [6]. As a result of the directional pulling forces exerted by force generators, the spindle aligns parallel to the polarity axis, slightly displaced towards the basal site. Upon cytokinesis, the fate determinants partition only to the smaller ganglion mother cell, which is positioned away from the neuroepithelium. Genetic studies revealed that the size difference between the neuroblast and the ganglion mother cell, and the unequal segregation of Prospero, are fundamental events in setting the correct lineage length and progeny fate [7].

Insights into the mechanistic basis of spindle coupling to cortical polarity in vertebrates have lagged behind those in flies and worms, mainly due to technical difficulties in isolating and studying stem cells. Yet recent evidence supports the notion that the spindle orientation machinery active in neuroblasts is conserved in mouse skin and neural progenitors, and is responsible for vertical divisions in lung distal epithelium [8]. At about day E12.5 of embryonic mouse development, progenitors of the epidermis start dividing vertically to promote skin stratification. Such vertical asymmetric divisions are promoted by the apical recruitment of NuMA:LGNI nsc complexes (the vertebrate counterpart of Mud:Pins:Go4) by Par6:Par3aPKC via mInsc (where ‘m’ indicates the mammalian orthologue of dlnsc), which results in apico-basal spindle alignment and generates one daughter cell placed above the epidermal layer (figure 1c) [9,10]. The situation is more sophisticated in neural stem cells, called radial ganglial cells in vertebrates. Radial glial cells are attached to the ventricular zone through a tiny apical end-foot, accounting for only about 2 to 3 per cent to the total cellular membrane, where Par proteins localize [11,12]. Seminal studies from the Huttner and Ffrench-Constant laboratories [13,14] revealed that in early embryogenesis apical neural progenitors mostly divide planarly, with the spindle parallel to the ventricular surface (figure 1d, left panel). Between E13 and E18, when mouse neurogenesis peaks, radial glial cells divide semi-planarly with a minor tilt in the spindle axis that is sufficient to determine the unequal inheritance of the apical foot domain and the basal process (figure 1d, right panel). Imaging analysis in the developing chicken neocortex revealed that NuMA:LGNI nsc are distributed in an equatorial belt above the spindle poles, and do not seem to co-localize with Par proteins [15]. No clear evidence is available for the precise cortical localization of mlnsc in radial glial cells, although it has been shown that its overexpression in mice at day E8.5 increases tilted neurogenic divisions, whereas its ablation causes radial glial expansion [16]. The prominent role of planar divisions in maintaining the population of apical neural progenitors in the developing central nervous system is also supported by knock-down experiments of LGNI nsc in chicken and mouse neuroepithelial cells, which result in randomization of the spindle axis and premature exit from the neuroepithelium, but do not compromise the replicative potential [17,18].

What do we know about the molecular mechanisms accounting for spindle coupling to cortical polarity? As briefly sketched earlier, for years, the simple model that was pushed forward to explain spindle orientation was that Par proteins, mlnsc, NuMA, LGNI nsc and Go4 would be part of the same macromolecular complex, apically localized in polarized asymmetric divisions, and capable of generating pulling forces on astral microtubules via the direct interaction between NuMA and the microtubule motor Dynamin/Dynactin [19]. This model stems from imaging analyses showing that this set of proteins localizes in a crescent above the apical spindle pole, and was further corroborated by coinmunoprecipitation experiments in which LGNI nsc:Go4 were found in association with Par3:mlnsc [20] and NuMA [21].

Recent biochemical and structural data revealed that mlnsc and NuMA are in fact competitive interactors of LGNI nsc [22,23]. This evidence challenges the notion that they belong to the same complex, and imposes its revision on the basis of the newly acquired knowledge. Here, we review the organizational and functional principles of the interactions of mlnsc and NuMA with LGNI nsc, and explain the molecular basis for their competition, emphasizing similarities and differences between Drosophila and vertebrate proteins. We also advance new hypotheses for the working principles of these proteins truly reflecting their biochemical properties.

3. Conserved architecture of LGNI nsc and Pins:Insc complexes

LGNI nsc and Pins share a homologous domain structure comprising eight tetra-tricopeptide repeats (TPRs) at the N-terminus and multiple GoLoco motifs at the C-terminus joined by a linker region of about 100 residues. TPRs consist of a couple of antiparallel α-helices, and are usually arranged in contiguous arrays forming superhelical scaffolds that mediate protein–protein interactions. Indeed, LGNI nscTPR has been shown to be responsible for the interaction with NuMA [21,24] and Lgl2 [25], and PinsTPR associates with Mud [26–29], mlnsc [4] and Canoe [30]. Recently, the topologies of binding of LGNI nscTPR/PinsTPR to mlnsc/dlnsc [22,31] and NuMA [23] have been unveiled.

The direct interaction of Pins/LGNI nsc with dlnsc/mlnsc is required for apico-basal spindle alignment in neuroblasts [2] and in mouse skin progenitors [9]. Deletion analysis revealed that the portion of fruitfly dlnsc encompassing residues 252–615, termed asymmetric-domain or dlnscASYM, is sufficient to recapitulate dlnsc functions during neuroblast asymmetric divisions [4,32]. The poor sequence similarity among Insc homologues makes it difficult to identify in silico a corresponding portion on the vertebrate proteins. Nonetheless, comparison of the crystallographic structures of Drosophila PinsTPR:dlnsc [22] with human and mouse LGNI nscTPR:mlnsc [23,31] revealed that the interface between the 40-residue peptide of Insc (InscPEPT hereafter) containing the high-affinity LGNI nsc-binding site and LGNI nscTPR is conserved throughout species (figure 2a,b). For clarity, we will use hlnsc when referring to the human protein. The crystallographic structures revealed that InscPEPT adopts an extended conformation lining within the inner groove of the superhelical TPR scaffold of LGNI nsc with an opposite orientation. This arrangement defines a modular interface. The first 12 residues of InscPEPT fold as an α-helix that packs perpendicular to the TPRs and contribute to the binding strength primarily via
hydrophobic interaction mediated by Trp313dInsc/Trp31hInsc (figure 3a, b, left panels). The central portion of InscPEPT is anchored on PinsTPR/LGNTPR by bidentate hydrogen bonds between Asn residues of the Leu–Gly–Asn (LGN) triplets of TPR4–5 and main chain carbonyls and nitrogen of Insc. In this region, the interaction is further strengthened by polar interactions between the negatively charged Glu-X-Glu motif of InscPEPT and invariant Arg side chains of Pins/LGN (figure 3a, b, central panels). The C-terminal portion of InscPEPT inserts Lys332dInsc/Lys50hInsc and Ile334dInsc/Ile52hInsc into two adjacent pockets formed by TPR1–2–3 (figure 3a, b, right panels). Although these lysine and isoleucine residues are fully conserved, their substitution does not affect the binding affinity. Interestingly, the structure of human LGNTPR:hInscPEPT [23], which has been determined with a longer Insc fragment than the fly one, shows that the hInsc chain folds back into a β-hairpin lining on the N-terminal TPRs of LGN. (c) A structure of mouse LGNTPR:NuMAPEPT (PDB ID 3RO2), showing that hInsc and NuMA (purple) occupy the same surface in the inner groove of the TPR domain. The C-terminal portion of NuMAPEPT adopts a helical conformation.

Figure 2. Architecture of PinsTPR/LGNTPR in complex with Insc and NuMA. (a) (i) Cartoon and (ii) surface representation of Drosophila PinsTPR:dInscPEPT (PDB ID 4A1S). Pins is shown in yellow and dInsc in blue. (b) Structure of human LGNTPR:hInscPEPT (PDB ID 3SF4) displayed with the same orientation as in (a), with LGN coloured grey. The longer hInsc fragment forms a β-hairpin lining on the N-terminal TPRs of LGN. (c) A structure of mouse LGNTPR:NuMAPEPT (PDB ID 3RO2), showing that hInsc and NuMA (purple) occupy the same surface in the inner groove of the TPR domain. The C-terminal portion of NuMAPEPT adopts a helical conformation.

4. Ubiquitous functions of NuMA:LGN:Gαi in mitotic spindle orientation

In all mitoses, the placement of the mitotic spindle relies on the interaction between NuMA and cortically localized LGN:Gαi complexes [33]. In Hela cells, NuMA:LGN:Gαi are distributed above both poles to stabilize the spindle and assist sister chromatid separation in anaphase. Myristoylated Gαi subunits recruit the complex at the cortex [21], while its restricted localization above the poles relies on a RanGTP-dependent gradient precluding membrane association in the proximity of the metaphase plate [34]. In this system as well as in skin progenitors, Abi-1 kinase orchestrates the coordination of LGN crescents with the spindle axis by phosphorylating NuMA on Tyr1774, with molecular details that are still unclear [35]. In oriented symmetrical divisions of epithelial cells, NuMA:LGN:Gαi complexes are restricted baso-laterally in order to keep the spindle horizontal, and do not localize with Par proteins. The mechanism that has been put forward to account for the apical exclusion of NuMA:LGN:Gαi in this system is the phosphorylation of Ser401LGN by apical aPKC that primes the association of LGN with 14-3-3, thus precluding the binding to cortical Gαi [36].

In polarized asymmetric mitosis, the NuMA:LGN:Gαi complex is thought to be recruited apically with Par3/Par6/aPKC via mInsc to unequally partition fate determinants. As previously outlined, this mechanism has been pushed forward to explain the spindle alignment to cortical polarity in fly neuroblasts and mouse skin progenitors, whereas radial glial cells seem to constitute an exception to this simplistic view. In our opinion, this apparent discrepancy can be reconciled, envisioning that a few mInsc-coordinated NuMA:LGN:Gαi complexes localized with Par proteins at the apical end-foot, but not detectable by immunostaining, might be sufficient to tilt the spindle axis even if the bulk...
Interestingly, in asymmetrically dividing Drosophila neuroblasts, the phosphorylation of Ser436Pins (corresponding to Ser401LGN) by Aurora-A has been reported to trigger a secondary microtubule-dependent spindle orientation pathway sustained by the phospho-specific association of Pins with membrane-associated Dlg [23, 37, 38], an association that can also occur when Pins is in complex with dInsc [39]. There is no clear evidence as to whether the pathway is conserved in vertebrates. In fruitflies’ neuroblasts, an additional player of NuMA:LGN:Gai is on an equatorial belt [15] (figure 1d).

![Diagram of interaction surfaces](http://rsob.royalsocietypublishing.org/)

**Figure 3.** A structural comparison of the interaction surface of dInsc/hInsc and NuMA with PinsTPR/LGNTPR. (a) Enlarged views of the modular interface between dInscPEPT and PinsTPR. Conserved residues contributing to the dimer interface are shown in balls-and-sticks, including the EPEInsc-motif in the central portion of the peptide. (b) Analogous close-ups of human hInscPEPT:LGNTPR, in which the additional C-terminal β-strand is visible. (c) Details of the NuMAPEPT-binding interface in the same LGNTPR regions displayed in (a,b). (d) A structure-based sequence alignment of InscPEPT and NuMAPEPT recapitulating the high-affinity interaction with LGN/ Pins. Residues engaged in chemically equivalent interactions with the TPR scaffold are coloured in red.
of the spindle orientation network is the actin-binding protein Canoe [40], which directly binds Pins, and has been implicated in Mud recruitment at the cortex in a RanGTP-dependent manner [30]. In vitro Canoe interacts directly with RanGTP; however, how this association may favour the localization of Mud is still unclear. It will be extremely interesting to test whether the orthologue Afadin plays an analogous role in vertebrates’ asymmetric divisions, as this interaction represents the first direct link between the acto-myosin cortex and the spindle-tethering machinery.

5. Structural organization of the NuMa:LGN assembly

It has long been known from biochemical studies that a 20 kDa C-terminal fragment of NuMA contains the LGNTPR-binding site [24], which partly overlaps with the microtubule-binding site [41], thus implying that the microtubule-organizing activity of NuMA and its function in spindle orientation are mutually exclusive. Recent structural evidence revealed that NuMA contacts the internal concave surface of LGNTPR with a short amino acid acidic stretch spanning residues 1886–1914 of the human protein (which we will refer to as NuMAPEPT), roughly occupying the same surface recognized by InsCPEPT (figure 2c) [23]. At the molecular level, NuMAPEPT runs parallel to the TPR super-helical axis, forming with its C-terminus a three-helix bundle with α1–α2 of LGN (figure 3c). At first glance, the only conserved motif between InsCPEPT and NuMAPEPT sequences is the central Glu–Glu–Glu motif. However, a careful inspection of the dimeric interface shows that several residues of the two peptides with analogous interacting potential are engaged in the same type of chemical bonds, and that their contributions sum up to create a substantially identical interaction network with LGNTPR (figure 3c). In particular, the Phe1886NuMA ring is positioned as Trp313InsC/Trp313InsD, whereas Arg1905NuMA and Ile1906NuMA insert into negatively charged and hydrophobic cavities of LGN in much the same way as Lys332InsC/Lys332InsD and Ile334InsC/Ile334InsD. Notably, the Glu–Pro–Glu motif of NuMAPEPT is two residues out of register when compared with the Glu–Glu–Glu motif of LGNTPR, which structurally aligns with the upstream Gln–Asp–Glu NuMA triplet (figure 3c,d). As InsCPEPT and NuMAPEPT occupy the same position on LGNTPR, we expect that designing LGNTPR mutants selectively impairing the binding either to mInsc or to NuMA will be a challenging exercise. It is worth pointing out that the common molecular signature described for the recognition of mInsc/dInsc and NuMA by LGNTPR/PinsTPR has not allowed the identification of a corresponding Pins-binding peptide on Mud. Consistent with the structural analysis, NuMA also binds LGNTPR.

6. NuMa and mInsc bind competitively to LGNTPR

The evidence that mInsc and NuMA share the same binding surface on LGNTPR depicts them as competitive interactors. Indeed, in several experimental settings, it has been proved that in vitro and in living cells the two proteins do not enter the same complex [22,23,39]. Measurements with human proteins suggest that InsCPEPT associates with LGNTPR with a fivefold to tenfold higher affinity than NuMAPEPT [22,31], whereas mouse proteins display similar binding strengths [23]. Although no quantification is available, full-length LGN:Goi also displays a preferential association with full-length mInsc than with NuMA [22]. The relation seems to be opposite for Drosophila proteins as Pins binds Mud better [39]. How the relative affinities impinge on the cross-talk between the mInsc-bound and the NuMA-bound LGN:Goi pools in living cells remains to be determined.

7. Opening of the LGN conformational switch

Besides competing with one another for the binding to LGNTPR, both NuMA and mInsc are capable of displacing the C-terminal portion of LGN, which has been shown to interact with the TPR domain in unliganded LGN [21,22,29]. The precise fragment of LGN C-terminus required for this intra-molecular interaction has not been mapped; what is known is that the GoLoco23 of Pins [29] and GoLoco34 of LGN (M. Mapelli 2011, unpublished data) form a complex with LGNTPR. On the basis of recent biochemical and structural data, we suspect LGNTPR has an inherent conformational flexibility that needs to be stabilized by association with an extended ligand, and therefore we expect the LGN C-terminus to bind LGNTPR with modalities similar to those described for mInsc and NuMA. The affinity between separately purified LGNTPR and GoLocos is in the micromolar range [29] (M. Mapelli 2011, unpublished data), suggesting that substoichiometric concentrations of NuMA and mInsc might be sufficient for the LGN switch conversion. Intriguingly, in vivo the activation of full-length LGN and Pins requires the synergistic binding of NuMA/ Mud and several Goi subunits [42,43], implying an active role of the linker region in maintaining LGN in the closed state. It is not known whether mInsc can trigger the LGN conformational transition in the absence of Goi. As the release of the intra-molecular interaction holding LGN in an inhibited closed conformation is a prerequisite for force generators’ assembly, we believe that elucidating the structural role of the linker region in closed LGN will be instrumental in figuring out the LGN activation mechanism.

8. A revised model for force generators’ assembly in asymmetric cell divisions

The competitive association of NuMA and mInsc with LGN contrasts with the notion that mInsc is the molecular bridge recruiting NuMA:LGN:Goi to polarity sites during asymmetric mitoses, and imposes a major revision of the current view for force generators’ localization and maintenance at the cortex. The more simplistic model that has been advanced [22,23] envisions the sequential binding of LGN first to Par3-bound mInsc and subsequently to NuMA (figure 4). In this view, in the early phases of mitosis, the higher affinity interaction with mInsc will be dominant in instructing the cortical distribution of LGN, and concomitantly will catalyse the conformational rearrangement required for the binding to several Goi subunits. If so, the functional role of mInsc would be to cluster and activate LGN at the membrane, a known mechanism able to trigger localized signalling pathways [44]. How
the transfer of LGN:Goi complexes from mInsc to NuMA during mitosis might be achieved remains totally unclear. Biochemical measurements indicate that there is about a fivefold difference in the binding strength of mInsc and NuMA to LGN, which we suggest could be overcome by addition of a few phospho-groups either to NuMA or LGN. None of the mitotic phosphorylations of NuMA recently reported affects the interaction with LGN [34,35,45,46], though a clear function has been assigned only to a few of them. An inherent question of the sequential-binding model is how the NuMA:LGN:Goi complexes that are assembled in the proximity of Par proteins are retained long enough at the correct sites to pull on astral microtubules with the proper direction. As mentioned, in fly neuroblasts, cortical Dlg binds to the phosphorylated linker region of Pins, providing an anchoring mechanism independent of Par proteins [38]. We believe that newly identified Pins/LGN interactors (such as the earlier-mentioned Canoe, as well as yet undiscovered effectors) may serve a similar purpose. Interestingly, ablation of α-catenin and β-integrin in skin progenitors causes misoriented divisions, implying that other signalling pathways not directly regulated by Par3:αPKC contribute to spindle positioning in this system. Alternatively, NuMA:LGN:Goi can be transient complexes, briefly pulling in the direction of Par proteins where they are assembled, and then dissociating before diffusing away by spontaneous drift of the Goi myristoyl groups inserted in the plasma membrane. It is known that LGN binds exclusively to GDP-loaded Goi [47], and that the conserved GEF Ric-8 catalyses the GDP exchange of Goi, which is essential to the spindle orientation process [48–51]. In the context of the sequential-binding model, the function of Ric-8 could be to assist the disruption of the NuMA:LGN:Goi\(_{\text{GDP}}\) subunits previously disengaged from Goi. Ric-8 may be assisted by a specific G-protein coupled receptor such as the Drosophila Tr1. At metaphase, most of the membrane-associated LGN:Goi\(_{\text{GDP}}\) is released from mInsc and enters a complex with dimeric NuMA, which in turn interacts with the minus-end-directed motor Dynein to pull on astral microtubules (MTs). At this stage, cortical anchoring of NuMA:LGN:Goi\(_{\text{GDP}}\) complexes can be strengthened by interactions between Ser406-phosphorylated LGN and Dlg, or between LGN and actin-bound Afadin. On the basis of the sequential model, NuMA:LGN:Goi\(_{\text{GDP}}\) assemble near Par complexes, but do not retain any positional information. To prevent mis-directional MT pulling caused by membrane-diffusion of NuMA:LGN:Goi\(_{\text{GDP}}\), it is possible that these complexes are short-lived and disassemble under the action of the Goi GEF Ric-8, and that new cycles of LGN recruitment by mInsc start until the spindle is properly aligned (dotted arrow).

In this system, the regulation of the Pins:Goi\(_{\text{GDP}}\) association by the G-protein coupled receptor Tr1 constitutes an extrinsic cue coordinating cortical polarity with tissue architecture as it instructs the organization of the apical domain at the site in contact with the neuroepithelium. The validation of this sequential/transient-binding model in living cells would greatly benefit from the availability of LGN mutants selectively impaired for mInsc or NuMA binding. The model predicts that LGN mutants unable to bind mInsc would phenocopy the spindle misorientation observed in dlnc/mlnsc-deficient neuroblasts or radial glia cells, whereas mutants deficient in NuMA binding would be recruited to Par proteins but fail to pull on astral microtubules. Furthermore, these selective mutations could be introduced into FRET sensors (such as the already-used YFP-LGN/Pins-CPF sensors [21,29]) to check whether the opening of the switch occurs upon Insc or NuMA binding. Given the major overlap between mInsc and NuMA binding sites, we anticipate that generating such LGN mutants will be a rather daunting task.

### 9. Conclusions

In the past few years, the prominent role of the spindle alignment in setting the balance between symmetric and asymmetric divisions of stem cells has fuelled intense research activities aimed at understanding the molecular mechanisms underpinning the process in several cellular systems. It is now clear that in fly neuroblasts, intrinsic and extrinsic cues synergize in positioning an asymmetric spindle, and this is a prerequisite for the correct fate and placement of daughter cells [7,53]. Attempts have been made to recapitulate in vertebrates what is known from genetic and imaging studies in fly neuroblasts, and this effort led to the conclusion that randomizing the progenitors’ spindle orientation impacts on neurogenetic programmes also in vertebrates [16–18]. Recent biochemical and structural evidence...
indicated an inconsistency in the established molecular model for spindle orientation, requiring more analyses to clarify the mechanistic interplay between mInsc and NuMA. Meanwhile, the number of interactors of the NuMA:LGN:Gαi complex and the way they regulate the spindle orientation in different cellular systems starts to become clear. This sets the stage for further investigations in vivo and in vitro aimed at delivering a coherent picture of how they function.

10. Acknowledgements

We are grateful to members of the Mapelli and Gonzalez laboratories for critical reading of the manuscript. Mapelli’s laboratory is funded by the Italian Association for Cancer Research (AIRC) and the Italian Ministry of Health; Gonzalez’s laboratory is funded by grants BFU2009-07975/BMC, CENIT ONCOLOGICA-20091016 and SGR Aguar 2009 CG041413.

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