Front. Med. 2022, 16(3): 339–357
https://doi.org/10.1007/s11684-022-0926-1

REVIEW

Fine-tuning cell organelle dynamics during mitosis by small GTPases

Zijian Zhang[1], Wei Zhang[2], Quentin Liu (✉)[1,3]

[1]Sun Yat-sen University Cancer Center; State Key Laboratory of Oncology in South China; Collaborative Innovation Center for Cancer Medicine, Guangzhou 510060, China; [2]Department of Clinical Immunology, The Third Affiliated Hospital, Sun Yat-sen University, Guangzhou 510630, China; [3]Institute of Cancer Stem Cell, Dalian Medical University, Dalian 116044, China

Abstract **During mitosis, the allocation of genetic material concurs with organelle transformation and distribution. The coordination of genetic material inheritance with organelle dynamics directs accurate mitotic progression, cell fate determination, and organismal homeostasis. Small GTPases belonging to the Ras superfamily regulate various cell organelles during division. Being the key regulators of membrane dynamics, the dysregulation of small GTPases is widely associated with cell organelle disruption in neoplastic and non-neoplastic diseases, such as cancer and Alzheimer's disease. Recent discoveries shed light on the molecular properties of small GTPases as sophisticated modulators of a remarkably complex and perfect adaptors for rapid structure reformation. This review collects current knowledge on small GTPases in the regulation of cell organelles during mitosis and highlights the mediator role of small GTPase in transducing cell cycle signaling to organelle dynamics during mitosis.**

Keywords small GTPase; cell organelle; mitosis

Introduction

During cell division, duplicated genetic material and other cellular components must be segregated before partitioning into two daughter cells [1–3]. The inheritance of chromosomes is under strict regulation and executed with high spatial and temporal control. However, how cell organelles respond to cell cycle signals and are dynamically orchestrated to ensure proper cell division remains unclear. Recently, with the help of technological advances, intensive studies found that various cell organelles actively participate in cell division through rapid changes in morphology and function to facilitate this process or at least not interfere with chromosome segregation. A plethora of proteins and dozens of distinct pathways are discovered to orchestrate organelle dynamics with cell division. Notably, small GTPases are found heavily involved in this progress (Table 1). Whether there lies a common mechanism that orchestrates organelle dynamics with cell division and whether small GTPases are uniform mediators that execute this sophisticated process are worthy of investigation.

Received: October 26, 2021; accepted: February 24, 2022
Correspondence: Quentin Liu, liuq9@mail.sysu.edu.cn

Small GTPases, a family of conserved proteins, are widely discovered to function as nodal points that integrate broad upstream regulatory inputs and disseminate broad effector outputs in distinct biological processes. Mostly residing in the cytosol, small GTPases (20–30 kDa) are homologous to the alpha subunit of heterotrimeric G-proteins (large G-proteins) [4]. But unlike the alpha subunit of heterotrimeric G-protein, a small GTPase can independently hydrolyze GTP to form guanosine diphosphate (GDP) [5]. Around 167 Ras superfamily proteins in human are divided into six prominent families on the basis of sequence identity and function: Ras, Rho, Rab, Arf, Ran, and Rag [6–8]. Small GTPases share a conserved conformational switch mechanism coordinating with guanine nucleotide exchange factors (GEFs) and GTPase-activating proteins (GAPs), which work in opposite ways to govern the cycle between two conformations of GDP-bound inactive and GTP-bound active states [9–12]. These mechanisms give small GTPases rapid on–off switches and subcellular location transfer characteristics. With abundant family members and various regulators and effectors, small GTPases are the perfect executor and adaptor for rapid structure reformation in coordination with cell division.

Table 1 Summary of small GTPases in the regulation of cell organelle dynamics during mitosis

Organelle	Small GTPase	Proposed function	References
Spindle apparatus	Ran	RanGTP recruits essential centrosome and kinetochore components and releases and activates spindle assembly factors to nucleate, bind, and organize nascent spindle microtubules	[13,36–41]
	Cdc42	Bi-orientation and stabilization of spindle microtubule attachment to kinetochores, spindle assembly, and spindle orientation	[42,43]
	RhoA	Maintenance of spindle orientation	[42]
	Rab5	Regulation of the astral microtubule size and spindle alignment	[45]
	Rab11	Bringing microtubule-nucleating factors and spindle pole proteins to spindle poles	[44,46,47]
	Arl8A, Arl8B	Centrosome maturation and chromosome segregation	[48,49]
	RalA	Regulation of the kinetochore–microtubule interaction in early mitosis	[50]
Plasma membrane	Rap1	Focal adhesion assembly–disassembly	[25,71,72]
	RhoA	Actomyosin cortex organization beneath the plasma membrane during mitosis	[73,76,77]
	Ran	Polar cortex relaxation and ingression furrow position	
	Rac1	Repolarization of the actomyosin cortex	[69,80]
ER & nuclear envelope	Rab5	ER membrane remodeling and NEBD. Rab5 depletion inhibits nuclear envelope disassembly	[108]
	Ran	Ran activities regulate microtubule dynamics and the mechanical rupture of nuclear envelope during NEBD. After division, Ran promotes the assembly of NPCs and vesicle fusion	[114,118–123]
	Cd42	Nuclear envelope sealing and ER remodeling	[126]
Golgi apparatus	Arf1	Participation in the Golgi cycle through the regulation of vesicle transportation	[96,133,134]
	Sar1	Participation in the Golgi cycle through the regulation of vesicle transportation	[135–139]
	Rab1	Reassembly of the Golgi complex after mitosis	[142]
	Rab6A′	Retrograde trafficking. Depletion causes metaphase blockage	[145]
Mitochondria	RalA	Promotion of mitochondrial fission during mitotic entry	[21]
	Arf1	Recruitment of PI(4)P-containing vesicles at ER-mitochondria contact site and promotion of mitochondrial fission	[152]
	Miro	Miro1 and Miro2 bind CENP-F and associate with microtubule-growing tips. Miro loss decreases the spreading of the mitochondrial network and causes cytokinesis-specific defects	[154]
Midbody	RhoA	Position of ingression furrow and membrane ingression and abscission	[161,169–172,175,176]
	Rac1	Membrane ingression. The overexpression of constitutively active Rac1 causes multinucleation and cytokinesis failure	[42,187,192]
	Rab1	Rab1 facilitates new membrane supplementation along the ingressing cleavage furrow	[191]
	Rab11	Through en dosome transport to facilitate furrow ingression and F-actin elimination for final abscission	[192,194,198,200,201]
	Rab35	Through endosome transport to facilitate F-actin elimination for final abscission	[194,200–202]
	Arf1	Golgi organization and Golgi output for ingression furrow function	[193]
	Arf6	Bridge stability and abscission	[65,204]
	RalA & RalB	RalA and RalB control the exocyst localization at the furrow and midbody, respectively. Their collaboration is required for abscission completion	[205,206]
Autophagosome	Rabs & Sec4	Autophagosome formation. Role in mitosis is unknown	[212–215]
	Rab7, Rab8B & Rab24	Autophagosome maturation. Role in mitosis is unknown	[213,214,216–219]
	Arfs & Sar1	Autophagosome biogenesis and cellular localization. Role in mitosis is unknown	[213,220]
Peroxisomes	Rho, Rab, Arf & Miro	In the interphase, small GTPases regulate peroxisome distribution and biogenesis. The disruption of spindle pole localization of peroxisomes impairs spindle orientation. The direct role in mitosis is unclear	[17,239–242]

The potential mediator role of small GTPases that link cell division with organelle dynamics is further highlighted by its ubiquitous but distinct organelle regulation functions. RanGTP concentration gradient restores the subtle control of spindle formation [13]. Rab and Arf families profoundly undertake intracellular vesicular transportation and the vesicle transportation processes continuously shaping ER and Golgi apparatus structures [14–20]. Recently, small organelles, which have long been considered disconnected from the genetic material division cycle but undergo stochastic partition, such as mitochondria, are found to coordinate with canonical cell division, and specific small GTPases emerge to be a potential mediator [21].

In this review, we compare the role of small GTPases in cell shaping, spindle formation, membrane-bound organelle (MBO), and membrane-less organelle (MLO) structuring and highlight the mediator role of small GTPase in transducing cell cycle signaling to organelle dynamics within the cell cycle. Given that small GTPases are conserved in sequences and have related functions among subfamilies, we focus on events during mammalian cell division and use examples from other eukaryotic organisms.

Regulation of small GTPases during cell division

Eukaryotic cells undergo extensive and reversible cellular reorganization covering multiple dimensions among cell division. Given the dynamic roles of small GTPases

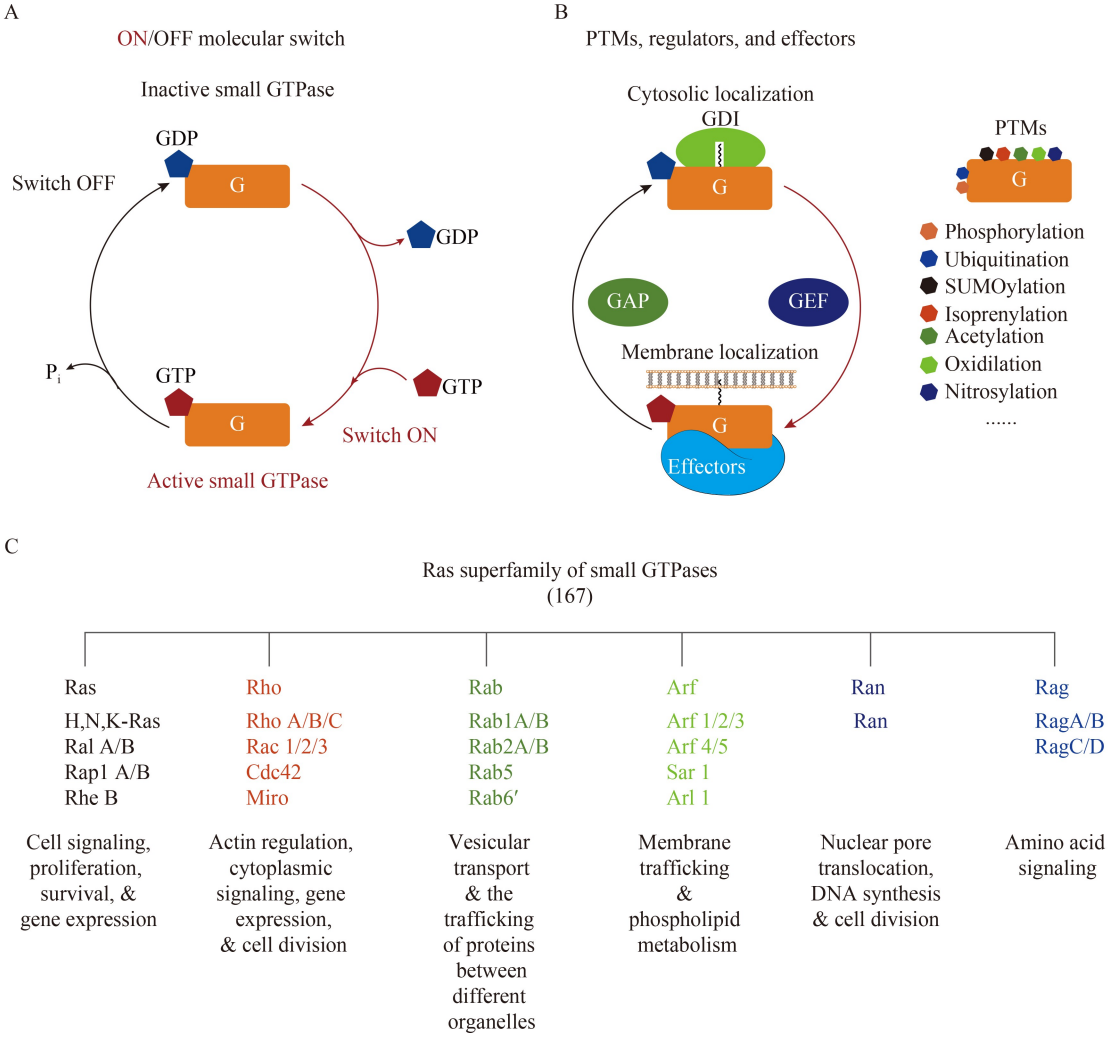

Fig. 1 Overview of small GTPases. (A) Molecular switch. Small GTPase cycle between the inactive (GDP-bound) and active (GTP-bound) states. Abbreviation: G, small GTPase. (B) PTMs, regulators, and effectors of small GTPases. GDP/GTP-bound form is regulated by guanine nucleotide exchange factors (GEFs) and GTPase-activating proteins (GAPs). Guanine–nucleotide dissociation inhibitors (GDIs) inhibit nucleotide dissociation and control small GTPases localization. Active GTPases interact with different effectors to mediate various cellular responses. PTMs can alert their activities. (C) RAS superfamily of small GTPases. The 167 RAS superfamily GTPases are classified into six families on the basis of sequence identity and cellular functions.

during different stages of cell division, mechanisms for their spatial and temporal regulation are crucial to ensure orderly conduct. The regulation of small GTPase activity, localization, and function has been found among interaction with GAPs and GEFs. Small GTPases show high affinity toward GTP and GDP, and their GDP/GTP alternation actuates a variety of functional switches that are pivotal for cell dynamics (Fig. 1A and 1B). GEFs and GAPs accelerate intrinsically sluggish GDP/GTP exchange and GTP hydrolysis speed by 10^5. For Ras, Rho, and Rab GTPases, this switch incorporates a membrane/cytosol alternation regulated by GDIs and GDI-like proteins. The post-translational modifications of small GTPases and their cofactors are also vital for their activation and function [9,22,23].

Phosphorylation is a universal protein modification in eukaryotic cells and plays critical roles in every aspect of cellular life. The cell cycle is a leading example as protein phosphorylation peaks during mitosis. Mitotic kinases cyclin-dependent kinase (CDK, CDK1 and CDK2), Aurora (AURKA and AURKB), and PLK (Polo-like kinase) families and Bub1, Haspin, and Mps1 drive the entry and progression through the division phase of the cell cycle [24]. Notably, the reversible phosphorylation of small GTPases, GEFs, and their GPAs is an essential regulatory mechanism that occurs through cell division. At the beginning, a rise in CDK1 activity activates RhoA and cell rounding by phosphorylating p190RhoGAP and Ect2 for mitotic entry. The bridge scission at the last step of cell division requires AURKB-mediated MgcRacGAP phosphorylation. In intermediate steps, the phosphorylation of small GTPases facilitates spindle formation and organelle dynamics. The important new findings of small GTPases related to spindle formation and organelle dynamics are described in the following sections.

Besides phosphor regulation, ubiquitination-directed proteolysis ensures the unidirectional progression of the cell cycle [25–27]. Interestingly, the ubiquitination of multiple small GTPases modifies their activities, relocalization, and degradation [22,27–29]. For example, a component of the E3 ubiquitin ligase parkin-dependent ubiquitination on conserved K38 residue enhances RILP–Rab7 binding (RILP is a Rab7-interacting lysosomal protein), thus regulating Rab7 activity [30]. HECT type E3 ubiquitin ligase Smurf1 regulates cell polarity and motility through targeting RhoA for ubiquitination and degradation [31]. Besides small GTPase itself, GAPs, GEFs, and GDIs are frequent targets of the ubiquitination machinery [28]. Further studies will be necessary to test the significance of small GTPase ubiquitination during mitosis.

Other modifications include prenylation by a prenyltransferase on the cysteine, and the methylation of the C-terminal cysteine by isoprenylcysteine carboxyl methyltransferase. Prenylation isoprenylcysteine is required for membrane targeting and localization of small GTPase [22,32,33]. These modifications may not be as easy or fast as phosphor or ubiquitin regulation in shifting small GTPase activity when confronting rapid cell division events. Still, their roles in cell division are also worth exploration.

Spindle apparatus

The most significant phenomenon of eukaryotic cell division is the establishment of microtubule (MT)-based bipolar spindle apparatus. The cellular spindle apparatus includes three main components, i.e., spindle MTs, condensed chromosomes, and centrosomes. These three parts coordinate with associated proteins to guarantee chromosome inheritance [34,35].

Dozens of small GTPases covering all five subfamilies (except Rag) localize along spindle MTs, chromosomes, around centrioles, and between kinetochore–MT contacting sites and directly mediate spindle formation, position, orientation, and proper function.

Ran, as the single member of its subfamily, functions in centrosome duplication, MT dynamics, chromosome alignment, kinetochore attachment, and nuclear envelope dynamic regulation [13]. As for the spindle apparatus, Ran regulates the life cycle of centrosomes, and the Ran gradient directs spindle MT organization and assembly [36]. In mitotic cells, PLK1 and PAK4 phosphorylate Ran protein on S135 [37,38], and PLK1 phosphorylates Ran-binding protein 1 (RANBP1). Phosphor-activated Ran and RANBP1 modulate Cyclin B1's function at the centrosome to facilitate MT nucleation and stabilization [36,39].

For the Rho subfamily, Rho GTPases are central modulators of cell morphogenesis through the remodeling of the cytoskeleton [40,41]. The role of Rho GTPases that marks cytokinesis in animal cell division has now extended to the metaphase in coordinating mitotic spindle formation and the bi-orient attachment of spindle MTs to the kinetochore. This subject has been extensively reviewed [42]. Cdc42 is a master regulator of cell polarity. During metaphase, Cdc42 localizes to the spindle and centrosomes, facilitating spindle orientation and formation for chromosome alignment [43]. Cell division signals are transmitted to Rho GTPase and cofactors by phosphorylation modification via AURKA/B and CDK1 kinases [42].

Rab and Arf proteins link membrane transport and cytoskeleton dynamics [17]. During spindle formation, endosomal transport facilitates centrosome maturation, bipolar spindle formation, orientation, positioning, and function. The spindle-associated Rabs have been extensively reviewed [44]. Briefly, several Rabs and interacting proteins associate with spindle apparatus during cell

division [45]. Rab5- and Rab11-positive endosomes localize on the mitotic spindle and at mitotic spindle poles (Fig. 2). Rab5, in association with dynein, regulates astral MT size and spindle alignment. Rab5/CENP-F form complexes adjacent to kinetochores, and the silencing of Rab5 increases aberrant and unattached kinetochores, which may be due to reduced CENP-F at kinetochores. Mitotic spindle poles are active sites in vesicular transportation. Rab11-positive endosomes are reported to be involved in spindle pole organization and orientation by bringing MT-nucleating factors and spindle pole proteins to poles [46,47]. For the Arf family, Arl8A and Arl8B bind to tubulin and localize with MTs on the spindle midzone in late mitosis and may function in maintaining centrosome integrity [48,49].

Ras GTPases are known as signaling nodes but do not directly participate in spindle structuring. However, a Ras subfamily member RalA is proven to have functional interaction with a chromosomal passenger complex (CPC) [50]. RalA and its CPC-localized GEF TD-60 contribute to the regulation of kinetochore–MT interaction in early mitosis. The loss of RalA causes AURKB activity loss at the centrosome and increases the interkinetochore stretch with perturbed spindle structures [50].

MLOs

MLOs belong to an unconventional class of organelles formed by phase separation but are not sealed with a phospholipid membrane [51–54]. Recent discoveries on phase separation revolutionized our understanding of MLO organization, molecular properties, physical features, and biological functions. DYRK3 kinase is found to diffuse MLOs at mitotic onset [55], extending the phase separation concept to cell division [52]. However, the dynamic regulation of most MLOs during mitosis except pericentriolar material (PCM) is largely unknown. PCM is a typical example of MLOs surrounding centrioles, which nucleate MTs for mitotic apparatus establishment [56,57]. Previous work demonstrated that Ran regulates multiple steps of the centrosome life cycle [36]. Briefly, Ran interacts with the PCM scaffolding protein AKAP450 at centrosomes and regulates mitotic MT nucleation and stabilization [58,59]. Mitotic kinases PLK1 and PAK4 phosphorylate Ran at S135 and switch Ran into Ran–GTP and RanBP1-binding state to promote MT nucleation [37,60].

Although MLOs are free of lipid membrane, membrane and factors regulating membrane trafficking steps are emerging as important components of MLO formation and function [52]. In yeast, small GTPase Arf1 mutation [19] and other secretory mutants promote stress granule (P-body) accumulation under stress, which are related to P-body secretion malfunction [61]. Membrane trafficking-associated small GTPases Rab5, Rab6′, and Rab11 are found on endosomes around spindle poles and contribute to spindle pole maturation [46,62–65]. These findings suggest a major role for the endocytic pathway and small GTPases in MLO regulation.

MBOs

Eukaryotic cells organize their cytoplasm into multiple compartments to accommodate increased cell size and life process complexity. The compartments that are surrounded by biological membranes are MBOs. In terms of cell division, organelles may utilize different strategies for reorganization and partition [1,2], and small GTPases are widely found to be involved in this process.

Plasma membrane

Cells undergo dramatic shape changes to facilitate genetic material partition and the formation of daughter cells [2,66,67]. The plasma membrane and its associated cytoskeleton underneath support massive shape changes from cell rounding to abscission at the end of cytokinesis. The plasma membrane lipid composition dramatically changes to facilitate cell division especially during cytokinesis [68,69]. Small GTPases especially Rho GTPases control cell shaping through their ability to modulate MT dynamics and the actin–myosin cytoskeleton.

Cell rounding

To enter mitosis, eukaryotes use a rounding process to meet geometric requirements and facilitate chromosome capture and spindle function [70]. Focal adhesions (FAs) that link the extracellular matrix with cell skeleton must dismantle to ensure cell rounding. A key regulator in FA dismantling is the Ras subfamily small GTPase Rap1 [25]. Rap1 inactivation facilitates FA disassembly by preventing the Rap1 effector RIAM complex formation and the integrin activator talin interaction (Fig. 2) [71,72]. FA dismantling allows G2 cells to pass through the "adhesion-dependent checkpoint" and entry to mitosis. FA dismantling inactivates the "adhesion-dependent checkpoint" through the DEPDC1B/RhoA/PTPRF axis. Briefly, DEPDC1B accumulates at the G2 phase, and by competing with RhoA for the interaction with PTPRF, DEPDC1B frees RhoA from PTPRF and RhoA nucleotide exchange factor GEF-H1 [73]. This mechanism promotes FA disassembly as cells enter prophase. The released RhoA then becomes available for ECT2-dependent activation at other sites of the PM and promotes actomyosin cortex formation in prophase. However, during this process, how the cell cycle signal is transduced to Rap1 for FA dismantling is still unknown.

Cell rounding in a confined environment *in vitro* needs

cytoskeleton disassembly and reorganization. The cytoskeleton forms a mitotic actomyosin network underneath the plasma membrane, increasing cortical rigidity and providing attachment sites for astral MTs to facilitate spindle position and function [70,74,75].

RhoA is a key element in the formation of the actomyosin cortex. At mitotic entry, ECT2 released from the nucleus activates RhoA. CDK1 and PLK1 phosphor activate ECT2 and increase its GEF function toward RhoA. Activated RhoA induces the retraction of the cell margin, generates nonbranched actin filaments through DIA, and activates myosin via ROCK [76,77].

Cell elongation and cytokinesis

After sister chromatins segregate, cells elongate and form a cleavage ingression furrow to finalize cell division. This stage of cell shape change uses the same set of proteins as in cytokinesis, ECT2, RhoA, DIA, actin, myosin, and anillin [78,79]. The drop of CDK1–Cyclin B1 activity at this stage of mitosis shifts RhoA localization, thus starting repolarization via GAP and GEF MgcRacGAP midzone localization. RhoA and Rac1, another Rho subfamily of small GTPase, establish a gradient for actomyosin cortex polarization.

Rho and Rab GTPases have well-established functions in cytokinesis, share lipid PTMs, and show specific lipid preferences. As the plasma membrane lipid composition dramatically changes in the cell cycle [68], their localization and interaction with regulators and effectors may also be affected. During anaphase, PtdIns(4,5)P2 and PtdIns(3,4,5)P3 enrich in the furrow and poles separately, and form a lipid gradient, leading to RhoA/Rac activity gradient for the repolarization of cortical actomyosin establishment [69,80]. The ingression process transforms the cell into a dumbbell shape with apparent surface area expansion.

Polar relaxation

A stable ingression furrow's position and function also require a reduction of contractility at polar cortex regions. Several signals may contribute to the relaxation of the cortex at opposing cell poles [67]. Among these regulating pathways, the establishment of a high Ran–GTP gradient at cell poles may be associated with polar relaxation. As chromosomes approach cell poles, the associated RCC1 activates Ran and then functions via importin β to regulate the activity and localization of a wide range of actin regulators [81–83].

Mitosis to interphase transition

Finally, cells process mitosis-to-interphase transition and reorganize interphase structures in new cells. With the degradation of Cyclin B1, protein phosphatases PP1 and PP2A direct lamin and/or nucleoporin dephosphorylation to re-establish the nuclear envelope (NE) boundary [84]. Furthermore, proteins, such as anillin, RacGAP1, and ECT2, released from the nucleus to facilitate mitotic cell structure are again isolated from the cytoplasm to re-establish interphase cell organization. The cell–matrix interaction is acquired through Rap1 reactivation, promoting the assembly of cell–substrate adhesion [25].

Endoplasmic reticulum (ER) and NE

Morphometric changes to the ER during division

The ER is a single MBO involved in critical cellular processes, including protein processing, lipid synthesis, and calcium homeostasis. Interphase ER is a contiguous MBO with distinct subdomains that vary in structures and functions [85–89]. During cell division, ER morphology shows dramatic reorganization, and its reconstruction is required for mitotic fidelity [90]. The maintenance and remodeling of ER morphology are dependent on a number of proteins, including membrane-bending protein reticulons (RTNs), the dynamin superfamily member atlastins, and cytoskeleton [91–93]. In addition, certain Rab GTPases, i.e., Rab10 and Rab18, mediate the interaction between the ER and motors, thus regulating tubular ER membrane dynamics [94,95]. The functional characterization of Rab GTPases in *C. elegans* reveals that the depletion of Rab5 phenocopies the ER structure from the depletion of the Rtn4a and DP1/NogoA with reduced ER sheets [96]. A recent study showed that ER-shaping proteins REEPs are required to preserve tubular ER structure during mitosis. The depletion of REEPs reduces ER curvature and increases sheet-like ER proportion [97]. REEP3 and REEP4 are also needed to clear ER from metaphase chromatins, preventing their premature association to ensure proper division and NE architecture [98]. How cell division signaling connects ER-shaping proteins, such as REEPs, and how these proteins respond remain an open question (Fig. 2).

NE breakdown (NEBD) and assembly

The NE is a part of the ER network that is shaped into a large bimembrane cisterna consisting of outer (ONM) and an inner (INM) nuclear membranes, which together isolate and protect chromatin from the cytoplasm environment during interphase. Following the CDK1 activity cycle, NE breaks down during prometaphase, and the reverse process re-establishes this barrier during mitotic exit. Both processes require the dynamic remodeling of the ER with cytoskeleton. This subject has been reviewed extensively [99–102].

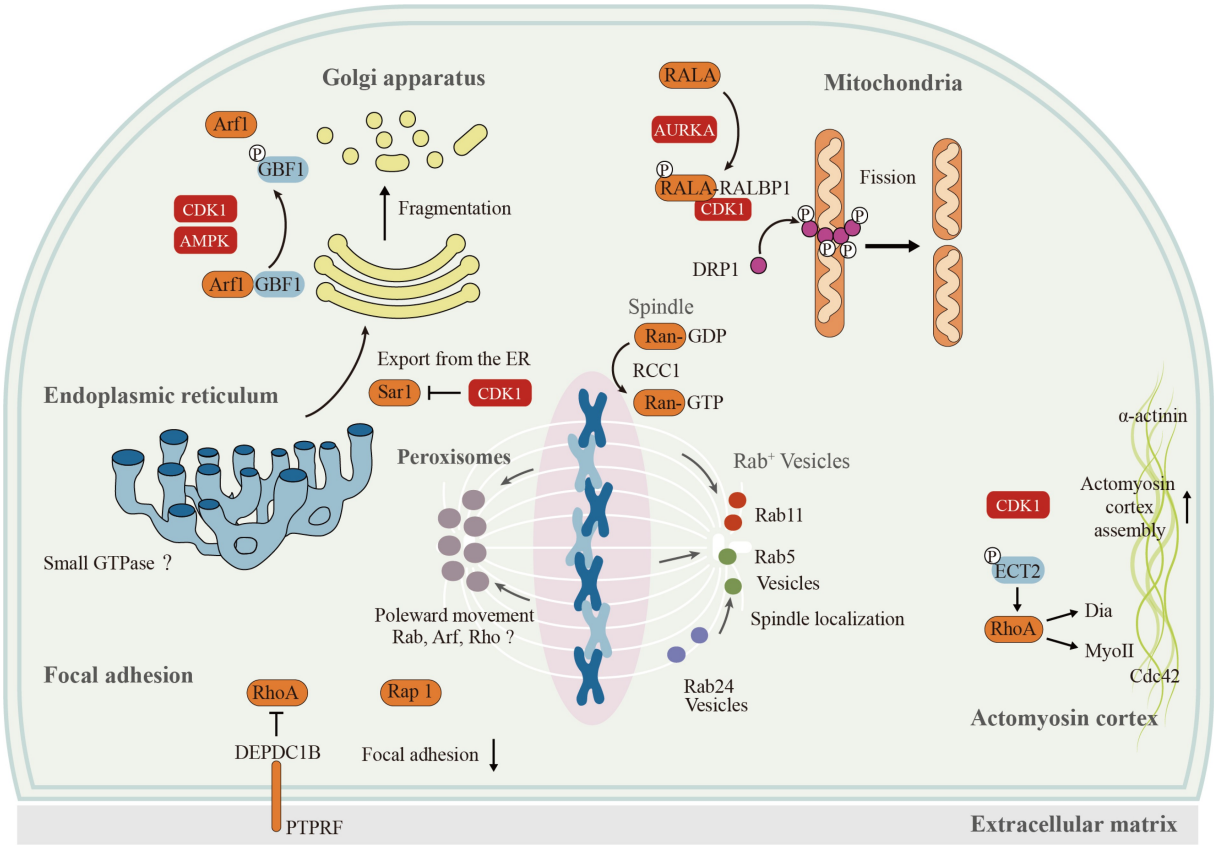

Fig. 2 Fine-tuning organelle dynamics by small GTPase during cell division. Golgi fragmentation: CDK1 mediates Sar1 inactivation during prophase and reduces membrane and protein export from the ER. Inactivation of Arf1 results in the release of COPI from Golgi and Golgi disperse. Certain Rabs, including Rab5, Rab11, and Rab24, bind and traffic mitotic proteins along microtubules for spindle formation. Mitochondrial fission: Mitotic kinase AURKA phosphorylates RalA and promotes DRP1-mediated mitochondria fission. Spindle formation: RanGTP formation around chromatin directs spindle assembly. Actomyosin cortex assembly: At mitotic entry, ECT2 released from nucleus activates RhoA. CDK1 and PLK1 phosphor activate ECT2 and increase its GEF function toward RhoA. Activated RhoA induces the retraction of the cell margin and generates nonbranched actin filaments through DIA and activates myosin via ROCK. Loss of FAs: FAs disassemble at late G2 through the inactivation of Rap1 and the local inhibition of RhoA signaling by DEPDC1B. Rab-positive vesicles: Rab-positive vesicles localize on the spindle and around centrosomes for spindle formation. Peroxisome: Peroxisomes cluster around spindle poles, and Rho GTPase Miro1 functions as an adaptor for microtubule-based peroxisome motility during interphase. However, whether small GTPases are required for peroxisome poleward gathering remain unknown. ER: At mitotic onset, ER "blends" with NE and Golgi. The mitotic inhibition of ER–MT linkers detaches ER from the cytoskeleton. How the ER dynamically coordinates with cell division is currently unclear. Abbreviations: FA, focal adhesions; ER, endoplasmic reticulum.

During interphase, the INM is widely tethered to chromatin and a meshwork of intermediate filaments [102,103]. CDK1-mediated phosphorylation drives NEBD via cytoskeletal contact disassociation and nuclear lamina dissolution [1,2,104–107]. Thus, NE is allowed to disengage from chromatin, and NE proteins redistribute into the mitotic ER. However, previous work suggested that ER membrane remodeling Rab5 is critical for NEBD [108]. Rab5 is a Rab subfamily small GTPase that functions in endocytosis and early endosome fusion [45,109,110]. In the *C. elegans* embryo model, the depletion of Rab5 reduces ER clusters and thickens tubules similar to the depletion of YOP-1/RET-1. The Rab5 depletion inhibits NE disassembly and generates total embryonic death. A previous study showed the conservative role of Rab5 in shaping ER in HeLa cells [108]. This study proposed a connection between ER and NEBD, and the peripheral ER structure is required to facilitate NE component diffusion into ER because the disruption of ER structure inhibits NEBD. This model on Rab5 leads to an interesting assumption that other small GTPases that regulate ER structure may also function in NEBD or NE reassembly. Another factor in NEBD is the mechanical force mediated by MTs and actin filaments that rupture membranes with lamina, thereby assisting NE disassembly [111–116]. This process also involves Ran activities in regulating MT dynamics during NEBD [114]. To comply with interphase functions, cells undergo another dramatic reorganization after division. One of the most significant changes during mitotic exit is the reformation of the NE [117]. First found in yeast, Ran has been identified as a key regulator in NE formation in several eukaryotes

[118–122]. At telophase, Ran in its GDP-bound conformation binds with chromatin surface to recruit RCC1, which subsequently activates Ran to a GTP-binding state. The spatial organization of RanGDP/RanGTP promotes the assembly of NPCs and vesicle fusion via interactions between RanGTP and importin-β to form NE with interphase structure and functions [123]. The COPII vesicular formation requires Sar1 and its effector Sec23/24 and Sec13/31 [124]. The effector Sec13 is also found in Nup84p complex in organizing nuclear pore complex formation [125]. A recent study in yeast found that Cdc42 regulates ESCRT disassembly and functions in NE sealing and ER fission after division [126].

Golgi apparatus

The Golgi apparatus is a central station for post-translational modifications and secretion. The quantitative proteomics analysis in rodent and human samples identified 348 Golgi and associated proteins, in which Rab and Arf with their associates make up 17% of total candidates [127]. Many other small GTPases from Ras and Rho subfamily show transient or permanent localization on the Golgi apparatus. Small GTPases are also actively involved in Golgi life cycles. In mammals, the Golgi apparatus is a continuous membranous system composed of stacks, and each stack has a *cis* entry face and a *trans* exit face connected by tubular bridges, i.e., the "Golgi ribbon" [128]. The behavior of the Golgi apparatus during cell cycle is recorded in mammalian cells. From the G1 phase to the S phase, the Golgi mass increases significantly. During cell division, the Golgi apparatus undergoes extensive fragmentation to assist its correct partitioning and inheritance. The mitotic phosphorylation of Golgi reassembly stacking proteins (GRASPs) by mitotic kinases at the C-terminal serine/proline-rich (SPR) inhibits their oligomerization and results in the separation of the Golgi cisternae [129]. After cell division, fragments undergo a reverse series of changes and rapidly re-establish the Golgi ribbon and polarization in the two daughter cells [130–132].

Golgi fragmentation and Golgi checkpoint

The Golgi apparatus fragmentation begins at the late G2/early prophase when the connected Golgi ribbon breaks into individual stacks. At metaphase, stacks further go through unstacking and vesiculation to form Golgi clusters [1,2]. During this process, a key step for Golgi sequential disassembly is the inactivation of small GTPases Arf1 and Sar1 that operate at the ER/Golgi interface (Fig. 2) [130]. Arf1 at the Golgi apparatus is inactivated by its GBF1, which is phosphor-inactivated by AMPK and CDK1 in mitosis [96,133]. The inactivation of Arf1 contributes to Golgi disassembly through the inhibition of Arf1 effector recruitment to membranes. COPI vesicles have been shown to participate in the retrieval of proteins from the Golgi back to the ER. The inactivation of Arf1 results in the release of COPI from Golgi and Golgi dispersion. The Arf1 effector Golgin160, the connector of Golgi membranes with dynein motors, is released from Golgi membranes as a direct consequence of Arf1 inactivation in mitosis, leading to loss of dynein from these membranes. This phenomenon correlates temporally with the Golgi apparatus becoming fragmented [134]. At ER exit sites, CDK1 mediates Sar1 inactivation during prophase and results in a reduction in membrane and protein export from the ER [135,136]. The active Sar1 GTP–GDP binding cycle recruits COPII coat proteins and other effectors, maintaining the ER export domain and supporting Golgi dynamic structuring. When expressing Sar1 T39N GDP-restricted mutant, ER export sites disappear, Golgi integral membrane proteins are trapped in the ER, and Golgi peripheral proteins are retargeted to the ER or cytoplasm, thus leading to the disappearance of Golgi or Golgi-like structure within cells [137–139].

Research on the mechanisms of Golgi fragmentation led to the striking discovery that the inhibition of the Golgi disassembly process induces a potent and persistent G2 block of cell cycle progression [130,140]. The blockage of Golgi fragmentation reduces AURKA activation and centrosome localization, which sequentially blocks G2/M master regulator CDK1–Cyclin B1. Therefore, the inheritance of the Golgi complex is actively participated in cell cycle and acts as an organelle-based cell cycle checkpoint, i.e., the Golgi checkpoint in monitoring proper organelle partition [141].

Reassembly of Golgi complex

In contrast to fragmentation, Golgi reformation occurs through the sequential reactivation of Sar1 and Arf1. The Sar1 reactivation re-establishes ER export domains first by recruiting Rab1, p115, SNAREs, and matrix proteins, which support its differentiation into ERGIC [142]. The activity of Arf1 and dozens of its effectors further differentiate newly formed membrane structure to morphologically and geographically specialized Golgi membranes distinct from ER [143]. The Golgi reconstruction after BFA treatment shows that the Rab GTPase-regulated targeting fusion pathways are required in Golgi recovery and *cis*-to-*trans* polarity [18]. The Rab-mediated Golgi polarization may also apply to Golgi reassembly in the cell cycle. In late mitosis, each daughter cell reassembles a pair of twin Golgi complexes at two distinct locations: a smaller cluster near the midbody and a bigger juxtanuclear compartment. Arf-associated GEF GBF1 phosphorylation and degradation allow a midbody-located cluster to migrate along the cell skeleton to the other twin, forming a single perinuclear Golgi ribbon. Expressing

nondegradable GBF1 or treating with GBF1 inhibitor BFA blocks cytokinesis and Golgi reformation [133,144].

Other Golgi-associated small GTPases have also been shown to have links to Golgi-based processes and mitotic progression. Rab6A′ regulates retrograde transport from late endosomes via the Golgi to the ER through its interaction with p150Glued and GAPCenA and participates in the transition from metaphase to anaphase during mitosis [145]. Together, these findings raise the possibility that the activities of these GTPases are relevant to the sophisticated process of mitotic Golgi dynamic regulation and constitute an organelle-based checkpoint participating mitotic entry, metaphase-to-anaphase transition, and cytokinesis.

Mitochondria

Mitochondria are considered semiautonomous organelles, and their growth and fission–fusion cycle can occur independently of the cell cycle [146]. However, recent studies proved that the mitochondria fission–fusion cycle and its distribution are coordinated with cell cycle (Fig. 2) [2,147]. Mitotic kinases CDK and AURKA regulate mitochondrial fission–fusion cycles by the phosphorylation of dynamin-related GTPase proteins (DRPs) [148,149]. AURKA induces the phosphorylation of RalA (a Ras subfamily member), promoting its effector RALBP1 to mitochondria during mitotic entry. RALBP1 then serves as a scaffold for CDK1-dependent activation of DRP1 [21]. Cells devoid of RalA show decreased cellular ATP levels and disrupted cytokinesis. Such an effect may be the consequence of impaired energy production as the fission blockage disrupts ATP production [150,151]. Recently, the last step of mitochondrial division has been shown to depend on the recruitment of the trans-Golgi network PI(4)P-containing vesicles at the ER–mitochondria contact site by Arf1 and its effector PI(4)KIIIb. The loss of Arf1 or PI(4)KIIIb prevents PI(4)P generation and leads to a hyperfused and branched mitochondrial network, which may be through disrupting the Arp2/3-dependent actin polymerization [152].

The fragmentation of the mitochondria helps stochastic mitochondrial inheritance. However, this phenomenon may not be the only factor because artificially disrupted cytoskeleton-mediated mitochondrial distribution leads to asymmetric cell division and mitotic defects [153,154]. The Arf1 and Rho subfamily small GTPase mitochondrial rho GTPase (Miro) oppositely regulates mitochondrial retrograde and anterograde movement [155]. During cytokinesis, mitochondria interact with growing MT tips and move toward the cleavage furrow. CENP-F (cytoskeletal-associated protein), which associates with MT-growing tips, is recruited to mitochondria by directly interacting with Miro1 and Miro2 via its C-terminal highly conserved domain [154]. Miro and CENP-F interaction peak at S/G2 and cytokinesis, remain low at mitosis. This phenomenon indicates a dynamic interaction and regulated process. The knockdown of Miro decreases the spreading of the mitochondrial network and shows cytokinesis-specific defects. In the opposite direction, active Arf1 and its GEF GBF1 physically interact with Miro and block Miro-dependent retrograde mitochondrial transportation [155]. The specific localization of the mitochondria is regulated to meet local energy demands [156]. Miro depletion induces mitochondria misallocation and cell division failure. These results suggest that the mitochondrial distribution coordinates with cell division. Altogether, small GTPases' function in the coordination of power supply, fission–fusion cycle control, and cytosolic distribution suggests a binary regulation connecting mitochondrial inheritance with the powering of cell chromosome partition. Cell cycle signals are predicted to implement on the Miro GTPase domain or CENP-F Miro-binding peptide, where serine and threonine residues are phosphorylated during the cell cycle [154,157–159]. GBF1 is inhibited through phosphorylation by AMPK, and the degradation of GBF1 is required for the inheritance of the Golgi apparatus and cytokinesis [133,144]. Thus, GBF1 may coordinate the Golgi apparatus and the mitochondrial network reorganization during cell division.

Midbody and membrane ingression

Midbody, a transient organelle, links two nascent daughter cells that form after furrow ingression during cytokinesis [160]. The cleavage furrow ingression compacts antiparallel midzone bundles into a 1–1.5 μm diameter structure, i.e., the midbody [161]. The midbody is rich in MT, MT-interacting proteins, and membrane-based proteins as its formation and final abscission require the cooperation of the cytoskeleton with the membrane system [162,163]. The spatial and temporal coordination of the Rho family GTPase with mitotic kinase and downstream effectors ensures accurate ingression, midbody position, and final abscission [42,164–167]. Recent studies highlighted the role of membrane and membrane trafficking during this process.

At the heart of cytokinesis in animal cells is the centralspindlin complex. The centralspindlin complex comprises two proteins: the kinesin-like protein Mitotic kinesin-like protein 1 and the Rho GTPase-activating protein (RhoGAP) CYK-4. Through its targeted localization to a narrow region of antiparallel MT overlap immediately following chromosome segregation, the centralspindlin initiates central spindle assembly. During cell division, the centralspindlin has several critical functions, including positioning the division plane, regulation of Rho family GTPases, and midbody assembly and abscission.

Position of ingression furrow

An ingression furrow is established immediately after chromosome segregation at the location where the chromosomes once localized during the metaphase to finalize cell division [79,160,168]. How cells precisely get the ingression furrow into position has drawn wide attention for decades as its functions in symmetric and asymmetric cell division and cell fate determination. The Rho small GTPase marks the narrow zone for ingression furrow as RhoA accumulates to the equatorial cortex ahead of furrow formation [169–171]. The activity of the equator cortex that recruits RhoA is strictly regulated by Rho GEFs (ECT2, GEF-H1, and Myo-GEF) and GAPs (MgcRacGAP, p190RhoGAP, and MP-GAP). ECT2 localizes to spindle midzone by interacting with the centralspindle complex, which depends on MgcRacGAP phosphorylation by mitotic kinase PLK1 [161]. Thus, Ect2 is stabilized in an active conformation to interact with RhoA. A detailed experiment in human cells shows that ECT2 membrane-binding is required and sufficient for cytokinesis [172].

Membrane ingression

Membrane ingression and invagination of the cell membrane are driven by a contractile ring composed of paralleled actin filaments and nonmuscle myosin II [173,174]. RhoA regulates the contractile ring in multiple aspects. RhoA stimulates actin polymerization and regulates myosin activity and other scaffold proteins. RhoA is a key regulator that controls actin polymerization by reliving formin autoinhibition [175,176] at the ingression position [169,171]. Formin proteins harbor two proline-rich forming homology domains, i.e., FH1 and FH2 [177], that control actin polymerization [177–180]. The mammalian formin mDia1 selectively binds with active RhoA and promotes actin polymerization [176] together with another actin cytoskeletal regulator profiling [180]. RhoA regulates myosin by activating Rho-kinase (ROCK) to phosphorylate the regulatory light chains of myosin-II. Three myosin-regulating kinases (and MLCK) are found to phosphorylate myosin at myosin regulatory light chain (MRLC) to activate myosin. ROCK and possibly Citron, but not MLKC, depend on RhoA to acquire the correct localization at the ingression site. The ROCK recruited by RhoA regulates myosin through phosphorylating MRLC at S19 [181]. MLC phosphorylation is regulated in part by myosin phosphatase (MYPT1), which can be phosphorylated at T853 by ROCK. ROCK-directed MYPT1 phosphorylation reduces phosphatase activity, thus maintaining myosin activity [182–184]. As for Citron kinase, which is believed to be activated by interacting with active RhoA and promoting the constriction of the actomyosin ring just like ROCK, it is later proven to be unnecessary for ingression but acts as an organizing center for the midbody [42,185,186]. Study on *Drosophila* and human cells show that Citron kinase is required for correct RhoA localization at cleavage, thus indicating its function as a regulator but not effector of RhoA. RhoA also regulates scaffold proteins anillin and septins in coordination with ingression besides actin and myosin II [42]. In contrast to RhoA, the other Rho subfamily member Rac1 acts as a negative regulator for contractile ring constriction [42]. Rac1 inactivation by MgcRacGAP abrogates MLCK inhibition by PAK1/2 and ARHGEF, thus sustaining myosin activity. Furthermore, the Rac1 inactivation prevents branched actin filament nucleation by inactivating the Arp2/3 complex, thus confining a narrow zone for proper actin–myosin function [187].

As mentioned before, cell surface area expansion during cytokinesis requires the transportation of membrane vesicles to be inserted at the cleavage site [188–190]. Likewise, the actomyosin ring function requires the timely delivery of regulatory proteins and remodeling factors required at different stages of this process. In *Drosophila* spermatocytes, Rab1 (*omt*) mutation disrupts cytokinesis. Rab1 organizes the Golgi-dependent secretion through the GOLPH3 complex and controls membrane trafficking to facilitate new membrane supplementation along the ingressing cleavage furrow [191]. Rab11 mutation, which disrupts the recycling endosome, also causes furrow ingression defects in a *Drosophila* model by regulating the rate of actin polymerization through the RhoGEF2–Rho1 (Rac1 in human) pathway [192]. Arf1 localizes to the Golgi apparatus and plays a central role in regulating the Golgi apparatus material flow. In the *Drosophila* model, an Asap–Arf1–Golgi pathway appears to fuel cleavage furrow ingression. Asap dominates Arf1 accumulation at Golgi for proper Golgi organization and the Golgi output further fueling ingression furrow [193]. The widespread participation of small GTPases around ingression sites together with their functions in membrane and cytoskeleton dynamics suggest that cytokinesis relies on membrane traffic to coordinate cytoskeletal elements and lipid-based membranes [194–197].

Abscission

The final step of cell division is the abscission that physically separates one linking protoplast into two independent daughter cells [78,162]. Abscission requires the disassembly of cortical actin in the intercellular bridge [198]. Similarly, this process is driven by RhoA inactivation, whereas Aurora B phosphorylates Rac GAP MgcRacGAP at S387 [199]. Several Rabs and Arfs are involved in this cell cycle step as vesicle trafficking dominates cytokinesis [200,201]. Rab11 and Rab35

endosomes ensure low F-actin levels required for scission at the abscission site [194]. Rab11 acts as an upstream regulator for RhoA inactivation in bridges. Rab11–FIP3 endosomes transport RhoA GAP p50RhoGAP to inhibit RhoA activities on actin polymerization. Rab11 or FIP3 depletion leads to F-actin accumulation at the bridge, delaying ESCRT-III filament assembly at the abscission site and abscission [198]. In addition, Rab35 endosome transports OCRL to reduce PtdIns(4,5)P2, which is required for F-actin polymerization [202]. In parallel to reducing polymerization, Rab35 also increases F-actin depolymerization via recruiting oxidoreductase MICAL1 at the intercellular bridge, which oxidizes methionine residues of F-actin and speeds up its disassembly [203]. Rab11 and Rab35 are well-established regulators in this process, and other small GTPases, such as Arf6, RalA/RalB, and several Rabs, are also present within midbody and bridges. Briefly, Arf6 forms a complex with the MKLP1 kinesin of the centralspindlin complex and concentrates at the midbody for bridge stability and abscission [65,204]. RalA and RalB control exocyst localization at the furrow and midbody, respectively, and their collaboration is required for abscission completion [205,206]. RNAi screening found that several Rab GTPases may play a modulatory role in abscission [207].

The cooperation between cell skeleton and vesicular traffic is a driving force behind cytokinesis. Plasma membrane lipids bring new perspectives into cytokinesis regulation. Lipid composition at furrow and bridge changes dramatically and is essential for ingression and abscission regions during cytokinesis [68,69,208]. PtdIns(4,5)P2 stabilize the bridge. Thus, for proper abscission, the PI5 phosphatase OCRL-mediated hydrolysis is required at the abscission site [209–211]. As previously mentioned, Rab35 endosomes drive OCRL's transportation and bridge localization [202].

Autophagosomes

Autophagosomes are double-membrane vesicles functioning in the lysosome-dependent degradation process. This process intersects with continuous and dynamic vesicle transportation, requiring small GTPases. For example, Rab and Arf GTPases regulate endocytic membrane trafficking pathways. Briefly, the Rab subfamily, Rab1, Rab5, Rab7, Rab9A, Rab11, Rab23, Rab32, Rab33B, and Sec4 function in autophagosome formation [212–215]. Rab7, Rab8B, and Rab24 regulate maturation [213,214,216–219]. The Arf family Arf1, Arf6, Arf8, and Sar1 determine its biogenesis and cellular localization [213,220]. In addition, other small GTPases outside Rab or Arf family, such as RalB, are involved. RalB regulates mammalian Atg1 ortholog (ULK1)-mediated formation of autophagosome [221], indicating that small GTPases are widely involved in autophagosome dynamic regulation. However, whether autophagy is active during division is still debated. A recent study proposed that nutrition status is uncoupled with autophagy because the interaction between lysosome resident Rag GTPase (a small group of Ras superfamily small GTPase [222,223] functioning in mTOR activation [224,225]) and RAPTOR is blocked by CDK1–Cyclin B-mediated phosphorylation [226]. This phenomenon may extend small GTPases from morphological regulation to biochemical processes. Current evidence also suggested that the phosphoregulation of small GTPase at mitosis entry relocates small GTPase and their cofactors, which may limit their autophagic membrane trafficking ability. The exquisite regulation of degradation may be required to avoid the unplanned degradation of exposed genetic content [2]. Further research on how these autophagosomes associated with small GTPases are functioning in mitosis and whether it is similar to that in interphase will provide knowledge regarding the mechanisms underlying autophagosome cell cycle regulation and help us understand the potential crosstalk between autophagosomes and cell division.

Lipid droplets

Lipid droplets are cytoplasmic lipid-rich storage organelles covered by a phospholipid monolayer [227–229]. Lipid droplets are important for membrane expansion and energy generation during cell division, thus its biogenesis and turnover may be carefully regulated along with the cell cycle [68,69,208,230]. In fission yeast, the number of lipid droplets increases during G2 phase and remains relatively constant after G2. In budding yeast, the collection of excess lipids into droplets is vital for successful cytokinesis [208]. A recent study observed the rapid dispersion of lipid droplets in mammalian cell lines during S phase [231]. However, no systematic analysis of lipid droplet distribution or functions during division is observed. Similar to autophagosomes, lipophagy and lipid droplet biogenesis together with its localization depend on Rabs and Arfs [232–234]. Thus, research on the mitotic regulation of lipid droplet-associated GTPases may give further insights into their binary coordination.

Peroxisomes

Peroxisomes are single MBOs involved in catabolism and reduction of reactive oxygen species [235]. Peroxisomes cluster around spindle poles and partition into daughter cells in a spindle pole-dependent manner in mammalian cells [236,237]. The symmetric distribution of peroxisomes coordinates with spindle orientation, and thus regulates cell growth/differentiation balance during epidermal development [238]. An important goal of future research is to identify the molecules that govern peroxisome

distribution in coordination with cell division. Small GTPases, like Rho, Rab, and Arf proteins, are the main regulators connecting membranes to cytoskeleton motors or adapters, potentiating their functions in this process [17,239]. In interphase, Rho GTPase Miro1 functions as an adaptor for MT-based peroxisome motility [240]. The binding of peroxisomes to MTs and actin is regulated by RhoA activities [241]. In addition to its distribution, peroxisome biogenesis, growth, and fission are tightly associated with small GTPases [242] (27 small GTPases identified in rat liver peroxisomes [243]). Further research is required to determine the role of small GTPases in regulating peroxisome dynamics in cell division.

Conclusions and perspectives

Small GTPases coordinate organelle reorganization with cell division

Unified regulation and cooperation between heterogeneous processes is the prerequisite and foundation of exquisite life activities. Small GTPases are identified as nodal points of cell signaling pathways. When we consider the processes of organelle dynamics in cell division, small GTPases also show extraordinary molecular features and functional properties to fit such sophisticated orchestration. First, small GTPase localization is highly compartmentalized [16,244–246]. Sufficient protein species enables various organelles or specific organelle domains to have a unique complement of small G proteins [6,247]. Second, small GTPases are liable to PTMs. Thus, they can receive cell cycle signals and transduce them to specific effectors, thus linking organelle dynamics to cell division [22,248]. Third, due to their tunable nature, small GTPases can shift between on and off states and translocate among locations to complex with diverse effectors that perform various functions, thus trimming organelles [9–11,248,249]. Additionally, highly related small GTPases can have subtle differences in their binding affinities for the same effector protein, thus helping us gain valuable insight into the fine-tuning of organelle structuring and membrane domain formation [250]. Several small GTPases are found as substrates of key mitotic kinases. In this vein, the pervasive crosstalk between mitosis-specific kinases and small GTPases is speculated. This regulation network, mitotic kinase–small GTPase, may constitute a regulation mechanism of organelle dynamics in coordination with genetic material partition during mitosis.

Small GTPase family expands along with the cell evolution

The origin of membrane organelles in eukaryotes is one of the research foci of evolutionary cell biology. Being the nodal component of the membrane system, the expansion of the small GTPase family with specified interacting proteins may be the prerequisite for the generation of increased organelle complexity and regulatory control in autogenously derived eukaryotic compartments. In bacteria and archaebacteria, which lack nucleus and MBO, few, if any, small GTPases are found. By contrast, small GTPases take around 0.6% of the whole genome of *Homo sapiens*. Significantly, the proportion peaks in unicellular organisms, which operate all life activities in a single cell and normally harbor a complicated and specialized cellular structure, e.g., 1.7% in *Naegleria gruberi* [251]. Naturally, specified organelles increase biological efficiency at the cost of regulation complexity especially during cell division. The analysis of small GTPase functions in organelle dynamics in cell growth and division may give directions toward organelle origination and mitosis evolution.

Acknowledgements

We would like to thank Mr. Christopher M. Lavender and Dr. Yuchen Zhang for critically reading our manuscript, and members of the Liu Q laboratory for scientific advice. Space constraints limited the number of citations. We apologize to those whose work we are unable to cite. This research work is supported by the National Key R&D Program of China (Nos. 2019YFA0110300 and 2017YFA0505600-04), the National Natural Science Foundation of China (Nos. 81820108024 and 81630005), the Innovative Research Team in University of Ministry of Education of China (No. IRT-17R15), and the Natural Science Foundation of Guangdong (Nos. 2016A030311038 and 2017A030313608).

Compliance with ethics guidelines

Zijian Zhang, Wei Zhang, and Quentin Liu declare no competing interest. This manuscript is a review article and does not involve a research protocol requiring approval by the relevant institutional review board or ethics committee.

References

1. Champion L, Linder MI, Kutay U. Cellular reorganization during mitotic entry. Trends Cell Biol 2017; 27(1): 26–41
2. Carlton JG, Jones H, Eggert US. Membrane and organelle dynamics during cell division. Nat Rev Mol Cell Biol 2020; 21(3): 151–166
3. Jongsma MLM, Berlin I, Neefjes J. On the move: organelle dynamics during mitosis. Trends Cell Biol 2015; 25(3): 112–124
4. Song S, Cong W, Zhou S, Shi Y, Dai W, Zhang H, Wang X, He B, Zhang Q. Small GTPases: structure, biological function and its interaction with nanoparticles. Asian J Pharm Sci 2019; 14(1): 30–39
5. Vetter IR. The structure of the G domain of the Ras superfamily.

In: Wittinghofer A. Ras Superfamily Small G Proteins: Biology and Mechanisms 1. Springer Vienna, 2014: 25-50
6. Wennerberg K, Rossman KL, Der CJ. The Ras superfamily at a glance. J Cell Sci 2005; 118(5): 843–846
7. Hodge RG, Schaefer A, Howard SV, Der CJ. RAS and RHO family GTPase mutations in cancer: twin sons of different mothers? Crit Rev Biochem Mol Biol 2020; 55(4): 386–407
8. Rojas AM, Fuentes G, Rausell A, Valencia A. The Ras protein superfamily: evolutionary tree and role of conserved amino acids. J Cell Biol. 2012; 196: 189–201
9. Cherfils J, Zeghouf M. Regulation of small GTPases by GEFs, GAPs, and GDIs. Physiol Rev 2013; 93(1): 269–309
10. Bos J, Rehmann H, Wittinghofer A. GEFs and GAPs: critical elements in the control of small G proteins. Cell 2007; 129(5): 865–877 Erratum in: Cell 2007; 130(2): 385
11. Cherfils J. GEFs and GAPs: mechanisms and structures. In: Wittinghofer A. Ras Superfamily Small G Proteins: Biology and Mechanisms 1. Springer Vienna; 2014: 51-63
12. Mishra AK, Lambright DG. Small GTPases and their GAPs. Biopolymers 2016; 105(8): 431–448
13. Clarke PR, Zhang C. Spatial and temporal coordination of mitosis by Ran GTPase. Nat Rev Mol Cell Biol 2008; 9(6): 464–477
14. Jackson CL, Bouvet S. Arfs at a glance. J Cell Sci 2014; 127(19): 4103–4109
15. Schwartz SL, Cao C, Pylypenko O, Rak A, Wandinger-Ness A. Rab GTPases at a glance. J Cell Sci 2007; 120(22): 3905–3910
16. D'Souza-Schorey C, Chavrier P. ARF proteins: roles in membrane traffic and beyond. Nat Rev Mol Cell Biol 2006; 7(5): 347–358
17. Kjos I, Vestre K, Guadagno NA, Borg Distefano M, Progida C. Rab and Arf proteins at the crossroad between membrane transport and cytoskeleton dynamics. Biochim Biophys Acta Mol Cell Res 2018; 1865(10): 1397–1409
18. Bannykh SI, Plutner H, Matteson J, Balch WE. The role of ARF1 and rab GTPases in polarization of the Golgi stack. Traffic 2005; 6(9): 803–819
19. Yahara N, Ueda T, Sato K, Nakano A. Multiple roles of Arf1 GTPase in the yeast exocytic and endocytic pathways. Mol Biol Cell 2001; 12(1): 221–238
20. Donaldson JG, Honda A, Weigert R. Multiple activities for Arf1 at the Golgi complex. Biochim Biophys Acta 2005; 1744(3): 364–373
21. Kashatus DF, Lim KH, Brady DC, Pershing NLKK, Cox AD, Counter CM. RALA and RALBP1 regulate mitochondrial fission at mitosis. Nat Cell Biol 2011; 13(9): 1108–1115
22. Shinde SR, Maddika S. Post translational modifications of Rab GTPases. Small GTPases 2018; 9(1-2): 49–56
23. Hodge RG, Ridley AJ. Regulating Rho GTPases and their regulators. Nat Rev Mol Cell Biol 2016; 17(8): 496–510
24. Nigg EA. Mitotic kinases as regulators of cell division and its checkpoints. Nat Rev Mol Cell Biol 2001; 2(1): 21–32
25. Dao VT, Dupuy AG, Gavet O, Caron E, de Gunzburg J. Dynamic changes in Rap1 activity are required for cell retraction and spreading during mitosis. J Cell Sci 2009; 122(16): 2996–3004
26. Glotzer M, Murray AW, Kirschner MW. Cyclin is degraded by the ubiquitin pathway. Nature 1991; 349(6305): 132–138
27. Lei Z, Wang J, Zhang L, Liu CH. Ubiquitination-dependent regulation of small GTPases in membrane trafficking: from cell biology to human diseases. Front Cell Dev Biol 2021; 9: 688352
28. de la Vega M, Burrows JF, Johnston JA. Ubiquitination: added complexity in Ras and Rho family GTPase function. Small GTPases 2011; 2(4): 192–201
29. Ding F, Yin Z, Wang HR. Ubiquitination in Rho signaling. Curr Top Med Chem 2011; 11(23): 2879–2887
30. Song P, Trajkovic K, Tsunemi T, Krainc D. Parkin modulates endosomal organization and function of the endo-lysosomal pathway. J Neurosci 2016; 36(8): 2425–2437
31. Wang H-R, Zhang Y, Ozdamar B, Ogunjimi AA, Alexandrova E, Thomsen GH, Wrana JL. Regulation of cell polarity and protrusion formation by targeting RhoA for degradation. Science 2003; 302(5651): 1775–1779
32. Seabra MC, Goldstein JL, Südhof TC, Brown MS. Rab geranylgeranyl transferase. A multisubunit enzyme that prenylates GTP-binding proteins terminating in Cys-X-Cys or Cys-Cys. J Biol Chem 1992; 267(20): 14497–14503
33. Leung KF, Baron R, Ali BR, Magee AI, Seabra MC. Rab GTPases containing a CAAX motif are processed post-geranylgeranylation by proteolysis and methylation. J Biol Chem 2007; 282(2): 1487–1497
34. Heald R, Khodjakov A. Thirty years of search and capture: the complex simplicity of mitotic spindle assembly. J Cell Biol 2015; 211(6): 1103–1111
35. O'Connell CB, Khodjakov AL. Cooperative mechanisms of mitotic spindle formation. J Cell Sci 2007; 120(10): 1717–1722
36. Lavia P. The GTPase RAN regulates multiple steps of the centrosome life cycle. Chromosome Res 2016; 24(1): 53–65
37. Feng Y, Yuan JH, Maloid SC, Fisher R, Copeland TD, Longo DL, Conrads TP, Veenstra TD, Ferris A, Hughes S, Dimitrov DS, Ferris DK. Polo-like kinase 1-mediated phosphorylation of the GTP-binding protein Ran is important for bipolar spindle formation. Biochem Biophys Res Commun 2006; 349(1): 144–152
38. Bompard G, Rabeharivelo G, Frank M, Cau J, Delsert C, Morin N. Subgroup II PAK-mediated phosphorylation regulates Ran activity during mitosis. J Cell Biol 2010; 190(5): 807–822
39. Tedeschi A, Ciciarello M, Mangiacasale R, Roscioli E, Rensen WM, Lavia P. RANBP1 localizes a subset of mitotic regulatory factors on spindle microtubules and regulates chromosome segregation in human cells. J Cell Sci 2007; 120(21): 3748–3761
40. Sit ST, Manser E. Rho GTPases and their role in organizing the actin cytoskeleton. J Cell Sci 2011; 124(5): 679–683
41. Müller PM, Rademacher J, Bagshaw RD, Wortmann C, Barth C, van Unen J, Alp KM, Giudice G, Eccles RL, Heinrich LE, Pascual-Vargas P, Sanchez-Castro M, Brandenburg L, Mbamalu G, Tucholska M, Spatt L, Czajkowski MT, Welke RW, Zhang S, Nguyen V, Rrustemi T, Trnka P, Freitag K, Larsen B, Popp O, Mertins P, Gingras AC, Roth FP, Colwill K, Bakal C, Pertz O, Pawson T, Petsalaki E, Rocks O. Systems analysis of RhoGEF and RhoGAP regulatory proteins reveals spatially organized RAC1 signalling from integrin adhesions. Nat Cell Biol 2020; 22(4): 498–511
42. Chircop M. Rho GTPases as regulators of mitosis and cytokinesis in mammalian cells. Small GTPases 2014; 5(2): e29770
43. Yasuda S, Taniguchi H, Oceguera-Yanez F, Ando Y, Watanabe S, Monypenny J, Narumiya S. An essential role of Cdc42-like GTPases in mitosis of HeLa cells. FEBS Lett 2006; 580(14):

3375–3380
44. Miserey-Lenkei S, Colombo MI. Small RAB GTPases regulate multiple steps of mitosis. Front Cell Dev Biol 2016; 4: 2
45. Lanzetti L. A novel function of Rab5 in mitosis. Small GTPases 2012; 3(3): 168–172
46. Hehnly H, Doxsey S. Rab11 endosomes contribute to mitotic spindle organization and orientation. Dev Cell 2014; 28(5): 497–507
47. Hobdy-Henderson KC, Hales CM, Lapierre LA, Cheney RE, Goldenring JR. Dynamics of the apical plasma membrane recycling system during cell division. Traffic 2003; 4(10): 681–693
48. Zhou C, Cunningham L, Marcus AI, Li Y, Kahn RA. Arl2 and Arl3 regulate different microtubule-dependent processes. Mol Biol Cell 2006; 17(5): 2476–2487
49. Okai T, Araki Y, Tada M, Tateno T, Kontani K, Katada T. Novel small GTPase subfamily capable of associating with tubulin is required for chromosome segregation. J Cell Sci 2004; 117(20): 4705–4715
50. Papini D, Langemeyer L, Abad MA, Kerr A, Samejima I, Eyers PA, Jeyaprakash AA, Higgins JMG, Barr FA, Earnshaw WC. TD-60 links RalA GTPase function to the CPC in mitosis. Nat Commun 2015; 6(1): 7678
51. Boeynaems S, Alberti S, Fawzi NL, Mittag T, Polymenidou M, Rousseau F, Schymkowitz J, Shorter J, Wolozin B, Van Den Bosch L, Tompa P, Fuxreiter M. Protein phase separation: a new phase in cell biology. Trends Cell Biol 2018; 28(6): 420–435
52. Zhang C, Rabouille C. Membrane-bound meet membraneless in health and disease. Cells 2019; 8(9): 1000
53. Nott TJ, Petsalaki E, Farber P, Jervis D, Fussner E, Plochowietz A, Craggs TD, Bazett-Jones DP, Pawson T, Forman-Kay JD, Baldwin AJ. Phase transition of a disordered nuage protein generates environmentally responsive membraneless organelles. Mol Cell 2015; 57(5): 936–947
54. Gomes E, Shorter J. The molecular language of membraneless organelles. J Biol Chem 2019; 294(18): 7115–7127
55. Rai AK, Chen JXX, Selbach M, Pelkmans L. Kinase-controlled phase transition of membraneless organelles in mitosis. Nature 2018; 559(7713): 211–216
56. Jiang H, Wang S, Huang Y, He X, Cui H, Zhu X, Zheng Y. Phase transition of spindle-associated protein regulate spindle apparatus assembly. Cell 2015; 163(1): 108–122
57. Woodruff JB, Ferreira Gomes B, Widlund PO, Mahamid J, Honigmann A, Hyman AA. The centrosome is a selective condensate that nucleates microtubules by concentrating tubulin. Cell 2017; 169(6): 1066–1077.e10
58. Keryer G, Witczak O, Delouvée A, Kemmner WA, Rouillard D, Taskén K, Bornens M. Dissociating the centrosomal matrix protein AKAP450 from centrioles impairs centriole duplication and cell cycle progression. Mol Biol Cell 2003; 14(6): 2436–2446
59. Keryer G, Di Fiore B, Celati C, Lechtreck KF, Mogensen M, Delouvée A, Lavia P, Bornens M, Tassin AM. Part of Ran is associated with AKAP450 at the centrosome: involvement in microtubule-organizing activity. Mol Biol Cell 2003; 14(10): 4260–4271
60. Bompard G, Rabeharivelo G, Cau J, Abrieu A, Delsert C, Morin N. P21-activated kinase 4 (PAK4) is required for metaphase spindle positioning and anchoring. Oncogene 2013; 32(7): 910–919
61. Kilchert C, Weidner J, Prescianotto-Baschong C, Spang A. Defects in the secretory pathway and high Ca^{2+} induce multiple P-bodies. Mol Biol Cell 2010; 21(15): 2624–2638
62. Serio G, Margaria V, Jensen S, Oldani A, Bartek J, Bussolino F, Lanzetti L. Small GTPase Rab5 participates in chromosome congression and regulates localization of the centromere-associated protein CENP-F to kinetochores. Proc Natl Acad Sci USA 2011; 108(42): 17337–17342
63. Zhang X, Hagen J, Muniz VP, Smith T, Coombs GS, Eischen CM, Mackie DI, Roman DL, Van Rheeden R, Darbro B, Tompkins VS, Quelle DE. RABL6A, a novel RAB-like protein, controls centrosome amplification and chromosome instability in primary fibroblasts. PLoS One 2013; 8(11): e80228
64. Hehnly H, Chen CTT, Powers CM, Liu HLL, Doxsey S. The centrosome regulates the Rab11-dependent recycling endosome pathway at appendages of the mother centriole. Curr Biol 2012; 22(20): 1944–1950
65. Takahashi S, Takei T, Koga H, Takatsu H, Shin HW, Nakayama K. Distinct roles of Rab11 and Arf6 in the regulation of Rab11-FIP3/arfophilin-1 localization in mitotic cells. Genes Cells 2011; 16(9): 938–950
66. Champion L, Linder MI, Kutay U. Cellular reorganization during mitotic entry. Trends Cell Biol 2017; 27(1): 26–41
67. Ramkumar N, Baum B. Coupling changes in cell shape to chromosome segregation. Nat Rev Mol Cell Biol 2016; 17(8): 511–521
68. Atilla-Gokcumen GE, Muro E, Relat-Goberna J, Sasse S, Bedigian A, Coughlin ML, Garcia-Manyes S, Eggert US. Dividing cells regulate their lipid composition and localization. Cell 2014; 156(3): 428–439
69. Storck EM, Özbalci C, Eggert US. Lipid cell biology: a focus on lipids in cell division. Annu Rev Biochem 2018; 87(1): 839–869
70. Théry M, Bornens M. Get round and stiff for mitosis. HFSP J 2008; 2(2): 65–71
71. Lee HS, Lim CJ, Puzon-McLaughlin W, Shattil SJ, Ginsberg MH. RIAM activates integrins by linking talin to ras GTPase membrane-targeting sequences. J Biol Chem 2009; 284(8): 5119–5127
72. Lafuente EM, van Puijenbroek AAFL, Krause M, Carman CV, Freeman GJ, Berezovskaya A, Constantine E, Springer TA, Gertler FB, Boussiotis VA. RIAM, an Ena/VASP and Profilin ligand, interacts with Rap1-GTP and mediates Rap1-induced adhesion. Dev Cell 2004; 7(4): 585–595
73. Marchesi S, Montani F, Deflorian G, D'Antuono R, Cuomo A, Bologna S, Mazzoccoli C, Bonaldi T, Di Fiore PP, Nicassio F. DEPDC1B coordinates de-adhesion events and cell-cycle progression at mitosis. Dev Cell 2014; 31(4): 420–433
74. Lancaster OM, Le Berre M, Dimitracopoulos A, Bonazzi D, Zlotek-Zlotkiewicz E, Picone R, Duke T, Piel M, Baum B. Mitotic rounding alters cell geometry to ensure efficient bipolar spindle formation. Dev Cell 2013; 25(3): 270–283
75. Chugh P, Paluch EK. The actin cortex at a glance. J Cell Sci 2018; 131(14): jcs186254
76. Arnold TR, Stephenson RE, Miller AL. Rho GTPases and actomyosin: partners in regulating epithelial cell-cell junction structure and function. Exp Cell Res 2017; 358(1): 20–30
77. Rosa A, Vlassaks E, Pichaud F, Baum B. Ect2/Pbl acts via Rho

and polarity proteins to direct the assembly of an isotropic actomyosin cortex upon mitotic entry. Dev Cell 2015; 32(5): 604–616
78. Mierzwa B, Gerlich DW. Cytokinetic abscission: molecular mechanisms and temporal control. Dev Cell 2014; 31(5): 525–538
79. Pollard TD, O'Shaughnessy B. Molecular mechanism of cytokinesis. Annu Rev Biochem 2019; 88(1): 661–689
80. Neto H, Collins LL, Gould GW. Vesicle trafficking and membrane remodelling in cytokinesis. Biochem J 2011; 437(1): 13–24
81. Kiyomitsu T, Cheeseman IM. Cortical dynein and asymmetric membrane elongation coordinately position the spindle in anaphase. Cell 2013; 154(2): 391–402
82. Kiyomitsu T, Cheeseman IM. Chromosome- and spindle-pole-derived signals generate an intrinsic code for spindle position and orientation. Nat Cell Biol 2012; 14(3): 311–317
83. Bird SL, Heald R, Weis K. RanGTP and CLASP1 cooperate to position the mitotic spindle. Mol Biol Cell 2013; 24(16): 2506–2514
84. Queralt E, Uhlmann F. Cdk-counteracting phosphatases unlock mitotic exit. Curr Opin Cell Biol 2008; 20(6): 661–668
85. Baumann O, Walz B. Endoplasmic reticulum of animal cells and its organization into structural and functional domains. Int Rev Cytol 2001; 205: 149–214
86. Friedman JR, Voeltz GK. The ER in 3D: a multifunctional dynamic membrane network. Trends Cell Biol 2011; 21(12): 709–717
87. Westrate LM, Lee JE, Prinz WA, Voeltz GK. Form follows function: the importance of endoplasmic reticulum shape. Annu Rev Biochem 2015; 84(1): 791–811
88. Schwarz DS, Blower MD. The endoplasmic reticulum: structure, function and response to cellular signaling. Cell Mol Life Sci 2016; 73(1): 79–94
89. English AR, Voeltz GK. Endoplasmic reticulum structure and interconnections with other organelles. Cold Spring Harb Perspect Biol 2013; 5(4): a013227
90. Merta H, Carrasquillo Rodríguez JW, Anjur-Dietrich MI, Vitale T, Granade ME, Harris TE, Needleman DJ, Bahmanyar S. Cell cycle regulation of ER membrane biogenesis protects against chromosome missegregation. Dev Cell 2021; 56(24): 3364–3379.e10
91. Oertle T, Klinger M, Stuermer CAO, Schwab ME. A reticular rhapsody: phylogenic evolution and nomenclature of the RTN/Nogo gene family. FASEB J 2003; 17(10): 1238–1247
92. Di Sano F, Bernardoni P, Piacentini M. The reticulons: guardians of the structure and function of the endoplasmic reticulum. Exp Cell Res 2012; 318(11): 1201–1207
93. Voeltz GK, Prinz WA, Shibata Y, Rist JM, Rapoport TA. A class of membrane proteins shaping the tubular endoplasmic reticulum. Cell 2006; 124(3): 573–586
94. Gerondopoulos A, Bastos RN, Yoshimura S, Anderson R, Carpanini S, Aligianis I, Handley MT, Barr FA. Rab18 and a Rab18 GEF complex are required for normal ER structure. J Cell Biol 2014; 205(5): 707–720
95. English AR, Voeltz GK. Rab10 GTPase regulates ER dynamics and morphology. Nat Cell Biol 2013; 15(2): 169–178
96. Morohashi Y, Balklava Z, Ball M, Hughes H, Lowe M. Phosphorylation and membrane dissociation of the ARF exchange factor GBF1 in mitosis. Biochem J 2010; 427(3): 401–412
97. Kumar D, Golchoubian B, Belevich I, Jokitalo E, Schlaitz ALL. REEP3 and REEP4 determine the tubular morphology of the endoplasmic reticulum during mitosis. Mol Biol Cell 2019; 30(12): 1377–1389
98. Schlaitz AL, Thompson J, Wong CCLL, Yates JR 3rd, Heald R. REEP3/4 ensure endoplasmic reticulum clearance from metaphase chromatin and proper nuclear envelope architecture. Dev Cell 2013; 26(3): 315–323
99. Arnone JT, Walters AD, Cohen-Fix O. The dynamic nature of the nuclear envelope: lessons from closed mitosis. Nucleus 2013; 4(4): 261–266
100. LaJoie D, Ullman KS. Coordinated events of nuclear assembly. Curr Opin Cell Biol 2017; 46: 39–45
101. Vietri M, Stenmark H, Campsteijn C. Closing a gap in the nuclear envelope. Curr Opin Cell Biol 2016; 40: 90–97
102. Hetzer MW. The nuclear envelope. Cold Spring Harb Perspect Biol 2010; 2(3): a000539
103. Prunuske AJ, Ullman KS. The nuclear envelope: form and reformation. Curr Opin Cell Biol 2006; 18(1): 108–116
104. Peter M, Nakagawa J, Dorée M, Labbé JC, Nigg EA. Identification of major nucleolar proteins as candidate mitotic substrates of cdc2 kinase. Cell 1990; 60(5): 791–801
105. Heald R, McKeon F. Mutations of phosphorylation sites in lamin A that prevent nuclear lamina disassembly in mitosis. Cell 1990; 61(4): 579–589
106. Torvaldson E, Kochin V, Eriksson JE. Phosphorylation of lamins determine their structural properties and signaling functions. Nucleus 2015; 6(3): 166–171
107. Martinez de Ilarduya O, Vicente-Carbajosa J, Sanchez de la Hoz P, Carbonero P. Sucrose synthase genes in barley. cDNA cloning of the Ss2 type and tissue-specific expression of Ss1 and Ss2. FEBS Lett 1993; 320(2): 177–181
108. Audhya A, Desai A, Oegema K. A role for Rab5 in structuring the endoplasmic reticulum. J Cell Biol 2007; 178(1): 43–56
109. Nielsen E, Severin F, Backer JM, Hyman AA, Zerial M. Rab5 regulates motility of early endosomes on microtubules. Nat Cell Biol 1999; 1(6): 376–382
110. Bucci C, Parton RG, Mather IH, Stunnenberg H, Simons K, Hoflack B, Zerial M. The small GTPase rab5 functions as a regulatory factor in the early endocytic pathway. Cell 1992; 70(5): 715–728
111. Cavazza T, Vernos I. The RanGTP pathway: from nucleo-cytoplasmic transport to spindle assembly and beyond. Front Cell Dev Biol 2016; 3: 82
112. Wesolowska N, Avilov I, Machado P, Geiss C, Kondo H, Mori M, Lénárt P. Actin assembly ruptures the nuclear envelope by prying the lamina away from nuclear pores and nuclear membranes in starfish oocytes. eLife 2020; 9: e49774
113. Penfield L, Wysolmerski B, Mauro M, Farhadifar R, Martinez MA, Biggs R, Wu HY, Broberg C, Needleman D, Bahmanyar S. Dynein pulling forces counteract lamin-mediated nuclear stability during nuclear envelope repair. Mol Biol Cell 2018; 29(7): 852–868
114. Mühlhäusser P, Kutay U. An *in vitro* nuclear disassembly system reveals a role for the RanGTPase system and microtubule-dependent steps in nuclear envelope breakdown. J Cell Biol 2007;

178(4): 595–610
115. Beaudouin J, Gerlich D, Daigle N, Eils R, Ellenberg J. Nuclear envelope breakdown proceeds by microtubule-induced tearing of the lamina. Cell 2002; 108(1): 83–96
116. Salina D, Bodoor K, Eckley DMM, Schroer TA, Rattner JBB, Burke B. Cytoplasmic dynein as a facilitator of nuclear envelope breakdown. Cell 2002; 108(1): 97–107
117. Sullivan M, Morgan DO. Finishing mitosis, one step at a time. Nat Rev Mol Cell Biol 2007; 8(11): 894–903
118. Zhang C, Clarke PR. Chromatin-independent nuclear envelope assembly induced by Ran GTPase in *Xenopus* egg extracts. Science 2000; 288(5470): 1429–1432
119. Hetzer M, Gruss OJ, Mattaj IW. The Ran GTPase as a marker of chromosome position in spindle formation and nuclear envelope assembly. Nat Cell Biol 2002; 4(7): E177–E184
120. Bamba C, Bobinnec Y, Fukuda M, Nishida E. The GTPase Ran regulates chromosome positioning and nuclear envelope assembly *in vivo*. Curr Biol 2002; 12(6): 503–507
121. Hetzer M, Bilbao-Cortés D, Walther TC, Gruss OJ, Mattaj IW. GTP hydrolysis by Ran is required for nuclear envelope assembly. Mol Cell 2000; 5(6): 1013–1024
122. Schellhaus AK, De Magistris P, Antonin W. Nuclear reformation at the end of mitosis. J Mol Biol 2016; 428(10Pt A): 1962–1985
123. Matchett KB, McFarlane S, Hamilton SE, Eltuhamy YSA, Davidson MA, Murray JT, Faheem AM, El-Tanani M. Ran GTPase in Nuclear Envelope Formation and Cancer Metastasis. Adv Exp Med Biol 2014; 773: 323–351
124. Townley AK, Feng Y, Schmidt K, Carter DA, Porter R, Verkade P, Stephens DJ. Efficient coupling of Sec23-Sec24 to Sec13-Sec31 drives COPII-dependent collagen secretion and is essential for normal craniofacial development. J Cell Sci 2008; 121(18): 3025–3034
125. Siniossoglou S, Lutzmann M, Santos-Rosa H, Leonard K, Mueller S, Aebi U, Hurt E. Structure and assembly of the Nup84p complex. J Cell Biol 2000; 149(1): 41–54
126. Lu MS, Drubin DG. Cdc42 GTPase regulates ESCRTs in nuclear envelope sealing and ER remodeling. J Cell Biol 2020; 219(8): e201910119
127. Chen X, Simon ES, Xiang Y, Kachman M, Andrews PC, Wang Y. Quantitative proteomics analysis of cell cycle-regulated Golgi disassembly and reassembly. J Biol Chem 2010; 285(10): 7197–7207
128. Klumperman J. Architecture of the mammalian Golgi. Cold Spring Harb Perspect Biol 2011; 3(7): a005181
129. Xiang Y, Wang Y. GRASP55 and GRASP65 play complementary and essential roles in Golgi cisternal stacking. J Cell Biol 2010; 188(2): 237–251
130. Colanzi A, Corda D. Mitosis controls the Golgi and the Golgi controls mitosis. Curr Opin Cell Biol 2007; 19(4): 386–393
131. Tang D, Wang Y. Cell cycle regulation of Golgi membrane dynamics. Trends Cell Biol 2013; 23(6): 296–304
132. Valente C, Colanzi A. Mechanisms and regulation of the mitotic inheritance of the Golgi complex. Front Cell Dev Biol 2015; 3: 79
133. Mao L, Li N, Guo Y, Xu X, Gao L, Xu Y, Zhou L, Liu W. AMPK phosphorylates GBF1 for mitotic Golgi disassembly. J Cell Sci 2013; 126(Pt 6): 1498–1505
134. Yadav S, Puthenveedu MA, Linstedt AD. Golgin160 recruits the dynein motor to position the Golgi apparatus. Dev Cell 2012; 23(1): 153–165
135. Kano F, Tanaka AR, Yamauchi S, Kondo H, Murata M. Cdc2 kinase-dependent disassembly of endoplasmic reticulum (ER) exit sites inhibits ER-to-Golgi vesicular transport during mitosis. Mol Biol Cell 2004; 15(9): 4289–4298
136. Prescott AR, Farmaki T, Thomson C, James J, Paccaud JP, Tang BL, Hong W, Quinn M, Ponnambalam S, Lucocq J. Evidence for prebudding arrest of ER export in animal cell mitosis and its role in generating Golgi partitioning intermediates. Traffic 2001; 2(5): 321–335
137. Stroud WJ, Jiang S, Jack G, Storrie B. Persistence of Golgi matrix distribution exhibits the same dependence on Sar1p activity as a Golgi glycosyltransferase. Traffic 2003; 4(9): 631–641
138. Ward TH, Polishchuk RS, Caplan S, Hirschberg K, Lippincott-Schwartz J. Maintenance of Golgi structure and function depends on the integrity of ER export. J Cell Biol 2001; 155(4): 557–570
139. Miles S, McManus H, Forsten KE, Storrie B. Evidence that the entire Golgi apparatus cycles in interphase HeLa cells: sensitivity of Golgi matrix proteins to an ER exit block. J Cell Biol 2001; 155(4): 543–556
140. Corda D, Barretta ML, Cervigni RI, Colanzi A. Golgi complex fragmentation in G2/M transition: an organelle-based cell-cycle checkpoint. IUBMB Life 2012; 64(8): 661–670
141. Persico A, Cervigni RI, Barretta ML, Corda D, Colanzi A. Golgi partitioning controls mitotic entry through Aurora-A kinase. Mol Biol Cell 2010; 21(21): 3708–3721
142. Altan-Bonnet N, Sougrat R, Lippincott-Schwartz J. Molecular basis for Golgi maintenance and biogenesis. Curr Opin Cell Biol 2004; 16(4): 364–372
143. Altan-Bonnet N, Sougrat R, Liu W, Snapp EL, Ward T, Lippincott-Schwartz J. Golgi inheritance in mammalian cells is mediated through endoplasmic reticulum export activities. Mol Biol Cell 2006; 17(2): 990–1005
144. Magliozzi R, Carrero ZI, Low TY, Yuniati L, Valdes-Quezada C, Kruiswijk F, van Wijk K, Heck AJR, Jackson CL, Guardavaccaro D. Inheritance of the Golgi apparatus and cytokinesis are controlled by degradation of GBF1. Cell Rep 2018; 23(11): 3381–3391.e4
145. Miserey-Lenkei S, Couëdel-Courteille A, Del Nery E, Bardin S, Piel M, Racine V, Sibarita JB, Perez F, Bornens M, Goud B. A role for the Rab6A′ GTPase in the inactivation of the Mad2-spindle checkpoint. EMBO J 2006; 25(2): 278–289
146. Mishra P, Chan DC. Mitochondrial dynamics and inheritance during cell division, development and disease. Nat Rev Mol Cell Biol 2014; 15(10): 634–646
147. Giacomello M, Pyakurel A, Glytsou C, Scorrano L. The cell biology of mitochondrial membrane dynamics. Nat Rev Mol Cell Biol 2020; 21(4): 204–224
148. Kashatus DF, Lim KH, Brady DC, Pershing NLK, Cox AD, Counter CM. RALA and RALBP1 regulate mitochondrial fission at mitosis. Nat Cell Biol 2011; 13(9): 1108–1115
149. Kanfer G, Kornmann B. Dynamics of the mitochondrial network during mitosis. Biochem Soc Trans 2016; 44(2): 510–516
150. Benard G, Bellance N, James D, Parrone P, Fernandez H, Letellier T, Rossignol R. Mitochondrial bioenergetics and structural network organization. J Cell Sci 2007; 120(5): 838–848
151. Parone PA, Da Cruz S, Tondera D, Mattenberger Y, James DI, Maechler P, Barja F, Martinou JC. Preventing mitochondrial

fission impairs mitochondrial function and leads to loss of mitochondrial DNA. PLoS One 2008; 3(9): e3257
152. Nagashima S, Tábara LC, Tilokani L, Paupe V, Anand H, Pogson JH, Zunino R, McBride HM, Prudent J. Golgi-derived PI(4)P-containing vesicles drive late steps of mitochondrial division. Science 2020; 367(6484): 1366–1371
153. Horbay R, Bilyy R. Mitochondrial dynamics during cell cycling. Apoptosis 2016; 21(12): 1327–1335
154. Kanfer G, Courthéoux T, Peterka M, Meier S, Soste M, Melnik A, Reis K, Aspenström P, Peter M, Picotti P, Kornmann B. Mitotic redistribution of the mitochondrial network by Miro and Cenp-F. Nat Commun 2015; 6(1): 8015
155. Walch L, Pellier E, Leng W, Lakisic G, Gautreau A, Contremoulins V, Verbavatz JM, Jackson CL. GBF1 and Arf1 interact with Miro and regulate mitochondrial positioning within cells. Sci Rep 2018; 8(1): 17121
156. Frederick RL, Shaw JM. Moving mitochondria: establishing distribution of an essential organelle. Traffic 2007; 8(12): 1668–1675
157. Kettenbach AN, Schweppe DK, Faherty BK, Pechenick D, Pletnev AA, Gerber SA. Quantitative phosphoproteomics identifies substrates and functional modules of Aurora and Polo-like kinase activities in mitotic cells. Sci Signal 2011; 4(179): rs5
158. Dephoure N, Zhou C, Villén J, Beausoleil SA, Bakalarski CE, Elledge SJ, Gygi SP. A quantitative atlas of mitotic phosphorylation. Proc Natl Acad Sci USA 2008; 105(31): 10762–10767
159. Malik R, Lenobel R, Santamaria A, Ries A, Nigg EA, Körner R. Quantitative analysis of the human spindle phosphoproteome at distinct mitotic stages. J Proteome Res 2009; 8(10): 4553–4563
160. D'Avino PP, Giansanti MG, Petronczki M. Cytokinesis in animal cells. Cold Spring Harb Perspect Biol 2015; 7(4): a015834
161. Kechad A, Jananji S, Ruella Y, Hickson GRX. Anillin acts as a bifunctional linker coordinating midbody ring biogenesis during cytokinesis. Curr Biol 2012; 22(3): 197–203
162. Steigemann P, Gerlich DW. Cytokinetic abscission: cellular dynamics at the midbody. Trends Cell Biol 2009; 19(11): 606–616
163. Hu CK, Coughlin M, Mitchison TJ. Midbody assembly and its regulation during cytokinesis. Mol Biol Cell 2012; 23(6): 1024–1034
164. Wadsworth P. Cytokinesis: Rho marks the spot. Curr Biol 2005; 15: R871–R874
165. Piekny A, Werner M, Glotzer M. Cytokinesis: welcome to the Rho zone. Trends Cell Biol 2005; 15(12): 651–658
166. Jordan SN, Canman JC. Rho GTPases in animal cell cytokinesis: an occupation by the one percent. Cytoskeleton (Hoboken) 2012; 69(11): 919–930
167. Narumiya S, Yasuda S. Rho GTPases in animal cell mitosis. Curr Opin Cell Biol 2006; 18(2): 199–205
168. Fraschini R. Cytokinesis in eukaryotic cells: the furrow complexity at a glance. Cells 2020; 9(2): 271
169. Bement WM, Benink HAHA, von Dassow G. A microtubule-dependent zone of active RhoA during cleavage plane specification. J Cell Biol 2005; 170(1): 91–101
170. Yüce O, Piekny A, Glotzer M. An ECT2-centralspindlin complex regulates the localization and function of RhoA. J Cell Biol 2005; 170(4): 571–582
171. Yoshizaki H, Ohba Y, Kurokawa K, Itoh RE, Nakamura T, Mochizuki N, Nagashima K, Matsuda M. Activity of Rho-family GTPases during cell division as visualized with FRET-based probes. J Cell Biol 2003; 162(2): 223–232
172. Kotýnková K, Su KC, West SC, Petronczki M. Plasma membrane association but not midzone recruitment of RhoGEF ECT2 is essential for cytokinesis. Cell Rep 2016; 17(10): 2672–2686
173. Schroeder TE. The contractile ring. I. Fine structure of dividing mammalian (HeLa) cells and the effects of cytochalasin B. Z Zellforsch Mikrosk Anat 1970; 109(4): 431–449
174. Schroeder TE. Actin in dividing cells: contractile ring filaments bind heavy meromyosin. Proc Natl Acad Sci USA 1973; 70(6): 1688–1692
175. Otomo T, Otomo C, Tomchick DR, Machius M, Rosen MK. Structural basis of Rho GTPase-mediated activation of the formin mDia1. Mol Cell 2005; 18(3): 273–281
176. Rose R, Weyand M, Lammers M, Ishizaki T, Ahmadian MR, Wittinghofer A. Structural and mechanistic insights into the interaction between Rho and mammalian Dia. Nature 2005; 435(7041): 513–518
177. Castrillon DH, Wasserman SA. Diaphanous is required for cytokinesis in *Drosophila* and shares domains of similarity with the products of the limb deformity gene. Development 1994; 120(12): 3367–3377
178. Evangelista M, Pruyne D, Amberg DC, Boone C, Bretscher A. Formins direct Arp2/3-independent actin filament assembly to polarize cell growth in yeast. Nat Cell Biol 2002; 4(3): 260–269
179. Sagot I, Rodal AA, Moseley J, Goode BL, Pellman D. An actin nucleation mechanism mediated by Bni1 and profilin. Nat Cell Biol 2002; 4(8): 626–631
180. Watanabe N, Madaule P, Reid T, Ishizaki T, Watanabe G, Kakizuka A, Saito Y, Nakao K, Jockusch BM, Narumiya S. p140mDia, a mammalian homolog of *Drosophila* diaphanous, is a target protein for Rho small GTPase and is a ligand for profilin. EMBO J 1997; 16(11): 3044–3056
181. Kawano Y, Fukata Y, Oshiro N, Amano M, Nakamura T, Ito M, Matsumura F, Inagaki M, Kaibuchi K. Phosphorylation of myosin-binding subunit (MBS) of myosin phosphatase by Rho-kinase *in vivo*. J Cell Biol 1999; 147(5): 1023–1038
182. Kosako H, Yoshida T, Matsumura F, Ishizaki T, Narumiya S, Inagaki M. Rho-kinase/ROCK is involved in cytokinesis through the phosphorylation of myosin light chain and not ezrin/radixin/moesin proteins at the cleavage furrow. Oncogene 2000; 19(52): 6059–6064
183. Yokoyama T, Goto H, Izawa I, Mizutani H, Inagaki M. Aurora-B and Rho-kinase/ROCK, the two cleavage furrow kinases, independently regulate the progression of cytokinesis: possible existence of a novel cleavage furrow kinase phosphorylates ezrin/radixin/moesin (ERM). Genes Cells 2005; 10(2): 127–137
184. Khasnis M, Nakatomi A, Gumpper K, Eto M. Reconstituted human myosin light chain phosphatase reveals distinct roles of two inhibitory phosphorylation sites of the regulatory subunit, MYPT1. Biochemistry 2014; 53(16): 2701–2709
185. Gai M, Camera P, Dema A, Bianchi F, Berto G, Scarpa E, Germena G, Di Cunto F. Citron kinase controls abscission through RhoA and anillin. Mol Biol Cell 2011; 22(20): 3768–3778
186. D'Avino PP. Citron kinase—renaissance of a neglected mitotic

kinase. J Cell Sci 2017; 130(10): 1701–1708
187. Canman JC, Lewellyn L, Laband K, Smerdon SJ, Desai A, Bowerman B, Oegema K. Inhibition of Rac by the GAP activity of centralspindlin is essential for cytokinesis. Science 2008; 322(5907): 1543–1546
188. Boucrot E, Kirchhausen T. Endosomal recycling controls plasma membrane area during mitosis. Proc Natl Acad Sci USA 2007; 104(19): 7939–7944
189. Ai E, Skop AR. Endosomal recycling regulation during cytokinesis. Commun Integr Biol 2009; 2(5): 444–447
190. Schiel JA, Prekeris R. Membrane dynamics during cytokinesis. Curr Opin Cell Biol 2013; 25(1): 92–98
191. Sechi S, Frappaolo A, Fraschini R, Capalbo L, Gottardo M, Belloni G, Glover DM, Wainman A, Giansanti MG. Rab1 interacts with GOLPH3 and controls Golgi structure and contractile ring constriction during cytokinesis in *Drosophila melanogaster*. Open Biol 2017; 7(1): 160257
192. Cao J, Albertson R, Riggs B, Field CM, Sullivan W. Nuf, a Rab11 effector, maintains cytokinetic furrow integrity by promoting local actin polymerization. J Cell Biol 2008; 182(2): 301–313
193. Rodrigues FF, Shao W, Harris TJC. The Arf GAP Asap promotes Arf1 function at the Golgi for cleavage furrow biosynthesis in *Drosophila*. Mol Biol Cell 2016; 27(20): 3143–3155
194. Frémont S, Echard A. Membrane traffic in the late steps of cytokinesis. Curr Biol 2018; 28(8): R458–R470
195. Albertson R, Riggs B, Sullivan W. Membrane traffic: a driving force in cytokinesis. Trends Cell Biol 2005; 15(2): 92–101
196. Montagnac G, Echard A, Chavrier P. Endocytic traffic in animal cell cytokinesis. Curr Opin Cell Biol 2008; 20(4): 454–461
197. Schiel JA, Childs C, Prekeris R. Endocytic transport and cytokinesis: from regulation of the cytoskeleton to midbody inheritance. Trends Cell Biol 2013; 23(7): 319–327
198. Schiel JA, Simon GC, Zaharris C, Weisz J, Castle D, Wu CC, Prekeris R. FIP3-endosome-dependent formation of the secondary ingression mediates ESCRT-III recruitment during cytokinesis. Nat Cell Biol 2012; 14(10): 1068–1078
199. Minoshima Y, Kawashima T, Hirose K, Tonozuka Y, Kawajiri A, Bao YC, Deng X, Tatsuka M, Narumiya S, May WS Jr, Nosaka T, Semba K, Inoue T, Satoh T, Inagaki M, Kitamura T. Phosphorylation by aurora B converts MgcRacGAP to a RhoGAP during cytokinesis. Dev Cell 2003; 4(4): 549–560
200. Yu X, Prekeris R, Gould GW. Role of endosomal Rab GTPases in cytokinesis. Eur J Cell Biol 2007; 86(1): 25–35
201. Hanai A, Ohgi M, Yagi C, Ueda T, Shin HW, Nakayama K. Class I Arfs (Arf1 and Arf3) and Arf6 are localized to the Flemming body and play important roles in cytokinesis. J Biochem 2016; 159(2): 201–208
202. Dambournet D, Machicoane M, Chesneau L, Sachse M, Rocancourt M, El Marjou A, Formstecher E, Salomon R, Goud B, Echard A. Rab35 GTPase and OCRL phosphatase remodel lipids and F-actin for successful cytokinesis. Nat Cell Biol 2011; 13(8): 981–988
203. Frémont S, Hammich H, Bai J, Wioland H, Klinkert K, Rocancourt M, Kikuti C, Stroebel D, Romet-Lemonne G, Pylypenko O, Houdusse A, Echard A. Oxidation of F-actin controls the terminal steps of cytokinesis. Nat Commun 2017; 8(1): 14528
204. Montagnac G, Sibarita JB, Loubéry S, Daviet L, Romao M, Raposo G, Chavrier P. ARF6 interacts with JIP4 to control a motor switch mechanism regulating endosome traffic in cytokinesis. Curr Biol 2009; 19(3): 184–195
205. Cascone I, Selimoglu R, Ozdemir C, Del Nery E, Yeaman C, White M, Camonis J. Distinct roles of RalA and RalB in the progression of cytokinesis are supported by distinct RalGEFs. EMBO J 2008; 27(18): 2375–2387
206. Chen XW, Inoue M, Hsu SC, Saltiel AR. RalA-exocyst-dependent recycling endosome trafficking is required for the completion of cytokinesis. J Biol Chem 2006; 281(50): 38609–38616
207. Neumann B, Walter T, Hériché JKK, Bulkescher J, Erfle H, Conrad C, Rogers P, Poser I, Held M, Liebel U, Cetin C, Sieckmann F, Pau G, Kabbe R, Wünsche A, Satagopam V, Schmitz MH, Chapuis C, Gerlich DW, Schneider R, Eils R, Huber W, Peters JM, Hyman AA, Durbin R, Pepperkok R, Ellenberg J. Phenotypic profiling of the human genome by time-lapse microscopy reveals cell division genes. Nature 2010; 464(7289): 721–727
208. Yang PL, Hsu TH, Wang CW, Chen RH. Lipid droplets maintain lipid homeostasis during anaphase for efficient cell separation in budding yeast. Mol Biol Cell 2016; 27(15): 2368–2380
209. Brill JA, Wong R, Wilde A. Phosphoinositide function in cytokinesis. Curr Biol 2011; 21(22): R930–R934
210. Ben El Kadhi K, Roubinet C, Solinet S, Emery G, Carréno S. The inositol 5-phosphatase dOCRL controls PI(4,5)P2 homeostasis and is necessary for cytokinesis. Curr Biol 2011; 21(12): 1074–1079
211. Field SJ, Madson N, Kerr ML, Galbraith KAA, Kennedy CE, Tahiliani M, Wilkins A, Cantley LC. PtdIns(4,5)P2 functions at the cleavage furrow during cytokinesis. Curr Biol 2005; 15(15): 1407–1412
212. Zoppino FCM, Militello RD, Slavin I, Álvarez C, Colombo MI. Autophagosome formation depends on the small GTPase Rab1 and functional ER exit sites. Traffic 2010; 11(9): 1246–1261
213. Ao X, Zou L, Wu Y. Regulation of autophagy by the Rab GTPase network. Cell Death Differ 2014; 21(3): 348–358
214. Chua CEL, Gan BQ, Tang BL. Involvement of members of the Rab family and related small GTPases in autophagosome formation and maturation. Cell Mol Life Sci 2011; 68(20): 3349–3358
215. Hutagalung AH, Novick PJ. Role of Rab GTPases in membrane traffic and cell physiology. Physiol Rev 2011; 91(1): 119–149
216. Ganley IG, Wong PM, Gammoh N, Jiang X. Distinct autophagosomal-lysosomal fusion mechanism revealed by thapsigargin-induced autophagy arrest. Mol Cell 2011; 42(6): 731–743
217. Pilli M, Arko-Mensah J, Ponpuak M, Roberts E, Master S, Mandell MA, Dupont N, Ornatowski W, Jiang S, Bradfute SB, Bruun JA, Hansen TE, Johansen T, Deretic V. TBK-1 promotes autophagy-mediated antimicrobial defense by controlling autophagosome maturation. Immunity 2012; 37(2): 223–234
218. Munafó DB, Colombo MI. Induction of autophagy causes dramatic changes in the subcellular distribution of GFP-Rab24. Traffic 2002; 3(7): 472–482
219. Sakurai A, Maruyama F, Funao J, Nozawa T, Aikawa C, Okahashi N, Shintani S, Hamada S, Ooshima T, Nakagawa I.

Specific behavior of intracellular *Streptococcus pyogenes* that has undergone autophagic degradation is associated with bacterial streptolysin O and host small G proteins Rab5 and Rab7. J Biol Chem 2010; 285(29): 22666–22675

220. Bento CF, Puri C, Moreau K, Rubinsztein DC. The role of membrane-trafficking small GTPases in the regulation of autophagy. J Cell Sci 2013; 126(5): 1059–1069
221. Bodemann BO, Orvedahl A, Cheng T, Ram RR, Ou YH, Formstecher E, Maiti M, Hazelett CC, Wauson EM, Balakireva M, Camonis JH, Yeaman C, Levine B, White MA. RalB and the exocyst mediate the cellular starvation response by direct activation of autophagosome assembly. Cell 2011; 144(2): 253–267
222. Nakashima N, Noguchi E, Nishimoto T. *Saccharomyces cerevisiae* putative G protein, Gtr1p, which forms complexes with itself and a novel protein designated as Gtr2p, negatively regulates the Ran/Gsp1p G protein cycle through Gtr2p. Genetics 1999; 152(3): 853–867
223. Sekiguchi T, Hirose E, Nakashima N, Ii M, Nishimoto T. Novel G proteins, Rag C and Rag D, interact with GTP-binding proteins, Rag A and Rag B. J Biol Chem 2001; 276(10): 7246–7257
224. Sancak Y, Bar-Peled L, Zoncu R, Markhard AL, Nada S, Sabatini DM. Ragulator-Rag complex targets mTORC1 to the lysosomal surface and is necessary for its activation by amino acids. Cell 2010; 141(2): 290–303
225. Sancak Y, Peterson TR, Shaul YD, Lindquist RA, Thoreen CC, Bar-Peled L, Sabatini DM. The rag GTPases bind raptor and mediate amino acid signaling to mTORC1. Science 2008; 320(5882): 1496–1501
226. Odle RI, Walker SA, Oxley D, Kidger AM, Balmanno K, Gilley R, Okkenhaug H, Florey O, Ktistakis NT, Cook SJ. An mTORC1-to-CDK1 switch maintains autophagy suppression during mitosis. Mol Cell 2020; 77(2): 228–240.e7
227. Thiam AR, Farese RV Jr, Walther TC. The biophysics and cell biology of lipid droplets. Nat Rev Mol Cell Biol 2013; 14(12): 775–786
228. Walther TC, Farese RV Jr. Lipid droplets and cellular lipid metabolism. Annu Rev Biochem 2012; 81(1): 687–714
229. Martin S, Parton RG. Lipid droplets: a unified view of a dynamic organelle. Nat Rev Mol Cell Biol 2006; 7(5): 373–378
230. Hashemi HF, Goodman JM. The life cycle of lipid droplets. Curr Opin Cell Biol 2015; 33: 119–124
231. Cruz ALS, Carrossini N, Teixeira LK, Ribeiro-Pinto LF, Bozza PT, Viola JPB. Cell cycle progression regulates biogenesis and cellular localization of lipid droplets. Mol Cell Biol 2019; 39(9): e00374–18
232. Tan R, Wang W, Wang S, Wang Z, Sun L, He W, Fan R, Zhou Y, Xu X, Hong W, Wang T. Small GTPase Rab40c associates with lipid droplets and modulates the biogenesis of lipid droplets. PLoS One 2013; 8(4): e63213
233. Ozeki S, Cheng J, Tauchi-Sato K, Hatano N, Taniguchi H, Fujimoto T. Rab18 localizes to lipid droplets and induces their close apposition to the endoplasmic reticulum-derived membrane. J Cell Sci 2005; 118(12): 2601–2611
234. Schroeder B, Schulze RJ, Weller SG, Sletten AC, Casey CA, McNiven MA. The small GTPase Rab7 as a central regulator of hepatocellular lipophagy. Hepatology 2015; 61(6): 1896–1907
235. Gabaldón T. Peroxisome diversity and evolution. Philos Trans R Soc Lond B Biol Sci 2010; 365(1541): 765–773
236. Knoblach B, Rachubinski RA. How peroxisomes partition between cells. A story of yeast, mammals and filamentous fungi. Curr Opin Cell Biol 2016; 41: 73–80
237. Nguyen T, Bjorkman J, Paton BC, Crane DI. Failure of microtubule-mediated peroxisome division and trafficking in disorders with reduced peroxisome abundance. J Cell Sci 2006; 119(4): 636–645
238. Asare A, Levorse J, Fuchs E. Coupling organelle inheritance with mitosis to balance growth and differentiation. Science 2017; 355(6342): eaah4701
239. Heasman SJ, Ridley AJ. Mammalian Rho GTPases: new insights into their functions from *in vivo* studies. Nat Rev Mol Cell Biol 2008; 9(9): 690–701
240. Castro IG, Richards DM, Metz J, Costello JL, Passmore JB, Schrader TA, Gouveia A, Ribeiro D, Schrader M. A role for mitochondrial Rho GTPase 1 (MIRO1) in motility and membrane dynamics of peroxisomes. Traffic 2018; 19(3): 229–242
241. Schollenberger L, Gronemeyer T, Huber CM, Lay D, Wiese S, Meyer HE, Warscheid B, Saffrich R, Peränen J, Gorgas K, Just WW. RhoA regulates peroxisome association to microtubules and the actin cytoskeleton. PLoS One 2010; 5(11): e13886
242. Just WW, Peränen J. Small GTPases in peroxisome dynamics. Biochim Biophys Acta 2016; 1863(5): 1006–1013
243. Gronemeyer T, Wiese S, Grinhagens S, Schollenberger L, Satyagraha A, Huber LA, Meyer HE, Warscheid B, Just WW. Localization of Rab proteins to peroxisomes: a proteomics and immunofluorescence study. FEBS Lett 2013; 587(4): 328–338
244. Zerial M, McBride H. Rab proteins as membrane organizers. Nat Rev Mol Cell Biol 2001; 2(2): 107–117
245. Cussac D, Leblanc P, L'Heritier A, Bertoglio J, Lang P, Kordon C, Enjalbert A, Saltarelli D. Rho proteins are localized with different membrane compartments involved in vesicular trafficking in anterior pituitary cells. Mol Cell Endocrinol 1996; 119(2): 195–206
246. Croisé P, Estay-Ahumada C, Gasman S, Ory S. Rho GTPases, phosphoinositides, and actin: a tripartite framework for efficient vesicular trafficking. Small GTPases 2014; 5(2): e29469
247. Wittinghofer A. Ras Superfamily Small G Proteins: Biology and Mechanisms 1: general features, signaling. Springer Vienna, 2014
248. Zhou B, Cox AD. Posttranslational modifications of small G proteins. In: Wittinghofer A. Ras Superfamily Small G Proteins: Biology and Mechanisms 1. Springer Vienna, 2014: 99–131
249. Barr F, Lambright DG. Rab GEFs and GAPs. Curr Opin Cell Biol 2010; 22(4): 461–470
250. Eathiraj S, Pan X, Ritacco C, Lambright DG. Structural basis of family-wide Rab GTPase recognition by rabenosyn-5. Nature 2005; 436(7049): 415–419
251. Spang A, Saw JH, Jørgensen SL, Zaremba-Niedzwiedzka K, Martijn J, Lind AE, van Eijk R, Schleper C, Guy L, Ettema TJG. Complex archaea that bridge the gap between prokaryotes and eukaryotes. Nature 2015; 521(7551): 173–179