

The Role of Actin-Binding Proteins in Breast Cancer Progression

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Abstract: Actin and actin-binding proteins (ABPs) regulate fundamental processes in cancer progression, including migration, invasion, and metastasis. Despite increasing evidence from in vitro and in vivo studies, the role and prognostic significance of actin and ABPs in breast cancer remain unclear due to the lack of a comprehensive review. This review, conducted in 2024 following PRISMA 2020 guidelines, systematically searched PubMed and Scopus using MeSH terms and text words to identify English-language original studies on actin and actin-binding proteins (ABPs) in breast cancer progression. Inclusion criteria were applied during title/abstract screening and full-text review, focusing on studies reporting cell migration, invasion, or metastasis. A total of 176 studies were included, comprising in vitro and in vivo models that investigated ABPs such as Fascin, Cofilin, and Mena, along with key signaling pathways like Rho GTPase, PI3K, and MAPK/ERK. Extracted data included cell lines, interventions, signaling pathways involved in actin or ABP regulation, the mechanism by which each intervention impacted actin remodeling or ABP expression, and outcomes such as migration, invasion, or metastasis. Prominent ABPs such as fascin, cofilin, and Mena were found to influence actin cytoskeletal dynamics, cell motility, and metastatic behavior. Findings highlight the prognostic relevance of ABPs and their therapeutic potential, although clinical translation remains limited by biological complexity and lack of standardized detection tools.

Keywords: actin, actin-binding proteins, biomarker, breast cancer, cancer progression

Introduction

Breast cancer is the most commonly diagnosed cancer among women worldwide and remains a significant cause of cancer-related mortality. According to GLOBOCAN, in 2022, there were nearly 2.3 million new cases and over 650,000 deaths due to breast cancer globally.¹ Despite advances in screening and treatment, challenges such as metastasis and therapeutic resistance continue to limit clinical outcomes. Tumor heterogeneity, shaped by genetic and epigenetic alterations, contributes to variability in treatment response and disease progression.² Moreover, invasive breast cancer can evade immune surveillance and adapt to the tumor microenvironment to support its survival and dissemination.³

As a result, tumor heterogeneity, therapeutic resistance, and immune evasion, contribute to delays in detecting disease progression, making it more challenging to assess prognosis accurately and initiate timely interventions. Delayed detection can lead to increased mortality rates, delayed treatment initiation, and potentially reduced survival rates for patients. Developing targeted therapies hinges on accurate and timely diagnosis, which could significantly impact patient outcomes and overall survival rates. Conventional prognostic tools such as mammography, ultrasound, Magnetic Resonance Imaging (MRI), and tissue biopsy are widely used in clinical settings. However, they present notable limitations, including low sensitivity in dense breast tissue, operator dependence, high costs, and invasive procedures.^{4,5}

The actin cytoskeleton is a critical component of eukaryotic cells, existing in two dynamic forms, G-actin (Globular actin) and F-actin (Filamentous actin), that interconvert to regulate cell shape and movement.⁶ G-actin is a monomeric protein that serves as the fundamental unit of F-actin. Through the process of actin polymerization, these monomers

assemble into dynamic actin filaments that play a crucial role in cell migration. This process predominantly occurs at the leading edge of the lamellipodium and begins with nucleation, where actin monomers form a stable nucleus assisted by actin-binding proteins such as formin and the Arp2/3 complex. This is followed by elongation, during which ATP-bound actin monomers are added to the barbed ends of filaments, a process supported by profilin. Meanwhile, cross-linking proteins such as filamin-A and α -actinin stabilize and stiffen the filaments, enabling them to exert force on the cell membrane. Actin filaments also undergo treadmilling, in which monomers are added at the barbed end and removed at the pointed end, maintaining filament dynamics. Regulation of this process involves thymosin β 4, which sequesters G-actin, capping proteins that control filament growth, and severing proteins like cofilin that generate new barbed ends, collectively enabling the formation of lamellipodia, filopodia, and pseudopodia necessary for cell movement.^{7,8} This dynamic remodeling is tightly controlled by actin-binding proteins (ABPs), which govern the polymerization, stabilization, and spatial organization of actin filaments.⁹ These include monomer-binding proteins, actin-nucleating proteins, polymerases, capping proteins, severing proteins, cross-linking proteins, bundling proteins, and branching proteins.¹⁰

In cancer, aberrant expression or regulation of ABPs contributes to increased motility, invasiveness, and drug resistance.¹¹ ABPs also play key roles in epithelial-to-mesenchymal transition (EMT), a process that facilitates metastasis and is associated with poor prognosis.^{11,12} Epithelial–mesenchymal transition (EMT) is a dynamic cellular program in which epithelial cells lose their apicobasal polarity and stable cell–cell adhesion while acquiring mesenchymal traits that enhance motility and invasiveness. A central event in EMT is the downregulation of E-cadherin, a key component of adherens junctions, whose loss destabilizes epithelial integrity and weakens intercellular cohesion. Concurrently, cells undergo cytoskeletal reorganization marked by the upregulation of vimentin, an intermediate filament protein that supports mesenchymal phenotypes by promoting EMT-associated transcriptional programs, facilitating microtubule polarization for directional migration, and maintaining cellular force balance. Together, the loss of E-cadherin–mediated adhesion and the gain of vimentin-dependent cytoskeletal plasticity enable cells to transition toward a migratory and invasive state characteristic of EMT.^{13–15} Additionally, actin-rich structures such as lamellipodia, filopodia, and invadopodia enable directional migration and invasion through the extracellular matrix, which is crucial for metastasis.^{16–19} Therefore, mutations or dysregulation of ABPs enhance cell motility, invasiveness, and metastatic potential, thereby accelerating cancer progression.

Given their central role in cancer cell migration, invasion, and cytoskeletal reorganization, actin and ABPs hold great potential as prognostic biomarkers in breast cancer. Several studies have linked specific ABPs to aggressive tumor behavior and treatment outcomes, yet their clinical utility remains underexplored. Unlike previous reviews that focus broadly on actin in cancer biology, this review specifically investigates the prognostic value of actin and ABPs in breast cancer. By highlighting mechanistic roles and relevant evidence from *in vitro* and *in vivo* studies, this review aims to uncover potential biomarkers that could improve early prognosis, risk stratification, and personalized treatment strategies. Ultimately, understanding actin dynamics may provide new avenues for clinical intervention and better patient outcomes.

Methods

The Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) 2020 guidelines were used. This review was conducted in 2024. This study is guided by the DSEO (Disease, Settings, Exposure, Outcome) research framework. The disease of interest (D) is breast cancer, examined in a global setting (S). The study focuses on actin (E) and its role in the progression of breast cancer (O), specifically in processes such as cell migration, cell invasion, and metastasis. A comprehensive literature search was conducted in PubMed and Scopus without year limitation to identify relevant studies investigating the role of actin and actin-binding proteins (ABPs) in breast cancer progression. The search was conducted in 2024 and followed a structured approach that combined Medical Subject Headings (MeSH) and free-text terms (Title/Abstract), with Boolean operators used to connect relevant domains: (1) actin cytoskeleton, (2) microfilament proteins, (3) breast cancer, and (4) progression/metastasis.

In PubMed, the search strategy utilized MeSH terms such as “Actin Cytoskeleton”, “Microfilament Proteins”, “Breast Neoplasms”, and “Neoplasm Metastasis”. Each MeSH term was expanded using a set of text words (Title/Abstract) to capture variations and synonyms found in the literature. For the actin cytoskeleton domain, text words included: Cytoskeletons, Actin, Cytoskeleton, Actin, Actin Filaments, Actin Filament, Filament, Actin, Filaments, Actin, Actin

Microfilaments, Actin Microfilament, Microfilament, Actin, and Microfilaments, Actin. For the microfilament proteins domain, terms such as Actin-Binding Proteins, Actin Binding Proteins, Binding Protein, Actin, Protein, Actin Binding, and Proteins, Actin-Binding were included. The breast cancer concept was addressed using both MeSH and text words (Title/Abstract), including: Breast Cancer, Breast Carcinoma, Breast Neoplasm, Breast Neoplasms, Breast Tumors, Mammary Cancer, Mammary Cancers, Breast Carcinomas, Breast Malignant Neoplasm(s), Malignant Tumor of Breast, Breast Malignant Tumor(s), Cancer of Breast, Cancer of the Breast, and Human Mammary Carcinomas. To identify studies discussing cancer progression or metastasis, terms such as Metastasis, Progressivity, Progressive, Continuing, Continuous, Growing, Developing, and Gradual were used alongside the MeSH term “Neoplasm Metastasis”. Initial search in PubMed applied filters to include only English-language articles, free full text, and to exclude reviews.

In Scopus, where MeSH terms are not available, equivalent free-text keywords were searched within the Title, Abstract, and Keyword fields. Boolean operators were applied consistently to combine synonymous terms within each concept using OR, and different concepts using AND. Initial search in Scopus was filtered to include only English-language articles, exclude review articles, and limited to “All Open Access” documents. The results were limited to articles published in English with full-text availability. Review articles, non-English papers, and documents without full-text access were excluded. The results were imported into Rayyan.ai for blinded screening, duplicate detection, and selection based on inclusion and exclusion criteria.

The selection of studies was conducted in two phases: (1) a screening of titles and abstracts and (2) a full-text evaluation. The initial screening was performed independently by two reviewers (RIH and KFA) using the Rayyan.ai platform, which facilitated blinded review and duplicate detection. Any uncertainties or disagreements regarding study inclusion during this phase were discussed with two additional reviewers (NMA and AFK) for clarification. In the second phase, full-text articles that passed the initial screening were reviewed by RIH, applying the same eligibility criteria. Any uncertainties or questions during this process were discussed with NMA and AFK. Specific reasons for exclusion such as irrelevant outcomes or populations were documented accordingly. This process followed the PRISMA 2020 flow diagram ([Supplementary Figure 1](#)), ensuring that all inclusion and exclusion steps were transparently reported. Extracted data were synthesized narratively and thematically, focusing on the mechanisms by which actin and ABPs influence breast cancer progression. Feedback on the manuscript draft was provided by NMA, AFK, and MBF to enhance clarity and scientific precision.

Results

A total of 362 studies were identified through preliminary database searches. The initial step in the process involved excluding articles based on their titles and abstracts. This led to the inclusion of 216 articles. In the subsequent screening phase, which involved a comprehensive evaluation of the complete text, several articles were excluded from the study because they did not provide any data or observations related to actin or ABPs. Alternatively, articles were excluded if they did not employ breast cancer cells as the primary model in their research. A total of 176 articles were included in the analysis. Of these, 167 studies utilized *in vitro* breast cancer models, with 59 also integrating *in vivo* validation. An additional nine studies employed *in vivo* models exclusively, such as murine xenografts and genetically engineered mouse models. The following Venn diagram offers a visual representation of the overlapping study designs observed among the included articles ([Supplementary Figure 2](#)).

Experimental manipulation of actin-regulatory pathways consistently demonstrates that breast cancer cell migration is governed by coordinated signaling networks that control cytoskeletal plasticity rather than actin abundance alone ([Supplementary Table 1](#)). Among these, the Rho family of GTPases; RhoA, Rac1, and Cdc42 acts as a central signaling hub translating extracellular stimuli into actin reorganization, as evidenced by marked alterations in migratory behavior following their inhibition or dominant-negative expression across multiple breast cancer models. Rac1 and Cdc42 are particularly critical for front-edge dynamics, where they drive lamellipodia and filopodia formation and enable persistent, directional migration.²⁰ In contrast, RhoA primarily regulates actomyosin contractility and stress fiber assembly. Its contribution to migration appears more context-dependent, reflecting its dual role in maintaining cytoskeletal integrity

and generating rear-end contractile forces, such that its disruption may variably enhance or suppress net cell movement depending on cellular context.

Beyond upstream signaling, proteins that directly regulate actin filament turnover are key determinants of migratory efficiency. Profilin-1, which facilitates actin polymerization by maintaining the ATP–actin monomer pool, exhibits a context-dependent role in invasiveness, while cofilin-mediated filament severing is essential for sustaining actin dynamics required for motility.^{21,22} In contrast, fascin functions as a dominant pro-migratory actin-bundling protein by stabilizing filopodia and invadopodia structures. Inhibition of fascin–actin interactions consistently suppresses migration and invasion across diverse breast cancer models, highlighting fascin as one of the most promising cytoskeletal targets for anti-metastatic intervention.^{23,24}

Hormonal and transcriptional programs further modulate actin remodeling in breast cancer. Steroid hormones, including estrogen, progestins, and androgens, markedly influence cytoskeletal organization in hormone receptor–positive tumors, underscoring the role of nuclear receptor signaling in licensing migratory competence.^{25–28} Similarly, activation of the TGF- β pathway promotes epithelial–mesenchymal transition (EMT), a process characterized by extensive actin cytoskeleton reprogramming, whereas inhibition of this axis reverses metastatic traits.^{29–31}

Finally, the actin cytoskeleton functions as an integrative platform for diverse environmental cues. Metabolic inputs such as glucose availability, mechanical signals from the extracellular matrix, pharmacological and natural compounds, and post-transcriptional regulation by microRNAs collectively fine-tune actin dynamics.^{32–40} Notably, several miRNAs simultaneously target multiple actin regulators, acting as endogenous suppressors of invasive cytoskeletal programs. Loss of these regulatory miRNAs may facilitate metastasis, while their restoration represents a promising strategy to restrain cancer cell motility by targeting the actin network at multiple levels.^{41,42} All associated data are summarized in [Supplementary Table 1](#) and [3](#).

Most in vitro studies have utilized breast cancer cell lines to assess the effects of gene modifications or novel compounds on actin cytoskeletal dynamics and actin-binding proteins (ABPs), particularly on cell migration and invasion. These findings were often extended in vivo using animal models, with primary outcomes focusing on tumor volume and lung metastasis. The characteristics of the included in vitro studies, including the cell lines used, types of interventions, key signaling pathways involved, evaluated biomarkers (particularly those related to actin and/or actin-binding proteins), and the observed effects on migration and/or invasion, are summarized in [Supplementary Table 1](#). The earliest in vitro studies exploring ABPs in breast cancer appeared in 1998, with the first in vivo studies in 2001, and research has continued to this day, showing ongoing interest in how actin cytoskeletal regulation affects cancer development and its potential clinical applications.

The most commonly used cell lines in vitro included MDA-MB-231, MCF-7, T47D, 4T1, and BT549, representing a spectrum of molecular subtypes from luminal A to triple-negative breast cancer. The frequency of breast cancer cell lines used across the included studies was summarized in [Supplementary Table 2](#). The experimental designs encompassed gene silencing (eg, RNA interference/short hairpin RNA knockdown), overexpression systems, and pharmacological interventions targeting actin polymerization or ABP function. In addition to phenotypic observations, functional assays assessing migration, invasion, morphology, and EMT markers were widely utilized. Despite the diverse study designs, a strong positive correlation was consistently found between the expression of several ABPs and increased migration, invasion, and metastasis. In contrast, several studies also reported that suppression or loss of specific ABPs led to reduced motility and invasive potential, highlighting the nuanced and context-dependent roles of these proteins.

Across the included studies, a recurrent set of ABP, notably Fascin, α -actinin, Arp2/3 complex, Cofilin, and Filamin A, were identified as key modulators of cell motility and cytoskeletal remodeling in breast cancer cells. Changes in F-actin polymerization status were commonly used as readouts of cytoskeletal remodeling. [Table 1](#) below summarizes the biomarkers evaluated for actin cytoskeletal dynamics across the included studies. The standard functional assessments employed included Boyden chamber and Matrigel invasion assays. Notably, suppression of ABP function or that of its upstream regulators consistently reduced the motility and invasive potential of cancer cells. In contrast, overexpression was commonly associated with enhanced migration, EMT, and metastatic spread. Conversely, the upregulation or expression of specific ABPs often resulted in the induction of EMT-like features and the promotion of cell dissemination. However, further analysis shows that ABPs can have varying effects. For example, while Filamin A downregulation has been shown to impair migration in several models, the role of Profilin-1 appears more complex. Reduced expression of Profilin-1 is in fact often associated with increased motility in breast cancer and other cancer cell types, whereas its overexpression tends to inhibit migration. These

Table 1 Frequency of Biomarkers Assessed in in vitro and in vivo Studies

Biomarker/Actin-Related Readout	In vitro	In vivo
Actin/F-actin organization	132	53
Fascin	8	4
Cofilin	5	3
Mena	5	7
MenaINV	3	5
Ezrin	3	0
Cortactin	3	0
Actinin	2	0
Profilin	2	2
Girdin	2	1
Filamin A	2	2
MRTFs	2	0
Moesin	1	0
Tensin	1	1
CNN1	1	1
L-plastin	1	0
MTSSI	1	0
Actin-related protein 2/3 complex (ARPC2)	1	1
WAVE3	1	0
Afadin	1	2
Talin	1	0
Transgelin	1	1
PARVA	1	0
NMIIA	1	0
Paxillin	1	1
Migfilin	1	0
Coronin-1C	1	0
CAPG	1	1
Vinculin	0	1
Anillin	0	1

Notes: Actin and F-actin were classified as structural readouts of cytoskeletal remodeling rather than molecular biomarkers. In vivo evidence was reported only when directly supported by experimentally validated animal studies identified through the predefined search strategy.

findings emphasize that Profilin-1 and Filamin A, though both actin-binding proteins, exert distinct and sometimes opposing effects on cancer cell behavior depending on the cellular context.

In vivo studies have yielded translational insights into the influence of actin or ABPs modulation on tumor progression within a complex physiological environment. Among the 68 studies incorporating animal models (59 in vitro and in vivo and 9 exclusively in vivo), the majority used orthotopic mouse models, in which human or murine breast cancer cells were injected into the mammary fat pad ([Supplementary Table 3](#)). The interventions were diverse, most commonly consisting of either gene knockout or overexpression strategies, or the administration of novel compounds that had not previously been tested in breast cancer models. These in vivo studies were typically built upon prior in vitro experiments using the same interventions. The most frequently utilized breast cancer cell lines in the in vivo models were identified as MDA-MB-231, 4T1, MCF-7, and MTLn3 ([Supplementary Table 2](#)).

Additionally, the most frequently used animal models were SCID mice. The most frequently evaluated biomarker was filamentous actin, with Mena, the most commonly studied actin-binding protein, being the most frequently studied ([Table 1](#)). The majority of studies concentrated on evaluating breast cancer metastasis to the lungs, with fewer studies additionally assessing tumor volume.

The following table ([Table 2](#)) presents a comprehensive overview of the signaling pathways that were the primary focus of the majority of investigations in the included studies. The table illustrates the number of studies that have

Table 2 Frequency of Signaling Pathways Investigated in in vitro and in vivo Studies

Pathway	In vitro	In vivo
Rho GTPase	67	20
Actin Binding Protein	23	13
PI3K	15	5
MAPK/ERK	14	7
LIMK/Cofilin	6	2
TGF- β / Smad Signaling Pathway (Canonical Pathway)	5	3
FAK/Src	5	2
NF- κ B	4	3
Non-canonical TGF- β Signaling Pathway (p38 MAPK Pathway)	2	0
Wnt/ β -catenin	1	0
HIF-1 signaling pathway	1	1
mTORC1/S6K	1	0
Src/ERK	1	0
JAK/STAT	1	0
Integrin/FAK	1	1
RAGE	1	1
miR-206/TWFI/MKLI-SRF/IL11	1	1
Hippo	1	0
Wnt/PCP	1	1
JNK/c-Jun	1	1
PKC/Src/Rho	1	0

investigated each pathway in both in vitro and in vivo contexts, providing insights into the molecular mechanisms frequently examined regarding actin cytoskeletal regulation and breast cancer progression. The findings, when considered as a whole, emphasize the pivotal role of actin dynamics and ABP regulation in the cellular behaviors that are fundamental to the progression of breast cancer. The uniformity of the findings across disparate models and pathways underscores their prospective value as prognostic indicators and therapeutic targets.

Fascin, Cofilin, Mena, MenaINV, Ezrin, and Cortactin consistently emerged as the most frequently studied ABPs. Likewise, although various signaling pathways were explored, only a few pathways such as Rho GTPase, PI3K, MAPK/ERK, and LIMK/Cofilin, appeared repeatedly across studies, yet without consistent temporal focus. In conclusion, while several ABPs and associated signaling pathways have been studied extensively in the context of breast cancer, it remains difficult to determine which specific ABP is most consistently favored or prioritized across studies. Most ABPs such as Fascin, Cofilin, Mena, MenaINV, Ezrin, and Cortactin tend to promote cancer cell migration and invasion when overexpressed. However, certain ABPs like Profilin-1 demonstrate the opposite, where increased expression is associated with reduced migratory behavior. This contrast highlights that not all ABPs uniformly enhance metastatic potential.

Discussion

This review highlights the central role of the actin cytoskeleton and its associated actin-binding proteins (ABPs) in regulating breast cancer progression. The dynamic remodeling of the actin cytoskeleton is essential for key processes such as cell migration, invasion, and metastasis, which are hallmarks of aggressive tumor behavior.^{43,44} While the functional involvement of ABPs such as Fascin, Cofilin, and Mena has been extensively characterized, their potential clinical relevance as prognostic or therapeutic biomarkers remains insufficiently elucidated in the current literature. These proteins facilitate the movement and penetration of cancer cells through the extracellular matrix, contributing to tumor dissemination. Notably, their expression levels are often elevated in highly invasive breast cancer subtypes, suggesting their potential value as biomarkers of disease progression and as targets for therapeutic intervention.

The shape and organization of filamentous actin (F-actin) critically influence breast cancer cell migration, invasion, and metastasis by forming specialized protrusions that facilitate movement and tissue penetration. These F-actin assemblies function as viscoelastic materials, combining resistance to flow with elastic energy storage, which enables cells to generate and sustain protrusive forces.⁴⁵ Lamellipodia, broad sheet-like F-actin networks at the leading edge of cells, generate protrusive forces through rapid actin polymerization, enabling directional migration in aggressive cancer cells.⁴³ Filopodia, thin finger-like F-actin bundles, extend beyond lamellipodia to sense the extracellular environment, guiding cell movement and enhancing adhesion to the extracellular matrix (ECM).^{46,47} Invadopodia, dense F-actin-rich protrusions, degrade the ECM via protease secretion, allowing cancer cells to breach tissue barriers and metastasize.^{48,49} The dynamic remodeling of F-actin within these structures determines their efficiency in promoting motility and invasion. Disrupting F-actin formation impairs these protrusions, reducing cell migration, invasion, and metastatic potential.

Among ABPs examined, fascin impacts actin by cross-linking (bundling) actin filaments into tightly packed, parallel bundles that support cellular protrusions such as filopodia. These filopodia act as dynamic sensory probes at the cell membrane, allowing cells to explore their microenvironment and facilitate processes such as migration and invasion.^{50–53} In addition, cofilin dynamically regulates actin by severing and depolymerizing filaments at low concentrations. Cofilin-1 binds along actin filaments, twisting their helical structure and inserting between actin subunits, which weakens lateral contacts and induces fractures, creating new barbed and pointed ends for polymerization and depolymerization.⁵⁴ Conversely, at high levels, it stabilizes filaments as cofilactin.⁵⁵ It indirectly supports actin bundling by generating free barbed ends and supplying monomers for polymerization, thereby facilitating structures such as lamellipodia (via rapid actin turnover) and filopodia (via localized remodeling). In lamellipodia, cofilin drives protrusion by creating new barbed ends, whereas in filopodia, it fine-tunes length and flexibility by balancing bundled and cofilactin states.^{56,57}

On the other hand, Mena promotes actin polymerization and filament elongation at lamellipodial edges and filopodia tips by protecting barbed ends from capping proteins, enhancing actin filament organization without direct bundling.^{58,59} This activity leads to the stabilization of membrane protrusions by organizing actin into parallel arrays, which indirectly supports the formation of bundled filopodia structures.⁶⁰ Mena, particularly its invasive isoform MenaINV, guides

directional migration (haptotaxis) by binding to $\alpha 5 \beta 1$ integrin, enhancing cancer cell sensitivity to fibronectin gradients through increased integrin association, FAK signaling, and actin polymerization, enabling tumor cells to migrate toward ECM-rich areas like blood vessels and metastatic sites.⁶¹ Collectively, these ABPs work synergistically to shape actin architecture that facilitates cancer cell migration and invasion during metastasis.

Numerous signaling pathways influence actin dynamics. Among them, the pathways most frequently identified in this review include the Rho GTPase, PI3K, MAPK/ERK, and LIMK/Cofilin Pathways (Figure 1). The Rho GTPase family, comprising RhoA, Rac1, and Cdc42, regulates the formation of actin filaments into stress fibers, lamellipodia, and filopodia, respectively. RhoA promotes stress fiber formation by activating ROCK, which stabilizes actin filaments through LIMK-dependent cofilin inhibition.^{62,63} ROCK functions downstream of RhoA to regulate actomyosin contractility and stress fiber formation by controlling myosin activity together with MLCK. ROCK inhibits myosin phosphatase through MYPT1 phosphorylation, thereby sustaining MLC phosphorylation at Ser19/Thr18 and enhancing non-muscle myosin II ATPase activity, which generates strong and stable contractile forces and promotes central/ventral stress fiber formation. In parallel, MLCK directly phosphorylates MLC at Ser19 to initiate myosin activation, primarily driving peripheral stress fibers that support dynamic protrusion and retraction at the cell edge. Through this coordinated action, MLCK provides localized and rapid myosin activation, while ROCK maintains and reinforces contractility, together managing stress fiber organization and cellular mechanical tension.⁶⁴

In contrast, Rac1 stimulates lamellipodia formation by activating the WAVE complex. WAVE, as part of the WAVE regulatory complex (WRC), which binds to the A- and D-sites of the WRC and induces a conformational change that releases the autoinhibited VCA domain. Once exposed, the V (WH2) motif of WAVE binds a G-actin monomer and

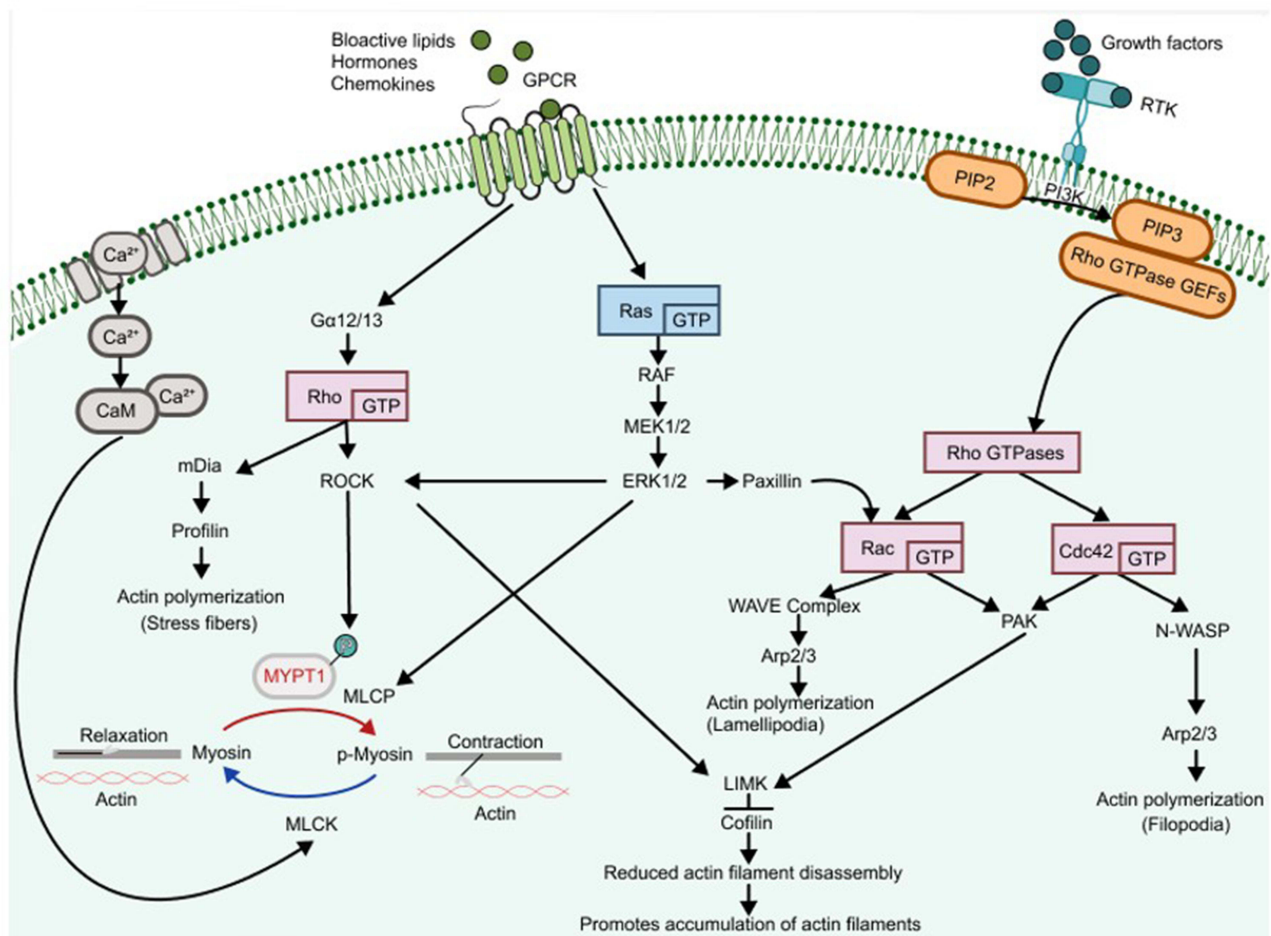


Figure 1 Schematic representation of key signaling pathways regulating actin cytoskeleton remodeling and actin-binding proteins in breast cancer progression.

delivers it directly to the inactive Arp2/3 complex, positioning the actin between Arp2 and Arp3. Simultaneously, the CA region binds Arp2/ARPC1 and Arp3, stabilizing their rearrangement into a short-pitch, actin-dimer-like configuration. The bound G-actin effectively bridges Arp2 and Arp3, promoting the rotation and alignment of Arp3 so that the complex mimics the first two subunits of a new filament. This stabilized nucleation seed then associates with a pre-existing “mother” filament, enabling rapid elongation of a new, branched “daughter” filament from the barbed end at approximately 70°, with additional actin monomers supplied to sustain growth.^{65–67} Meanwhile, Cdc42 regulates filopodia assembly by activating N-WASP, another Arp2/3 activator, which nucleates actin filaments that bundle into parallel arrays, enabling directional sensing and polarized migration.^{62,63}

The PI3K pathway drives actin cytoskeletal remodeling through its lipid mediators PIP2 (phosphatidylinositol 4,5-bisphosphate) and PIP3 (phosphatidylinositol 3,4,5-trisphosphate), with PI3K phosphorylating PIP2 to PIP3, which engage PH domain-containing GEFs to activate Rho GTPases (Rac1 and Cdc42).^{68,69} Rac1 signaling also leads to PAK activation, which in turn activates LIMK, blocking cofilin’s ability to break down actin filaments and thereby helping to maintain cytoskeletal structure.^{69–71} The PI3K/AKT pathway indirectly regulates RhoA-mediated actin remodeling by inhibiting GSK-3 β through serine-9 phosphorylation. Ser9 phosphorylation creates a pseudosubstrate that blocks the kinase active site, thereby reducing GSK-3 β dependent phosphorylation of cytoskeletal regulators such as APC and β -catenin. When active, GSK-3 β suppresses APC and CLIP-170/CLASP mediated microtubule–actin interactions, favoring RhoA/ROCK driven stress fiber formation while limiting protrusive activity and cell migration.^{72–74}

By coordinating both the creation of new actin branches and the protection of existing filaments, this PI3K driven process generates the sustained membrane protrusions that allow cancer cells to move directionally and invade surrounding tissues during metastasis.

The MAPK/ERK pathway coordinates cell migration by linking focal adhesion turnover and actin remodeling through paxillin and Rac signaling. Upon activation, ERK1/2 phosphorylates paxillin, enhancing its role as a scaffold at focal adhesions and promoting dynamic adhesion turnover. Phosphorylated paxillin recruits Rac-specific GEFs such as DOCK180 and PIX, leading to localized Rac activation at the cell’s leading edge. Active Rac stimulates actin polymerization via the WAVE/Arp2/3 complex, driving lamellipodia formation and membrane protrusion. This ERK/paxillin/Rac signaling axis enables spatial coordination of protrusive and adhesive forces, supporting directed migration.⁷⁵

Most of the experimental studies included in this review have utilized gene knockdown techniques to investigate the therapeutic potential of targeting ABPs and their regulators. Silencing or knockdown of genes such as Mena, Fascin, Filamin A, Profilin, and Palladin has resulted in reduced motility and invasion of breast cancer cells in both in vitro and/or in vivo models.^{21,24,61,76–78} Additionally, several actin/ABP-targeting compounds have been identified that interfere with actin dynamics or ABP function. Chelidonine disrupts actin cytoskeleton reorganization, Vitamin C inhibits F-actin assembly, and Telocinobufagin induces the collapse of actin filaments.^{79–81} SH-479, a derivative of betulinic acid, alters microfilament architecture, while NP-G2-044 specifically inhibits fascin activity.^{82,83} These compounds suppress breast cancer cell migration and/or invasion in vitro (eg, chelidonine, vitamin C, SH-479, Telocinobufagin), while NP-G2-044 demonstrates anti-metastatic efficacy in preclinical animal models. Their ability to effectively target actin/ABP involved in breast cancer progression makes them promising candidates for breast cancer therapy. However, current direct pharmacological targeting of actin itself is associated with significant cytotoxicity due to its essential role in normal cellular function, limiting its clinical applicability in cancer therapy. These findings are primarily supported by studies employing well-established breast cancer models. In vitro experiments frequently utilized MDA-MB-231, MCF-7, T47D, 4T1, and BT549 cell lines, while in vivo investigations commonly involved MDA-MB-231, 4T1, MCF-7, and MTLn3 models, which were inoculated into animal models to establish primary tumors. Importantly, in vivo studies further validate these mechanistic findings, demonstrating that modulation of ABP expression—either via overexpression, knockdown, or pharmacological inhibition—consistently alters metastatic potential and tumor burden in orthotopic and xenograft mouse models. For instance, inhibition of Mena or Cofilin using small interfering RNA (siRNA) has been shown to significantly reduce lung metastasis and intravasation, underscoring the translational relevance of these targets. This RNA interference–based approach selectively degrades Mena- or Cofilin-specific mRNAs, leading to reduced protein expression and impaired metastatic potential.^{22,84}

The current clinical study on actin-binding proteins in breast cancer has reached a significant milestone. Transcriptome analyses and tissue-based studies using datasets such as TCGA and METABRIC have identified several ABPs as potential prognostic markers. Among them, cofilin-1, shows a strong association with metastatic potential.⁸⁵ Other ABPs, including transgelin, fascin, and MenaINV, have also demonstrated clinical relevance in relation to disease progression.^{61,86–88} A small number of studies have explored ABPs as circulating biomarkers. For example, elevated serum levels of Actinin-4 are associated with aggressive disease features such as higher tumor grade and lymph node involvement, suggesting potential for non-invasive diagnostics.⁸⁹ However, therapeutic applications remain limited. To date, only one ABP-targeting compound, the fascin inhibitor NP-G2-044, has progressed into Phase I and II clinical trials. This shows that several actin-binding proteins are associated with breast cancer prognosis and metastasis, with limited evidence supporting their use as circulating biomarkers, while only one ABP-targeting therapy has advanced to early-phase clinical trials.

Among the actin-related components and ABPs investigated in breast cancer, actin itself remains the most extensively analyzed biomarker, particularly in relation to F-actin. Among specific ABPs, Fascin, Cofilin, Mena, MenaINV, and Profilin are the most frequently studied due to their critical roles in reorganizing the cytoskeleton and promoting cancer cell motility. In vivo models, especially those involving Mena and MenaINV, highlight their roles in metastasis. The pathways most commonly associated with ABP activity include the Rho GTPase pathway, which regulates actin-based structures such as lamellipodia, filopodia, and stress fibers through key effectors like Rac1, Cdc42, and RhoA. Other prominent signaling pathways include PI3K and MAPK/ERK, which facilitate actin remodeling through mechanisms such as LIMK-mediated cofilin regulation, activation of the Arp2/3 complex, and regulation of focal adhesion dynamics. Together, these actin regulators and pathways underscore the importance of cytoskeletal remodeling in breast cancer progression, supporting their potential as prognostic biomarkers and therapeutic targets.

Despite promising findings, several barriers continue to hinder the clinical translation of ABPs research in breast cancer. The research landscape remains fragmented, with many studies investigating different ABPs without a consistent or strategic direction. A significant methodological limitation is the overreliance on TNBC models, particularly the MDA-MB-231 cell line, while other molecular subtypes such as HER2-positive and luminal B are significantly under-represented. This imbalance reduces the generalizability of findings across the diverse landscape of breast cancer. Moreover, only a limited number of studies have explored how ABPs interact with the tumor microenvironment, including critical components such as extracellular matrix stiffness, structural proteins, and immune cell infiltration, which are known to influence tumor progression and therapeutic response.

Beyond experimental design issues, the biological complexity and context-dependent roles of ABPs further complicate their clinical application. ABP expression and function vary across different breast cancer subtypes and disease stages, contributing to inconsistent outcomes in both prognostic and therapeutic studies. The lack of standardized, clinically validated assays for detecting ABP levels adds another layer of difficulty, especially given that ABP expression can be dynamically regulated by microenvironmental factors such as scaffold stiffness.³³ Although certain ABPs show promise as biomarkers, their inconsistent behavior across tumor contexts undermines their reliability in clinical practice. Tumor heterogeneity further complicates their use, as ABP expression varies across breast cancer subtypes and stages.⁹⁰

On the therapeutic side, efforts to target actin and ABPs face significant challenges due to their fundamental roles in essential cellular processes. Actin and ABPs are involved in critical physiological functions, including muscle contraction in the heart and skeletal muscles, making systemic modulation risky due to potential cardiotoxicity.¹¹ Their pleiotropic involvement in numerous signaling pathways further complicates the design of selective drugs. Although preclinical models have demonstrated that disrupting the actin cytoskeleton can suppress cancer cell migration and invasion, achieving tumor-specific effects without damaging normal tissues remains a significant challenge. Moving forward, the development of effective therapies will depend on strategies that can precisely target cancer-specific actin dynamics while preserving essential functions in healthy cells.

Despite the current limitations, growing research continues to unveil promising opportunities for leveraging actin and ABPs in breast cancer management. Advances in targeted drug delivery systems, such as nanoparticle-based drug delivery, offer the potential to inhibit tumor-associated ABP functions while minimizing systemic toxicity selectively.^{91–93} Furthermore, the integration of ABPs into multi-omics approaches and machine learning models may

enhance their utility as prognostic or predictive biomarkers, especially in stratifying patients based on metastatic risk or treatment response. Circulating ABPs such as Actinin-4 also hold promise in the development of minimally invasive diagnostic tools, enabling early detection or disease monitoring through liquid biopsy.⁸⁹ In addition, combinatorial strategies that incorporate ABP-targeting agents alongside chemotherapy or immunotherapy are being explored to enhance therapeutic outcomes.⁹⁴ Taken together, the current body of evidence highlights the multifaceted role of actin cytoskeletal regulators in promoting breast cancer aggressiveness. Further exploration into their prognostic value, especially when integrated with molecular subtype stratification, may yield clinically actionable biomarkers to enhance precision oncology approaches in breast cancer management.^{95–233}

Conclusion

This review emphasizes that remodeling of the actin cytoskeleton, driven by key actin-binding proteins (ABPs) and various signaling pathways, plays a vital role in breast cancer progression by regulating cell motility and invasion. Numerous in vitro and in vivo studies consistently highlight the crucial roles of ABPs such as Fascin, Cofilin, and Mena, along with signaling pathways like Rho GTPase, PI3K, and MAPK/ERK, in mediating actin cytoskeletal changes that promote breast cancer progression. Despite these consistent findings, several challenges hinder the clinical application of ABP-related research. Tumor heterogeneity, the diverse functions of ABPs, and the absence of standardized detection methods limit their use as universal biomarkers or therapeutic targets. Additionally, because actin and ABPs are involved in essential physiological processes, systemic targeting raises concerns about potential toxicity. However, emerging strategies such as nanoparticle-based drug delivery, ABP-targeting agents like fascin inhibitors, and incorporating ABPs into biomarker tools like liquid biopsies and molecular profiling present promising approaches that could unlock the clinical potential of actin dynamics for personalized breast cancer treatment.

Abbreviations

ABP, actin-binding protein; APC, adenomatous polyposis coli; Arp2/3, actin-related protein 2/3; Cdc42, cell division cycle 42; CLASP, cytoplasmic linker-associated protein; CLIP-170, cytoplasmic linker protein of 170 kDa; DOCK180, dedicator of cytokinesis 180; DSEO, Disease, Settings, Exposure, Outcome; ECM, extracellular matrix; EMT, epithelial-to-mesenchymal transition; ERK, extracellular signal-regulated kinase; FAK, focal adhesion kinase; GEF, guanine nucleotide exchange factor; GSK-3 β , glycogen synthase kinase-3 β ; HER2, human epidermal growth factor receptor 2; LIMK, LIM domain kinase; MAPK, mitogen-activated protein kinase; mDia, mammalian diaphanous; METABRIC, Molecular Taxonomy of Breast Cancer International Consortium; MeSH, Medical Subject Headings; MRI, Magnetic Resonance Imaging; N-WASP, neuronal Wiskott-Aldrich syndrome protein; PI3K, phosphoinositide 3-kinase; PIX, PAK-interacting exchange factor; PIP2, phosphatidylinositol 4,5-bisphosphate; PIP3, phosphatidylinositol 3,4,5-trisphosphate; PRISMA, Preferred Reporting Items for Systematic Reviews and Meta-Analyses; ROCK, Rho-associated protein kinase; SCID, severe combined immunodeficiency; TCGA, The Cancer Genome Atlas; TNBC, triple-negative breast cancer; WAVE, Wiskott-Aldrich syndrome protein family verprolin-homologous protein.

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