

# Chapter 1

## Steroid Receptor Coactivators (SRCs) as Integrators of Multiple Signaling Pathways in Cancer Progression

Weiwen Long and Bert W. O'Malley

**Abstract** Steroid receptor coactivators (SRCs), including SRC-1, SRC-2, and SRC-3, mediate transcriptional activities of nuclear receptors and other transcription factors. SRCs' activities and functions are regulated by multiple signaling pathways, including those of hormones, growth factors, and cytokines, and are determined by post-translational modifications, including phosphorylation, ubiquitination, sumoylation, acetylation, and methylation. SRCs integrate signals from a variety of pathways that regulate multiple cellular processes such as metabolism, reproduction, and growth. For the growth response, they regulate proliferation, survival, migration, and invasion, and promote tumor development and metastasis. SRCs are highly dysregulated in many types of cancers at multiple levels including gene amplification, mutation, and mRNA/protein overexpression. Alterations of SRCs are frequently associated with advanced tumor progression and drug resistance. As such, SRCs are important prognostic cancer biomarkers and could serve as therapeutic targets for cancer therapy.

**Keywords** Steroid receptor coactivators (SRCs) • Nuclear receptor • Gene transcription • Posttranslational modifications • Signaling pathways • Tumorigenesis • Cancer metastasis • Drug targeting

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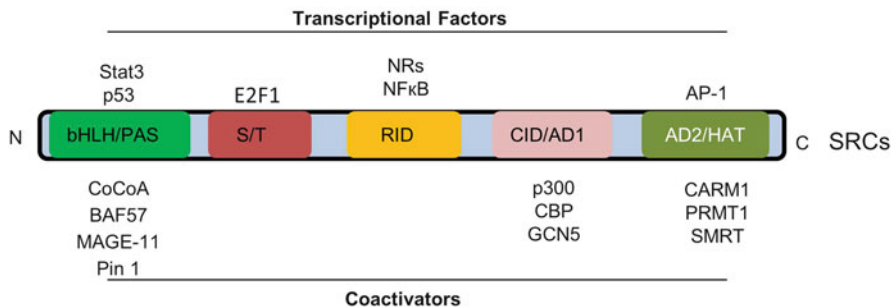
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## 1.1 Introduction

The p160 steroid receptor coactivator (SRC) family, consisting of SRC-1, SRC-2, and SRC-3, were originally identified as transcriptional coactivators of nuclear hormone receptors (NRs) for estrogen, progesterone, and androgen. SRC-1, also known as nuclear receptor coactivator 1 (NCOA1), was cloned and characterized as the first NR coactivator in 1995 [1]. SRC-2, also known as NCOA2, GRIP1 (glucocorticoid receptor interacting protein 1), and TIF2 (transcriptional intermediary factor 2), was identified soon after the cloning of SRC-1 [2, 3]. SRC-3 was then identified by several laboratories nearly in the same year of 1997, and was provided with different names [4–7]: AIB1 (amplified in breast cancer 1), p/CIP (p300/CBP interacting protein), RAC3 (RAR-associated coactivator 3), ACTR (activator of thyroid and retinoic acid receptor), and TRAM1 (thyroid receptor activator molecule 1). Since the discovery of the first coactivator (SRC-1) in 1995, a substantial number of studies have been conducted to elucidate the molecular actions of SRCs in normal physiology and pathology. In this chapter, we will focus on the cancer-related functions of SRCs and the underlying molecular mechanisms, thereby highlighting the molecular structures and functional interacting partners of SRCs, the regulation of SRCs' activities by posttranslational modifications (PTMs), and the integration of multiple oncogenic signaling pathways by SRCs that promote tumor development and progression.

## 1.2 Structures and Transcriptional Interacting Partners of SRCs

SRC proteins share a common structure that contains five functional domains/regions (Fig. 1.1): the N-terminal basic helix-loop-helix-Per/ARNT/Sim (bHLH/PAS) domain, the serine/threonine rich (S/T) domain, the nuclear receptor interacting domain (RID), the CBP(cAMP-response element binding protein-binding protein) interacting domain (CID) or activation domain 1 (AD1), and the activation domain 2 (AD2) or the histone acetyltransferase (HAT) domain at the C-terminus [10, 11]. Each domain has different interacting partners that confer various functions (Fig. 1.1). The bHLH/PAS domain harbors nuclear localization signals (NLS) and is the most conserved region. This domain is also termed activation domain 3 (AD3) as it is responsible for the interaction of SRCs with multiple co-coactivators and non-NR transcriptional factors. CoCoA was shown to interact with SRC-2 through the bHLH/PAS domain and work cooperatively with p300/CBP co-coactivators to regulate NR-mediated gene transcription [12]. hBrm-associated factor 57 (BAF57), a core component of SNI/SWF chromatin remodeling complex, binds to the bHLH/PAS domain of SRCs and bridges the SNI/SWF chromatin remodeling complex to ER/SRCs transcription complex to promote estrogen-responsive gene transcription [13]. Melanoma antigen gene protein-A11 (MAGE-11) interacts with both TIF2 and AR and potentiates AR transcriptional activity probably through stabilizing the AR-TIF2 transcription complex on the target gene



**Fig. 1.1** Structural domains and transcriptional interacting partners of SRCs. SRC proteins contain five functional domains: the N-terminal bHLH/PAS domain, the serine/threonine rich (*S/T*) domain, the nuclear receptor interacting domain (*RID*), the p300/CBP interacting domain (*CID*) or activation domain 1 (*AD1*), and the C-terminal activation domain 2 (*AD2*). SRC-1 and SRC-3 harbor a histone acetyltransferase domain (*HAT*) in the C-terminus. A representative list of transcriptional interacting partners within each domain of SRCs are indicated above (for interacting transcriptional factors) or below (for interacting coactivators) the structure. Interacting proteins are referenced from [8, 9] and as mentioned in the text

promoter [14]. The bHLH/PAS domain also mediates the interaction of SRCs with several non-NR transcription factors such as Stat3 [15] and p53 [16] that are important factors in cancer.

The *S/T*-rich domains of SRCs are frequently targeted by protein kinases and phosphatases, which regulate SRC protein stability and activity [17]. The *S/T*-rich domain of SRC-3 mediates its interaction with E2F1, an essential transcription factor in cell cycle control [18]. SRCs bind to NRs through the *RID* domain that harbors three “LXXLL” NR-binding motifs where “L” represents leucine residue and “X” denotes any amino acid [19, 20]. The interactions of SRCs with NRs are either hormone-dependent or hormone-independent based upon the NRs that SRCs are bound to and the growth conditions. Besides mediating the interaction with NRs, the *RID* domain of SRC-3 is important for its interaction with NFκB [21]. Following the binding to NRs, SRCs recruit p300/CBP histone acetyltransferases through the *CID* domain, which promotes chromatin remodeling and the recruitment of general transcription machinery [5, 22–24]. In the C-terminus of SRCs resides the activation domain 2 (*AD2*) that recruits CARM1 and PRMT1 methyltransferases [25, 26]. Interestingly, the C-terminus of SRC-1 and SRC-3 also contains a *HAT* domain [6, 27], but its functional substrates remain to be substantiated. In addition, the C-terminus was shown to mediate the interaction of SRCs with AP-1 transcription factors that play critical roles in cancer cell proliferation and invasion [28].

Of note, SRCs also have been shown to interact with other oncogenic transcription factors such as Rb [29] and HIF1α [30], and to potentiate activities of these transcription factors, although it is unclear which precise domains within SRCs are required for these interactions. Taken together, SRCs interact with a variety of transcriptional factors and coregulators through their five functional domains, suggesting that SRCs are important molecules that integrate diverse cellular processes.

### 1.3 Molecular Codes of SRCs: PTMs Targeted by Multiple Signaling Pathways

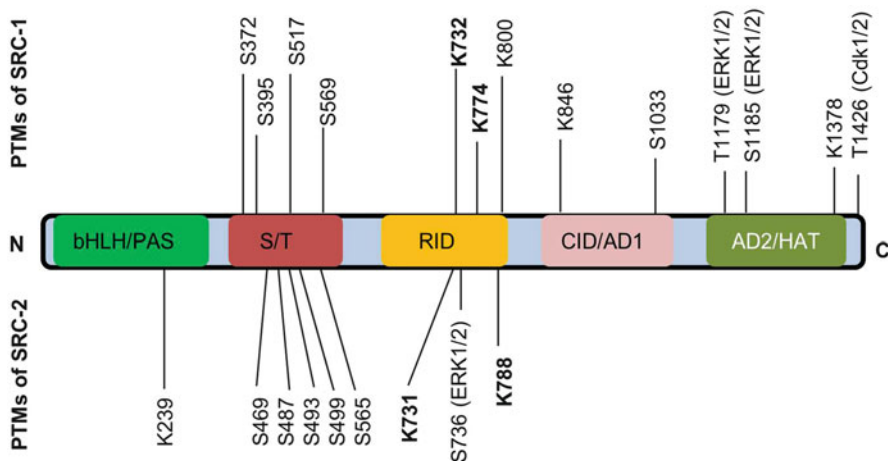
As coactivators of a variety of transcription factors, the activity and functions of SRCs are regulated by multiple signaling pathways. The molecular regulation of SRCs' activity and functions are determined by post-translational modifications (PTMs, Figs. 1.2 and 1.3), including phosphorylation, ubiquitination, sumoylation, acetylation, and methylation, all of which coordinately regulate SRCs' cellular localization, stability, and the interactions with their functional partners.

### 1.4 Phosphorylations

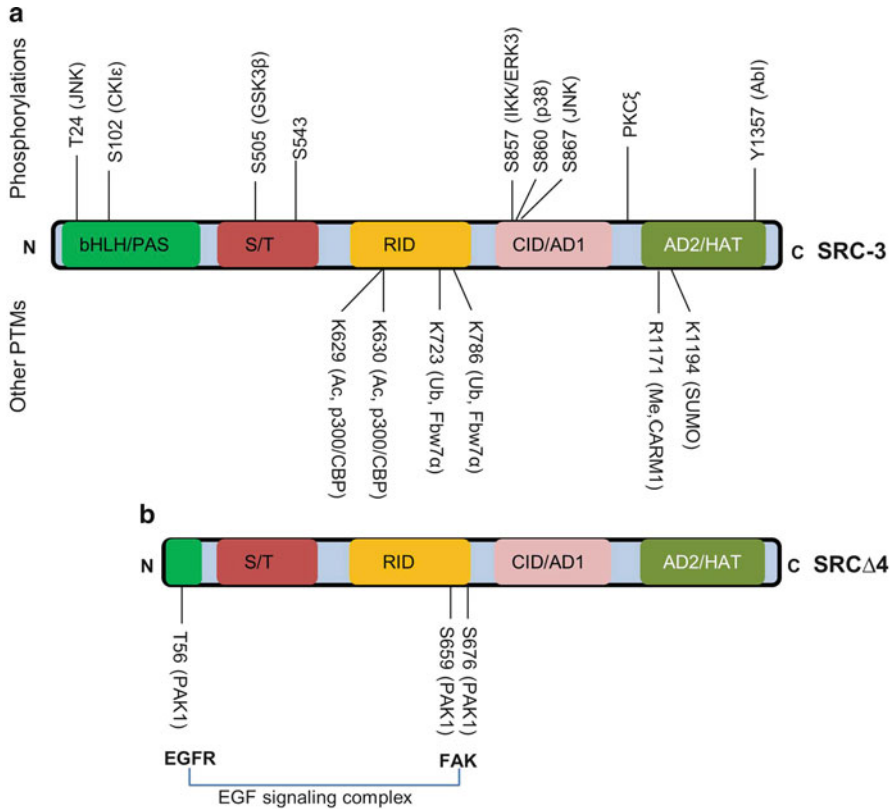
SRCs are phosphorylated by protein kinases in response to multiple signals including hormones, growth factors, and cytokines. These signals work independently or in concert to regulate SRCs' activities and functions.

### 1.5 Hormone-Induced Phosphorylations of SRCs

Hormones stimulate target gene transcription not only by activating hormone receptors via direct binding, but also by activating protein kinases that subsequently phosphorylate hormone receptors and coregulators including SRCs (Fig. 1.4). Hormones

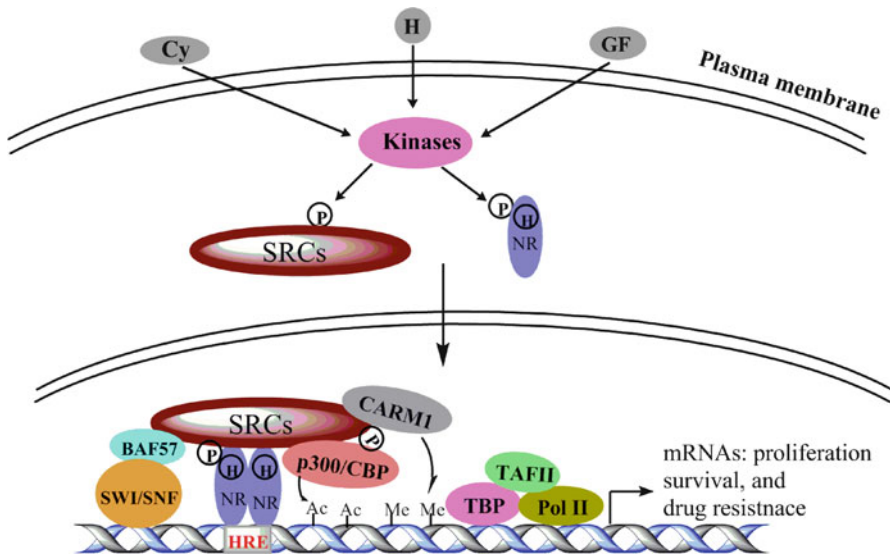


**Fig. 1.2** PTMs of SRC-1 and SRC-2. Some identified serine (S) and threonine (T) phosphorylation sites and sumoylated lysine (K) residues of SRC-1 and SRC-2 are indicated in the schematic structure. In the “( )” are shown certain kinases that target the specific phosphorylation residues. The two conserved sumoylation sites within RID domain of SRCs are shown in *bold*



**Fig. 1.3** PTMs of SRC-3 and SRC-3Δ4. **(a)** Selected phosphorylation sites of serine (S), threonine (T), or tyrosine (Y), lysine (K) residues with ubiquitination (Ub), sumoylation (SUMO), or acetylation (Ac), and arginine (R) residue with methylation (Me) of SRC-3 are indicated in the schematic structures. In the “( )” are also shown certain modifying enzymes for each specific PTM. Both K723 and K786 are sumoylation sites as well that are conserved in SRCs. **(b)** Phosphorylation codes of SRC-3Δ4 that are targeted by PAK1 for EGF signal transduction to FAK. PAK1 phosphorylates SRC-3Δ4 at T56, which mediates the interaction with EGFR, and at S659 and S676, which is important for the interaction with FAK. See the text for details (It should be noted that SRC-3 contains over 50 different PTMs that have been identified by a variety of techniques)

such as estrogen, progesterone, androgen, and glucocorticoid stimulate the activation of multiple kinases such as ERK1/2, Akt, p38, and JNK; rapid activations of these kinases by hormones are referred to as non-genomic signaling in contrast to direct actions of the receptors on the nuclear genome [31]. In response to E2 stimulation, SRC-3 is phosphorylated at multiple residues including T24 in the N-terminus, S505 and S543 in the S/T-rich region, and S857, S860, and S867 in the RID region [32]. E2-induced phosphorylation of SRC-3 occurs acutely (within minutes) and is dependent on ERα [33]. Phosphorylations at these residues promote the interaction of SRC-3 with ERα and CBP, and augment SRC-3’s transcriptional activity.



**Fig. 1.4** SRCs-mediated hormone signaling and the cross-talk with growth factor and cytokine signals in regulating NR target gene expression. Upon the binding of hormone (*H*), nuclear receptors (*NRs*) dimerize and bind to the hormone responsive element (*HRE*) of target genes. SRCs coactivate gene transcription by interacting with DNA-bound NRs and then recruiting secondary coactivators including p300/CBP histone acetyltransferases and CARM1/PRMT1 histone methyltransferases. p300/CBP and CARM1/PRMT1 elicit histone acetylation (*Ac*) and methylation (*Me*), respectively, both of which facilitates the assembly of the general transcriptional machinery consisting of TBP, TAFIIs, and Pol II, and the subsequent gene transcription. SRCs also are capable of recruiting SWI/SNF chromatin remodeling complex via BAF57 and further potentiate gene transcription. The transcriptional activities of SRCs and NRs are regulated by multiple signaling pathways including those of cytokines (*Cy*), growth factors (*GF*), and non-genomic hormone actions, mainly through protein kinase-mediated phosphorylations (*P*) that are important for the interactions of SRCs with NRs and other coactivators

Interestingly, while androgen/AR induces SRC-3 phosphorylations similar to E2/ ER $\alpha$ , progesterone/PR is unable to do so, suggesting there is ligand/receptor/coactivator specificity in hormone-induced SRC phosphorylations. In agreement with this notion, SRC-2 is a primary coactivator for glucocorticoid receptor (GR) and is phosphorylated upon the stimulation of dexamethasone at five residues (S469, S487, S493, S499, and S565) in the S/T-rich region and one residue (S736) in the RID region [34]. Phosphorylations of SRC-2 facilitate GR transcriptional activity. Similarly, progesterone/PR stimulates SRC-1 phosphorylations that are important for SRC-1 transcription activity (Weiwen Long and Bert O'Malley, unpublished data). Collectively, these findings demonstrate that phosphorylations of SRCs serve as an integrating link between non-genomic and genomic actions of hormones.

## 1.6 Phosphorylations of SRCs Induced by Cytokines and Growth Factors

SRCs also are phosphorylated upon stimulation by growth factors and/or cytokines, which facilitates their functions in coactivating NR-mediated gene expression in both ligand-dependent and ligand-independent mechanisms; these stimulations serve as important molecular mechanisms for anti-hormone resistance during cancer therapy. SRC-1 is phosphorylated at T1179 and S1185 by MAPK upon stimulation by interleukin 6 (IL-6) and co-activates AR in a ligand-independent manner in prostate cancer cells [35]. Interestingly IL-4 promotes PP2A-directed dephosphorylation of SRC-1 which is important for SRC-1/Stat6-regulated IL-4 target gene expression in Ramos B lymphoma cells [36]. Cytokines such as TNF $\alpha$  stimulate IKK-directed phosphorylation of SRC-3 which potentiates NF $\kappa$ B-mediated gene expression in breast cancer cells [32, 37].

SRC-1, SRC-2, and SRC-3 all are known to be regulated by growth factor signals. Epidermal growth factor (EGF) stimulates ERK2-directed phosphorylations of SRC-1 that are important for the interaction of SRC-1 with CBP in PR-dependent transactivation [38]. T1426 in AD2 of SRC-1 is targeted by Cdk1 and Cdk2, and this phosphorylation is important for PR/SRC-1-mediated cell cycle control [39]. SRC-2 is phosphorylated at S736 by EGF stimulation, and S736-phosphorylated SRC-2 promotes AR-dependent but ligand-independent transactivation, suggesting a potential role of SRC-2-mediated cross-talk between growth factor signaling and AR signaling in recurrent prostate cancer progression [40]. SRC-3 activity is tightly regulated by growth factor signaling. Both EGF and IGF-1 stimulate SRC-3 phosphorylation at tyrosine 1357 (Y1357) that is directed by AbI kinase in breast cancer and lung cancer cells [41]. Phosphorylation of Y1357 is critical for SRC-3 oncogenic activity in coactivating ER $\alpha$  and NF $\kappa$ B and promoting anchorage-independent cancer cell growth. Heregulin 1 $\beta$ , an EGF-like growth factor, stimulates SRC-3 phosphorylation through ERBB2 oncogenic kinase [42] which is implicated in the breast cancer tamoxifen resistance. cAMP/PKA signaling also induces SRC-1 and SRC-2 phosphorylation and potentiates NR-mediated transactivation in a ligand-independent manner [43, 44].

## 1.7 Phosphorylation Codes for SRC-3 $\Delta$ 4 Acting as an EGF Signaling Adaptor

SRC-3 $\Delta$ 4 is a splicing variant of SRC-3 with the deletion of exon 4 (Fig. 1.3b) [45, 46]. In comparison with full-length SRC-3 protein, SRC-3 $\Delta$ 4 lacks an N-terminal bHLH/PAS region that harbors the NLS. Consequently, SRC-3 $\Delta$ 4 primarily localizes in the cell cytosol due to its absence of an NLS. Upon EGF stimulation, PAK1 phosphorylates SRC-3 $\Delta$ 4 on T56 at the N-terminus and S659 and S676 within the RID region. Phosphorylations of SRC-3 $\Delta$ 4 promote its localization to the plasma membrane region where it interacts with EGFR through the N-terminus, which is

mediated by T56 phosphorylation, and with FAK through the RID region, which is mediated by phosphorylations of S659 and S676 (Fig. 1.3b). SRC-3 $\Delta$ 4 mediates the interaction between EGFR and FAK, thereby promoting EGF-induced c-Src activation and FAK phosphorylation on Y925, which in turn drives cancer cell migration and metastasis.

## 1.8 Ubiquitination and Its Regulation by Phosphorylation

Ubiquitination plays an essential role in regulating the stability and functions of SRC proteins. Ubiquitination of SRCs is frequently dependent on phosphorylations of specific residues that mediate the interaction of SRCs with the ubiquitin E3 ligases. The stability and activity of SRC-3 have been shown to be regulated by several protein kinase signals that are coupled to different E3 ligase complexes. GSK3 $\beta$  phosphorylates SRC-3 at S505 in the S/T-rich region, which is required for the binding of Fbw7 $\alpha$ , a component of the SCF (Skp, Cullin, F-box protein containing) E3 ligase complex. SRC-3 is then ubiquitinated by SCF<sup>Fbw7 $\alpha$</sup>  at lysine 723 (K723) and K786 that are within the receptor-interacting domain. Interestingly, mono-ubiquitinations at K723 and K786 enhance the interaction of SRC-3 with ER $\alpha$ , ER $\alpha$ 's phosphorylation at S118, and expression of the target genes in response to E2 stimulation [47]. Subsequent poly-ubiquitinations then lead to the degradation of SRC-3 and termination of SRC-3/ER $\alpha$ -regulated gene transcription. Ubiquitination-coupled activation of SRC-3 is also manifested by retinoic acid (RA) signaling, which involves the phosphorylation of SRC-3 at S860 by RA-activated p38, the subsequent phospho-S860-mediated recruitment of Cullin 3-based E3 ligase, ubiquitination of SRC-3, and finally activation of SRC-3/RAR-regulated gene transcription [48, 49]. In addition, SRC-3 protein stability and activity are regulated by a phospho-dependent degron that is located in the N-terminal bHLH/PAS region [50, 51]. Ser102 in the degron is phosphorylated by CKI (casein kinase I), which is required for the recruitment of a speckle-type POZ protein (SPOP)-based E3 ligase complex and the subsequent ubiquitination and turnover of SRC-3. Interestingly, phosphatases PP2A and PP1 target phosphorylated Ser102 and inhibit SRC-3 protein ubiquitination [50].

In addition to ubiquitin-dependent proteasomal degradation pathways, SRC-3 protein turnover is regulated by an ubiquitin-independent mechanism [52]. Importantly, PKC $\zeta$  phosphorylates multiple residues in an acidic fragment that is important for the interaction of SRC-3 with the C8 subunit of the 20S proteasome, and enhances SRC-3 protein stability by inhibiting both ubiquitin-dependent and ubiquitin-independent proteolytic pathways [53].

In contrast with the extensive study on SRC-3, much less is known about the regulation of ubiquitination and stability of SRC-1 and SRC-2. However, a single nucleotide polymorphism (SNP) P1272S was shown to increase SRC-1 protein stability by disrupting a potential GSK3 $\beta$ -directed phospho-dependent degradation



code in the AD2 region of SRC-1 [54]. Although no specific phosphorylation and ubiquitination sites were revealed, an ubiquitination-coupled activation mechanism for SRC-2 was shown to be regulated by cAMP/PKA signaling [44].

## 1.9 Sumoylation

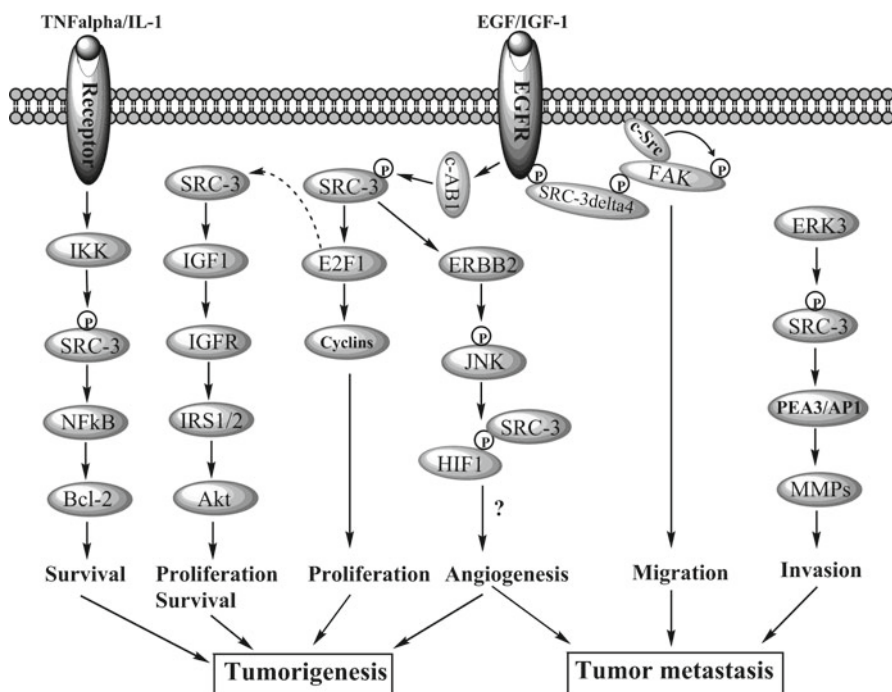
Sumoylation is a type of PTM that involves an addition of small ubiquitin-like modifier (SUMO) to the lysine residues of proteins [55]. In spite of its structural and enzymatic processing similarities to ubiquitination, sumoylation often alters a protein's binding affinity with the associating partners or its subcellular localization rather than degradation. All of the SRCs were shown to be sumoylated on two conserved lysine residues of the nuclear receptor-interacting domains (Figs. 1.2 and 1.3); sumoylations alter the interaction of SRCs with NRs and their transcriptional activities [56]. However, while sumoylations enhance the interaction of SRC-1 and SRC-2 with PR and AR respectively [57, 58], and their retention and transactivity in the nucleus, SRC-3 transactivity is attenuated by sumoylations at K723 and K786 [47]. As aforementioned, K723 and K786 of SRC-3 are ubiquitination sites as well, and the ubiquitinations on these sites are important for the interaction of SRC-3 with ER $\alpha$  and their transactivity. As such, the attenuation of SRC-3 transactivity by sumoylations at K723 and K786 is likely due to the competitive blocking of ubiquitinations on these two sites. Although the regulation of SRCs' sumoylations by phosphorylations have not been reported to date, both SRC-2 and SRC-3 harbor a phosphorylation-dependent sumoylation motif (PDSF)  $\psi$ KxE $\times$ SP (where  $\psi$  is a large hydrophobic residue) that has been characterized in heat shock factor 1 (HSF-1) and MEF2A transcription factors [59, 60]. S736 within the PDSF of SRC-2 is a phosphorylation site targeted by EGF/ERK1/2 signaling [40], and K731 is a sumoylation site that enhances SRC-2 transactivity [58]. It would be of interest to determine whether this is a *bona fide* PDSF that plays a role in SRC-2 activity.

## 1.10 Acetylation and Methylation

SRCs act as bridging factors to recruit histone acetyltransferases such as p300/CBP and histone methyltransferases such as CARM1/PRMT1 to DNA-bound NRs to remodel chromatin and regulate gene transcription (Fig. 1.4). Interestingly, these histone modifying enzymes target not only histones but also SRCs and NRs [61–64]. SRCs were shown to be acetylated by p300 [61] and methylated by CARM1 upon E2 stimulation [63, 64]. While histone acetylation and methylation facilitate the assembly of the transcription machinery and subsequent gene transcription, acetylation or methylation of SRC-3 leads to the dissociation of NRs/cofactors complex and the termination of gene transcription.

## 1.11 Molecular Actions of SRCs in Cancer Cells In Vitro and in Mouse Tumor Models In Vivo: SRCs as Integrators of Multiple Signaling Pathways

SRCs, in particular SRC-3, function as important mediators and integrators of a variety of oncogenic signaling (e.g., hormones, growth factors, and cytokines) pathways to regulate virtually every aspect of cellular processes: proliferation, survival, migration, and invasion (Figs. 1.4 and 1.5). Hormone signaling acts independently



**Fig. 1.5** SRC-3 integrates multiple signaling pathways to promote tumorigenesis and metastasis. Besides its regulation of hormone signaling as illustrated in Fig. 1.4, SRC-3 integrates multiple growth factor and cytokine signaling pathways to regulate a variety of cancer cell processes. Only a subset of these pathways are illustrated in Fig 1.5. In response to TNF $\alpha$ /IL-1 signals, SRC-3 is phosphorylated by IKKs and coactivates NF $\kappa$ B-mediated Bcl-2 expression for cancer cell survival. SRC-3 upregulates the expression of multiple components of IGF1-IGFR-PI3K/Akt pathway that is important for both cancer cell proliferation and survival. Upon EGF or IGF-1 stimulation, SRC-3 is targeted by protein kinases including c-AB1, and then coactivates E2F1-mediated expression of cell cycle genes including cyclins E and A. SRC-3 itself is a target gene of E2F-1 (indicated by a *dashed arrow*), and upregulation of SRC-3 by E2F-1 might boost other signaling pathways regulated by SRC-3, for example, the IGF1/Akt pathway. SRC-3 is also important for the activation (phosphorylations) of ERBB2 and EGFR and the downstream kinases such as JNK, and plays a role in tumor angiogenesis, likely by coactivating HIF1. In addition, SRC-3 $\Delta$ 4 acts as an EGF signaling adaptor by bridging EGFR to FAK, and promotes EGF-induced FAK phosphorylations and cancer cell migration. Furthermore, SRC-3 is targeted by ERK3 kinase and coactivates PEA-3/AP-1-mediated MMP gene expression for promoting cell invasion

or synergistically with growth factor or cytokine signaling to regulate these cellular processes in which SRCs play important, integrating roles (Fig. 1.4). The actions of SRCs are exquisitely regulated by PTMs (mainly phosphorylations) that are stimulated by the oncogenic signals. Increased growth factor and/or cytokine signaling hijack SRCs to drive the progression of cancer cells from hormone-dependent to hormone-independent growth and elicit anti-hormone resistance, for example, anti-estrogen resistance in breast cancer. Based on the expression status of hormone receptors (mainly ER and PR) and growth factor tyrosine kinase receptors (mainly ERBB2 and EGFR) and the origin of cancer cells, breast cancers can be classified as 4 subtypes [65, 66]: luminal A ( $ER^+ PR^+ ERBB2^-$ ), luminal B ( $ER^+ PR^+ ERBB2^+$ ), ERBB2-enriched ( $ER^- PR^- ERBB2^{++}$ ), and basal-like (also known as triple-negative,  $ER^- PR^- ERBB2^-$ ). Accompanied by enhanced growth factor signaling, luminal A subtype can progress to luminal B and further to ERBB2-enriched subtype, which leads to advanced cancer phenotype and increased anti-estrogen resistance. Basal-like breast cancer cells often have upregulated EGFR expression and high aggressiveness. As discussed below, SRC-1 and SRC-3 play critical functions in all four subtypes of breast cancer, whereas the roles of SRC-2 are minor.

## 1.12 SRCs with Hormones/NRs-Mediated Signaling

### 1.12.1 Estrogen/ER Signaling in Breast Cancer

Both SRC-1 and SRC-3 act as coactivators of  $ER\alpha$  to mediate estradiol signaling in promoting breast cancer cell proliferation and survival. SRC-1 is important for estradiol-induced cell proliferation of MCF-7, a breast cancer cell line of luminal A subtype [67–69]. Depletion of SRC-1 differentially affected E2-inducible genes: with a significant decrease in the expression of pS2 and stromal cell-derived factor 1 (SDF-1) but little effect on c-Myc [69]. Both MCF-7 and T47D (another breast cancer cell line of luminal A subtype) overexpress SRC-3. Depletion of SRC-3 in these cells diminishes the expression of estrogen/ER target genes including cyclin D1, c-Myc, and Bcl-2, and inhibits cell proliferation but increases apoptosis [70, 71]. Consequently, depletion of SRC-3 in MCF-7 cells inhibits estrogen-induced colony formation in soft agar and xenograft tumor growth in nude mice [72]. E2 exerts non-genomic signaling by activating multiple kinases including ERK1/2 and  $IKK\alpha$ . E2-induced phosphorylations of SRC-3 via ERK1/2 and  $IKK\alpha$  are critical for SRC-3's activity in promoting the expression of E2 target genes such as cyclin D1 and c-Myc [32, 73]. The functional relationship between SRC-3 and  $ER\alpha$  in tumorigenesis was revealed in a mouse mammary tumor virus (MMTV)-SRC-3 transgenic mouse model [74]. Transgenic overexpression of SRC-3 induced tumors primarily in mammary glands but also in other organs including uterus and lung, suggesting SRC-3 is a *bona fide* oncogene. Ovariectomy in MMTV-SRC-3 mice greatly decreased mammary tumor formation, and genetic deletion of  $ER\alpha$  in MMTV-SRC-3 mice by crossing with  $ER\alpha$ -null mice completely abolished mammary tumor formation [75]. Taken together, these findings suggest that SRC-3 and possibly SRC-1 are critical for E2/ER signaling in promoting breast cancer progression.

### ***1.12.2 Androgen/AR Signaling in Prostate Cancer***

While estrogen/ER signaling is critical for the progression of breast cancer, androgen/AR signaling plays an essential role in hormone responsive prostate cancer. All of three SRC members have been shown to coactivate AR to mediate androgen signaling in prostate cancer cells. Depletion of either SRC-1 [76], SRC-2 [77, 78], or SRC-3 [79, 80] significantly decreases androgen-dependent AR transcriptional activity and LNCaP prostate cancer cell growth in culture and in xenograft tumor mouse models. On the contrary, overexpression of SRC-3 or SRC-2 in LNCaP greatly enhances the responsiveness of AR to androgen or to ligand-independent stimulation and promotes cell growth.

### **1.13 Interplay of SRCs with ERBB2 Signaling: Anti-estrogen Resistance in Breast Cancer**

ERBB2, a member of the EGFR family, is an oncogenic protein that is frequently overexpressed in advanced breast cancer. ERBB2 overexpression promotes tumor progression, and is highly associated with the progression of ER-positive breast cancer cells from estrogen-dependent to estrogen-independent growth; the overexpression is concomitant with the gain of resistance to anti-estrogen drugs [81]. Both SRC-1 and SRC-3, in concert with ERBB2, play a critical role during these processes. Genetic loss of SRC-3 completely suppressed MMTV-ERBB2 induced mouse mammary tumor formation in association with a remarkable decrease in phosphorylations of ERBB2 and the downstream kinases JNK and Akt [82]. Interestingly, tumor angiogenesis also was curtailed significantly due to the loss of SRC-3. SRC-3 was confirmed as a pro-angiogenic factor recently [83] and acts as a coactivator of HIF1 $\alpha$  [30]. While loss of SRC-1 did not significantly decrease the average tumor number formed in MMTV-ERBB2 transgenic mice, it increased tumor latency and greatly inhibited tumor metastasis to the lung [84]. Under cell culture conditions, stable exogenous expression of ERBB2 in MCF-7 elicits an estrogen-independent cell growth and resistance to tamoxifen, both of which were significantly inhibited by depletion of SRC-3 [42]. A similar synergistic role of ERBB2 with SRC-3 or SRC-1 was shown in BT474, a luminal-B subtype of breast cancer cell line with overexpression of ERBB2 [85, 86]. ERBB2 overexpression activates the downstream kinases ERK1/2, JNK, and Akt that phosphorylate ER $\alpha$  and SRCs, which leads to activation of ER $\alpha$  under low concentration or even in the absence of estrogen [42, 87]. In addition to ER $\alpha$ , SRC-3 and SRC-1 interact with and coactivate other transcription factors such as Ets and PEA3 to promote cancer cell growth and invasion in response to enhanced ERBB2 signaling [88, 89]. Conversely, SRC-3 positively regulates ERBB2 expression by competing with PAX-2 (a repressor of ERBB2 gene expression) for the binding to the ER $\alpha$ -bound site of the ERBB2 gene [90]. These findings suggest a positive feedback between ERBB2 and SRC-3 that regulates breast cancer cell proliferation and anti-estrogen resistance.

## 1.14 Interplay Between SRCs and EGFR Signaling: From the Membrane to the Nucleus

EGF/EGFR signaling is implicated in multiple cancers including those of breast, prostate, and lung. EGF signaling stimulates SRCs' phosphorylation and activation; activated SRCs then work with transcriptional factors including E2F-1, ETS, and AP-1 to regulate cell proliferation, migration, and invasion (Fig. 1.5).

In breast cancer, increased EGFR signaling is frequently associated with the invasive and triple-negative phenotype. In a triple negative breast cancer cell line MDA-MB231, SRC-3 and its N-terminus-deleted isoform SRC-3Δ4 elegantly regulate distinct aspects of the EGF signaling at different cellular locations (Fig. 1.5). SRC-3Δ4 acts as a signaling adaptor bridging EGFR to FAK at the plasma membrane to mediate activation of FAK and promote cell migration upon the EGF signal [46]. SRC-3 is phosphorylated by Ab1 kinase at Y1357 in response to EGF stimulation, and this phosphorylation is important for SRC-3's function in coactivating AP-1 and E2F1 in the nucleus and promoting cell growth [41]. Intriguingly, EGFR tyrosine phosphorylation and activity is regulated by SRC-3. Depletion of SRC-3 greatly decreased EGF-induced EGFR tyrosine phosphorylation, which led to decreased JNK kinase activity and growth inhibition of MDAMB231 cells [91]. While the detailed molecular mechanism is unclear, downregulation of tyrosine phosphatases by SRC-3 partly contributes to an increase of EGFR phosphorylation.

In prostate cancer, enhanced EGFR signaling is highly associated with castration-resistant (androgen-independent) cancer progression. On one hand, EGF signaling stimulates AR tyrosine phosphorylation (Y534) via c-Src kinase [92], and AR tyrosine phosphorylation promotes its nuclear localization and transactivity. On the other hand, EGF signaling targets SRCs via MAPK-directed phosphorylations. For example, SRC-2 is phosphorylated at S736 by EGF stimulation, and S736-phosphorylated SRC-2 promotes AR-dependent but androgen-independent transactivation [40]. Together, EGF signaling stimulates AR/SRCs' transactivity and promotes prostate cancer cell growth in culture and tumor growth in castrated mice [40, 92].

## 1.15 Regulation of IGF-1/Akt Signaling by SRC-3 and SRC-1

IGF-1/Akt signaling is another molecular pathway that is regulated by SRCs and is critical for SRCs' oncogenic functions (Fig. 1.5). The IGF-1/Akt signaling pathway initiates with the binding of IGF-1 to its receptor (IGF-1R) on the cell membrane and the subsequent activation of IGF-1R by auto-tyrosine phosphorylation, followed by the recruitment of insulin receptor substrate (IRS) proteins and IRS-mediated activation of the phosphatidylinositol 3-kinase (PI3K)/Akt pathway [93]. SRC-3 regulates the expression levels of multiple components of the IGF-1/Akt pathway, including IGF-1/IGF-2, IGF-1R, IRS-1/IRS-2, and Akt in breast cancer cells [94] and prostate cancer cells [95], thereby regulating the activities/

phosphorylations of IGF-1R and Akt and promoting cancer cell proliferation and anchorage-independent cell growth. The regulation of IGF-1/Akt signaling by SRC-3 was corroborated *in vivo*. Increased IGF-1 expression and activation of IGF-1R, Akt, and mTOR was seen in MMTV-AIB1 (SRC-3) transgenic mice, which led to spontaneous mammary tumor formation [74]. In contrast, genetic depletion of SRC-3 in v-Ha-Ras transgenic mice caused a remarkable decrease in tumor initiation and metastasis to the lung, partly due to decreased expression of IRS-1 and IRS-2 and the attenuated Akt activity [96]. Loss of SRC-1 did not affect primary mammary tumor growth, but greatly decreased tumor metastasis to the lung in MMTV-polyoma middle T antigen (PyMT) transgenic mice by downregulating ERBB2 expression and Akt phosphorylation [97].

## 1.16 Interplay of SRCs with Cytokine Signaling in Promoting Cancer Cell Aggressiveness

IL-6 signaling promotes castration-resistant prostate cancer progression by activating AR in an androgen-independent mechanism [98–100]. Besides the direct effect on AR, IL-6 signaling modulates SRCs' activity as well. SRC-1 phosphorylation by MAPK in response to IL-6 is important for ligand-independent activation of AR [35]. In addition, upregulation of SRC-2 in LNCaP cells upon long-term treatment with IL-6 is associated with acquired resistance to bicalutamide, an anti-androgen drug [101]. Conversely, cytokine production can be regulated by SRCs. For example, SRC-1 upregulates colony-stimulating factor-1 (CSF-1) expression and promotes the recruitment of macrophages to the tumor site, which contributes to tumor metastasis [97].

SRC-3 is phosphorylated upon the stimulation of cytokines such as TNF $\alpha$  and IL-1 $\beta$  [32, 37]. Phosphorylations of SRC-3 stimulate the interactions of SRC-3 with ER $\alpha$  and NF $\kappa$ B, which are important for TNF $\alpha$ -induced cyclin D1 expression and cell proliferation [102]. Interestingly, SRC-3 was shown to interact with translational repressors TIA1 (T cell restricted antigen 1) and TIAR (TIA1 related homologue) and regulate the translation of TNF $\alpha$  and interleukin 1 mRNAs [103], for which the implication in cancer is unclear at present.

A recent study revealed an intriguing interplay between a cleaved isoform of SRC-1 and TNF $\alpha$  signaling during endometriosis [104] which shed new light on the roles of SRCs in inflammation-associated diseases such as cancers. Endometriosis is an inflammation-driven disease that is initiated by the migration of endometrial cells to distal sites. While TNF $\alpha$  is well-known as a critical driving factor for endometriosis, it is less clear how the intrinsic pro-apoptotic activity of TNF $\alpha$  is silenced during this process. It is shown in this interesting study that TNF $\alpha$ -induced MMP9 cleaves SRC-1 at Pro-790, and the c-terminus of cleaved SRC-1 promotes endometriosis by blocking caspase8-mediated apoptosis and by stimulating

epithelial-to-mesenchymal transition (EMT) for increased invasiveness. Given the positive associations of both SRC-1 and inflammation with advanced and metastatic tumor stages, cytokine signaling and SRC-1 conceivably could synergistically promote cancer progression and metastasis following similar mechanisms as shown in endometriosis. Indeed, SRC-1 was shown to positively regulate TWIST, a master regulator of EMT, thereby promoting tumor cell migration/invasion and metastasis [89]. It would be interesting to determine whether SRC-1 undergoes proteolytic cleavage to produce the cleaved isoform during cancer progression and whether this cleaved form of SRC-1 is responsible for the upregulation of TWIST and EMT-associated tumor cell migration and invasion.

### **1.17 Phospho-dependent Regulation of SRC-3 by an Atypical MAPK for Cancer Cell Invasion**

SRC-3 promotes cancer cell invasion by coactivating PEA-3- and AP-1-regulated matrix metalloproteinase (MMP) expression [105–107], but the invasive signals to SRC-3 and the molecular regulation of SRC-3 proinvasive activity were not elucidated until a recent study that revealed a phospho-dependent regulation of SRC-3 proinvasive activity by an atypical MAPK ERK3 (Fig. 1.5) [108]. ERK3 was identified as an interacting partner of SRC-3 by immunoprecipitation-mass spectrometry (IP-MS) analyses. ERK3 phosphorylates SRC-3 at serine 857 (S857), and this ERK3-mediated phosphorylation at S857 is essential for SRC-3's interaction with the ETS transcription factor PEA3, promoting upregulation of matrix metalloproteinase (MMP) gene expression and proinvasive activity in lung cancer cells. ERK3/SRC-3 signaling drives cancer cells to invade and form tumors in the lung. As such, this study not only revealed a molecular mechanism for regulating SRC-3 proinvasive activity, but also identified a novel oncogenic function for ERK3 in promoting lung cancer invasiveness.

### **1.18 Alterations of SRCs and the Clinical Implications in Cancers**

As transcriptional coactivators integrating multiple signaling pathways to regulate cancer cell proliferation, survival, migration, and invasion, SRCs are highly dysregulated in a variety of cancers including breast cancer, prostate cancer, endometrial cancer, ovarian cancer, lung cancer, colorectal cancer, liver cancer, and pancreatic cancer. Alterations of SRCs, including primarily gene amplification, mRNA or protein overexpression, are implicated in cancer progression and metastasis and tumor resistance to therapeutic interventions.

## 1.19 Gene Amplification

Gene amplification is one of the fundamental features for defining an oncogene. SRC genes, in particular SRC-3 (also known as AIB1-Amplified in breast cancer gene 1), are amplified in multiple human cancers. Gain of copy numbers of SRC-1 and SRC-2 genes were reported in a recent study with a cohort of 218 prostate tumors consisting of 181 primaries and 37 metastases [109]. Of particular note, SRC-2 gene amplification was detected in 8 % of primary tumors and 37 % of metastases. Gain of SRC-2 expression is associated with increased rates of prostate tumor recurrence. SRC-3 gene amplification has been shown in multiple cancers including breast cancer (with 5–10 % frequency [4, 110]), ovarian cancer (with 7–25 % frequency [110, 111]), colorectal cancer (with 10–32 % frequency [112, 113]), lung cancer (with 8.2–27 % frequency [114, 115]), and hepatocellular cancer (40 % frequency, [116]). SRC-3 gene amplification contributes to upregulation of SRC-3 mRNA and protein in cancers, and is positively correlated with advanced tumor stages.

## 1.20 Mutations

In contrast to high frequencies of gene amplification and mRNA/protein overexpression, gene mutation of SRCs is rarely detected in cancers. Even though a few point mutations of SRC-1 [117] and SRC-2 [109] were identified in tumors, the frequency is very low (~1 %) and the pathological association is undetermined. Interestingly, a fusion between MOZ (monocytic leukemia zinc finger) gene and TIF2 (SRC-2) gene has been repeatedly detected in acute myeloid leukemia [118–120]. MOZ-TIF2 fusion protein retains the PHD zinc finger domain and the MYST domain of MOZ and the CBP-interacting domain (CID) and activation domain 2 (AD2) of TIF2. The recruitment of p300/CBP via the CID of MOZ-TIF2 is essential for leukemogenesis of the fusion gene [120].

## 1.21 Upregulation of mRNA and Proteins

Expression of SRCs, in particular SRC-3 and SRC-1, are frequently upregulated in a variety of cancers. SRC-3 is the second most overexpressed oncogene among all human cancers, second only to c-myc. Upregulation of SRCs is often co-current with elevated protein kinase signaling, which indicates high tumor grade, increased tumor invasiveness, and tumor resistance to therapeutic treatments. A substantial number of studies have investigated the expression and clinical implication of SRCs in a variety of cancers, with focus mostly on breast cancer and prostate cancer.



## 1.22 Breast Cancer

Breast cancer progression relies on two major signaling pathways: hormone (e.g. E2/ER $\alpha$ ) signaling and epidermal growth factor signaling pathways [81]. Antihormonal drugs (e.g. tamoxifen, an estradiol antagonist, and letrozole, an anti-aromatase inhibitor) have been commonly used for treating ER/PR-positive breast cancers. However, antihormone resistance (either naïve or acquired resistance after therapy) and associated cancer recurrence have been major obstacles for curing breast cancer patients. The acquisition of resistance to antihormonal drugs is often associated with a transition of hormone signaling-dependent to growth factor signaling-dependent tumor growth [121, 122]. SRC-1 and SRC-3 are overexpressed at high frequency in breast cancer, and their overexpression is implicated both in hormone-dependent and in hormone-independent breast cancer progression and metastasis.

SRC-1 expression has been shown to be significantly increased in around 19–30 % breast tumors [123–125]. In line with its primary role in promoting cancer cell migration and invasion *in vitro* and tumor metastasis in animal models, upregulation of SRC-1 is highly correlated with lymph node metastasis and poor disease-free survival (DFS) of breast cancer patients [88, 126]. Another important role for SRC-1 is the regulation of cancer cell sensitivity to anti-hormone drugs. Indeed, SRC-1 expression has been demonstrated as a predictor of anti-estrogen resistance and/or tumor recurrence following therapy [125, 126].

The implication of SRC-3 expression in breast cancer progression has been extensively studied. From various separate studies [4, 72, 124, 127, 128], overexpression of SRC-3 mRNA and protein has been shown in the range of from 13 % to 74 % of breast tumors, with an average of around 50 % overexpression rate. In agreement with the broad roles of SRC-3 in regulating cancer cell proliferation, survival, migration, and invasion in cultured cells and in animal models, overexpression of SRC-3 is positively associated with advanced tumor grade, increased tumor invasiveness and metastasis, and worse DFS in both ER $\alpha$ -positive and ER $\alpha$ -negative breast tumors [4, 87, 124, 127]. SRC-3 overexpression is frequently associated with enhanced protein kinase signaling. Tyrosine kinase receptor ERBB2 is frequently amplified (gene copy) and overexpressed (mRNA and protein) in cancers [129], with the highest frequency in breast cancer (~25 %). Simultaneous overexpression of SRC-3 and ERBB2 are reported in several studies [87, 128, 130, 131], and their co-overexpression indicates increased tumor resistance to tamoxifen treatment and increased tumor recurrence. Although the regulation of the IGF1R/Akt signaling pathway by SRC-3 has been well demonstrated by cell culture studies and mouse mammary gland tumor models, the correlation between these two has not been shown in tumor studies of breast cancer patients. Given the frequent alterations of both of these two factors in breast cancer, it is of high clinical significance to investigate the association of SRC-3 and IGF1R/Akt signaling pathways and their implications in cancer progression in more detail.

In contrast with ample evidence for the critical roles of SRC-1 and SRC-3 in breast cancer progression and metastasis, few studies have provided conclusive data to support a definite role for SRC-2 in breast cancer.

### 1.23 Prostate Cancer

Androgen/AR signaling plays a critical role in the initiation and progression of prostate cancer, and has been a major therapeutic target for treating this disease [132, 133]. Androgen ablation therapy (mainly by chemical castration) effectively inhibits tumor growth during the initial treatment. Unfortunately, most tumors relapse and become resistant to androgen ablation therapy. Castration-resistant cancer progression or recurrence is frequently associated with an advanced and metastatic tumor phenotype and has been a major obstacle for curing prostate cancer. AR and its target genes are commonly expressed in and are believed to drive recurrent prostate cancers [134]. In addition to AR gene mutations and AR overexpression, alterations in AR coactivators including SRCs and upregulation of growth factor signaling are two other major molecular mechanisms for castration-resistant tumor progression [135]. While genetic alterations of the SRC-1 gene are rare in prostate tumors, upregulation of SRC-1 has been shown by a few studies [76, 117, 136]. Upregulation of SRC-1 protein is associated with lymph node metastasis [76] and tumor recurrence after androgen deprivation therapy [117, 136]. Like SRC-1, SRC-2 expression is highly increased in recurrent prostate tumors following androgen deprivation therapy [117, 136]. More importantly, a recent study showed that elevated SRC-2 expression, probably due to SRC-2 gene amplification, was detected in both primary and metastatic prostate tumors [109]. Similar findings were reported for SRC-3 in prostate cancer [79, 106, 137, 138]. Upregulation of SRC-3 is positively correlated with increased Akt activity in prostate tumors [79, 138], which affirms a positive regulatory role of SRC-3 in Akt signaling in prostate cancer.

### 1.24 Lung Cancer

SRC-3 functions as an oncogene in lung cancer. Transgenic overexpression of SRC-3 in mice causes spontaneous lung tumor formation [74]. SRC-3 gene amplification and protein overproduction were shown in as high as 27 % of non-small cell lung cancers (NSCLCs) in one study [115]; overexpression correlates with poor disease free and overall survival. Interestingly, ERK3, a kinase that phosphorylates SRC-3 and confers SRC-3 pro-invasive activity in lung cancer cells, was shown to be highly upregulated in lung cancer [108]. Overexpression of SRC-3 protein in lung cancer also was reported in two other studies [139, 140]. The implications of SRC-1 and SRC-2 in lung cancer are not known.

In addition to the cancer types discussed above, SRC-3 has been shown to be overexpressed in many other cancers: a 64 % overexpression rate in high grade ovarian tumors [141], a 67 % overexpression rate in hepatocellular carcinomas [116], a 35 % overexpression rate in colorectal carcinomas [112], and a nearly 70 % overexpression frequency in pancreatic tumors [142].

## **1.25 Tumor Suppressor Functions of SRC-3 and SRC-2 in Specific Tissue Context**

In contrast with the ample evidence for SRC-3's function as an oncogene in a multitude of cancers, deletion of the SRC-3 gene promotes proliferation of lymphocytes and induces spontaneous malignant B-cell lymphoma upon aging in mice [143]. Similarly, while SRC-2 has been identified as an oncogene in prostate cancer, a recent study revealed a tumor suppressor role for SRC-2 in liver cancer [144]. Although the molecular mechanisms underlying the unexpected tumor-suppressing roles of SRC-2 and SRC-3 are not understood, these findings suggest that SRCs, as transcriptional coactivators, can regulate cell proliferation and survival either positively or negatively, depending upon the cell- and tissue context.

## **1.26 SRCs as Prognostic Biomarkers and Therapeutic Drug Targets**

Increased expression and activities of SRCs not only are implicated in cancer progression and metastasis, but also are positively associated with drug resistance, including anti-estrogen resistance in breast cancer [87, 123, 125, 145, 146], resistance to EGFR inhibitors in lung cancer [115]), and resistance to chemotherapeutic drugs such as cisplatin and doxorubicin [30, 147, 148]. Hence, novel therapeutic drugs targeting SRCs might be utilized individually or in combination with other therapeutic drugs for treating cancers in different subtypes and at different stages.

## **1.27 Targeting SRCs by Intervening NR-SRC Interactions**

The binding of SRCs with NRs via SRCs' 'LXXLL' NR interacting motifs is critical for their transcriptional activity. In addition, the flanking amino acids of the 'LXXLL' motif are shown to confer an order of specificity on differential NR/SRCs interactions. On the basis of these molecular mechanisms, there have been efforts to develop peptides containing LXXLL motifs or identifying small molecules that can disrupt the interactions between NRs and SRCs. A screening of the phage display

library identified peptides that specifically and effectively inhibit ER $\alpha$  or ER $\beta$  transactivity [149–151], but it was unclear what specific ER/SRC interaction(s) was affected by these peptides. Soon after this, a peptide specifically blocking the interaction of SRC-2 with TR $\beta$  [152] and other peptides preventing the binding of SRC-1 with ER $\alpha$  or ER $\beta$  [153, 154] were identified utilizing a similar strategy. In addition, small molecule inhibitors (SMIs) were identified for targeting SRCs' interaction with ER $\alpha$  [155] and TR $\beta$  [156]. Although these identified peptides or SMIs were shown to efficiently inhibit NRs' transactivity, their efficacy on NR/SRCs-mediated cell functions were not evaluated in animals.

## 1.28 Small Molecule Inhibitors Targeting SRCs for Degradation

Since overexpression of SRC proteins, in particular SRC-3, is highly associated with advanced tumor progression and drug resistance, a potentially more effective strategy would be to identify small molecules that directly target SRCs and downregulate SRCs' protein stability and activities. Based on this idea, a recent study identified a SMI for SRC-1 and SRC-3 by both activity-based and stability-based screening assays [157]. This proof-of-principle drug, gossypol, downregulates the stability and activities of both SRC-1 and SRC-3 via direct binding, but is less selective for SRC-2 and other cofactors. Importantly, gossypol greatly increases the response of cancer cells to inhibitors of growth factor signaling, including MEK inhibitor AZD6244, EGFR inhibitor AG1478, and IGF-1R inhibitor AG1024. This study demonstrates that SRCs are accessible therapeutic targets to SMIs and encourages additional high throughput screenings for identifying drugs targeting SRCs.

SRCs also can serve as diagnostic and prognostic biomarkers, as they are altered in cancers at multiple levels including gene amplification, mRNA/protein overexpression, and protein posttranslational modifications. Of particular interest is the phosphorylation of SRC-3 at S857. S857 appears to be a hotspot that is targeted by multiple kinases and confers to SRC-3 and SRC-3 $\Delta$ 4 a variety of oncogenic functions: augmentation of cancer cell motility when targeted by PAK-1 [46], increase of cancer cell invasion when targeted by ERK3 [108], and gain of chemotherapeutic drug resistance when targeted by IKK [30]. It is of significant clinical interest to test whether phosphorylation on this site is positively associated with human cancer progression and metastasis, thereby serving as a diagnostic and/or prognostic tumor biomarker.

## 1.29 Conclusion and Perspective

Cancer cells must acquire a variety of capabilities for tumor initiation, uncontrolled outgrowth, invasion of surroundings, and metastasis to the distant organs. Hanahan and Weinberg have summarized these required capabilities as eight hallmarks of

cancer: sustaining proliferative signaling, evading growth suppressors, resisting cell death, enabling replicative immortality, inducing angiogenesis, activating invasion and metastasis, and two more recently recognized hallmarks-reprogramming of energy metabolism and evading immune destruction [158]. Despite little information on the roles of SRCs in those two emerging hallmarks, substantial evidence exists that SRCs act as integrators for the other hallmarks, thereby making great contributions to cancer cells for acquisition of these hallmarks. It has been recognized that cancer cells reprogram energy metabolism to provide fuels and biosynthetic intermediates (nucleosides and amino acids) for uncontrolled cell growth and/or invasion by enhancing energy consumption from glycolysis [159]. Although the roles of SRCs in reprogramming energy metabolism of cancer cells have not been revealed, a number of studies, mostly by using SRC knock-out animals, have shown that SRCs are critical regulators of energy metabolism of glucose and lipids [160–166]. SRC-1 has distinct functions in cell metabolism of white and brown adipose tissues: loss of SRC-1 renders animals more susceptible to high fat diet-induced obesity, whereas loss of SRC-2 or SRC-3 confers protection against it. As such, future work on SRCs in cancer cell metabolism is warranted and should provide new insights on the molecular mechanisms by which SRCs alter the cues for uncontrolled growth and aggressiveness of cancers.

Evading immune destruction and harnessing tumor-associated inflammation is another hallmark that is important for cancer progression. The roles of SRCs in this process have been scarce but surely are worthy of investigations. Although their exact roles in tumor-associated inflammation remain to be determined, SRCs are engaged in cytokine signaling and inflammation. As mentioned above, SRCs are activated (phosphorylated) by cytokine signaling and function as coactivators of NF $\kappa$ B and/or Stats to positively regulate cytokine signaling in cancer cells [32, 35, 37, 101, 102] and in animal models of inflammation-associated disease [104, 167–169]. Hence, it would be of clinical significance to determine in more detail the roles of SRCs in the underlying molecular mechanisms of tumor-associated inflammation. Finally, as our recent proof-of-principle study demonstrates that SRCs are accessible therapeutic targets for SMIs, more effort should be put on future high throughput screenings for therapeutic drugs targeting SRCs for cancers.

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