



Molecular Cochaperones: Tumor Growth and Cancer Treatment

Citation

Calderwood, Stuart K. 2013. "Molecular Cochaperones: Tumor Growth and Cancer Treatment." *Scientifica* 2013 (1): 217513. doi:10.1155/2013/217513. <http://dx.doi.org/10.1155/2013/217513>.

Published Version

doi:10.1155/2013/217513

Permanent link

<http://nrs.harvard.edu/urn-3:HUL.InstRepos:11879066>

Terms of Use

This article was downloaded from Harvard University's DASH repository, and is made available under the terms and conditions applicable to Other Posted Material, as set forth at <http://nrs.harvard.edu/urn-3:HUL.InstRepos:dash.current.terms-of-use#LAA>

Share Your Story

The Harvard community has made this article openly available. Please share how this access benefits you. [Submit a story](#).

[Accessibility](#)

Review Article

Molecular Cochaperones: Tumor Growth and Cancer Treatment

Stuart K. Calderwood

Division of Molecular and Cellular Biology, Department of Radiation Oncology, Beth Israel Deaconess Medical Center, Harvard Medical School, 99 Brookline Avenue, Boston, MA 02215, USA

Correspondence should be addressed to Stuart K. Calderwood; scalderw@bidmc.harvard.edu

Received 11 February 2013; Accepted 1 April 2013

Academic Editors: M. H. Manjili and Y. Oji

Copyright © 2013 Stuart K. Calderwood. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Molecular chaperones play important roles in all cellular organisms by maintaining the proteome in an optimally folded state. They appear to be at a premium in cancer cells whose evolution along the malignant pathways requires the fostering of cohorts of mutant proteins that are employed to overcome tumor suppressive regulation. To function at significant rates in cells, HSPs interact with cochaperones, proteins that assist in catalyzing individual steps in molecular chaperoning as well as in posttranslational modification and intracellular localization. We review current knowledge regarding the roles of chaperones such as heat shock protein 90 (Hsp90) and Hsp70 and their cochaperones in cancer. Cochaperones are potential targets for cancer therapy in themselves and can be used to assess the likely prognosis of individual malignancies. Hsp70 cochaperones Bag1, Bag3, and Hop play significant roles in the etiology of some cancers as do Hsp90 cochaperones Aha1, p23, Cdc37, and FKBP1. Others such as the J domain protein family, HspBP1, TTC4, and FKBP1 appear to be associated with more benign tumor phenotypes. The key importance of cochaperones for many pathways of protein folding in cancer suggests high promise for the future development of novel pharmaceutical agents.

1. Introduction

Chaperones/HSPs. Molecular chaperones are a diverse group of proteins involved in the maintenance of other “client” proteins in folded and active conformations in all cellular organisms [1–5]. The term molecular chaperone is however generally reserved for proteins with a dedicated role in protein folding and refolding derived from the *HSPA* (HSP70), *HSPB* (small HSP), *HSPD* (Hsp60), *HSPC* (Hsp90), and *HSPH* (large HSP) gene families originally discovered as heat shock protein (HSP) genes [2, 6]. Products of these genes direct the folding of much of the proteome, resulting in the formation of proteins or protein complexes capable of metabolic functions in the cell. A subset of these proteins is also expressed at high levels in cells after proteotoxic stresses such as exposure to heat shock, heavy metals, alcohols and sodium arsenite [7–10]. Hence, they came to be known as heat shock proteins [7, 10]. Proteotoxic stresses lead to abundant levels of unfolded, aggregated, and ubiquitinated proteins, and cells respond to such an insult by abundant synthesis

of HSPs capable of resolving these perturbations to the proteome [11]. These proteins are known to increase cell survival after stress both through direct chaperoning of malformed proteins as well as inhibition of programmed cell death [12–14]. Altered demand for molecular chaperones is also associated with human diseases. For instance, in age-related degenerative diseases, aggregation-prone proteins accumulate and appear to exhaust the capacity of the molecular chaperone system [15–17]. Of more relevance for the current review, accumulation of mutated and overexpressed oncoproteins in cancer also leads to a demand for molecular chaperones and elevated levels of HSPs is characterize many malignancies [18–20]. This dependence on molecular chaperones appears to be a soft spot in the armor of the cancer cells and has led to the development of drugs aimed at depleting molecular chaperones and degrading the cancer proteome, leading to loss of viability of the tumors [21, 22]. In addition to their role in chaperoning the cancer cell proteome, HSPs are essential for evasion of a number of pathways of cell inactivation. For instance Hsp70 is involved in the inhibition of both caspase dependent apoptosis and senescence, key pathways in tumor

TABLE I: Cochaperones.

Name	Function	Conserved domain	Role in cancer	Associated proteins	Reference
Hsp70					
JDP	Substrate selection	J	Supp	—	[101–105]
HspBP1	Nucleotide exchange	—	Supp	—	[96–99]
Bag1	Nucleotide exchange	BAG, UBL	Onc		[92]
Bag3	Nucleotide exchange	BAG, WW	Onc	HspB8	[90, 91, 93]
Hop	Adaptor	TPR	Onc	TDB proteins	[107–109]
Hsp90					
Sgt1	Substrate selection	CHORD	—	Hsp70	[116–119]
P23	ATPase inhibitor	p23	Onc	—	[112–115]
Aha1	ATPase inhibitor	Aha1	Onc	—	[131, 132]
Cdc37	ATPase inhibitor	Hsp90 bd	Onc	Kinases	[120–129]
Hop	Adaptor	TPR	Onc	TDB	[107–109]
Cyp40	Immunophilin	TPR, PPIase	—	TDB	[32, 134]
FKBP1	Immunophilin	TPR, PPIase	Onc	TDB	[135, 136]
FKBP2	Immunophilin	TPR, PPIase	Onc	TDB, dynein	[134, 137, 138]
PP5	Protein phosphatase	TPR	—	TDB	[139–147]
TTC4	Adaptor, replication	TPR	Supp	TDB, Myst, MOF	[148–153]
TTC5	Adaptor, transcription	TPR	—	TDB, p300	[88, 154–157]
XAP2	Nuclear receptors	TPR	—	TDB	[158–161]

suppression [14, 23–25]. The mechanisms which underlie the elevated expression of molecular chaperones of the *HSPA* and *HSPD* families in cancer are currently unclear but may involve the dysregulation of transcription factor HSF1 first shown to couple stress to HSP transcription [8, 26]. HSF1 is elevated and becomes activated in a wide range of cancers, its expression is coupled to the severity of disease, and it has been shown to be coupled to upstream signaling pathways in the malignant cell [27–31].

Cochaperones. As with many cellular proteins with dynamic function, HSP molecular chaperones do not appear to work alone and require the assistance of accessory proteins, known in this case as cochaperones [1, 3, 32–35] (Table 1). Three particular classes of chaperone appear of high significance in cancer and these include the *HSPA*, *HSPB*, and *HSPC* families [19]. We will discuss here the *HSPA* and *HSPC* molecular chaperone families and the associated co-chaperones. Each HSP class appears to be regulated by an individual cohort of co-chaperones and these molecules that may be significant factors in cancer and carcinogenesis and potential targets for therapy.

Much has been discovered regarding the molecular and biochemical properties of *HSPA* family members such as Hsp70 and Hsc70. Hsp70 family members are described as being regulated by a bidirectional heterotropic allosteric mechanism by a tautology between target polypeptides and adenosine nucleotides [3, 36]. Thus Hsp70, family proteins contain two major functional domains including an N-terminal nucleotide binding region and a C-terminal region that can interact with the hydrophobic residues in partially unfolded proteins (client binding domain) [5, 36–39] (Figure 1). “Empty” Hsp70 contains ATP in its N-terminal

domain, and in this form the C-terminal domain can interact with suitably unfolded clients [3]. Binding is stabilized when the uptake of clients in the C-terminal domain triggers the ATPase activity of the N domain [3]. Clients are subsequently released, usually when refolded. This mechanism has been proposed to involve at least two modes of action, including (1) through stable “holding” of the client, Hsp70 maintains the levels of free unfolded client low enough to prevent aggregation; (2) inducing local unfolding in client protein domains and thus overcoming kinetic barriers to the native folded state. In the cell these biochemical properties of Hsp70 and Co. is regulated by co-chaperones that can couple activity to cell physiology/pathology [32, 40].

For Hsp70, co-chaperones include a large family of J domain proteins that can bind to specific substrates and foster association of such clients with Hsp70 [40, 41]. These proteins contain a J domain capable of interacting with the ATP domain of the Hsp70s and a client binding domain that can associate with unfolded proteins and transfer them to the client binding site of Hsp70, resulting in a multifold stimulation in the ATPase activity of client-bound Hsp70 [41–43]. There are at least 49 members of the human J domain protein family [44–46]. Following the “client holding” stage of the cycle, the next step is client release and perhaps refolding. In order for Hsp70 to release clients, ADP must dissociate from the N-terminal domain, a relatively gradual reaction that can however be strongly stimulated by nucleotide exchange factors such as BAG domain proteins [45–48]. The BAG (Bcl2-associated athanogene) domain interacts with the ATPase domain of Hsp70 and stimulates ADP release permitting client efflux by allosteric regulation of the N-terminal domain [47, 48]. Other nucleotide exchange factors include HspBP1 [49, 50]. The cytoplasmic members

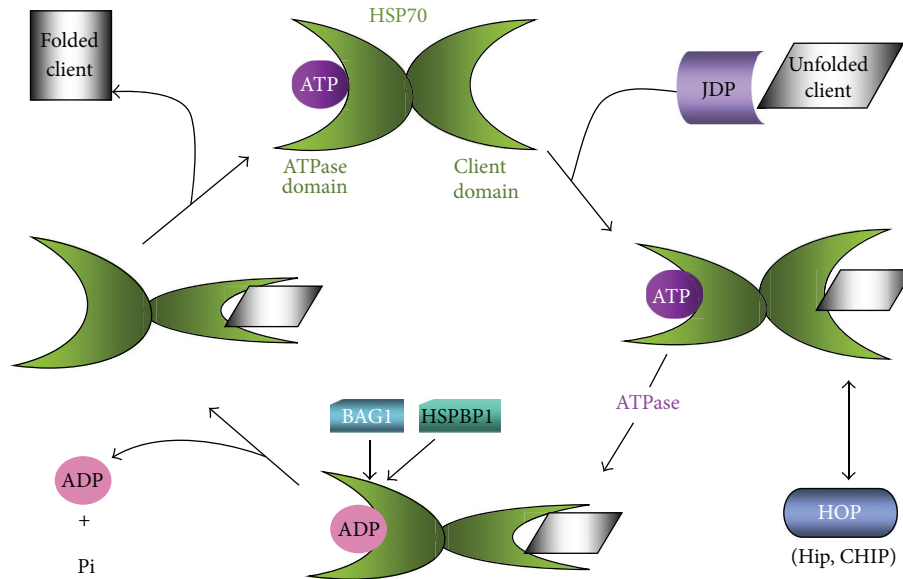


FIGURE 1: Reaction cycle for Hsp70 family polypeptides. Hsp70 proteins are portrayed as consisting of two major functional domains, including an N-terminal ATPase domain and a C-terminal client protein binding domain. When ATP occupies the ATPase domain, the C-terminal client protein-binding domain has weak affinity for clients. In the first step in chaperoning, the client protein (here depicted as unfolded) associated with a J domain protein (JDP) is able to bind Hsp70. This interaction causes allosteric changes in the N-terminal ATPase domain, ATP hydrolysis, and tight binding of substrate. Release of the client is then associated with nucleotide exchange loss of ADP and phosphate and replacement with ATP. In order to occur at a significant rate in cells nucleotide exchange factors such as Bag1 and HspBP1 are required. Released client is depicted as “folded.” However, the precise nature of the processes involved in achieving this state are not clear. We also show an alternative fate for Hsp70 client complexes involving the scaffold protein Hop. Hop can bind the extreme C-terminus of Hsp70 and couple it to other proteins such as Hsp90. Clients can thus be passed from Hsp70 to Hsp90 in a coordinated folding process.

of the hspa family also contain a TPR domain binding (TDB) site at the extreme C-terminus. The TPR (tetratricopeptide) domain is a protein interaction motif found in a range of proteins many of which interact with molecular chaperones Hsp70 and Hsp90 [51]. In the case of Hsp70, such TPR domain proteins include the scaffold protein Hop/Sti (Hop: Hsp70/Hsp90 organizing protein) and the ubiquitin E3 ligase CHIP [52–54].

HSPC (Hsp90) proteins, although bearing minimal sequence conservation with the HSPA family, have some biochemical properties in common with the Hsp70 proteins [55–57]. The HSPC family includes four major members, including two cytoplasmic proteins Hsp90 α and Hsp90 β , an ER resident member glucose-regulated protein 94 (grp94) and a mitochondrially located member TRAP1 [57–60]. Hsp90 α and Hsp90 β are of most significance in cancer where they are expressed to very high levels and are significant targets for drug development [18, 21, 61, 62]. These molecules have in common with Hsp70 the ability to bind and hydrolyze ATP and to bind and modify the conformations of clients [63]. Hsp90 proteins function as dimers and the ATP binding, and hydrolysis cycles regulate dimerization and client binding as with Hsp70 [56, 64–67]. The nature of the client interaction domain is not entirely clear although it is thought to bind the amino acid and middle domains on the outside of the dimer [68, 69]. In addition, cytoplasmic Hsp90 proteins also contain a TPR domain binding site at the C-terminus. Hsp90 interacts with an array of co-chaperones.

These include p23/Sba1, a protein with intrinsic chaperone activity that stabilizes the closed conformation of Hsp90 by inhibiting ATPase activity and thus prolongs interaction with clients such as steroid hormones [70, 71]. Another key co-chaperone is p50/*Cell Division Cycle 37* (Cdc37) that binds the N-terminal ATP binding domain, inhibits ATPase activity, and is of particular significance in interaction with protein kinases [72–75]. While p23 and Cdc37 appear to function by stabilizing Hsp90 client interactions, another co-chaperone Sgt1 appears to function at the beginning of the cycle binding ATP-free Hsp90 and helping to recruit clients to the chaperone in an analogous way to the function of JDPs in Hsp70 [76]. The other core co-chaperone is *Activator of the Hsp90 ATPase* (Aha1), a protein that binds Hsp90 in the middle domain and triggers ATPase activity and perhaps dissociation of clients [77, 78]. In addition to this core group, a large array of TPR domain co-chaperones bind to the C-terminus TDB motif of Hsp90 and can modulate chaperoning functions in specific clients, including scaffold protein Hop, protein phosphatase PP5, immunophilins FKBP1, FKBP2, Cyp4, and TPR domain proteins TTC4, TTC5, and XAP2/AIPL1 [68].

The TBD motifs of Hsp70 and Hsp90 proteins are key to determining the role of both proteins in intracellular protein quality control as well as more subtle interaction with bound clients. When Hsp70 binds to the multiple TPR domain scaffold protein Hop on its specific recognition site, Hsp90 can also bind to another TPR motif in Hop [79, 80]. Such coupling permits a coordinated pathway of remodeling of some clients,

with initial folding of nascent proteins by Hsp70/HDJ complexes commencing on the ribosome, preceding fine tuning of client conformation by Hsp90/p23/Cdc37/immunophilin complexes and full maturation of functional polypeptides [73]. Alternatively, protein quality control can be biased towards proteolysis and disposal of damaged proteins when the E3 ligase CHIP binds the TBD motifs of either Hsp70 or Hsp90 [54, 81, 82]. Triage between the various arms of protein quality control involves complex regulatory decision making. For instance, formation of the Hsp70/Hop/Hsp90 complex is favored by the nucleotide exchange factor Bag1 [45]. Alternatively, Bag3 favors the disposal of polyubiquitinated proteins by macroautophagy [83, 84]. As mentioned above, Hsp90 can bind a range of co-chaperones through the C-terminal TBD motif and can affect changes in phosphorylation of clients by PP5 and maturation of clients such as steroid hormones by immunophilins Cyp40, FKBP1, and FKBP2 [68]. Although the immunophilins are able to effect proline isomerization as a basic function, these properties do not seem essential in Hsp90 cochaperone mode [85, 86]. Other mechanisms seem to be involved. TTC 5 is an interesting molecule with potentially profound roles in cell physiology. This protein contains 6 TPR motifs and binds to transcriptional co-activators, activating transcription by factors such as p53 and HSF1 [87, 88]. Binding to the TBD motifs on Hsp70 or Hsp90 might thus permit coupling of protein unfolding in stress or quality control to transcriptional remodeling.

2. Hsp70 Cochaperones and Cancer

2.1. BAG Domain Proteins. As mentioned above, BAG domain proteins (Bag1-6) can associate with the nucleotide binding domain of Hsp70 family members, stimulate nucleotide exchange, and thus promote molecular chaperone activity (Figure 1) [3]. Bag1-6 are multidomain proteins, each of which contains the Hsp70-binding BAG domain close to the C-terminus [46, 47, 89, 90]. The two family members with most significance in cancer appear to be Bag1 and Bag3. Bag1 also contains a UBL domain that can bind polyubiquitinated proteins and indeed has been shown to bias protein quality control towards proteolytic degradation through its ability to bind polyubiquitinated proteins [3]. Bag3 contains WW and proline rich repeat sequences that appear to permit it to interact with cell signaling molecules [46]. Indeed, Bag3 can interact with the molecular chaperone HspB8 and mediate macroautophagy [83]. Another difference between Bag1 and Bag3 is that while Bag1 is constitutively expressed, Bag3 is conditionally inducible and indeed responds to the stress-inducible transcription factor HSF1 [91]. Elevated expression of Bag1 and Bag3 in each case signals a poor prognosis for cancer bearing patients. This effect may be related to the ability of BAG/Hsp70 complexes to inhibit apoptosis [90–92]. Indeed double knockdown of Bag1 and Bag3 in acute myeloid leukemia caused loss of antiapoptotic proteins Bcl2, Bcl-XL, Mcl1, and phosphor-ERK1/2 [92]. The roles of Bag1 and Bag3 are somewhat complicated by their opposing role in protein quality control, with Bag1/Hsp70 favoring proteasomal degradation of clients (such as BCR-ABL oncoproteins)

and Bag3 competing for binding to Hsp70 and deterring entry into the proteasome pathway [45, 46]. For instance, complexing of Bag3 with Hsp70 can protect oncogenic IKK gamma from proteasomal degradation, increase flux through the NF kappa B pathway, and increase cell growth and survival [93].

2.2. HspBP1. Similar to the BAG domain proteins, HspBP1 is also a nucleotide exchange factor that can stimulate the ATPase cycle of Hsp70 (Figure 1). Although both proteins induce nucleotide exchange, the mechanisms employed for this activity appear to involve contrasting interactions with the ATPase domain [94]. In addition, HspBP1 appears to be able to oppose the proteolytic pathway of protein quality control and binding of the protein to the ATPase domain of Hsp70 inhibits the ubiquitin ligase activity of CHIP when attached to the TBP domain of Hsp70 [95]. In contrast to the BAG proteins, HspBP1 appears to play a suppressive role in a number of types of cancer [96]. HspBP1 levels are elevated in breast tissue and inversely related to aggressiveness [96]. In addition some chemotherapeutic agents can increase cytotoxicity by inhibiting Hsp70 function [97]. Hsp70 appears to inhibit a unique pathway of cell death in tumor cells involving lysosomal membrane permeabilization and activation of caspase 3 [98, 99]. HspBP1 appears to oppose this Hsp70-regulated pathway [97].

2.3. J Domain Proteins. JDPs are the most abundant family of Hsp70 co-chaperones with at least 49 members [44]. The founder member of the family is the *E. coli* DNAJ, which along with the prokaryotic Hsp70 (DnaK) and nucleotide exchange factor (Grpe) is responsible for the bacterial Hsp70 cycle as in Figure 1 [55, 100]. JDPs characteristically function by locating client proteins and ensuring their tight binding to Hsp70 [3, 44]. This is assisted by the ability of JDPs to stimulate the ATPase activity of the Hsp70 chaperone and lock the client into the closed peptide binding domain [44]. All JDPs contain the 70 amino acid J domain, which is essential for interaction of the protein with Hsp70. There are three families of JDP, including types I, II, and III [44]. JDPs tend to be either elevated to distinctly high levels or deregulated in cancer [101]. However, the majority of JDP, at least in studies carried out so far, appear to be tumor suppressive in nature [44]. Notable examples of tumor suppressive JDP include TID1/DNAJA3 that functions in the mitochondrial matrix as an inhibitor of carcinogenesis and *mammalian relative of DnaJ* (MRJ) that negatively regulates breast cancer malignancy and reduces b-catenin signaling [102–105].

2.4. Hop. Hop, also known as STI1, mediates Hsp70/Hsp90 interactions through their TBD domains [106] (Figure 1). Only a limited amount of information is available regarding the possible involvement of Hop in cancer. However, increased levels of Hop were observed in human colon cancer, associated with increased Hsp70, Hsp90, and Hop/Hsp70/Hsp90 complexes [107]. Hop expression is also increased in hepatocellular carcinoma [108]. Interestingly,

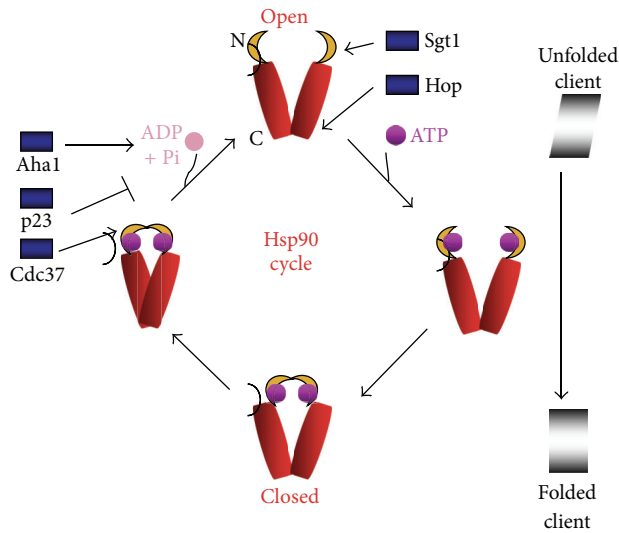


FIGURE 2: Reaction Cycle for Hsp90. Hsp90 functions as a dimer in a cycle of client binding, ATP binding, ATPase activity, and nucleotide exchange as with Hsp70. The dimers are in an open conformation when empty and a more closed conformation when ATP binds. Substrate binding is assisted by co-chaperone Sgt1. For Hsp90, in which prolonged “holding” of clients seems an important component of its cellular function, the co-chaperones p23 and Cdc37 inhibit ATPase activity and stabilize Hsp90 client complexes. For nucleotide exchange to take place after ATPase activity eventually occurs, Aha1 functions as an exchange factor. As with Hsp70, triage of the protein between pathways of protein quality control involves scaffold protein Hop that binds the C-terminal TPR domain-binding motif (TBD). Through the TBP, Hsp90 can interact with a range of TPR domain containing co-chaperones that regulate intracellular function.

knockdown of Hop by RNA targeting in pancreatic cancer cells reduced the levels of proteins that have been previously isolated as Hsp90 clients in cancer such as HER2, Bcr-Abl, c-Met, and v-Src, suggesting that Hop ablation in cancer cells could be functionally similar to Hsp90 inhibition which decreases tumor growth by reducing levels of key oncoproteins [18, 22, 109]. As mentioned above, Hop is a poly-TPR domain scaffold protein that couples Hsp90 to the Hsp70 folding cycle as well as to other co-chaperones, and loss of Hop may be functionally similar to deletion of the TBP domain of Hsp90, a modification that ablates chaperone function [106]. In addition, Hop knockdown also led to the loss of matrix metalloproteinase 2 (MMP-2) and a decrease in cancer cell migration, also consonant with a permissive role for Hop in cancer progression [109]. Hop is thus a co-chaperone for both Hsp70 and Hsp90, a coordinator of Hsp70/Hsp90 interaction, a scaffold for binding of other co-chaperones, and a potential target in cancer.

3. Hsp90 Cochaperones and Cancer

3.1. *P23*. P23 is an inhibitor of the ATPase activity of Hsp90 (Figure 2) and through this function can promote sustained interaction between hsp90 and a wide range of clients such as

steroid hormone receptors and HSF1 [70, 110]. Recent studies point to a role for p23 in tumor progression and cancer formation. High levels of p23 were associated with increased metastasis in breast cancer and indicated a poor prognosis including enhanced disease recurrence [111]. In addition, p23 targets genes involved in drug resistance and metastasis such as PMP22, ABCC3, AGR2, Sox2, TM4SF1, and NUPR were expressed to high levels in p23 overexpressing mammary carcinoma cells [111]. p23 could also be involved in the incidence of prostate cancer as a key component of the androgen receptor activity [112]. Interestingly, these effects may involve both Hsp90-dependent and Hsp90-independent effects. Hsp90-independent roles for p23 have been shown previously [113]. Another mechanism for increasing cancer incidence may involve inhibition of apoptosis in malignant cells. p23 is overexpressed in acute lymphoblastic leukemia (ALL) and functions as an inhibitor of chemotherapy induced apoptosis [114]. These effects may be connected to loss of the microRNA species has-miR-101 in childhood ALL cases and concomitant p23 dysregulation [114]. Interestingly, a novel plant product known as gedunin has been isolated that can bind p23, block its chaperoning and transcriptional activities, and lead to programmed cell death in malignant cells [115].

3.2. *Sgt1*. Sgt1 is a CHORD domain protein that acts early in the ATPase cycle of Hsp90 and may help to recruit client proteins in a similar manner to JDP for Hsp70 [116]. In addition, Sgt1 can bind to Hsp70 leading to the formation of an Sgt1/Hsp90/Hsp70 chaperone complex important in the function of leucine rich repeat proteins [117]. However, although Sgt1 shares sequence similarities with p23, few reports of a role for the protein in cancer are currently available. Sgt1 seems to be an important HSP co-chaperone in innate immune signaling through the intracellular NLR pathway and in kinetochore function [118, 119].

3.3. *P50/Cdc37*. Cdc37 appears to play a highly significant role in cancer and its forced expression in transgenic mice leads to prostatic hyperplasia and, when expressed in conjunction with the oncogene c-Myc, to prostate cancer [120, 121]. Cdc37 is also expressed to high level in other types of malignancy such as anaplastic large cell lymphoma, acute myelocytic leukemia, hepatocellular carcinoma, and multiple myeloma [122–125]. The key biochemical function of Cdc37 appears to slow down the ATPase cycle of the Hsp90 complex and extend the holding time of the client [73]. Cdc37 and Hsp90 form triple complexes with many proteins, being associated with protein kinases in particular [126, 127]. Such protein kinases include a long list of enzymes involved in promoting cell growth, including receptor tyrosine kinases epidermal growth factor (EGFR) and MET, nonreceptor tyrosine kinases SRC and LCK, and serine/threonine kinases RAF1, AKT1, IKK CDC2, and CDK2 (see [73, 74]). Not surprisingly, reduction in Cdc37 levels by RNA interference had a profound effect in reducing tumor cell growth [128, 129]. In prostate carcinoma, Cdc37 knockdown inactivated cell growth and sensitized tumors to Hsp90 inhibitors [128]. It is not clear why Cdc37 is selectively carcinogenic in

prostate as opposed to other tissues. One possibility is that the androgen receptor, one of the few nonkinase clients of Cdc37, is activated by elevated levels of Cdc37 [130]. However, Cdc37 knockdown inhibited growth of androgen receptor negative Prostate Carcinoma (PC-3 and DU-145) as effectively as it affected androgen-requiring LnCap cells [128]. In these cells, Cdc37 effectively inhibited both the ERK and Akt pathways as well as EGFR signaling [128] (J. Cheng & S.K. Calderwood, in preparation). Cdc37 therefore seems to be a strong molecular candidate for targeted therapy, particularly in prostate carcinoma [73].

3.4. Aha1. While many chaperones function to slow down the ATPase cycle of Hsp90, Aha1 triggers ATPase activity and release of client proteins from the complex [77]. Despite this, Aha1 appears to be involved in increasing the activity of c-Src by Hsp90 chaperone machines and maintaining signaling activity [131]. Aha1 mRNA levels are elevated in lymphoblast and testicular germ cells, although few studies have addressed levels in cancer [132]. However, Aha1 concentrations appear high in promyelocytic leukemia and Daudi Burkett's lymphoma cells [132]. Holmes et al. studied Aha1 protein levels in a range of human cancer cells and found markedly different levels in the different cell lines [133]. Treatment with the Hsp90 inhibitory drug 17-AAG increased Aha1 levels, an effect that appeared to reflect the activation of HSF1 by the Hsp90 ablation [133]. As might be predicted, reduction in Aha1 levels led to sensitization of cells to 17-AAG [133].

4. Hsp90 Interaction with TPR Domain Proteins

A number of proteins have been shown to bind to the TBD domains of Hsp90, including the scaffold protein Hop as mentioned above. These interactions have been intensively studied in regard to the regulation of steroid hormone receptors [63]. Hsp90 and co-chaperones are thought to be continuously required to maintain proteins such as glucocorticoid receptor (GR), mineralocorticoid receptor, and progesterone receptor in stable conformations receptive to activation by their respective ligands [32, 63, 134]. Receptors such as estrogen receptor and androgen receptor appear less prone to regulation by chaperone complexes [134]. TPR domain proteins that interact with the C-terminal TBD of Hsp90 include protein phosphatase 5 (PP5), immunophilins FKBP1/2 and Cyp40, and TPR additional domain proteins such as TTC4, TTC5, TPR2, XAP2, and AIPL1 [134].

Protein Phosphatase 5 (PP5). PP5 is a serine/threonine phosphatase and is a member of the PPP phosphatase family that also includes PPI and PPA2 [139–141]. Clearly, association with a protein phosphatase has considerable potential for modulating the properties of Hsp90 complexes. Indeed, binding of PP5 to Hsp90 has potentially pleiotropic effects as the enzyme may modify the phosphorylation of Hsp90 itself as well as modulating phosphorylated sites on other co-chaperones and on its bound clients [142, 143]. PP5 can dephosphorylate Hsp90 and thus positively regulate

its molecular chaperone activities [142, 144]. In addition, Hsp90-bound PP5 dephosphorylates the key co-chaperone Cdc37 on the residue serine 13, essential for intracellular function and thus reduces its ability to chaperone some of its many kinase clients [145]. The metabolic activities of chaperoned clients may be positively or negatively regulated by Hsp90-associated PP5, depending on the nature of the phosphorylation sites involved. For instance, in lipogenesis, PP5 can simultaneously activate GR and repress Peroxisome Proliferator Activated Receptor- γ (PPAR- γ) through dephosphorylation of certain serine residues [140]. In addition, Hsp90-PP5 interactions also influence cell cycle progression and DNA repair pathways through dephosphorylation of key Ser/Thr residues in DNA-dependent protein kinase and ATR [146, 147]. Thus, PP5 may play a key role in regulating many aspects of chaperone complexes in cancer although it is currently not clear what the overall effect of Hsp90-associated PP5 might be.

Immunophilins. Immunophilins are proteins that bind to immunosuppressive drugs such as cyclosporine and FK506 and have common domains with peptidyl-prolyl cis-trans isomerase (PPIase) activity [162]. At least three immunophilins with TPR domains, FKBP1, FKBP2, and Cyp40, are known to bind the TBD of Hsp90 and act as co-chaperones [68]. Cyp40 is present in complexes between Hsp90 and a number of steroid hormones such as GR and PR and increased transcriptional activity of the hormones when overexpressed [134, 163]. Activity appears to require the TPR and PPIase domains although a role for PPIase activity in the co-chaperone properties of Cyp40 has not been demonstrated [85, 86]. Cyp40 and other immunophilins may play a role in hormone-dependent malignancies such as prostate and breast cancer. Cyp40 and FKBP1 are elevated in prostate cancer compared to normal cells, positively regulate androgen dependent prostate cancer growth, and increase AR-dependent transcription [164, 165]. Growth of such cancers is suppressed by cyclosporine A and FK506, the immunophilin ligands that inhibited several stages of AR signaling [164, 165]. It had been shown previously that Cyp40 and FKBP2 are increased in mammary carcinoma cells by estradiol and that the antiestrogen drug ICI 182, 780 antagonized these increases [166].

FK506 binding proteins (FKBPs) including FKBP1 and FKBP2 are related proteins that, like Cyp40, contain a PPIase domain closely apposed to a TPR domain [135, 136]. As with Cyp40, co-chaperone activity is associated with the PPIase domain but does not require PPIase activity [137]. For FKBP2 at least, sequences in the PPIase domain may interact with the ligand binding domain of Hsp90 [137]. FKBP2 may function by increasing nuclear transport through interaction with the motor protein dynein. Although structurally similar, these two Hsp90 co-chaperones appear to have opposing effects on nuclear receptor transcriptional activity, with the tightly binding FKBP1 inhibiting activity and the more loosely associated FKBP2 activating at least in the case of MR, GR, PR and AR [134, 137]. These immunophilins may compete for binding to nuclear receptor-chaperone complexes through differential binding to the TBD of Hsp90, and for instances

FKBP2 can reverse the inhibitory effects of FKBP1 on GR activity [167]. However, Cyp40 was unable to oppose the trans-inhibitory effects of FKBP1 [134]. Recently another member of the FKBP family has emerged FKBP-like or FKBP1 that may have high significance in cancer [138, 168, 169]. FKBP1 has a conserved TPR domain although the PPLase domain is divergent compared with FKBP1, 2 [138].

As mentioned above-immunophilins appear to be significant in hormone-dependent cancer, and FKBP1 in particular is enriched in prostate cancer as opposed to benign tumors and stimulates androgen-dependent transcription and growth [164–166, 170, 171]. FKBP2 appears to play a role in breast cancer and treatment with estradiol led to a 14-fold increase in expression [166]. FKBP1 is associated with ER in breast cancer, and increased levels of the protein indicate a good prognosis in the case of this disease [138].

TTC4. Tetratricopeptide 4 (TTC4) is another TPR domain protein and was originally discovered in a screen for loss of heterozygosity in the chromosomal 1p31 region associated with breast cancer and was thus implicated as a tumor suppressor gene [148, 149]. TTC4 appears to function in the nucleus and has been implicated as a component of a complex containing the histone acetyltransferase MYST/MOF and in the assembly of transcriptional initiation factor TFIIB [149–152]. TTC4 is also a potential Hsp90 binding protein and appears to have an important role in linking Hsp90 function to replication [153], TTC4 may thus have a role in multiple nuclear functions including transcription and replication and these may be linked to its tumor suppressor properties.

TTC5. Tetratricopeptide 5 (TTC5) also known as stress-responsive activator of p300 (Strap) contains six TPR domains, and with these multiple interaction domains could thus play a role as a scaffold protein in a similar way to Hop [87, 88]. TTC5/Strap binds to the histone acetylase p300 and is implicated in the activation of transcription in response to stresses such as DNA damage and heat shock [88, 154, 155]. p300 is a cofactor for a wide range of transcription factors, as well as forming complexes with an array of other proteins and can modify both the associated factors as well as histone H4 by acetylation [156]. Indeed, TTC5/Strap is implicated in the regulation of GR as with other co-chaperones such as Cyp40, FKBP1, and FKBP2 and could potentially couple molecular chaperones and stress to transcriptional activation [157]. TTC5/Strap may thus play a role in transcriptional regulation during stress responses to heat shock or DNA damage although currently no evidence appears to link this co-chaperone to cancer.

XAP2/AIP. Another TPR domain containing Hsp90 binding co-chaperone is XAP2, also known as AIP [158]. This protein is a member of the immunophilin family and regulates activity of steroid hormone receptors such as the aryl hydrocarbon receptor and the estrogen receptor α (ER α) [159, 160]. The co-chaperone could potentially play a role in breast cancer through its negative regulation of ER α [159]. ER can stimulate

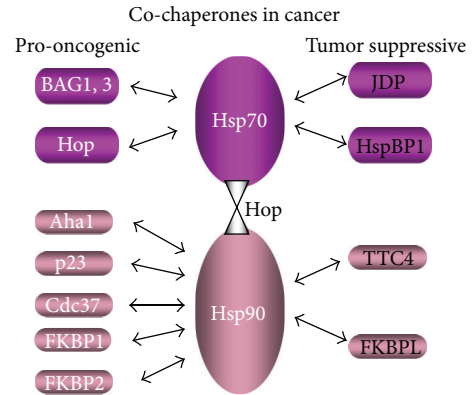


FIGURE 3: Oncogenic or tumor suppressive influence of molecular co-chaperones. (Hop is shown twice in the cartoon to depict its role in bridging Hsp70 and Hsp90 as well as its pro-oncogenic influence).

mammary cancer growth but can also function as an inhibitor of metastasis, and its exact role in cancer would thus be difficult to predict [161].

5. Overview: Cochaperones and Cancer

As co-chaperones are essential for significant molecular chaperone activity *in vitro*, one might predict a uniform pro-cancer role for these molecules as with the primary chaperones. However, their role in cancer appears to be complex. It is thus evident that a number of co-chaperones are overexpressed in cancers and signal a poor prognosis in patients and may be candidates for the development of novel approaches to cancer therapy. Hop, p23, p50/Cdc37, Aha1, FKBP1, and FKBP2 appear to be intimately involved in the chaperoning of molecules involved in cancer incidence and progression (Figure 3). Cancers appear to become addicted to these co-chaperones in a similar way to their dependence on the primary chaperones, requiring these cofactors to maintain elevated levels of oncogenes which are often mutated during carcinogenesis [18, 21]. In addition, the BAG domain proteins appear to indicate a poor prognosis for cancer patients due to their *inhibition of apoptosis*—one of the key hallmarks of cancer [172, 173]. However, a sizable number of the co-chaperones, including HspBP1, the JDP family proteins, FKBP1, and TTC4 appear to signal a good prognosis in cancer suggesting that they may have tumor suppressive functions (Figure 3). As mentioned above, TTC4 in particular was identified in a loss of heterozygosity screen for tumor suppressor genes.

6. Molecular Chaperones and Cochaperones in Cancer Treatment

The targeting of Hsp90 in cancer was initially stimulated by the availability of drugs such as geldanamycin and radicicol that bind to and inhibit its ATPase domain [174, 175]. Hsp90 has since become a heavily targeted molecule, and several

generations of anticancer drugs including the 17-allylamino-17-demethoxygeldanamycin (17-AAG) showed promise in cancer treatment [176, 177]. More modern synthetic drugs have recently become available that have solved some of the early problems with drug toxicity, and progress in this area can be expected [174]. Hsp70/HSPA family members also have considerable promise as targets in cancer and proteins such as Hsp72, Hsp70.2, and mortalin are increased in breast cancer and when inhibited elicit apoptosis [178–180]. In addition, the Hsp70 family members appear essential in chaperoning oncogenic proteins as is observed with Hsp90, and compounds capable of inhibiting the Hsp70 chaperones are beginning to emerge [181]. In addition, a recent pharmacological study of AR signaling using gene expression profiling indicated two more classes of drugs that might inhibit chaperone/co-chaperone interactions. Two drug families, centering on the natural compounds celastrol and gedunin, were uncovered [182]. Celastrol was shown to disrupt the function of the Hsp90/Cdc37 complex, a key growth-requiring pathway in prostate cancer and thus is a promising agent for this disease [183]. The drug is however somewhat lacking in specificity and also directly inhibits κ B kinase and the proteasome as well as activating HSF1 [184]. As mentioned above, gedunin inhibits p23, another prooncogenic Hsp90 co-chaperone [115]. Therefore, although in its infancy, the concept of targeting co-chaperones in cancer treatment seems feasible and practical.

Acknowledgment

This work was supported by NIH Research Grants RO-ICA047407, R01CA119045, and RO-ICA094397.

References

- [1] S. Lindquist and E. A. Craig, “The heat-shock proteins,” *Annual Review of Genetics*, vol. 22, pp. 631–677, 1988.
- [2] R. J. Ellis, “Protein misassembly: macromolecular crowding and molecular chaperones,” *Advances in Experimental Medicine and Biology*, vol. 594, pp. 1–13, 2007.
- [3] M. P. Mayer and B. Bukau, “Hsp70 chaperones: cellular functions and molecular mechanism,” *Cellular and Molecular Life Sciences*, vol. 62, no. 6, pp. 670–684, 2005.
- [4] E. Guisbert, C. Herman, C. Z. Lu, and C. A. Gross, “A chaperone network controls the heat shock response in *E. coli*,” *Genes and Development*, vol. 18, no. 22, pp. 2812–2821, 2004.
- [5] K. Liberek, D. Skowrya, M. Zylicz, C. Johnson, and C. Georgopoulos, “The *Escherichia coli* DnaK chaperone, the 70-kDa heat shock protein eukaryotic equivalent, changes conformation upon ATP hydrolysis, thus triggering its dissociation from a bound target protein,” *The Journal of Biological Chemistry*, vol. 266, no. 22, pp. 14491–14496, 1991.
- [6] H. H. Kampinga, J. Hageman, M. J. Vos et al., “Guidelines for the nomenclature of the human heat shock proteins,” *Cell Stress and Chaperones*, vol. 14, no. 1, pp. 105–111, 2009.
- [7] E. A. Craig, “The heat shock response,” *CRC Critical Reviews in Biochemistry*, vol. 18, no. 3, pp. 239–280, 1985.
- [8] S. K. Calderwood, Y. Xie, X. Wang et al., “Signal transduction pathways leading to heat shock transcription,” *Signal Transduction Insights*, vol. 2, pp. 13–24, 2010.
- [9] F. M. Ritossa, “Experimental activation of specific loci in polytene chromosomes of *Drosophila*,” *Experimental Cell Research*, vol. 35, no. 3, pp. 601–607, 1964.
- [10] F. Ritossa, “A new puffing pattern induced by temperature shock and DNP in *Drosophila*,” *Experientia*, vol. 18, no. 12, pp. 571–573, 1962.
- [11] Y. Zhang and S. K. Calderwood, “Autophagy, protein aggregation and hyperthermia: a mini-review,” *International Journal of Hyperthermia*, vol. 27, no. 5, pp. 409–414, 2011.
- [12] G. C. Li and Z. Werb, “Correlation between synthesis of heat shock proteins and development of thermotolerance in Chinese hamster fibroblasts,” *Proceedings of the National Academy of Sciences of the United States of America*, vol. 79, no. 10, pp. 3218–3222, 1982.
- [13] J. R. Subject, J. J. Sciandra, and R. J. Johnson, “Heat shock proteins and thermotolerance; a comparison of induction kinetics,” *The British Journal of Radiology*, vol. 55, no. 656, pp. 579–584, 1982.
- [14] V. L. Gabai, A. B. Meriin, D. D. Mosser et al., “Hsp70 prevents activation of stress kinases: a novel pathway of cellular thermotolerance,” *The Journal of Biological Chemistry*, vol. 272, no. 29, pp. 18033–18037, 1997.
- [15] M. Y. Sherman and A. L. Goldberg, “Cellular defenses against unfolded proteins: a cell biologist thinks about neurodegenerative diseases,” *Neuron*, vol. 29, no. 1, pp. 15–32, 2001.
- [16] K. F. Winklhofer, J. Tatzelt, and C. Haass, “The two faces of protein misfolding: gain- and loss-of-function in neurodegenerative diseases,” *EMBO Journal*, vol. 27, no. 2, pp. 336–349, 2008.
- [17] S. K. Calderwood, A. Murshid, and T. Prince, “The shock of aging: molecular chaperones and the heat shock response in longevity and aging—a mini-review,” *Gerontology*, vol. 55, no. 5, pp. 550–558, 2009.
- [18] L. Whitesell and S. L. Lindquist, “HSP90 and the chaperoning of cancer,” *Nature Reviews Cancer*, vol. 5, no. 10, pp. 761–772, 2005.
- [19] D. R. Ciocca, A. P. Arrigo, and S. K. Calderwood, “Heat shock proteins and heat shock factor 1 in carcinogenesis and tumor development: an update,” *Archives of Toxicology*, vol. 87, no. 1, pp. 19–48, 2013.
- [20] D. R. Ciocca and S. K. Calderwood, “Heat shock proteins in cancer: diagnostic, prognostic, predictive, and treatment implications,” *Cell Stress and Chaperones*, vol. 10, no. 2, pp. 86–103, 2005.
- [21] J. Trepel, M. Mollapour, G. Giaccone, and L. Neckers, “Targeting the dynamic HSP90 complex in cancer,” *Nature Reviews Cancer*, vol. 10, no. 8, pp. 537–549, 2010.
- [22] L. Neckers, “Hsp90 inhibitors as novel cancer chemotherapeutic agents,” *Trends in Molecular Medicine*, vol. 8, no. 4, pp. S55–S61, 2002.
- [23] V. L. Gabai, J. A. Yaglom, T. Waldman, and M. Y. Sherman, “Heat shock protein Hsp72 controls oncogene-induced senescence pathways in cancer cells,” *Molecular and Cellular Biology*, vol. 29, no. 2, pp. 559–569, 2009.
- [24] C. O’Callaghan-Sunol, V. L. Gabai, and M. Y. Sherman, “Hsp27 modulates p53 signaling and suppresses cellular senescence,” *Cancer Research*, vol. 67, no. 24, pp. 11779–11788, 2007.
- [25] H. M. Beere, “‘The stress of dying’: the role of heat shock proteins in the regulation of apoptosis,” *Journal of Cell Science*, vol. 117, no. 13, pp. 2641–2651, 2004.
- [26] C. Wu, “Heat shock transcription factors: structure and regulation,” *Annual Review of Cell and Developmental Biology*, vol. 11, pp. 441–469, 1995.

- [27] C. Dai, L. Whitesell, A. B. Rogers, and S. Lindquist, "Heat shock factor 1 is a powerful multifaceted modifier of carcinogenesis," *Cell*, vol. 130, no. 6, pp. 1005–1018, 2007.
- [28] M. A. Khaleque, A. Bharti, J. Gong et al., "Heat shock factor 1 represses estrogen-dependent transcription through association with MTA1," *Oncogene*, vol. 27, no. 13, pp. 1886–1893, 2008.
- [29] M. A. Khaleque, A. Bharti, D. Sawyer et al., "Induction of heat shock proteins by heregulin β 1 leads to protection from apoptosis and anchorage-independent growth," *Oncogene*, vol. 24, no. 43, pp. 6564–6573, 2005.
- [30] S. Santagata, R. Hu, N. U. Lin et al., "High levels of nuclear heat-shock factor 1 (HSF1) are associated with poor prognosis in breast cancer," *Proceedings of the National Academy of Sciences of the United States of America*, vol. 108, no. 45, pp. 18378–18383, 2011.
- [31] S. K. Calderwood, "HSF1, a versatile factor in tumorigenesis," *Current Molecular Medicine*, vol. 12, no. 9, pp. 1102–1107, 2012.
- [32] J. L. Johnson, "Evolution and function of diverse Hsp90 homologs and cochaperone proteins," *Biochimica et Biophysica Acta*, vol. 1823, no. 3, pp. 607–613, 2012.
- [33] H. Rampelt, M. P. Mayer, and B. Bukau, "Nucleotide exchange factors for Hsp70 chaperones," *Methods in Molecular Biology*, vol. 787, pp. 83–91, 2011.
- [34] J. C. Young, V. R. Agashe, K. Siegers, and F. U. Hartl, "Pathways of chaperone-mediated protein folding in the cytosol," *Nature Reviews Molecular Cell Biology*, vol. 5, no. 10, pp. 781–791, 2004.
- [35] J. C. Young, J. M. Barral, and F. U. Hartl, "More than folding: localized functions of cytosolic chaperones," *Trends in Biochemical Sciences*, vol. 28, no. 10, pp. 541–547, 2003.
- [36] K. P. da Silva and J. C. Borges, "The molecular chaperone Hsp70 family members function by a bidirectional heterotropic allosteric mechanism," *Protein and Peptide Letters*, vol. 18, no. 2, pp. 132–142, 2011.
- [37] K. M. Flaherty, C. DeLuca-Flaherty, and D. B. McKay, "Three-dimensional structure of the ATPase fragment of a 70K heat-shock cognate protein," *Nature*, vol. 346, no. 6285, pp. 623–628, 1990.
- [38] G. C. Flynn, T. G. Chappell, and J. E. Rothman, "Peptide binding and release by proteins implicated as catalysts of protein assembly," *Science*, vol. 245, no. 4916, pp. 385–390, 1989.
- [39] R. Schlecht, A. H. Erbse, B. Bukau, and M. P. Mayer, "Mechanics of Hsp70 chaperones enables differential interaction with client proteins," *Nature Structural and Molecular Biology*, vol. 18, no. 3, pp. 345–351, 2011.
- [40] S. K. Sharma, P. Christen, and P. Goloubinoff, "Disaggregating chaperones: an unfolding story," *Current Protein and Peptide Science*, vol. 10, no. 5, pp. 432–446, 2009.
- [41] J. P. Chapple, J. van der Spuy, S. Poopalasundaram, and M. E. Cheetham, "Neuronal DnaJ proteins HSP1a and HSP1b: a role in linking the Hsp70 chaperone machine to the ubiquitin-proteasome system?" *Biochemical Society Transactions*, vol. 32, no. 4, pp. 640–642, 2004.
- [42] F. Hennessy, M. E. Cheetham, H. W. Dirr, and G. L. Blatch, "Analysis of the levels of conservation of the J domain among the various types of DnaJ-like proteins," *Cell Stress and Chaperones*, vol. 5, no. 4, pp. 347–358, 2000.
- [43] F. Hennessy, W. S. Nicoll, R. Zimmermann, M. E. Cheetham, and G. L. Blatch, "Not all J domains are created equal: implications for the specificity of Hsp40-Hsp70 interactions," *Protein Science*, vol. 14, no. 7, pp. 1697–1709, 2005.
- [44] J. N. Sterrenberg, G. L. Blatch, and A. L. Edkins, "Human DnaJ in cancer and stem cells," *Cancer Letters*, vol. 312, no. 2, pp. 129–142, 2011.
- [45] F. Tsukahara and Y. Maru, "Bag1 directly routes immature BCR-ABL for proteasomal degradation," *Blood*, vol. 116, no. 18, pp. 3582–3592, 2010.
- [46] A. Rosati, V. Graziano, V. de Laurenzi, M. Pascale, and M. C. Turco, "BAG3: a multifaceted protein that regulates major cell pathways," *Cell Death and Disease*, vol. 2, no. 4, article e141, 2011.
- [47] S. Takayama, Z. Xie, and J. C. Reed, "An evolutionarily conserved family of Hsp70/Hsc70 molecular chaperone regulators," *The Journal of Biological Chemistry*, vol. 274, no. 2, pp. 781–786, 1999.
- [48] S. Takayama and J. C. Reed, "Molecular chaperone targeting and regulation by BAG family proteins," *Nature Cell Biology*, vol. 3, no. 10, pp. E237–E241, 2001.
- [49] M. Kabani, C. McLellan, D. A. Raynes, V. Guerriero, and J. L. Brodsky, "HspBP1, a homologue of the yeast Fes1 and Sls1 proteins, is an Hsc70 nucleotide exchange factor," *FEBS Letters*, vol. 531, no. 2, pp. 339–342, 2002.
- [50] M. Kabani, J. M. Beckerich, and J. L. Brodsky, "Nucleotide exchange factor for the yeast Hsp70 molecular chaperone Ssa1p," *Molecular and Cellular Biology*, vol. 22, no. 13, pp. 4677–4689, 2002.
- [51] C. Scheuffler, A. Brinker, G. Bourenkov et al., "Structure of TPR domain-peptide complexes: critical elements in the assembly of the Hsp70-Hsp90 multichaperone machine," *Cell*, vol. 101, no. 2, pp. 199–210, 2000.
- [52] H. Wegele, M. Haslbeck, J. Reinstein, and J. Buchner, "StiI is a novel activator of the Ssa proteins," *The Journal of Biological Chemistry*, vol. 278, no. 28, pp. 25970–25976, 2003.
- [53] C. Prodromou, G. Siligardi, R. O'Brien et al., "Regulation of Hsp90 ATPase activity by tetratricopeptide repeat (TPR)-domain co-chaperones," *EMBO Journal*, vol. 18, no. 3, pp. 754–762, 1999.
- [54] C. A. Ballinger, P. Connell, Y. Wu et al., "Identification of CHIP, a novel tetratricopeptide repeat-containing protein that interacts with heat shock proteins and negatively regulates chaperone functions," *Molecular and Cellular Biology*, vol. 19, no. 6, pp. 4535–4545, 1999.
- [55] K. Liberek, C. Georgopoulos, and M. Zylicz, "Role of the *Escherichia coli* DnaK and DnaJ heat shock proteins in the initiation of bacteriophage λ DNA replication," *Proceedings of the National Academy of Sciences of the United States of America*, vol. 85, no. 18, pp. 6632–6636, 1988.
- [56] B. Panaretou, C. Prodromou, S. M. Roe et al., "ATP binding and hydrolysis are essential to the function of the Hsp90 molecular chaperone in vivo," *EMBO Journal*, vol. 17, no. 16, pp. 4829–4836, 1998.
- [57] S. E. Jackson, "Hsp90: structure and function," *Topics in Current Chemistry*, vol. 328, pp. 155–240, 2013.
- [58] M. F. N. Rosser, B. M. Trotta, M. R. Marshall, B. Berwin, and C. V. Nicchitta, "Adenosine nucleotides and the regulation of GRP94-client protein interactions," *Biochemistry*, vol. 43, no. 27, pp. 8835–8845, 2004.
- [59] D. C. Altieri, G. S. Stein, J. B. Lian, and L. R. Languino, "TRAP-1, the mitochondrial Hsp90," *Biochimica et Biophysica Acta*, vol. 1823, no. 3, pp. 767–773, 2012.
- [60] S. J. Felts, B. A. L. Owen, P. Nguyen, J. Trepel, D. B. Donner, and D. O. Toft, "The hsp90-related protein TRAP1 is a mitochondrial protein with distinct functional properties," *The Journal of Biological Chemistry*, vol. 275, no. 5, pp. 3305–3312, 2000.

- [61] L. Neckers and S. P. Ivy, "Heat shock protein 90," *Current Opinion in Oncology*, vol. 15, no. 6, pp. 419–424, 2003.
- [62] P. Workman, F. Burrows, L. Neckers, and N. Rosen, "Drugging the cancer chaperone HSP90: combinatorial therapeutic exploitation of oncogene addiction and tumor stress," *Annals of the New York Academy of Sciences*, vol. 1113, pp. 202–216, 2007.
- [63] W. B. Pratt and D. O. Toft, "Regulation of signaling protein function and trafficking by the hsp90/hsp70-based chaperone machinery," *Experimental Biology and Medicine*, vol. 228, no. 2, pp. 111–133, 2003.
- [64] M. M. U. Ali, S. Mark Roe, C. K. Vaughan et al., "Crystal structure of an Hsp90-nucleotide-p23/Sba1 closed chaperone complex," *Nature*, vol. 440, no. 7087, pp. 1013–1017, 2006.
- [65] P. Meyer, C. Prodromou, B. Hu et al., "Structural and functional analysis of the middle segment of Hsp90: implications for ATP hydrolysis and client protein and cochaperone interactions," *Molecular Cell*, vol. 11, no. 3, pp. 647–658, 2003.
- [66] N. Wayne and D. N. Bolon, "Dimerization of Hsp90 is required for in vivo function: design and analysis of monomers and dimers," *The Journal of Biological Chemistry*, vol. 282, no. 48, pp. 35386–35395, 2007.
- [67] N. Wayne, P. Mishra, and D. N. Bolon, "Hsp90 and client protein maturation," *Methods in Molecular Biology*, vol. 787, pp. 33–44, 2011.
- [68] M. B. Cox and J. L. Johnson, "The role of p23, Hop, immunophilins, and other co-chaperones in regulating Hsp90 function," *Methods in Molecular Biology*, vol. 787, pp. 45–66, 2011.
- [69] C. K. Vaughan, U. Gohlke, F. Sobott et al., "Structure of an Hsp90-Cdc37-Cdk4 complex," *Molecular Cell*, vol. 23, no. 5, pp. 697–707, 2006.
- [70] S. H. McLaughlin, F. Sobott, Z. P. Yao et al., "The co-chaperone p23 arrests the Hsp90 ATPase cycle to trap client proteins," *Journal of Molecular Biology*, vol. 356, no. 3, pp. 746–758, 2006.
- [71] K. Richter, S. Walter, and J. Buchner, "The co-chaperone Sba1 connects the ATPase reaction of Hsp90 to the progression of the chaperone cycle," *Journal of Molecular Biology*, vol. 342, no. 5, pp. 1403–1413, 2004.
- [72] N. Grammatikakis, J. H. Lin, A. Grammatikakis, P. N. Tschlis, and B. H. Cochran, "p50(cdc37) acting in concert with Hsp90 is required for Raf-1 function," *Molecular and Cellular Biology*, vol. 19, no. 3, pp. 1661–1672, 1999.
- [73] P. J. Gray Jr., T. Prince, J. Cheng, M. A. Stevenson, and S. K. Calderwood, "Targeting the oncogene and kinome chaperone CDC37," *Nature Reviews Cancer*, vol. 8, no. 7, pp. 491–495, 2008.
- [74] A. K. Mandal, M. A. Theodoraki, N. B. Nillegoda, and A. J. Caplan, "Role of molecular chaperones in biogenesis of the protein kinome," *Methods in Molecular Biology*, vol. 787, pp. 75–81, 2012.
- [75] R. Matts and A. J. Caplan, *Cdc37 and Protein Kinase Folding*, Springer, Dordrecht, The Netherlands, 2007.
- [76] M. G. Catlett and K. B. Kaplan, "Sgt1p is a unique co-chaperone that acts as a client adaptor to link Hsp90 to Skp1p," *The Journal of Biological Chemistry*, vol. 281, no. 44, pp. 33739–33748, 2006.
- [77] M. P. Mayer, R. Nikolay, and B. Bukau, "Aha, another regulator for Hsp90 chaperones," *Molecular Cell*, vol. 10, no. 6, pp. 1255–1256, 2002.
- [78] M. Retzlaff, F. Hagn, L. Mitschke et al., "Asymmetric activation of the Hsp90 dimer by its cochaperone Aha1," *Molecular Cell*, vol. 37, no. 3, pp. 344–354, 2010.
- [79] J. van der Spuy, M. E. Cheetham, H. W. Dirr, and G. L. Blatch, "The cochaperone murine stress-inducible protein 1: overexpression, purification, and characterization," *Protein Expression and Purification*, vol. 21, no. 3, pp. 462–469, 2001.
- [80] A. B. Schmid, S. Lagleder, M. A. Grawert et al., "The architecture of functional modules in the Hsp90 co-chaperone Sti1/Hop," *EMBO Journal*, vol. 31, pp. 1506–1517, 2012.
- [81] M. Zhang, M. Windheim, S. M. Roe et al., "Chaperoned ubiquitylation—crystal structures of the CHIP U box E3 ubiquitin ligase and a CHIP-Ubc13-Uev1a complex," *Molecular Cell*, vol. 20, no. 4, pp. 525–538, 2005.
- [82] M. Stankiewicz, R. Nikolay, V. Rybin, and M. P. Mayer, "CHIP participates in protein triage decisions by preferentially ubiquitinating Hsp70-bound substrates," *FEBS Journal*, vol. 277, no. 16, pp. 3353–3367, 2010.
- [83] S. Carra, S. J. Seguin, and J. Landry, "HspB8 and Bag3: a new chaperone complex targeting misfolded proteins to macroautophagy," *Autophagy*, vol. 4, no. 2, pp. 237–239, 2008.
- [84] M. Gamberdinger, A. M. Kaya, U. Wolfrum, A. M. Clement, and C. Behl, "BAG3 mediates chaperone-based aggresome-targeting and selective autophagy of misfolded proteins," *EMBO Reports*, vol. 12, no. 2, pp. 149–156, 2011.
- [85] A. A. Duina, J. A. Marsh, R. B. Kurtz, H. C. J. Chang, S. Lindquist, and R. F. Gaber, "The peptidyl-prolyl isomerase domain of the Cyp-40 cyclophilin homolog Cpr7 is not required to support growth or glucocorticoid receptor activity in *Saccharomyces cerevisiae*," *The Journal of Biological Chemistry*, vol. 273, no. 18, pp. 10819–10822, 1998.
- [86] D. Mok, R. K. Allan, A. Carrello, K. Wangoo, M. D. Walkinshaw, and T. Ratajczak, "The chaperone function of cyclophilin 40 maps to a cleft between the prolyl isomerase and tetratricopeptide repeat domains," *FEBS Letters*, vol. 580, no. 11, pp. 2761–2768, 2006.
- [87] C. Demonacos, M. Krstic-Demonacos, and N. B. la Thangue, "A TPR motif cofactor contributes to p300 activity in the p53 response," *Molecular Cell*, vol. 8, no. 1, pp. 71–84, 2001.
- [88] C. Demonacos, M. Krstic-Demonacos, L. Smith et al., "A new effector pathway links ATM kinase with the DNA damage response," *Nature Cell Biology*, vol. 6, no. 10, pp. 968–976, 2004.
- [89] L. Brive, S. Takayama, K. Briknarova et al., "The carboxyl-terminal lobe of Hsc70 ATPase domain is sufficient for binding to BAG1," *Biochemical and Biophysical Research Communications*, vol. 289, no. 5, pp. 1099–1105, 2001.
- [90] J. K. Stuart, D. G. Myszka, L. Joss et al., "Characterization of interactions between the anti-apoptotic protein BAG-1 and Hsc70 molecular chaperones," *The Journal of Biological Chemistry*, vol. 273, no. 35, pp. 22506–22514, 1998.
- [91] S. Franceschelli, A. Rosati, R. Leroise, S. de Nicola, M. C. Turco, and M. Pascale, "bag3 gene expression is regulated by heat shock factor 1," *Journal of Cellular Physiology*, vol. 215, no. 3, pp. 575–577, 2008.
- [92] S. Aveic, M. Pigazzi, and G. Basso, "BAG1: the guardian of anti-apoptotic proteins in acute myeloid leukemia," *PLoS ONE*, vol. 6, no. 10, Article ID e26097, 2011.
- [93] M. Ammirante, A. Rosati, C. Arra et al., "IKKγ protein is a target of BAG3 regulatory activity in human tumor growth," *Proceedings of the National Academy of Sciences of the United States of America*, vol. 107, no. 16, pp. 7497–7502, 2010.
- [94] Y. Shomura, Z. Dragovic, H. C. Chang et al., "Regulation of Hsp70 function by HspBP1: structural analysis reveals an alternate mechanism for Hsp70 nucleotide exchange," *Molecular Cell*, vol. 17, no. 3, pp. 367–379, 2005.

- [95] S. Alberti, K. Böhse, V. Arndt, A. Schmitz, and J. Höhfeld, "The cochaperone HspBP1 inhibits the CHIP ubiquitin ligase and stimulates the maturation of the cystic fibrosis transmembrane conductance regulator," *Molecular Biology of the Cell*, vol. 15, no. 9, pp. 4003–4010, 2004.
- [96] A. P. Souza, C. Albuquerque, C. Torronteguy et al., "HspBP1 levels are elevated in breast tumor tissue and inversely related to tumor aggressiveness," *Cell Stress and Chaperones*, vol. 14, no. 3, pp. 301–310, 2009.
- [97] S. Tanimura, A. I. Hirano, J. Hashizume et al., "Anticancer drugs up-regulate HspBP1 and thereby antagonize the prosurvival function of Hsp70 in tumor cells," *The Journal of Biological Chemistry*, vol. 282, no. 49, pp. 35430–35439, 2007.
- [98] N. Fehrenbacher and M. Jäättelä, "Lysosomes as targets for cancer therapy," *Cancer Research*, vol. 65, no. 8, pp. 2993–2995, 2005.
- [99] J. Nylandsted, M. Gyrd-Hansen, A. Danielewicz et al., "Heat shock protein 70 promotes cell survival by inhibiting lysosomal membrane permeabilization," *Journal of Experimental Medicine*, vol. 200, no. 4, pp. 425–435, 2004.
- [100] D. Straus, W. Walter, and C. A. Gross, "DnaK, DnaJ, and GrpE heat shock proteins negatively regulate heat shock gene expression by controlling the synthesis and stability of σ^{32} ," *Genes and Development*, vol. 4, no. 12, pp. 2202–2209, 1990.
- [101] H. Isomoto, M. Oka, Y. Yano et al., "Expression of heat shock protein (Hsp) 70 and Hsp 40 in gastric cancer," *Cancer Letters*, vol. 198, no. 2, pp. 219–228, 2003.
- [102] A. Mitra, R. A. Fillmore, B. J. Metge et al., "Large isoform of MRJ (DNAJB6) reduces malignant activity of breast cancer," *Breast Cancer Research*, vol. 10, no. 2, article R22, 2008.
- [103] A. Mitra, L. A. Shevde, and R. S. Samant, "Multi-faceted role of HSP40 in cancer," *Clinical and Experimental Metastasis*, vol. 26, no. 6, pp. 559–567, 2009.
- [104] I. Canamasas, A. Debes, P. G. Natali, and U. Kurzik-Dumke, "Understanding human cancer using *Drosophila*. Tid47, a cytosolic product of the DnaJ-like tumor suppressor gene *l(2)tid*, is a novel molecular partner of patched related to skin cancer," *The Journal of Biological Chemistry*, vol. 278, no. 33, pp. 30952–30960, 2003.
- [105] U. Kurzik-Dumke, D. Gundacker, M. Rentrop, and E. Gateff, "Tumor suppression in *Drosophila* is causally related to the function of the lethal(2)tumorous imaginal discs gene, a dnaJ homolog," *Developmental Genetics*, vol. 16, no. 1, pp. 64–76, 1995.
- [106] P. E. Carrigan, L. A. Sikkink, D. F. Smith, and M. Ramirez-Alvarado, "Domain:domain interactions within Hop, the Hsp70/Hsp90 organizing protein, are required for protein stability and structure," *Protein Science*, vol. 15, no. 3, pp. 522–532, 2006.
- [107] H. Kubota, S. Yamamoto, E. Itoh et al., "Increased expression of co-chaperone HOP with HSP90 and HSC70 and complex formation in human colonic carcinoma," *Cell Stress and Chaperones*, vol. 15, no. 6, pp. 1003–1011, 2010.
- [108] W. Sun, B. Xing, Y. Sun et al., "Proteome analysis of hepatocellular carcinoma by two-dimensional difference gel electrophoresis," *Molecular and Cellular Proteomics*, vol. 6, no. 10, pp. 1798–1808, 2007.
- [109] N. Walsh, A. Larkin, N. Swan et al., "RNAi knockdown of Hop (Hsp70/Hsp90 organising protein) decreases invasion via MMP-2 down regulation," *Cancer Letters*, vol. 306, no. 2, pp. 180–189, 2011.
- [110] B. C. Freeman, S. J. Felts, D. O. Toft, and K. R. Yamamoto, "The p23 molecular chaperones act at a late step in intracellular receptor action to differentially affect ligand efficacies," *Genes and Development*, vol. 14, no. 4, pp. 422–434, 2000.
- [111] N. E. Simpson, W. M. Lambert, R. Watkins et al., "High levels of Hsp90 cochaperone p23 promote tumor progression and poor prognosis in breast cancer by increasing lymph node metastases and drug resistance," *Cancer Research*, vol. 70, no. 21, pp. 8446–8456, 2010.
- [112] V. Reebye, L. Q. Cano, D. N. Lavery et al., "Role of the HSP90-associated cochaperone p23 in enhancing activity of the androgen receptor and significance for prostate cancer," *Molecular Endocrinology*, vol. 26, no. 10, pp. 1694–1706, 2012.
- [113] T. Prince and L. Neckers, "A network of its own: the unique interactome of the Hsp90 cochaperone, Sba1/p23," *Molecular Cell*, vol. 43, no. 2, pp. 159–160, 2011.
- [114] X. Liu, L. Zou, L. Zhu et al., "miRNA mediated up-regulation of cochaperone p23 acts as an anti-apoptotic factor in childhood acute lymphoblastic leukemia," *Leukemia Research*, vol. 36, no. 9, pp. 1098–1104, 2012.
- [115] C. A. Patwardhan, A. Fauq, L. B. Peterson, C. Miller, B. S. Blagg, and A. Chadli, "Gedunin inactivates the co-chaperone p23 causing cancer cell death by apoptosis," *The Journal of Biological Chemistry*, vol. 288, no. 10, pp. 7313–7325, 2013.
- [116] M. Zabka, W. Leśniak, W. Prus, J. Kuźnicki, and A. Filipiek, "Sgt1 has co-chaperone properties and is up-regulated by heat shock," *Biochemical and Biophysical Research Communications*, vol. 370, no. 1, pp. 179–183, 2008.
- [117] J. Stuttmann, J. E. Parker, and L. D. Noël, "Staying in the fold: the SGT1/chaperone machinery in maintenance and evolution of leucine-rich repeat proteins," *Plant Signaling and Behavior*, vol. 3, no. 5, pp. 283–285, 2008.
- [118] M. Zhang, Y. Kadota, C. Prodromou, K. Shirasu, and L. H. Pearl, "Structural basis for assembly of Hsp90-Sgt1-CHORD protein complexes: implications for chaperoning of NLR innate immunity receptors," *Molecular Cell*, vol. 39, no. 2, pp. 269–281, 2010.
- [119] A. E. Davies and K. B. Kaplan, "Hsp90-Sgt1 and Skp1 target human Mis12 complexes to ensure efficient formation of kinetochore-microtubule binding sites," *Journal of Cell Biology*, vol. 189, no. 2, pp. 261–274, 2010.
- [120] L. Stepanova, M. Finegold, F. DeMayo, E. V. Schmidt, and J. W. Harper, "The oncoprotein kinase chaperone CDC37 functions as an oncogene in mice and collaborates with both c-myc and cyclin D1 in transformation of multiple tissues," *Molecular and Cellular Biology*, vol. 20, no. 12, pp. 4462–4473, 2000.
- [121] L. Stepanova, G. Yang, F. DeMayo et al., "Induction of human Cdc37 in prostate cancer correlates with the ability of targeted Cdc37 expression to promote prostatic hyperplasia," *Oncogene*, vol. 19, no. 18, pp. 2186–2193, 2000.
- [122] S. Casas, J. Ollila, A. Aventín, M. Vihinen, J. Sierra, and S. Knuutila, "Changes in apoptosis-related pathways in acute myelocytic leukemia," *Cancer Genetics and Cytogenetics*, vol. 146, no. 2, pp. 89–101, 2003.
- [123] F. Feo, M. R. de Miglio, M. M. Simile et al., "Hepatocellular carcinoma as a complex polygenic disease. Interpretive analysis of recent developments on genetic predisposition," *Biochimica et Biophysica Acta*, vol. 1765, no. 2, pp. 126–147, 2006.
- [124] Y. Katayama, A. Sakai, Y. Okikawa et al., "Cyclin D1 overexpression is not a specific grouping marker, but may collaborate with CDC37 in myeloma cells," *International Journal of Oncology*, vol. 25, no. 3, pp. 579–595, 2004.

- [125] M. A. Thompson, J. Stumph, S. E. Henrickson et al., "Differential gene expression in anaplastic lymphoma kinase-positive and anaplastic lymphoma kinase-negative anaplastic large cell lymphomas," *Human Pathology*, vol. 36, no. 5, pp. 494–504, 2005.
- [126] A. J. Caplan, A. K. Mandal, and M. A. Theodoraki, "Molecular chaperones and protein kinase quality control," *Trends in Cell Biology*, vol. 17, no. 2, pp. 87–92, 2007.
- [127] A. K. Mandal, P. Lee, J. A. Chen et al., "Cdc37 has distinct roles in protein kinase quality control that protect nascent chains from degradation and promote posttranslational maturation," *Journal of Cell Biology*, vol. 176, no. 3, pp. 319–328, 2007.
- [128] P. J. Gray Jr., M. A. Stevenson, and S. K. Calderwood, "Targeting Cdc37 inhibits multiple signaling pathways and induces growth arrest in prostate cancer cells," *Cancer Research*, vol. 67, no. 24, pp. 11942–11950, 2007.
- [129] J. R. Smith, P. A. Clarke, E. De Billy, and P. Workman, "Silencing the cochaperone CDC37 destabilizes kinase clients and sensitizes cancer cells to HSP90 inhibitors," *Oncogene*, vol. 28, no. 2, pp. 157–169, 2009.
- [130] K. Robzyk, H. Oen, G. Buchanan et al., "Uncoupling of hormone-dependence from chaperone-dependence in the L701H mutation of the androgen receptor," *Molecular and Cellular Endocrinology*, vol. 268, no. 1-2, pp. 67–74, 2007.
- [131] L. H. Pearl and C. Prodromou, "Structure, function, and mechanism of the Hsp90 molecular chaperone," *Advances in Protein Chemistry*, vol. 59, pp. 157–186, 2001.
- [132] A. I. Su, T. Wiltshire, S. Batalov et al., "A gene atlas of the mouse and human protein-encoding transcriptomes," *Proceedings of the National Academy of Sciences of the United States of America*, vol. 101, no. 16, pp. 6062–6067, 2004.
- [133] J. L. Holmes, S. Y. Sharp, S. Hobbs, and P. Workman, "Silencing of HSP90 cochaperone AHA1 expression decreases client protein activation and increases cellular sensitivity to the HSP90 inhibitor 17-allylamino-17-demethoxygeldanamycin," *Cancer Research*, vol. 68, no. 4, pp. 1188–1197, 2008.
- [134] J. P. Schülke, G. M. Wochnik, I. Lang-Rollin et al., "Differential impact of tetratricopeptide repeat proteins on the steroid hormone receptors," *PLoS ONE*, vol. 5, no. 7, p. e11717, 2010.
- [135] J. G. Scammell, W. B. Denny, D. L. Valentine, and D. F. Smith, "Overexpression of the FK506-binding immunophilin FKBP51 is the common cause of glucocorticoid resistance in three New World primates," *General and Comparative Endocrinology*, vol. 124, no. 2, pp. 152–165, 2001.
- [136] W. B. Denny, D. L. Valentine, P. D. Reynolds, D. F. Smith, and J. G. Scammell, "Squirrel monkey immunophilin FKBP51 is a potent inhibitor of glucocorticoid receptor binding," *Endocrinology*, vol. 141, no. 11, pp. 4107–4113, 2000.
- [137] D. L. Riggs, M. B. Cox, H. L. Tardif, M. Hessling, J. Buchner, and D. F. Smith, "Nocatalytic role of the FKBP52 peptidyl-prolyl isomerase domain in the regulation of steroid hormone signaling," *Molecular and Cellular Biology*, vol. 27, no. 24, pp. 8658–8669, 2007.
- [138] H. D. McKeen, D. J. Brennan, S. Hegarty et al., "The emerging role of FK506-binding proteins as cancer biomarkers: a focus on FKBP5," *Biochemical Society Transactions*, vol. 39, no. 2, pp. 663–668, 2011.
- [139] M. Chinkers, "Targeting of a distinctive protein-serine phosphatase to the protein kinase-like domain of the atrial natriuretic peptide receptor," *Proceedings of the National Academy of Sciences of the United States of America*, vol. 91, no. 23, pp. 11075–11079, 1994.
- [140] T. D. Hinds Jr., L. A. Stechschulte, H. A. Cash et al., "Protein phosphatase 5 mediates lipid metabolism through reciprocal control of glucocorticoid receptor and peroxisome proliferator-activated receptor-gamma (PPAR γ)," *The Journal of Biological Chemistry*, vol. 286, no. 50, pp. 42911–42922, 2011.
- [141] T. D. Hinds Jr. and E. R. Sánchez, "Protein phosphatase 5," *International Journal of Biochemistry and Cell Biology*, vol. 40, no. 11, pp. 2358–2362, 2008.
- [142] M. Mollapour, S. Tsutsumi, A. W. Truman et al., "Threonine 22 phosphorylation attenuates Hsp90 interaction with cochaperones and affects its chaperone activity," *Molecular Cell*, vol. 41, no. 6, pp. 672–681, 2011.
- [143] M. Mollapour and L. Neckers, "Post-translational modifications of Hsp90 and their contributions to chaperone regulation," *Biochimica et Biophysica Acta*, vol. 1823, no. 3, pp. 648–655, 2012.
- [144] S. K. Wandinger, M. H. Suhre, H. Wegele, and J. Buchner, "The phosphatase Ppt1 is a dedicated regulator of the molecular chaperone Hsp90," *EMBO Journal*, vol. 25, no. 2, pp. 367–376, 2006.
- [145] C. K. Vaughan, M. Mollapour, J. R. Smith et al., "Hsp90-dependent activation of protein kinases is regulated by chaperone-targeted dephosphorylation of Cdc37," *Molecular Cell*, vol. 31, no. 6, pp. 886–895, 2008.
- [146] T. Wechsler, B. P. C. Chen, R. Harper et al., "DNA-PKcs function regulated specifically by protein phosphatase 5," *Proceedings of the National Academy of Sciences of the United States of America*, vol. 101, no. 5, pp. 1247–1252, 2004.
- [147] Y. Kang, H. M. Cheong, J. H. Lee et al., "Protein phosphatase 5 is necessary for ATR-mediated DNA repair," *Biochemical and Biophysical Research Communications*, vol. 404, no. 1, pp. 476–481, 2011.
- [148] M. Poetsch, T. Dittberner, J. K. Cowell, and C. Woelckhaus, "TTC4, a novel candidate tumor suppressor gene at 1p31 is often mutated in malignant melanoma of the skin," *Oncogene*, vol. 19, no. 50, pp. 5817–5820, 2000.
- [149] G. Su, T. Roberts, and J. K. Cowell, "TTC4, a novel human gene containing the tetratricopeptide repeat and mapping to the region of chromosome 1p31 that is frequently deleted in sporadic breast cancer," *Genomics*, vol. 55, no. 2, pp. 157–163, 1999.
- [150] R. I. Dmitriev, I. A. Okkelman, R. A. Abdulin, M. I. Shakhparonov, and N. B. Pestov, "Nuclear transport of protein TTC4 depends on the cell cycle," *Cell and Tissue Research*, vol. 336, no. 3, pp. 521–527, 2009.
- [151] R. I. Dmitriev, T. V. Korneenko, A. A. Bessonov, M. I. Shakhparonov, N. N. Modyanov, and N. B. Pestov, "Characterization of hampin/MSL1 as a node in the nuclear interactome," *Biochemical and Biophysical Research Communications*, vol. 355, no. 4, pp. 1051–1057, 2007.
- [152] R. D. Moir and I. M. Willis, "Tetratricopeptide repeats of TFC4 and a limiting step in the assembly of the initiation factor TFIIB," *Advances in Protein Chemistry*, vol. 67, pp. 93–121, 2004.
- [153] G. Crevel, D. Bennett, and S. Cotterill, "The human TPR protein TTC4 is a putative Hsp90 co-chaperone which interacts with CDC6 and shows alterations in transformed cells," *PLoS ONE*, vol. 3, no. 3, Article ID e1737, 2008.
- [154] D. Xu, L. P. Zalmas, and N. B. la Thangue, "A transcription cofactor required for the heat-shock response," *EMBO Reports*, vol. 9, no. 7, pp. 662–669, 2008.
- [155] D. Xu and N. B. la Thangue, "Strap: a versatile transcription cofactor," *Cell Cycle*, vol. 7, no. 16, pp. 2456–2457, 2008.

- [156] Y. Zhang, A. Murshid, T. Prince, and S. K. Calderwood, "Protein kinase A regulates molecular chaperone transcription and protein aggregation," *PLoS ONE*, vol. 6, no. 12, Article ID e28950, 2011.
- [157] L. Davies, E. Paraskevopoulou, M. Sadeq et al., "Regulation of glucocorticoid receptor activity by a stress responsive transcriptional cofactor," *Molecular Endocrinology*, vol. 25, no. 1, pp. 58–71, 2011.
- [158] N. Kuzhandaivelu, Y. S. Cong, C. Inouye, W. M. Yang, and E. Seto, "XAP2, a novel hepatitis B virus X-associated protein that inhibits X transactivation," *Nucleic Acids Research*, vol. 24, no. 23, pp. 4741–4750, 1996.
- [159] W. Cai, T. V. Kramarova, P. Berg, M. Korbonits, and I. Pongratz, "The immunophilin-like protein XAP2 is a negative regulator of estrogen signaling through interaction with estrogen receptor α ," *PLoS ONE*, vol. 6, no. 10, Article ID e25201, 2011.
- [160] Z. Yin, E. C. Henry, and T. A. Gasiewicz, "(-)-epigallocatechin-3-gallate is a novel Hsp90 inhibitor," *Biochemistry*, vol. 48, no. 2, pp. 336–345, 2009.
- [161] A. Mazumdar, R. A. Wang, S. K. Mishra et al., "Transcriptional repression of oestrogen receptor by metastasis-associated protein 1 corepressor," *Nature Cell Biology*, vol. 3, no. 1, pp. 30–37, 2001.
- [162] P. Romano, Z. He, and S. Luan, "Introducing immunophilins. From organ transplantation to plant biology," *Plant Physiology*, vol. 134, no. 4, pp. 1241–1243, 2004.
- [163] A. A. Duina, H. C. J. Chang, J. A. Marsh, S. Lindquist, and R. F. Gaber, "A cyclophilin function in Hsp90-dependent signal transduction," *Science*, vol. 274, no. 5293, pp. 1713–1715, 1996.
- [164] S. Periyasamy, M. Warriar, M. P. M. Tillekeratne, W. Shou, and E. R. Sanchez, "The immunophilin ligands cyclosporin A and FK506 suppress prostate cancer cell growth by androgen receptor-dependent and -independent mechanisms," *Endocrinology*, vol. 148, no. 10, pp. 4716–4726, 2007.
- [165] S. Periyasamy, T. Hinds Jr., L. Shemshedini, W. Shou, and E. R. Sanchez, "FKBP51 and Cyp40 are positive regulators of androgen-dependent prostate cancer cell growth and the targets of FK506 and cyclosporin A," *Oncogene*, vol. 29, no. 11, pp. 1691–1701, 2010.
- [166] P. Kumar, P. J. Mark, B. K. Ward, R. F. Minchin, and T. Ratajczak, "Estradiol-regulated expression of the immunophilins cyclophilin 40 and FKBP52 in MCF-7 breast cancer cells," *Biochemical and Biophysical Research Communications*, vol. 284, no. 1, pp. 219–225, 2001.
- [167] G. M. Wochnik, J. Rüegg, G. A. Abel, U. Schmidt, F. Holsboer, and T. Rein, "FK506-binding proteins 51 and 52 differentially regulate dynein interaction and nuclear translocation of the glucocorticoid receptor in mammalian cells," *The Journal of Biological Chemistry*, vol. 280, no. 6, pp. 4609–4616, 2005.
- [168] H. D. McKeen, K. McAlpine, A. Valentine et al., "A novel FK506-like binding protein interacts with the glucocorticoid receptor and regulates steroid receptor signaling," *Endocrinology*, vol. 149, no. 11, pp. 5724–5734, 2008.
- [169] H. D. McKeen, C. Byrne, P. V. Jithesh et al., "FKBPL regulates estrogen receptor signaling and determines response to endocrine therapy," *Cancer Research*, vol. 70, no. 3, pp. 1090–1100, 2010.
- [170] A. M. Velasco, K. A. Gillis, Y. Li et al., "Identification and validation of novel androgen-regulated genes in prostate cancer," *Endocrinology*, vol. 145, no. 8, pp. 3913–3924, 2004.
- [171] L. Ni, C. S. Yang, D. Gioeli, H. Frierson, D. O. Toft, and B. M. Paschal, "FKBP51 promotes assembly of the Hsp90 chaperone complex and regulates androgen receptor signaling in prostate cancer cells," *Molecular and Cellular Biology*, vol. 30, no. 5, pp. 1243–1253, 2010.
- [172] D. Hanahan and R. A. Weinberg, "The hallmarks of cancer," *Cell*, vol. 100, no. 1, pp. 57–70, 2000.
- [173] D. Hanahan and R. A. Weinberg, "Hallmarks of cancer: the next generation," *Cell*, vol. 144, no. 5, pp. 646–674, 2011.
- [174] L. Neckers and P. Workman, "Hsp90 molecular chaperone inhibitors: are we there yet?" *Clinical Cancer Research*, vol. 18, pp. 64–76, 2012.
- [175] L. Whitesell, E. G. Mimnaugh, B. de Costa, C. E. Myers, and L. M. Neckers, "Inhibition of heat shock protein HSP90-pp60(v-src) heteroprotein complex formation by benzoquinone ansamycins: essential role for stress proteins in oncogenic transformation," *Proceedings of the National Academy of Sciences of the United States of America*, vol. 91, no. 18, pp. 8324–8328, 1994.
- [176] S. Modi, A. Stopeck, H. Linden et al., "HSP90 inhibition is effective in breast cancer: a phase II trial of tanespimycin (17-AAG) plus trastuzumab in patients with HER2-positive metastatic breast cancer progressing on trastuzumab," *Clinical Cancer Research*, vol. 17, no. 15, pp. 5132–5139, 2011.
- [177] S. Modi, A. T. Stopeck, M. S. Gordon et al., "Combination of trastuzumab and tanespimycin (17-AAG, KOS-953) is safe and active in trastuzumab-refractory HER-2-overexpressing breast cancer: a phase I dose-escalation study," *Journal of Clinical Oncology*, vol. 25, no. 34, pp. 5410–5417, 2007.
- [178] M. Rohde, M. Daugaard, M. H. Jensen, K. Helin, J. Nylandsted, and M. Jäättelä, "Members of the heat-shock protein 70 family promote cancer cell growth by distinct mechanisms," *Genes and Development*, vol. 19, no. 5, pp. 570–582, 2005.
- [179] R. Wadhwa, K. Taira, and S. C. Kaul, "An Hsp70 family chaperone, mortalin/mthsp70/PBP74/Grp75: what, when, and where?" *Cell Stress and Chaperones*, vol. 7, no. 3, pp. 309–316, 2002.
- [180] M. V. Powers, P. A. Clarke, and P. Workman, "Dual targeting of HSC70 and HSP72 inhibits HSP90 function and induces tumor-specific apoptosis," *Cancer Cell*, vol. 14, no. 3, pp. 250–262, 2008.
- [181] M. V. Powers, K. Jones, C. Barillari, I. Westwood, R. L. M. van Montfort, and P. Workman, "Targeting HSP70: the second potentially druggable heat shock protein and molecular chaperone?" *Cell Cycle*, vol. 9, no. 8, pp. 1542–1550, 2010.
- [182] H. Hieronymus, J. Lamb, K. N. Ross et al., "Gene expression signature-based chemical prediction identifies a novel class of HSP90 pathway modulators," *Cancer Cell*, vol. 10, no. 4, pp. 321–330, 2006.
- [183] T. Zhang, A. Hamza, X. Cao et al., "A novel Hsp90 inhibitor to disrupt Hsp90/Cdc37 complex against pancreatic cancer cells," *Molecular Cancer Therapeutics*, vol. 7, no. 1, pp. 162–170, 2008.
- [184] A. Salminen, M. Lehtonen, T. Paimela, and K. Kaarniranta, "Celastrol: molecular targets of Thunder God Vine," *Biochemical and Biophysical Research Communications*, vol. 394, no. 3, pp. 439–442, 2010.