

**Desmin and its molecular chaperone, the α B-crystallin:
how post-translational modifications modulate their functions
in heart and skeletal muscles?**

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ABSTRACT

Maintenance of the highly organized striated muscle tissue requires a cell-wide dynamic network through protein-protein interactions providing an effective mechanochemical integrator of morphology and function. Through a continuous and complex trans-cytoplasmic network, desmin intermediate filaments ensure this essential role in heart and in skeletal muscle. Besides their role in the maintenance of cell shape and architecture (permitting contractile activity efficiency and conferring resistance towards mechanical stress), desmin intermediate filaments are also key actors of cell and tissue homeostasis. Desmin participates to several cellular processes such as differentiation, apoptosis, intracellular signalisation, mechanotransduction, vesicle trafficking, organelle biogenesis and/or positioning, calcium homeostasis, protein homeostasis, cell adhesion, metabolism and gene expression. Desmin intermediate filaments assembly requires α B-crystallin, a small heat shock protein. Over its chaperone activity, α B-crystallin is involved in several cellular functions such as cell integrity, cytoskeleton stabilization, apoptosis, autophagy, differentiation, mitochondria function or aggresome formation. Importantly, both proteins are known to be strongly associated to the aetiology of several cardiac and skeletal muscles pathologies related to desmin filaments disorganisation and a strong disturbance of desmin interactome. Note that these key proteins of cytoskeleton architecture are extensively modified by post-translational modifications that could affect their functional properties. Therefore, we reviewed in the herein paper the impact of post-translational modifications on the modulation of cellular functions of desmin and its molecular chaperone, the α B-crystallin.

KEYWORDS: intermediate filaments, desmin, α B-crystallin, phosphorylation, O-GlcNAcylation, striated muscles.

ABBREVIATIONS

AA: amino acid

ACD: “ α -crystallin” domain

ADPRT: ADP ribosyl transferase

CamKII: calcium-calmodulin-dependant protein kinase II

Cdk1: cyclin-dependant kinase 1

CTE: C-terminal extension

GSK3: glycogen synthase kinase 3

HSP: heat shock protein

IFs: intermediate filaments

IXI/V: Ile-X-Ile/Val motif

KO: knock-out

MAPK: mitogen activated protein kinase

MAPKAP: MAPK activated protein kinase

MFm: myofibrillar myopathy

NTD: N-terminal domain

OGA: O-GlcNAcase, N-acetyl- β -D-glucosaminidase

O-GlcNAcylation: O-N-acetyl- β -D-glucosaminylation

OGT: O-GlcNAc transferase, Uridine diphospho-N-acetylglucosamine polypeptide β -N-acetylglucosaminyl-transferase

PAK: p21-activated kinase

PKA: cAMP-dependent protein kinase

PKC: calcium/phospholipid-dependant kinase

PP1: protein phosphatase 1

PTM(s): post-translational modification(s)

ROK: p160 Rho kinase

sHSP: small heat shock protein

UPS: ubiquitin proteasome system

1. THE SARCOMERIC CYTOSKELETON

The striated muscle, whose organization is highly complex through an intricate interconnected cytoskeletal network, is an efficient machinery composed of specialized myofibrils that convert chemical energy into mechanical work [1-3]. The sarcomere, the functional contractile unit of striated muscle, is delimited by two Z-discs and corresponds to a strictly and complex macromolecular assembly requiring precise and regulated localization of their constitutive proteins. It results from regular arrangement of two key filaments, the thin and the thick filaments mainly composed of actin and myosin, motor proteins at the origin of the contraction and the generation of force. Titin completes this sarcomeric organization; this giant protein, a genuine scaffold protein, permits the anchoring of several protein partners regulating thus their subsarcomeric position and modulates the intracellular signalling pathways as a function of contractile activity [4]. While thin and thick filaments interact to generate the contraction force, other proteins constitute an intricate and interconnected network, termed nowadays “sarcomeric cytoskeleton” [2] whose role is the regulation of sarcomere function to ensure its efficient work. Amazingly, although the contractile apparatus must be maintained in almost crystalline order, this framework is not passive or static. Instead, this semi-crystalline organized structure is highly dynamic and the constituted components are in a required equilibrium with constant coordinated changes in structural protein homeostasis as well as in its assembly and maintenance.

Intermediate filaments (IFs), a large family of around 70 members [5], are essential actors of the substantial and elaborated cytoskeletal network with a crucial role in the maintenance of cell shape and architecture, conferring resistance of cells towards mechanical stress [6-8]. They also contribute to the structuration of cells thanks to their interaction with organelles [9, 10], but also the organization of cells into tissues since IFs interact with adhesive structures such as focal adhesions or desmosomes [11]. Initially considered as static structure, it is now well admitted that IFs are on the contrary highly dynamic, able to respond rapidly to changes in cellular activities. Post-translational modifications (PTMs) are strong regulators of IFs dynamics since they could interfere for the fine modulation of the IFs dynamics and interactions in response to signalling pathways [12-17]. Thus, beyond their mechanical role, IFs are a nodal point within cells because of their interactions with a growing number of proteins, in particular proteins of signalling pathways [18, 19]; therefore, IFs are both targets and active contributors of intracellular signalling. As modifiers and organizers of signalling, IFs contribute to dynamic cell behaviour (*e.g.* development, cell division, cell proliferation, cell migration, cell adhesion, aging, apoptosis) and in larger extent to tissue homeostasis (*e.g.* regeneration, wound healing, inflammation, immune response) [12, 20-23]. Moreover, some studies describe that IFs can also be localized at the surface of the plasma membrane or released in the extracellular environment in different physiological and pathological conditions [24-26]. Indeed, the type III IFs vimentin was identified outside the cell where it serves as an attachment site for viral proteins, highlighting the role of the IFs

in viral infection [27, 28]. Importantly, it is now reported that IFs are involved in around 80 human diseases [29-32].

2. THE DESMIN INTERMEDIATE FILAMENTS

2.1. Roles of desmin filaments

Desmin, a 470-amino acids protein whose predicted molecular weight is 53.5 kDa (UniProtKB/Swiss-Prot entry: P17661 for human desmin), is the major protein of type III IFs in adult striated muscle cells, representing 2% and 0.35% of total proteins in heart and skeletal muscles, respectively [33]. Desmin is present in various cell types, such as smooth muscle cells, liver stellate cells, cardiac Purkinje fibres, vascular pericytes, Sertoli cells and primary lung fibroblasts [34-39]. Encoded by *DES* gene on 2q35 in human, desmin shares a tripartite organization, with a head, an α -helical rod and a tail from N- to C-terminus (**Table I, figure 1**); this organization is common to type III IFs family regrouping desmin, vimentin, glial fibrillary acidic protein, peripherin and syncoilin [40].

More specifically, for desmin, the rod domain plays a role in desmin polymerization and consists of four α -helix domains (termed 1A, 1B, 2A and 2B) separated by three linkers (L1, L12 and L2). However, it should be mentioned that only flexible segments L1 and L12 are now considered as linkers [40-43]. In addition to this rod domain, desmin head is involved in polymerization process too but also in IFs assembly while the tail is more specifically involved in the global organization of desmin IFs within the filamentous network presenting visco-elasticity properties [44-46]. Desmin is a highly insoluble protein that assembles through a multi-steps process: (i) two monomers of desmin dimerize within a parallel-oriented coiled-coil formation of the central rod domain; (ii) two coiled-coil dimers join together in an anti-parallel manner to form tetramer; and (iii) the lateral parallel assembly of tetramers leads to filaments of around 60 nm length and 16 nm diameter corresponding to unit-length filaments (ULFs) [8, 40, 47, 48]. The ULFs spontaneously assemble by annealing end-to-end to form incrementally longer filaments, leading at term to intermediate filaments of several hundred nanometres length and 10 nm width. Finally, these desmin IFs constitute a tridimensional filamentous network, anchoring a myriad of proteins within a complex interactome.

The desmin interactome is vast [49-52], desmin interacting with IFs and IFs-associated proteins, sarcomeric and membrane-associated proteins and also with heat shock proteins or signalling proteins [47, 49]. Thus, through specific interactions with a plethora of structural proteins, desmin forms a continuous transcytoplasmic network around Z-discs, maintaining the lateral alignment of myofibrils while tethering them to sarcolemma through costameres and organelles membrane, in particular nuclei, mitochondria and sarcoplasmic reticulum [3, 53]. This coupling of myofibrils to sarcolemma and mitochondria is essential for force transmission and mechanotransduction while maintaining the muscle cell integrity, and permits the optimization of energy use by myofibrils during the contraction

mechanism [3, 10, 40]. Thus, through the constitution of a tridimensional latticework and anchoring of myofibrils and organelles, desmin ensures the maintenance of cell shape and architecture, the preservation of muscle integrity, permitting efficient contractile activity and conferring resistance towards mechanical stress [49, 51, 54, 55]. Desmin IFs are also key actors of cell homeostasis and survival because of their implication in several cellular processes such as differentiation, repairing process, apoptosis, intracellular signalisation, mechanotransduction, vesicle trafficking, organelle biogenesis and/or positioning, calcium homeostasis, protein homeostasis, cell adhesion, metabolism and gene expression [3, 49, 50, 56-60]. Two independent desmin knock-out (KO) mice were obtained in 1996 by using exon 1 interruption strategy [61, 62]. These murine KO models support the essential role of desmin in muscle physiology. Indeed, in desmin null mice, the absence of desmin in muscle leads to the disruption of muscle architecture with strong abnormalities in myofibers characterized by a misalignment of myofibrils. As consequence, myofibrils integrity is lost, associated to a perturbation of sarcolemmal anchoring of myofibrils, abnormal mitochondrial localization and function, apoptosis and degeneration while endurance and muscle force decreased [59, 62-65]. Surprisingly, the desmin null mice are viable and fertile, and myofibrillogenesis and early stages of differentiation occur properly; however, during regeneration, the proliferation and the fusion delay while the second wave of myofibrillogenesis is abortive [58, 59, 64, 66, 67]. Since desmin is also found in cardiac intercalated disks and in skeletal muscle myotendinous and neuromuscular junctions, an abnormal morphology of intercalated disks and neuromuscular junction are also observed in desmin null mice [47, 63, 66]. Moreover, recent studies have assigned new roles to the desmin filaments as regulators of cell adhesion [60] and modifiers of dystrophic muscle [68].

2.2. Desmin network abnormalities and associated muscular and cardiac disorders

Mutations or impaired expression of desmin (primary desmin alteration) are closely associated to dramatic myofibrillar dysfunction and desmin is strongly associated to the aetiology of muscle pathologies, especially heart (*e.g.* dilated cardiomyopathy, hypertrophic cardiomyopathy, restrictive cardiomyopathy) and skeletal muscle diseases, in particular myofibrillar myopathies, a class of rare striated muscles diseases [3, 11, 49, 50, 54, 55, 69, 70]. It should also be noticed that desmin IFs remodelling (corresponding to secondary desmin alteration) is associated to aging and various disorders such as obesity, type II diabetes, sleep apnoea, asthma, dysphagia, hypoxia-induced pulmonary hypertension, muscle wasting, LMNA cardiomyopathy and Friedreich Ataxia, leading to cytoskeleton abnormalities and changes in muscle structure and/or function [48, 71-78]. Several case reports link desmin immunoreactivity abnormalities to diverse muscle pathologies such as congenital myopathy, developmental myopathies, adult onset myotubular myopathy, spheroid body myopathy, dystrophinopathies, cardiomyopathies or granulo-filamentous body myopathy, desmin being often localized toward cytoplasmic bodies and aggregates [79-90]. At the end of 1990s, Goldfarb et al.

described three missense mutations (A337P, A360P and N393I) in desmin gene associated with familial mild cardiac and adult-onset skeletal myopathy [91]. Several missense mutations, splice site or frame-shift mutations or deletions in *DES* gene were identified thereafter [92-105] (for review, see [47, 48, 50, 55, 106]). Importantly, these mutations could have repercussions on desmin structure, IFs assembly and/or organization and by extension on desmin IFs architecture [107]. A meta-analysis performed on 40 different mutations of *DES* gene (159 mutation carriers) revealed that 74% of patients presented myopathy or muscle weakness, 49% a combination of skeletal and cardiac signs and 26% suffer also from respiratory insufficiency [106]. The smooth muscle defects such as dysfunction of intestine or bladder are observed in some patients carrying desmin mutations [108, 109]. It is worth to note that the majority of these *DES* mutations occur predominantly in 2B domain, essential for IFs assembly, in particular in patients with neurological signs whereas predominant cardiological phenotype is rather linked to head and tail domains mutations [106]. These desmin-related myopathies (OMIM 601419), also referring as desminopathies, a subset of myofibrillar myopathies (MFMs), are characterized by strong morphological changes in striated muscle resulting from myofibril disintegration and abnormal accumulation of desmin among other structural and sarcomeric proteins (*e.g.* myotilin, filamin C, plectin, synemin, HSP27, α B-crystallin, dystrophin) [47]. Even if some mutations of *DES* gene are not characterized by abnormal protein aggregation [48], these ectopic desmin aggregates presenting subsarcolemmal and/or sarcoplasmic location are a hallmark of desminopathies and in larger extent, MFMs [110, 111]. As a consequence, desmin function is lost while toxic aggregates, that are seeding-competent amyloid aggregates of desmin, accumulate and persist within muscle fibres [112, 113]. The desmin network disorganization and destructuration have dramatic cellular repercussions since they are closely associated to improper mitochondrial function, loss of cell adhesion and cell-cell communication, fibrosis and inflammation [47, 50, 114]. Thus, desmin mutations lead to disruption of desmin cytoskeleton and mitochondrial abnormalities in terms of distribution, shape, number and function [115-117]. Finally, due to the role of desmin as scaffold for plethora of myofibrillar and signalling proteins, mutations of desmin could have repercussions on the function of the associated proteins that interact or co-interact within the desmin interactome. Indeed, when desmin aggregates in MFMs, numerous myofibrillar proteins co-aggregate such as α B-crystallin, filamin C, actinin, vimentin, synemin or myopalladin among others, leading to their mislocalization and/or the loss of their function [118-120]. Consequently, desmin mutants could affect several cellular processes depending on the mutation, such as proteasomal activity and autophagy (and in larger extent, protein homeostasis); in addition, cell stiffness changes due to the loss of interaction with nebulin and actin filaments [56, 121-125]. Thus, desmin-related myopathies (*i.e.* desminopathies) result from mutation in the desmin gene, but could also be consecutive to desmin cleavage and/or post-translational modifications (PTMs) changes leading to a dysfunctional desmin network [50, 105, 126-128].

2.3. The post-translational modifications of desmin

Desmin is the target of several PTMs [40, 71], the well-known and the most studied being phosphorylation. Desmin phosphorylation was firstly described four decades ago [129, 130], and phosphorylation of the head domain (**figure 1**) is often associated to IFs disassembly and solubilisation [131]. In addition, the change of the charge environment due to the addition of one or more negative charge(s) could also modify the interaction between desmin and its partner(s). Desmin is phosphorylated by several kinases, connecting desmin to different cellular processes such as cell division, myoblast differentiation or muscle contraction [71].

Among these kinases, Rho-associated kinase (also termed ROK or p160^{ROCK}), a member of the Rho family GTPase-dependant kinase, is involved in the regulation of muscle metabolism and differentiation while its activity increases after exercise [132-134]. Rho kinase phosphorylates desmin on threonines 17, 76 and 77 [135, 136], the phosphorylated desmin losing its ability to form 10 nm filaments. Similar observation was done when desmin is incubated with PAK (p21-Activated Kinase) that phosphorylates desmin mainly on the head domain [137]. PAK is a Ser/Thr kinase regulated by the Ras-related small G-proteins Cdc42/Rac1 involved in the regulation of cell cycle, cell survival, differentiation, cytoskeleton dynamics, muscle contractility and muscle regeneration [138-141]. However, even if similar consequences are observed on desmin depolymerisation when phosphorylated by ROK or PAK, modified sites are not the same since PAK phosphorylates serine residues whereas Rho kinase targets threonine residues [137]. These data support that specific kinases targeting different sites could impact the desmin function in a similar manner, increasing thus the regulatory potential for desmin organization and remodelling in response to specific cellular signals.

Desmin is also targeted by kinases involved in cell cycle regulation; among them, Aurora kinase B and Cdk1 phosphorylate desmin on Ser12/Thr17/Ser60 and Ser7/Ser28/Ser32, respectively [136, 142-144]. Interestingly, using phosphorylation site- and state-specific antibodies [145-147], Makiyama and co-workers showed a spatio-temporal regulation of desmin phosphorylation on Ser32 during cell cycle in muscle cells. More specifically, they observed that phosphorylation on Ser32 occurs in the whole cytoplasm during the prometaphase to metaphase transition, leading to efficient separation of desmin IFs during mitosis [142]. They also demonstrated that desmin phosphorylation on Ser60 by Aurora-B and on Thr76 by Rho kinase occurs during late mitosis (from anaphase to telophase) specifically at the cleavage furrow [142], suggesting a fine spatio-temporal regulation of desmin IFs through the differential and coordinated recruitment of kinases. It is worth to note that hyperphosphorylation of Ser32 resulting from hyperactivation of Cdk-1 in Drp/MC mice (a model of dynamin-related protein 1 overexpression in skeletal muscle) modifies desmin network, leading to mechanotransduction impairment while biogenesis and maintenance of mitochondria are altered [144].

The non-helical N-terminal domain is also phosphorylated by PKC (calcium/phospholipid-dependant protein kinase) and PKA (cAMP-dependent protein kinase) [148-150]. Several sites, more

specifically on Ser13, Ser30, Ser39 and Ser57 (chicken sequence) were identified to be phosphorylated by PKC, corresponding to Ser13, Ser48 and Ser68 on human desmin [71, 149], while PKA phosphorylates desmin on Ser30, Ser36 and Ser51, corresponding to Ser45 and Ser60 on human desmin [71, 148]. The PKC family is a major mediator of signalling pathways regulating a large panel of cell functions (*e.g.* proliferation, differentiation, apoptosis) and is involved in detrimental consequences of several striated muscle diseases, particularly in heart (heart failure, myocardial infarction, atherosclerosis, cardiac hypertrophy or laminopathies) [151-156]. When PKC is activated, it phosphorylates desmin, leading to IFs disassembly while proliferation and differentiation are inhibited [157-159]. The desmin IFs turnover is also strongly impacted by protein kinase A through inhibition of polymerization; interestingly, the fusion of myoblasts into myotubes decreases [148, 160]. Lastly, CamKII was also reported to phosphorylate desmin, but nor the impact on desmin nor the modified site are known [71, 161, 162].

Phosphorylation is a reversible PTM; unsurprisingly, protein phosphatases contribute to the regulation of desmin phosphorylation and are involved in the organization and reorganization of IFs. Indeed, it was demonstrated that protein phosphatases inhibitors dramatically alter IFs, leading to the loss of cytoskeletal integrity [163, 164]. In contrast to phosphorylation inducing filaments disassembly, phosphatase treatment leads to the reassembly of the desmin [150]. In the same way, it was shown that PP1 (type 1 protein phosphatase) antagonizes with Rho kinase to finely regulate the phosphorylation turnover on desmin filaments, and in larger extent, the exchange of desmin subunits between the soluble pool and the filamentous desmin [165].

In addition to phosphorylation, assembly-disassembly of desmin filaments is regulated by ADP-ribosylation. Desmin is a substrate for ADP-ribosyl transferase and the modification occurs in the head domain (Arg48 and 68 on turkey desmin, corresponding to Arg58 and 73 on human desmin). Once ADP-ribosylated, desmin does not form the typical 10 nm-diameter filaments [71, 166-168]. Interestingly, it was shown that ADP-ribosylation is a mechanism modulating phosphorylation by PKA and is involved in muscle cells differentiation [166, 169].

At least, desmin is also post-translationally modified by an atypical glycosylation: the O-N-acetyl- β -D-glucosaminylation (O-GlcNAcylation) [170]. O-GlcNAcylation corresponds to the transfer of a unique monosaccharide, the N-acetyl-D-glucosamine, on serine or threonine hydroxyl group of a protein; O-GlcNAcylation is highly dynamic and reversible, presenting a dynamic interplay with phosphorylation. It is highly abundant on cytoskeletal proteins, and among them, desmin is glycosylated on Ser460 in tail domain [171-173]; probably other glycosylation sites exist on desmin but remain to be discovered. Even though it was demonstrated that O-GlcNAcylation is involved in organization and reorganization of skeletal muscle sarcomere, partly through the modulation of interaction of desmin and its molecular chaperone, the α B-crystallin, the precise role of O-GlcNAcylation remains uncharacterized [174]. However, since O-GlcNAcylation was demonstrated to modulate the phosphorylation level of IFs [162, 175, 176] and increases keratins solubility [14, 177], ubiquitination

and proteasomal degradation of these IFs proteins [178], it is legitimate to consider that O-GlcNAcylation could exert a key role in the regulation of desmin network organization. In this way, the link between O-GlcNAcylation and desmin network was recently established. Indeed, it was shown that global change of O-GlcNAcylation level in C2C12 skeletal muscle cells is associated to a differential partition of desmin toward cytoskeleton; interestingly, the correlation with desmin phosphorylation was clearly established, suggesting that a dynamic and complex interplay may occur on desmin to modulated its behaviour [162].

2.4. Aberrant modifications of desmin: a link between PTMs and the physiopathology of muscle disorders?

Desmin could be non-enzymatically modified in detrimental physiological conditions; in this way, it was shown that desmin is a preferential target of advanced glycation end (AGE) products in dilated cardiomyopathy [179]. Furthermore, oxidative stress strongly affects desmin, leading to desmin cytoskeleton reorganisation and aggregation [69, 180] (**figure 2**). Desmin has been observed to be oxidized and nitrated within protein aggregates [111, 181, 182], and interestingly, antioxidant treatment prevents aggregation of desmin in cellular models of desminopathies submitted to various stresses [183]. It was suggested that these aberrant modifications make desmin untargeted by the ubiquitin-proteasome system, leading to the impairment of abnormal desmin degradation and at terms to desmin aggregation [111]. On another note, misregulated ubiquitination of desmin is associated to desmin degradation and is involved in the physiopathology of skeletal muscle atrophy, abnormal phosphorylation preceding the ubiquitination by TRIM32 [184, 185]. In this way, it was demonstrated that phosphorylation by GSK-3 β , a kinase activated in fasting conditions [186], is the initial step for desmin IFs degradation in muscle atrophy. Once activated, GSK-3 β phosphorylates desmin on Ser32, permitting subsequently its ubiquitination and degradation by calpain-1 [143, 184, 185, 187]. It is worth to note that additional site of phosphorylation linked to detrimental conditions for heart diseases was identified in head domain on the Ser28 [127, 179, 188] (**figure 2**).

While some desmin mutations linked to desmin-related myopathies correspond to phosphorylated sites, such as S6F or S12F in the head domain [55], abnormal desmin phosphorylation was linked to several cardiac diseases [126, 179, 188, 189] (**figure 2**). In this way, the phosphorylated form of desmin could be consider as a tissue marker of heart failure, and this phosphorylation increase is linked to desmin aggregation and cleavage by calpain or caspase [126, 127, 143, 190]. Importantly, the Ser32 phosphorylation was identified to be pivotal in the priming nucleation process leading to the formation of preamyloid oligomers [143]. As mentioned previously, Ser32 is also targeted by cyclin-dependant kinases [142, 144]. Interestingly, overexpression of several cyclin-dependant kinases is noticed in MFMs biopsies [191-193], suggesting that desmin hyperphosphorylation and the resulting IFs disassembly could be involved in the pathogenesis of desmin-related myopathies. In the same way, PKC

activity increase is described in a model of cardiomyopathic hamster heart, a model of myocardial disease resulting in chronic congestive heart failure [157]. In addition, desmin hyperphosphorylation occurs in some desminopathies [194, 195] while certain kinase isoforms expression increases in muscle fibres from patients suffering from myofibrillar myopathies [193, 196]; the phosphorylated fragments of desmin are closely associated with the amyloid-like oligomers deposition [188] (**figure 2**). However, no hypothesis concerning the role of the increase of desmin phosphorylation has been proposed, and it is now clear that the impact of desmin PTMs remains underexploited in myofibrillar myopathies.

Finally, the O-GlcNAc site on desmin corresponds to a mutated site closely associated to the development of desminopathies [173]. Furthermore, it is worth to note that in heart failure, a dynamic interplay was observed between phosphorylation and O-GlcNAcylation on desmin, phosphorylation increasing while O-GlcNAcylation decreases [190] (**figure 2**).

3. α B-CRYSTALLIN, THE MOLECULAR CHAPERONE OF DESMIN

3.1. *Structure and properties of the α B-crystallin*

The crystallins, regrouping α -, β - and γ -crystallin, were identified over a century ago as the major proteins in eye lens (around 90% of total protein content of the ocular lens) [197]. Among the different classes of crystallins, the α -crystallins regroup the α A- and α B-crystallins, encoded by two genes coming from a gene duplication event and presenting 57% sequence homology [198]. While the α A-crystallin is mainly expressed in eye lens, the α B-crystallin (encoded by the *CRYAB* gene located at the locus 11q23.1) is widespread expressed in various non-lenticular tissue, in particular heart, skeletal muscle (more specifically in the high oxidative type I fibres) and brain. Moreover, it has a significantly higher concentration in adult than in foetal tissues as demonstrated in rat [199-204]. They are for a long time classified as small Heat Shock Proteins (sHSP) due to their capacity to suppress aggregation of proteins, permitting the protection of eye lens from severe and deleterious consequences of protein aggregation [205, 206]. Although members of this protein superfamily differ according to their sequence and size, they share common characteristics, in particular: (i) a low molecular weight between 15 and 40 kDa; (ii) a tripartite structure with the “ α -crystallin” domain (ACD), a signature consensus sequence; (iii) the association with up to 50 subunits within polydisperse homo- and hetero-oligomers of about 10-25 nm diameter; (iv) a dynamic quaternary structure; (v) their induction consecutively to various cellular stresses; and (vi) their chaperone activity permitting the suppression of protein aggregation [199, 207-210].

The α B-crystallin (UniProtKB/Swiss-Prot entry: P02511 for human α -crystallin B chain) presents a common tripartite structure, composed of a conserved and central ACD, the hallmark of sHSP family, flanked with variable N-terminal domain (NTD) and a short C-terminal extension (CTE) [211, 212] (**Table 1, figure 3**). The ACD of α B-crystallin, covering around 80 amino acids, is characterized by a

predominance of β -strands that permit to form rapidly a stable dimer [197, 213-216]; this dimer is sufficient for *in vitro* chaperone activity, supporting that the multimeric state of α B-crystallin is not required for chaperone activity [214, 217]. In physiological conditions, soluble multimeric α B-crystallin complexes are formed; in contrast, in stress conditions, the α B-crystallin multimers dissociate to form smaller oligomers while the NTD and the CTE become available for recognition of the client proteins and the binding of the unfolded proteins (see below) [218]. For example, when pH varies from 7.5 to 6.8 (during cardiac ischemia, acidosis occurs), the ACD undergoes a transition from dimeric status to monomeric one, permitting so the α B-crystallin to act optimally [219]; at pH 6.8, the affinity of α B-crystallin for desmin increases, allowing so the preservation of IFs integrity in detrimental conditions for cardiac cells. The NTD is around 60 amino acids, particularly rich in hydrophobic amino acids [211]; the propensity of NTD to aggregate when expressed alone suggests that NTD hydrophobicity might be involved in the recognition of exposed hydrophobic domains of unfolded proteins, facilitating their capture [208]. Lastly, due to its modification by phosphorylation, the NTD contributes to conformational changes of α B-crystallin and the regulation of the chaperone activity; this point will be addressed hereinafter. Furthermore, the CTE is a short unstructured sequence of around 20 amino acids highly flexible, hydrophilic and accessible to solvent; consequently, the CTE contributes to the solubility of α B-crystallin under chaperone and non-chaperone conditions [197, 220-222]. The CTE contains the highly conserved IXI/V motif (Ile-Pro-Ile for α B-crystallin) that could interact with the neighbouring ACD domain; it is also involved in the formation and the solubility of oligomers [197, 211, 212, 223, 224]. Supporting the key role of CTE, it was demonstrated that its truncation or mutation leads to myofibrillar myopathies [225]. Importantly, the flanking NTD and CTE are required for solubility and stability of α B-crystallin, delay the amyloid fibril formation and contribute to the interaction with target proteins during the chaperone activity [221, 226]. Thus, although the ACD bears the chaperone activity, the N- and C-terminal regions of α B-crystallin are also involved in fibril disaggregation [227].

3.2. The cellular functions of α B-crystallin

Proteome is inherently metastable since the protein folding is intrinsically error-prone, and its integrity absolutely requires to be maintained; this corresponds to protein homeostasis or proteostasis [228-231]. A fundamental aspect of proteostasis is the maintenance of protein solubility; if not, proteins aggregate consecutively to the exposure and the interaction of hydrophobic amino acids/domains that are normally buried within proteins [228, 229, 232-234]. As a consequence, proteotoxicity results from abnormal accumulation of protein aggregates (extracellular amyloid deposits or intracellular inclusions); highly deleterious for cell and tissues, proteotoxicity is involved in a wide range of proteinopathies, sometimes termed as conformational diseases [233-238].

To ensure this protein equilibrium, cells use interconnected factors within the proteostasis network [231]; among them, molecular chaperones are critical players and guardians of the proteome's stability

and integrity. They are defined as “any protein that interacts with and aids in the folding or assembly of another protein without being part of its final structure” [229]; moreover, besides their role in *de novo* protein folding, molecular chaperones also contribute to aggregates unbundling and the refolding of stress-denaturated proteins. Many of molecular chaperones are logically heat shock proteins since they are synthesized under stress conditions that destabilize a subset of proteins [229]. The chaperone network regroups members fulfilling three main activities: (i) the “foldase” activity, assisting the protein refolding; (ii) the “holdase” activity, forming stable complexes with misfolded proteins and preventing protein aggregation; and (iii) the “translocase” activity, permitting the correct location of proteins [230, 239-241]. A further classification could also be considered, based on the energy dependence of the molecular chaperones: (i) the ATP-dependant chaperones, usually “foldases” such as HSP60, HSP70, HSP90, DnaK and GroEL, that need ATP hydrolysis for recognition and refolding of the targeted proteins; and (ii) the ATP-independent chaperone, usually “holdases”, preventing protein aggregation in an energy-independent way [239]. Archetypical “holdases” are sHSP that recognize misfolded proteins before cooperating with “foldase” chaperones to refold proteins or disintegrate the protein aggregates [211, 212, 230, 241-244]. Acting as the first line of defence against protein aggregation, they are qualified as the “paramedics” of the cell [216].

The α B-crystallin is an integral part of proteostasis system. Under various stresses leading to destabilization of proteins (oxidation, heat increase, pH changes, etc...), it interacts in an ATP-independent manner with the unfolded proteins to correct their conformation and can disrupt the unfolding process through the stabilization of the unfolded target proteins while facilitating their refolding thanks to its chaperone activity [221]. Importantly, it was demonstrated that the α B-crystallin interacts with amyloid oligomers, prevents the fibrillation of several target proteins, and mediates the amyloid dissolution and the depolymerisation of aggregation-prone proteins such as α -synuclein, β 2-microglobulin or amyloid β -peptide [240, 241, 245-249]. To ensure its molecular chaperone function, a key step is the recognition and the interaction with target proteins. Several interactive sequences are identified in α B-crystallin, two of them being located into the NTD, four in the ACD, and one in the CTE (**figure 3**) [250]. Substantially, these interactive sequences exert dual roles since they could mediate the subunit-subunit interactions involved in α B-crystallin assembly and also the interactions with client proteins [251]. However, several data support that the interaction between the chaperone and the target proteins involves several interaction domains while an interaction domain could contribute to the interaction of α B-crystallin with various proteins target (**figure 3**). For instance, the NTD or the ACD are the preferred interaction sites in some cases while in some other, both domains are needed for the chaperone activity [222, 250-257].

The α B-crystallin recognizes a broad spectrum of cellular proteins including proteins involved in apoptosis, cell-cell adhesion and cytoskeleton organization [242, 254, 258-260]. Consequently, over its role as guardian of proteome stability, the α B-crystallin also plays a critical role in the regulation and the modulation of several cellular functions such as cell integrity, apoptosis, autophagy, differentiation,

mitochondria function, aggresome formation, and cytoskeleton stabilization [261-265]; this last point will be explored thereafter. Thus, the α B-crystallin exerts anti-apoptotic activity through inhibition of caspase-3 and PARP, and by preventing the translocation of Bax and Bcl-2 and the activation of the RAS pathway [264, 266-272]. This anti-apoptotic effect of α B-crystallin is also demonstrated in the C2C12 skeletal muscle cell line and in neonatal mouse cardiomyocytes [273, 274]; in the same way, the overexpression of α B-crystallin in transgenic mice is closely associated to decrease of apoptosis and necrosis in cardiomyocytes [275]. Cytoprotective effects of α B-crystallin are also noticed in C2C12 myoblasts exposed to TNF- α [276]. Over its cytoprotective effects, the α B-crystallin seems to be involved in myogenic process since its expression ten-fold increases during skeletal muscle development and differentiation [277, 278] while its expression decreases in aging, closely linked to impaired proteostasis [279]. It modulates the activity of MyoD and delays the myogenic differentiation [280, 281] while C2C12 myoblasts deficient in α B-crystallin fail to form myotubes [282]. Finally, it should be mentioned that α B-crystallin is also detected in extracellular fluids where it binds inflammatory molecules and platelets [283], and it is demonstrated that the chaperone releasing occurs through exosomes under specific stress conditions [284].

3.3. α B-crystallin and cytoskeleton protection: focus on desmin network

As mentioned previously, sarcomere is a highly complex and dynamic structure requiring continuous protein turnover and assembly. The “sarcomat”, a protein control quality system of the sarcomere, relies on two main components, one of them being the UPS (ubiquitin proteasome system) permitting to target specific proteins for their degradation [285-287]. In addition, to ensure sarcomere homeostasis and its protection against stressors such as the contraction (*i.e.* mechanical stress), the prime function of striated muscle, chaperones dynamically associate with target proteins through a dynamic interplay [285, 286, 288]. Several chaperones are known to interact with the sarcomere, ensuring its assembly and its stabilization, and among them, the α B-crystallin interacts with actin [289, 290], myosin [291], titin [292, 293], and importantly with desmin [285, 290]. It should also be mentioned that actin for example, that is subject to both polymerization and aggregation, is the target of several chaperones that overlap (GimC, TRiC, HSP27, and α B-crystallin), suggesting a cooperative interplay between several chaperones [285]. It is worth to note that the α B-crystallin also interacts with the ubiquitin ligase FBX4, a F-box-containing protein component of the SCF complex (SKP1/Cul1/F-box) [294]. This suggests that, in addition to its role in the prevention of protein misfolding, the α B-crystallin also interplays with the UPS for the degradation of target proteins [285].

Through its involvement in microtubules and IFs dynamics, the α B-crystallin remains essential to cell shape maintenance and in mechano-biology [295], permitting the muscle cells protection toward mechanical stress [288, 296]. It is worth to note that α B-crystallin displays sarcomeric localization, in

particular on Z-disks and I-bands of skeletal muscle and cardiac sarcomeres where proteins are continuously submitted to mechanical stress [278, 297-299]; these interactions occur in both basal and stress conditions [288]. It should be mentioned that over its cytosolic distribution, α B-crystallin could be also located in subnuclear compartment [300]. Importantly, it is shown that α B-crystallin maintains the myosin enzymatic activity while preventing its aggregation under heat stress, suggesting that over its role in myofibrillogenesis and the maintenance of cytoskeleton integrity, the small molecular chaperone also sustains muscle performance [291]. Moreover, physical activity, considered as a physiological stressor, leads to a strong increase of different HSPs permitting the protection of muscle toward heat, oxidative and mechanical stresses resulting from exercise [301]. It is demonstrated that accumulation of the α B-crystallin preferentially occurred to Z-disks, to membrane scaffolding proteins and to desmin IFs [302, 303]. In addition, the increased expression of α B-crystallin facilitates the remodelling of trained skeletal muscle (*i.e.* protein synthesis and the resulting hypertrophy, and metabolic adaptation, in particular mitochondrial activity) [301]. This could explain why the expression of the α B-crystallin depends on the muscle phenotype, of the type of contraction (eccentric, concentric or isometric) and also depends on the training protocol (resistance *versus* endurance) [303-309].

As for microtubules and microfilaments, the IFs organization depends on the competence of the sHSP [285, 310]. Indeed, since these large complex structures have a propensity to misfold and/or aggregate, they need to be chaperoned. Interestingly, it is shown that the molecular chaperone could interact both with IFs and with soluble subunits, suggesting that it could be involved in the modulation of IFs assembly and remodelling as well as in the inter-filament interactions [310-314]. Thus, upon stress, the IFs network dynamically remodels while the α B-crystallin is concomitantly recruited on IFs proteins [311, 315]. The α B-crystallin interacts with desmin to inhibit both its assembly and its aggregation [311], and the assembly of desmin as well as the formation of desmin network requires the α B-crystallin [316, 317]. Over the role in assembly and stabilization of desmin IFs, the interplay between desmin and α B-crystallin is involved in the mitochondria homeostasis and cell viability [119, 318]. Interestingly, the morphology of desmin filaments impacts the binding of the α B-crystallin which mainly occurs on the C-terminal domain of desmin (442-453 amino acids sequence), underlining the sensor properties of α B-crystallin that is able to detect changes in the surface topology of desmin IFs [314]. Importantly, desmin mutants in the C-terminal domain, harbouring critical binding sites for α B-crystallin, have opposing effects on the binding of the molecular chaperone. Thus, the mutation I451M leads to a decreased α B-crystallin binding while the sample viscosity increased, supporting that the filament-filament interaction is enhanced. In contrast, the mutation R454W (a mutant causing desminopathy such as the I451M mutant) is correlated with an increase of the binding of α B-crystallin along the surface of the filament [314].

The α B-crystallin presents several bioactive interactive sequences modulating the sensitivity, the selectivity and in larger extent the activity of the molecular chaperone [319]. Using protein pin array,

Ghosh and co-workers identified interactive sequences on the α B-crystallin depending on its protein partners. They have identified seven interactive sequences involved in chaperone activity; five of them overlap with interactive sequences involved in subunit-subunit interaction, suggesting a dual function for some interactive sequences in multimerization of α B-crystallin and in its chaperone activity (**figure 3**) [250]. Several interactive sequences are involved in the regulation of α B-crystallin activity and in the recognition of protein targets [254]. These interactive sequences could have different repercussion on the interacting proteins. As example, five interactive sequences are involved in the interaction with tubulin (**figure 3**); two of them promote microtubule assembly while inhibiting their disassembly, one of them inhibits both microtubule assembly and disassembly, and the two remaining sequences have little or no effect on microtubule assembly and disassembly [320]. In fact, the effect of the molecular chaperone on microtubule assembly depends on the ratio of α B-crystallin to tubulin: favourable ratio ($1:4 < \text{ratio} < 2:1$) promotes microtubule assembly while unfavourable ratio ($< 1:4$ or $> 2:1$ corresponding so to low or high concentration of the molecular chaperone) inhibits the filament assembly. A similar effect was observed for actin [321]. All these data suggest that in unstressed conditions, the α B-crystallin could interact with filaments for their stabilization; in contrast, upon stress conditions, the molecular chaperone dissociates from filaments to interact with the unfolded proteins. Finally, for desmin, several interactive sequences are identified [321, 322]; among them, the peptide $^{113}\text{FISREFHR}^{120}$ has a strong affinity for desmin. This point is reinforced by the fact that the R120G mutant of α B-crystallin, presenting abnormal interaction with the target protein, leads to protein aggregation and disorganisation of desmin network in cardiomyopathy and in desmin-related myopathy [317, 323, 324].

While modulating the desmin network viscosity, the main function of the α B-crystallin is to prevent the improper self-assembly of desmin IFs that could lead to desmin filaments aggregation [119, 322]. Supporting this role of α B-crystallin in preventing desmin IFs aggregation, Elliott and co-workers have demonstrated that α B-crystallin alleviates desmin aggregation *in vitro* [119]. It is worth to note that if the molecular chaperone is missing, or if the recognition between desmin and its molecular chaperone is altered, desmin forms stable misfolded oligomers that accumulate within the cell [112, 314, 325]. The most relevant finding supporting the essential role of sHSP and IFs interaction is illustrated by the phenotype resulting from sHSP mutation. Indeed, the mutation of sHSP mimics the IFs aggregation phenotype related to IFs diseases [312]. Interestingly, some post-translationally modified sites are located into or close to some of the interactive domains (**figure 3**), suggesting a key role of PTMs in the modulation of the molecular chaperone functions. This important point will be also considered and discussed below.

3.4. The post-translational modifications of α B-crystallin

Three major phosphorylation sites are described on α B-crystallin: the serines 19, 45 and 59 that are localized into the NTD. While the Ser45 and the Ser59 are phosphorylated by p42/44 MAPK and

MAPKAP2/3, respectively, the kinase responsible of the Ser19 phosphorylation remains to be identified [326-328]. As mentioned previously, the α B-crystallin forms large polydisperse oligomers assemblies in equilibrium with smaller-assembly species, the oligomers containing a variable number of subunits; the NTD is mainly responsible of their assembly and their dynamic distribution [223, 277]. It is reported that serine phosphorylation is involved in the shift of higher-order oligomers toward smaller activated ones, in correlation with the enhancement of substrate binding [197, 224]. Once p38 MAPK stress transduction pathways activated, the N-terminal domain is phosphorylated and sHSP disassemble; interestingly, this is correlated with partition of the chaperone toward insoluble protein materials [286, 289, 329-331]. The α B-crystallin phosphorylation varies according to cellular demands or stress conditions, leading to activity profile changes [328]. Thus, several *in cellulo* studies have reported an increase of phosphorylation of the α B-crystallin following stresses [276, 289, 332-335]. However, phosphorylation changes are observed consecutively to several pathologies such as ischemia-reperfusion, chronic hyperglycaemia, congestive heart failure, cardioplegia or myocardial infarction [286, 336-342] or during skeletal muscle healing [343].

In fact, the phosphorylation of α B-crystallin has beneficial outcomes to counteract stress; however, if stress occurs for a long-time duration, the phosphorylation, which becomes irreversible, induces deleterious effects [262]. Among the seven interactive sequences of the α B-crystallin (**figure 2**), the ⁵⁷APSWFDTG⁶⁴ peptide which has a strong interaction with actin harbours the Ser59 that is known to be phosphorylated in stress conditions, increasing the interaction between the α B-crystallin and cytoskeleton [321]. In the same way, several studies have reported that upon stress conditions, Ser59 is involved in the colocalization of α B-crystallin with actin microfilaments, microtubules and intermediates filaments, permitting the stabilization and the preservation of the cytoskeleton [289, 328, 332, 334, 337]. Through its involvement in microtubules and IFs dynamics, the α B-crystallin remains essential for cell shape maintenance and in mechano-biology [295], permitting the muscle cells protection toward mechanical stress [288, 296]. As mentioned previously, α B-crystallin displays a sarcomeric localization (in particular on Z-disks and I-bands) where proteins are continuously submitted to mechanical stress. Thus, it makes sense that phosphorylation of α B-crystallin is increased during exercise in myocardium as well as in skeletal muscle [301, 304, 334, 344]. However, while lengthening contraction is often correlated to increase of α B-crystallin phosphorylation, it is shown that the cytoskeleton translocation is independent of the phosphorylation of the molecular chaperone [308]. In this way, while preconditioning and cardiac ischemia lead to α B-crystallin phosphorylation on Ser45 and Ser59 and translocation to contractile apparatus, reperfusion is linked to the dissociation of α B-crystallin from the contractile apparatus but without any correlation with the dephosphorylation of the chaperone [336, 341, 345]. This suggests that phosphorylation alone could not explain the translocation of the chaperone toward the cytoskeleton. In the same way, it is reported that both unphosphorylated

and phosphorylated forms of α B-crystallin are equally efficient to prevent the assembly of some IFs proteins, in particular GFAP and vimentin [310].

It is worth to note that numerous studies exclusively focused on Ser59 phosphorylation without considering simultaneously all the aforementioned sites. However, the relationship between the phosphorylation of α B-crystallin and its molecular chaperone activity is sometimes contradictory. It seems that the modulation of the chaperone activity and the interaction with the target protein depend on the phosphorylation pattern [346, 347]. Supporting this complex interplay between phosphosites, a study of Singh et al. shows a differential kinetic of phosphorylation for Ser45 and Ser59. Indeed, they observed that upon heat stress of H9c2 cardiac cells line, the phosphorylated Ser59 remains constant the first 30 minutes of stress and increases thereafter; interestingly, they observed a peak of phosphorylation on Ser59 in the soluble fraction up to 30 minutes and a decrease afterwards [289]. In contrast, the phosphorylation of Ser45 shows a gradual decrease in the soluble fraction while it increases in the insoluble fraction up to 60 minutes after which it decreases. While these data support the correlation between α B-crystallin phosphorylation, interaction with actin fibres and the partition of the chaperone toward insoluble material in stress conditions, they also suggest that phosphorylation differentially occurs at different sites which may have an impact on the interaction with actin fibres [289]. The phosphorylation of α B-crystallin on a given site could also affect the subcellular localization of the chaperone. In this way, in human myocardium after cardioplegia and cardiopulmonary bypass, Clements and coworkers observed a preferential localization of Ser59 phosphorylated α B-crystallin on Z-disks and I-bands, while the phosphorylated forms on Ser45 and Ser19 are preferentially localized to cell periphery/membrane and intercalated discs, respectively [340]. Lastly, while the phosphorylation of α B-crystallin is closely linked to cytoskeleton translocation, certain studies have shown that the phosphorylated α B-crystallin localized into the mitochondria in myocardium in models of ischemia or myocardial infarction [339, 348, 349]. It should be mentioned that phosphorylation occurs once α B-crystallin is translocated into mitochondria.

The α B-crystallin is also modified by O-GlcNAcylation, the turnover of the monosaccharide on the protein backbone being highly dynamic [350, 351]. Initially identified to be O-GlcNAcylated in lens, the O-GlcNAcylation of the α B-crystallin is known in heart and in skeletal muscle since 1996 and 2004, respectively [351, 352]. The main O-GlcNAcylation site of the molecular chaperone is found on the CTE, especially on the Thr170 [351]; additional site is described on Thr162 in C2C12 skeletal muscle cells line [173]. In this cell line, it was demonstrated that O-GlcNAcylation is involved in the remodelling of sarcomeric cytoskeleton through the modulation of protein-protein interactions including the interaction between desmin and the α B-crystallin [174]. It is now well admitted that O-GlcNAcylation mediates the regulation of protein-protein interactions [353, 354], reinforcing the potential role of O-GlcNAcylation in the binding of α B-crystallin on desmin. In this way, the O-GlcNAcylation sites are located closed to or into the $^{163}\text{REEKPAVTAAPK}^{174}$ interactive sequence with desmin (**figure 3**); it is thus legitimate to propose the O-GlcNAcylation as a modulator of desmin/ α B-

crystallin interaction. Interestingly, it is demonstrated in cardiomyocytes that O-GlcNAcylation of the α B-crystallin is involved in stress-induced translocation to cytoskeleton and in cytoprotection [355]. More specifically, in stressed cardiomyocytes, the O-GlcNAcylation of α B-crystallin increases while the O-GlcNAcylated α B-crystallin translocates to insoluble material; in contrast, the T170A mutant partially translocates while the cell survival decreases, supporting the pivotal role of Thr170 O-GlcNAcylation [355]. While O-GlcNAcylation occurs on both phosphorylated and non-phosphorylated α B-crystallin [351], Krishnamoorthy et al. showed that the T170A mutant is robustly phosphorylated on Ser45 and Ser59 compared with the wild-type α B-crystallin while, surprisingly, the mutant translocates less when phosphorylated [355]. Finally, over its role in the α B-crystallin translocation and interaction with protein partners, additional key roles could be devoted to O-GlcNAcylation of the sHSP. In particular, O-GlcNAcylation which modifies α B-crystallin close to the regulatory IXI/V domain, could also modulate its chaperone activity; in this way, Balana et al. demonstrated that O-GlcNAcylation could enhance the anti-amyloid chaperone activity of α B-crystallin toward α -synuclein [356]. Lastly, α B-crystallin is released in extracellular compartment through exosomes [357, 358] and it seems that O-GlcNAcylation, linked to the non-phosphorylation of α B-crystallin, regulates the exosomal secretion of the molecular chaperone [359]. This is demonstrated in glioma cells, but to our knowledge, there is no data about the secretion of phosphorylated and/or O-GlcNAcylated forms of α B-crystallin in striated muscle cells/tissue.

In addition to phosphorylation and O-GlcNAcylation, the α B-crystallin also brings other PTMs. Thus, non-enzymatic deamidation could occur on Asn78 and Asn146, affecting the chaperone activity of α B-crystallin, in particular for the N146D [360]. Deamidation leads to the appearance of a negative charge in place of a neutral amide group. Consequently, the stability and the solubility of α B-crystallin change, the extent of deamidated α B-crystallin increasing in the water-insoluble fraction [360, 361]. While this post-translational change is mainly described in lens and in the physiopathology of cataract, the deamidation of α B-crystallin is also reported in ischemic myocardium [342, 362]. It should be noticed that the α B-crystallin could be also modified by succinylation, acetylation, glycation, oxidation or carbamylation, and it could be truncated [363-368]; to our knowledge it has not been determined whether these PTMs could modify the α B-crystallin in skeletal muscle and in heart. Moreover, while the main sites are nowadays well-characterized and prominent in the literature, other sites could be modified on the α B-crystallin. Thus, 9 sites of lysine acetylation, 4 O-GlcNAc sites and 13 phosphorylation sites are identified on standard bovine α B-crystallin [369], and a multitude of sites that could be post-translationally modified also exist on α B-crystallin, in particular through phosphorylation [368, 370]. This plethora of potentially modified sites dramatically increases the complexity of the PTMs forms of α B-crystallin.

3.5. The α B-crystallin in physiopathological conditions

The α B-crystallin accumulates in several diseases, particularly in those involving abnormal protein aggregation. Moreover, a dysfunction of the chaperone is closely linked to the physiopathology of several disorders such as cardiovascular pathologies (desmin-related and dilated cardiomyopathies, ischemia/reperfusion), neurodegenerative disorders (Alzheimer's, Huntington's and amyotrophic lateral sclerosis among others), cancer, cataract, myofibrillar myopathies and inflammation related diseases [211, 371-374]. It was also established that the sHSP expression and/or subcellular localization change in several muscle diseases such as GNE myopathy (GNE: UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine-kinase), core myopathies, dystrophinopathies, or myofibrillar myopathies [375-378]. Numerous mutations of α B-crystallin are identified in skeletal muscle and/or heart diseases: the R120G mutation in desmin-related myopathy (myofibrillar myopathy and hypertrophic cardiomyopathy), the R157H in dilated cardiomyopathy, the Q151X and the 464delCT in myofibrillar myopathy, the 343delT in early-onset skeletal myopathy, the G154S in the late-onset distal myopathy and dilated cardiomyopathy, the D109H and the D109A in myofibrillar myopathy and dilated cardiomyopathy, the D109G in axial myopathy and restrictive cardiomyopathy, the 176Wext*19 in dilated cardiomyopathy, and the M1x and the S21Ala*24 in infantile myofibrillar myopathies [225, 277, 323, 324, 368, 379-390]. The mutations could have repercussions on skeletal muscle and/or myocardium, often together with cataract. Pathologies resulting from α B-crystallin mutation correspond to α B-crystallinopathies, presenting the typical characteristics of myofibrillar myopathies with the hallmark of protein aggregates including desmin and α B-crystallin, myofibrillar disorganization and the presence of vacuoles [277, 391-396]. In some case, hyperphosphorylation of α B-crystallin is reported, as well as changes in chaperone activity (gain-of-function or loss-of-function), oligomerization of the chaperone and/or change in its distribution (for review, see [374, 389, 390, 394, 397]). Concerning PTMs, it is worth to note that phosphorylation changes are observed consecutively to several pathologies such as ischemia-reperfusion, chronic hyperglycaemia, congestive heart failure, cardioplegia or myocardial infarction [286, 336-342]. In contrast, while phosphorylation of HSP27 was proposed to be a diagnostic tool to differentiate primary desminopathies from myofibrillar myopathies, no phosphorylation changes were observed in biopsies of patients for α B-crystallin [398].

Importantly and as mentioned previously, the mutation of sHSP mimics the IFs aggregation phenotype related to IFs diseases [312]. Thus, the mutation in the *CRYAB* gene which results from the replacement of arginine residue at the position 120 (a residue essential for the quaternary structure and function of α B-crystallin [399]) by a glycine residue (mutation R120G) leads to a desmin-related myopathy, an inherited disease characterized by desmin aggregation in skeletal and cardiac muscles [324]. This disease is closely linked to limb, neck, trunk and facial muscle weakness associated to cardiac dysfunction leading to cardiomyopathy [324, 400]. In addition, all protective functions dedicated to the wild-type α B-crystallin are lost when the mutant expresses, such as differentiation, apoptosis, aggresome formation, mitochondrial function and ubiquitin-proteasome system while desmin filaments are affected and aggregate leading to impaired myofibrils alignment [317, 325, 401-404]. It is also

demonstrated that R120G mutant is hyperphosphorylated while its interaction with other HSP is modified; this hyperphosphorylation appears as an important aspect of the pathogenicity of the mutant [330, 405, 406].

4. CONCLUDING REMARKS

In light of the role of α B-crystallin in the maintenance of protein homeostasis, modulation of expression and/or activity of molecular chaperone emerges to prevent, alleviate or cure the conformational diseases not only in striated muscle but also in neurological disorders or in cancer [407, 408]. *In vitro* studies have demonstrated that the sHSP could exert protective effects on skeletal muscle cells and cardiomyocytes submitted to various stresses [276, 334, 409-417]. Importantly, expression of α B-crystallin with the R120G mutant promotes the protein aggregation in C2C12 cells while overexpression of α B-crystallin in a mouse model of desminopathies counteracts the desmin function loss since it restores the mitochondrial homeostasis and rescues cardiomyocytes from death [318, 418]. In the same way, the development of dilated cardiomyopathy is attenuated when α B-crystallin is overexpressed in a mouse model presenting a mutation in the *LMNA* gene [77]. The protective role of α B-crystallin is highlighted with experiments demonstrating that its overexpression alleviates muscular dystrophy and other wasting conditions while heart has a better recovery after ischemia [275, 419]. Thus, α B-crystallin emerges as a new great therapeutic tool against protein aggregation and the resulting proteotoxicity. Interestingly, physical activity is shown to have beneficial effects to prevent skeletal muscle weakness, partially through the protective effect of α B-crystallin on myofibrils in models of adjuvant-induced arthritis, idiopathic inflammatory myopathies and muscle atrophy [420-422]. The beneficial effects of exercise are also observed in R120G desmin-related myopathy [423]. As mentioned in the herein paper, exercise modulates expression and/or phosphorylation of α B-crystallin in relation to the translocation of α B-crystallin to cytoskeleton and the cytoprotective effects; the expression/phosphorylation of α B-crystallin in correlation with the type of exercise is extensively reviewed by Dimauro and Caporossi, as well as the beneficial effects induced by exercise to alleviate muscle diseases [424].

In addition, tuning the phosphorylation of α B-crystallin in a spatio-temporal way could provide a powerful therapeutic strategy to counteract proteotoxicity and restore proteostasis [328, 425, 426]. Moreover, compounds which modulate α B-crystallin phosphorylation have been tested and proposed as a putative attractive therapeutic approach in neurodegenerative disorders [426]. Furthermore, since the interactive sequences could exert specific effect on cellular processes, for example microtubule assembly, the α B-crystallin peptides could be considered as new therapeutics for cancer, Alzheimer's disease and taupathies [320]. In this way, it is demonstrated that bioactive peptides synthesized from the interactive sequences of α B-crystallin target the toxic intermediates of amyloidogenic proteins and

decrease their fibrillation [427]. However, the precise framework of α B-crystallin PTMs needs to be clarified. Indeed, dynamic interplay should exist between PTMs, and it remains essential to determine precisely their role on α B-crystallin functions, in particular chaperone function and/or proteins targeting.

In addition, it remains also essential to better characterize the PTMs pattern and/or changes on the proteins targeted by α B-crystallin, in particular desmin. Indeed, as discussed hereinbefore, the desmin, preserving the muscle integrity, is fundamental for contractile activity and muscle function [3, 40]. Supporting this fundamental role of desmin in muscle physiology when mutated (nowadays, around 50 mutations are identified on desmin gene), the cytoskeletal network turns extremely disorganized while protein aggregates (including desmin) accumulate in myofibrils. These desmin-related disorders result from mutation in the desmin gene, cleavage of desmin, and/or changes on PTMs (in particular phosphorylation and/or kinases dysregulation) [50, 55, 128, 143]. In addition, desmin is O-GlcNAcylated on a serine of the C-terminal domain; however, it is not excluded that other O-GlcNAc sites could exist on desmin. Interestingly, a modification in the number or the linkage of O-GlcNAc moieties are closely associated to the physiopathology of several diseases, and the involvement of O-GlcNAcylation in neurodegenerative disorders, cancer, cardiovascular diseases or type II diabetes have been clearly demonstrated [428-431]. Importantly O-GlcNAcylation and neuromuscular pathologies are also closely linked, in particular in type I spinal amyotrophy, polymyositis, dermatomyositis, sporadic inclusion body myositis, muscular dystrophies, neurogenic muscular atrophy, rhabdomyolysis, and distal myopathy with rimmed vacuoles; the O-GlcNAc modification is also demonstrated to be involved in skeletal muscle atrophy [432-435]. Thus, it would be of interest to investigate whether O-GlcNAcylation could change on desmin or its chaperone in skeletal muscle and heart diseases.

Lastly, it was demonstrated that O-GlcNAcylation could be involved in the modulation of the desmin/ α B-crystallin interaction [173, 174], but the dynamic interplay between phosphorylation and O-GlcNAcylation on desmin and its molecular chaperone remains misunderstood nowadays. Deciphering finely this interplay on two essential proteins of striated muscle cytoskeleton will bring new insights for a better understanding of the physiology of striated muscle and the physiopathology of disorders such as desmin-related diseases. Moreover, considering PTMs is a great challenge nowadays and opens a new research field in the world of molecular chaperone and their target proteins; it could permit the emergence of new therapeutic interventions for striated muscle diseases.

ACKNOWLEDGEMENTS

This research was funded by the AFM-Téléthon (Association Française contre les myopathies). CCB, OA and CC were supported by AFM-Téléthon (contract number: 21011, 22142 and 22054 for CCB, OA and CC, respectively). NB is a recipient from the Lille University Hospital Center and the Region Haut-de-France.

CONFLICT OF INTEREST

The authors declare that they have no conflict of interest.

AUTHORS CONTRIBUTION

Conceptualization, C.C.B. and O.A.; writing-original draft preparation, C.C.B., C.C., N.B.; review and editing, C.C.B., C.C., N.B., O.A., B.B. All authors are the guarantors of the article jointly and have read and agreed to the published version of the manuscript.

FIGURES LEGEND

Figure 1: Representative scheme of desmin structure. Are indicated the head, the α -helical rod and the tail domains of the desmin. The N-terminal domain is magnified with the indication of the amino acid sequences of human desmin (UniProtKB/Swiss-Prot entry: P17661, Homo sapiens), mouse desmin (UniProtKB/Swiss-Prot entry: P31001, Mus musculus) and chicken desmin (UniProtKB/Swiss-Prot entry: P02542, Gallus gallus). The amino acids in red correspond to phosphorylation sites, those in green to ADP-ribosylation sites. The O-GlcNAcylation site in the C-terminal domain is indicated in blue.

Figure 2: Aberrant post-translational modifications of desmin and α B-crystallin in the physiopathology of striated muscle disorders. The structural organization of the sarcomere and desmin IFs of healthy muscle is depicted at the centre of the recapitulative scheme. Main aberrant PTMs are represented in diseased muscle and also their involvement in the physiopathology of several striated muscle pathologies and their consequences on the structural organization of sarcomere and desmin IFs. For diseased muscle, the scheme is divided in four parts for diseased muscle, corresponding to the link between muscle disorders and a default of desmin phosphorylation (in blue) and/or O-GlcNAcylation (in pink), desmin non-enzymatic modifications (in green), or hyperphosphorylation of α B-crystallin (in yellow).

Figure 3: Representative scheme of the structure of α B-crystallin. Are indicated the N-terminal domain, the α -crystallin domain, the IXI motif and the C-terminal extension. The phosphorylated sites are indicated in red, the O-GlcNAcylation sites in blue. The seven interactive sequences are represented in green, and those involved in the interaction of α B-crystallin with tubulin, desmin and actin are represented in blue, red and yellow, respectively. Note the overlap of the interactive sequences between themselves (black dotted lines), and the position of post-translational modifications within these sequences (red dotted lines).

Table 1: Main characteristics of human desmin and its molecular chaperone, the α B-crystallin.

Characteristics	Desmin		α B-crystallin	
UniProtKB/Swiss-Prot entry	P17661		P02511	
Gene	<i>DES</i>		<i>CRYAB</i>	
Chromosome	2q35		11q23.1	
Molecular weight	53.5 kDa		20.1 kDa	
Number of amino acids	470 AA		175 AA	
Protein class	Class III intermediate filament protein		sHSP	
Major role	Cytoskeleton organization; filamentous 3D network	[3, 44-46, 49, 51, 53-55]	Proteostasis; molecular chaperone	[228-231]
Other cellular functions	Differentiation, apoptosis, intracellular signalisation, mechano-transduction, vesicle trafficking, organelle biogenesis and/or positioning, calcium homeostasis, protein homeostasis, cell adhesion, metabolism, gene expression	[3, 49, 50, 56-60]	Cell integrity, cell shape maintenance, apoptosis, autophagy, differentiation, mitochondria function, aggresome formation, and cytoskeleton stabilization	[242, 254, 258-265]
Main post-translational modifications	Phosphorylation, O-GlcNAcylation, ADP-ribosylation, glycation, oxidation, nitration, ubiquitination	See Table 2 for more details and references	Phosphorylation, O-GlcNAcylation, deamidation, succinylation, acetylation, glycation, truncation, oxidation, carbamylation	See Table 2 for more details and references
Associated Pathologies	<u>Primary desmin alteration:</u> Dilated cardiomyopathy, hypertrophic cardiomyopathy, arrhythmogenic right ventricular cardiomyopathy, restrictive cardiomyopathy, desmin-related myopathies, myofibrillar	[3, 11, 49, 50, 54, 55, 69, 70, 79-90]	<u>Striated muscle diseases:</u> Restrictive cardiomyopathy, dilated cardiomyopathy, hypertrophic cardiomyopathy, ischemia-reperfusion, myofibrillar myopathies, α B-crystallinopathies, desmin-related myopathy, GNE myopathy, core	[225, 277, 323, 324, 368, 375-396]

	myopathies, desminopathies		myopathies, dystrophinopathies, early-onset skeletal myopathy, late-onset distal myopathy, axial myopathy, infantile myofibrillar myopathies.	
	<u>Secondary desmin alteration:</u> Aging, heart failure, obesity, type II diabetes, sleep apnoea, asthma, dysphagia, hypoxia- induced pulmonary hypertension, muscle wasting, LMNA cardiomyopathy, Friedreich Ataxia	[48, 71- 78]	<u>Other diseases:</u> Neurodegenerative disorders (Alzheimer's, Huntington's and amyotrophic lateral sclerosis among others), cancer, cataract, inflammation related diseases	[211, 371- 374]

Table 2: Main post-translational modifications on human desmin. The involved enzymes and the amino acid(s) bearing the modification are indicated, as well as the effect of the modification on the desmin. Non-enzymatic modifications are also mentioned. For each reference, it is indicated whether data result from *in vitro* (#), *in cellulo* (§) and *in vivo* (*) experiments, or from studies of human biopsies (§)

Enzyme	Abbreviation	PTM sites	Modification	Effect on desmin	Ref
ADP-ribosyl transferase	ADPRT	Arg58, Arg73	ADP-ribosylation	Desmin IFs dynamics; depolymerisation. Modulation of phosphorylation by PKA; involvement in differentiation	[166 [#] , 167 [#] , 168 [#]]
Aurora kinase B	Aurora-B	Ser12, Thr17, Ser60	Phosphorylation	Desmin IFs dynamics during cell cycle	[136 ^{#§}]
Calcium-calmodulin-dependent protein kinase II	CamKII	Unknown	Phosphorylation	Unknown	[161 [#] , 162 [§]]
Calcium / phospholipid-dependant kinase	PKC, Protein kinase C	Ser13, Ser48, Ser68	Phosphorylation	Desmin IFs dynamics; depolymerisation. Inhibition of proliferation and differentiation	[149 [#]]
cAMP-dependent protein kinase	PKA, Protein kinase A	Ser45, Ser60	Phosphorylation	Desmin IFs dynamics; depolymerisation. Inhibition of differentiation	[148 [#]]
Cyclin-dependant kinase 1	Cdk1	Ser7, Ser28, Ser32	Phosphorylation	Desmin IFs dynamics; separation of desmin IFs. Hyperphosphorylation on Ser32 leads to desmin IFs alteration	[142 ^{#*} , 144 [*]]
E3 ubiquitin ligase TRIM32	TRIM32	Unknown	Ubiquitination	Desmin turnover; muscle atrophy	[185 [*]]
Glycogen synthase kinase-3 beta	GSK-3 β	Ser32	Phosphorylation	Initial step for desmin IFs degradation; precedes ubiquitination	[143 ^{§*} , 185 [*] , 187 [*]]
N-acetyl- β -D-glucosaminidase	OGA, O-GlcNAcase	/	Deglycosylation	Regulation of O-GlcNAc moieties turnover	[170 [*]]
p21-Activated Kinase	PAK	Head domain	Phosphorylation	Desmin IFs dynamics; depolymerisation	[137 [#]]
Protein phosphatase 1	PP1	/	Dephosphorylation	Reassembly of desmin IFs; fine regulation of phosphorylation turnover	[165 [#]]

Rho-associated kinase	ROK	Thr 17, Thr76, Thr77	Phosphorylation	Desmin IFs dynamics; depolymerisation	[135 [#] , 136 ^{#§}]
Uridine diphospho-N-acetylglucosamine polypeptide β -N-acetylglucosaminyl-transferase	OGT, O-GlcNAc transferase	Ser460	O-GlcNAcylation	Unknown; modulation of interaction with protein partners?	[162 [§] , 170 [*] , 173 [§] , 174 [§]]
Non-enzymatic modification		Unknown	Glycooxidation (Advanced glycation end products)	Dilated cardiomyopathy	[179 [*]]
		Unknown	Oxidation	Cytoskeleton reorganization and desmin aggregation	[181 [*] , 182 [*]]
		Unknown	Nitration	Cytoskeleton reorganization and desmin aggregation	[181 [*] , 182 [*]]

The modified aminoacid(s) was(were) numbered including the starting methionine in protein sequence.

Table 3: Main post-translational modifications on human α B-crystallin. The involved enzymes and the amino acid(s) bearing the modification are indicated, as well as the effect of the modification on the α B-crystallin. Non-enzymatic modifications are also mentioned. For each reference, it is indicated whether data result from *in vitro* (#), *in cellulo* (§) and *in vivo* (*) experiments, or from studies of human biopsies (*).

Enzyme	Abbreviation	PTM sites	Modification	Effect on α B-crystallin	Ref
Lysine acetyl transferase	KAT	Lys92	Acetylation [†]	Modulation of structure and function of the chaperone	[364 ^{#§}]
MAPK activated protein kinase 2/3	MAPKAP2/3	Ser59	Phosphorylation	Phosphorylated in stress conditions; interaction with cytoskeleton; partition toward insoluble fraction	[289 [§] , 332 [§] , 334 ^{#*} , 337 [*]]
N-acetyl- β -D-glucosaminidase	OGA, O-GlcNAcase	Thr162, Thr170	Deglycosylation	Regulation of O-GlcNAc moieties turnover	[174 [§]]
p42/44 Mitogen activated protein kinase	P42/44 MAPK	Ser45	Phosphorylation	Phosphorylated in stress conditions; interaction with cytoskeleton; partition toward insoluble fraction	[289 [§] , 336 [*] , 341 [*] , 345 [*]]
Acyltransferase	Acyl CoA transferase	Lys72, Lys90, Lys92, K166, K175	Succinylation [†]	Modulation of chaperone activity. Note that non-enzymatic succinylation may occur on lysine	[363 [*]]
Unknown	/	Ser19	Phosphorylation	Subcellular localization?	[340 [*]]
Uridine diphospho-N-acetylglucosamine polypeptide β -N-acetylglucosaminyl-transferase	OGT, O-GlcNAc transferase	Thr162, Thr170	O-GlcNAcylation	Partition toward insoluble material; modulation of chaperone activity; exosomal secretion; modulation of interaction with protein partners?	[173 [§] , 174 [§] , 350 ^{**} , 351 ^{§*} , 352 [*] , 355 [§] , 356 ^{#*} , 359 [§]]
Non-enzymatic modification		Gln26, Asn78, Gln108, Asn146	Deamidation	Changes of stability, solubility and chaperone activity	[342 [*] , 360 [#] , 361 [*] , 362 [*] , 368]
		Lys92, Glu164, Lys166, Lys175	Carbamylation [†]	Modification of protein conformation and aggregation. <i>In vivo</i> carbamylase?	[367 [*] , 368]

[†] Indicates PTMs described on α B-crystallin, but it is unknown whether they occur in heart and/or skeletal muscle. Note that several other PTMs are described on the molecular chaperone but not indicated in the herein table (for review, see [368]).

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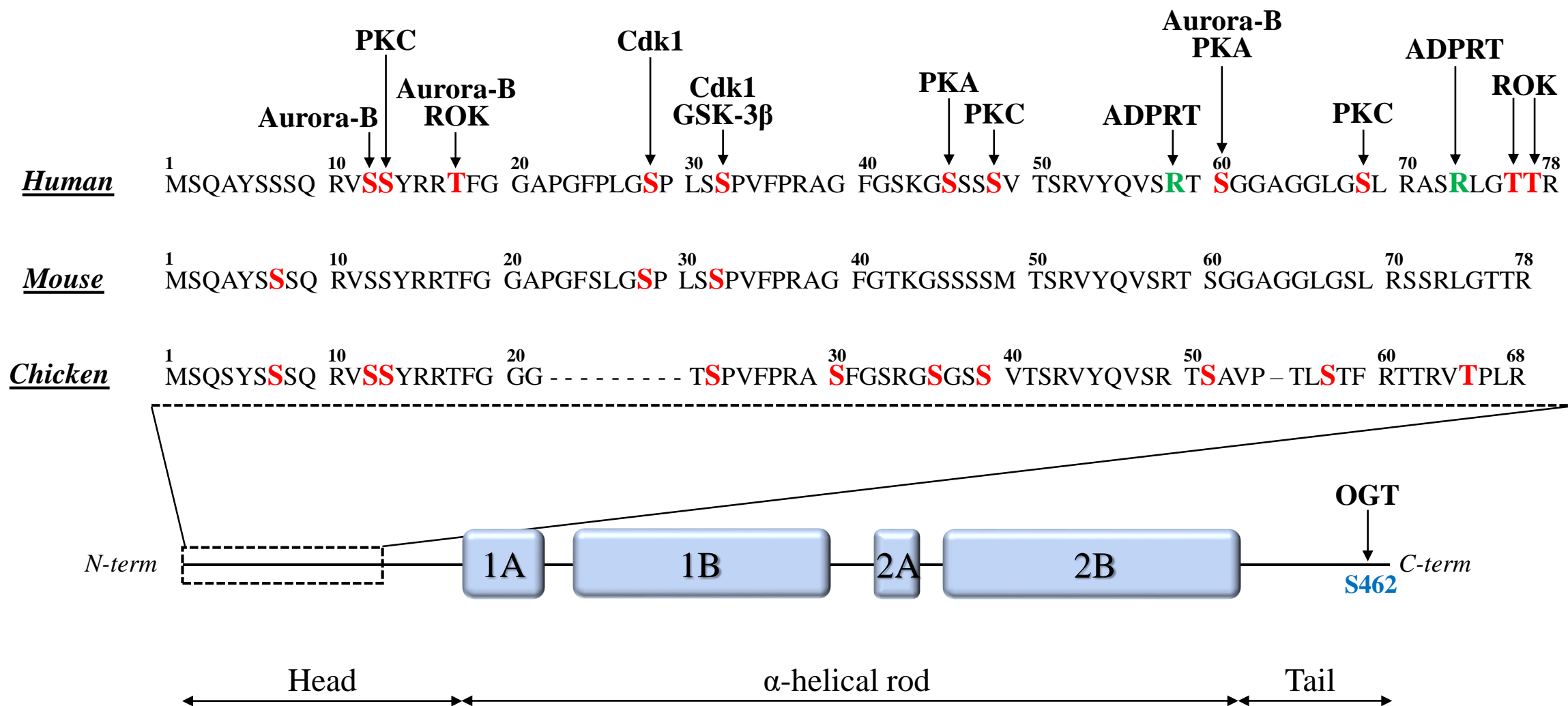
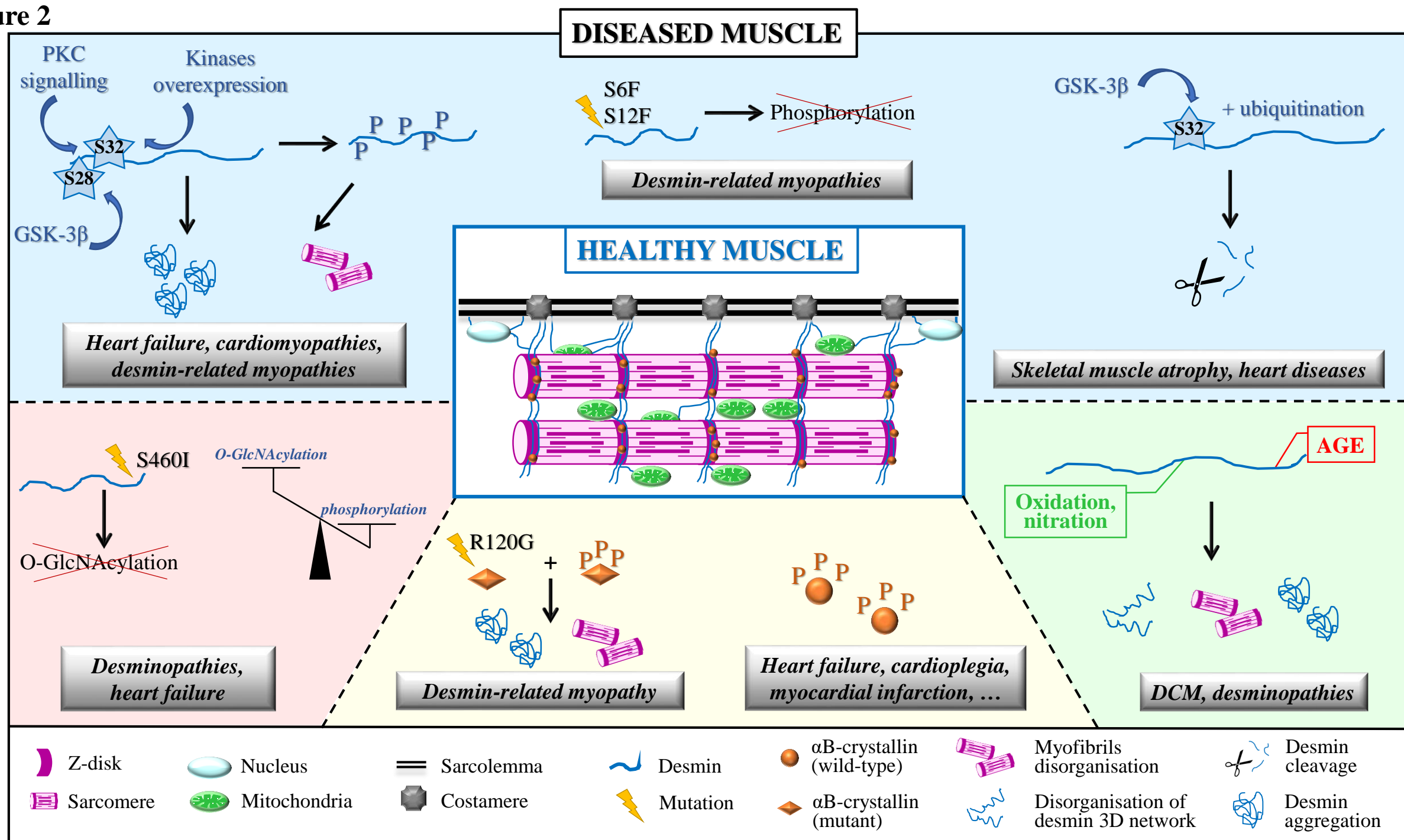


Figure 1

Figure 2



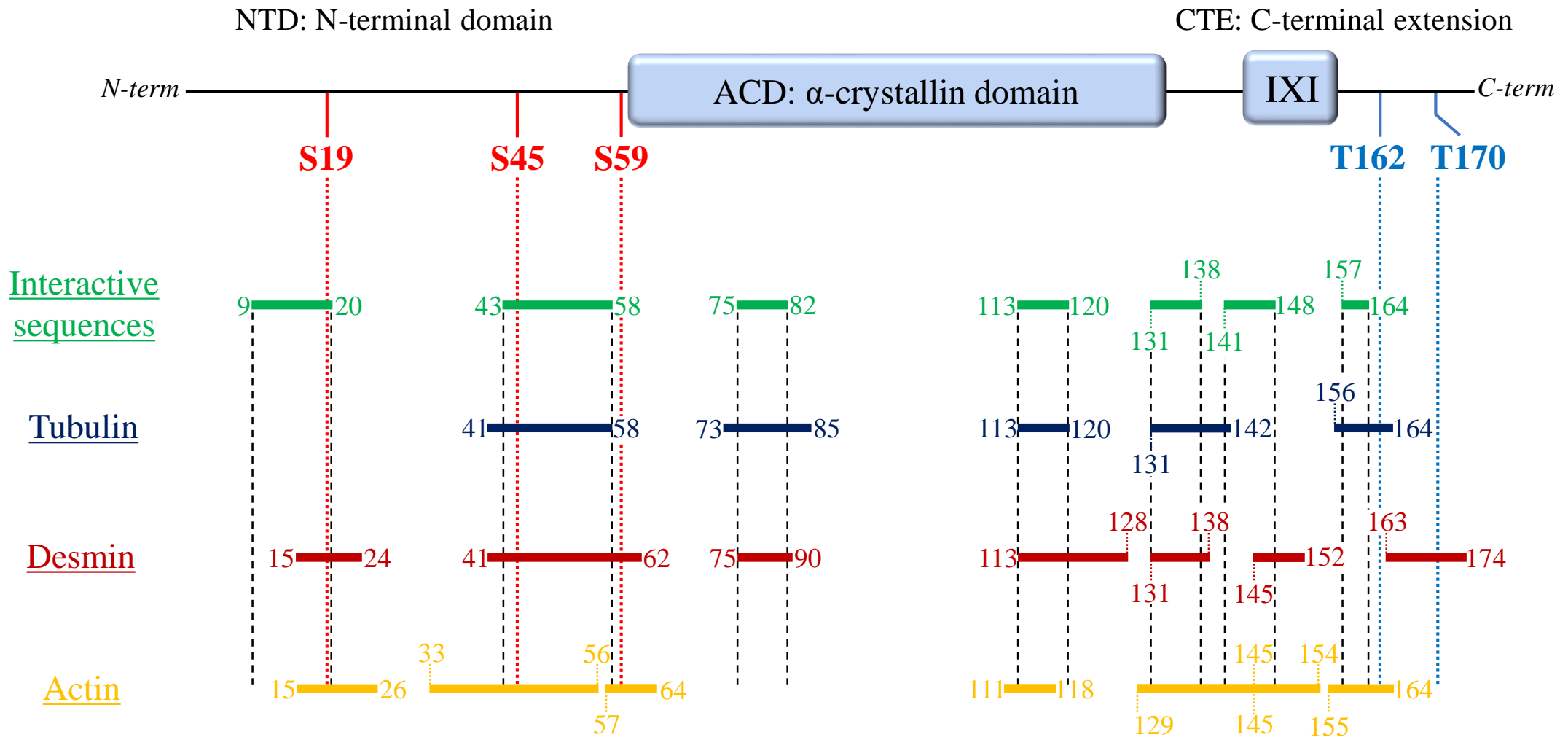


Figure 3