Molecular mechanisms of GSK3β-driven modulation of ABLIM1 and titin interactions in cardiac muscle

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December 8, 2024

1 Abstract

The heart adapts to cardiac demand through a variety of mechanisms. Some of these adaptations include chemical modifications of myofilament proteins responsible for cell contraction. Interestingly, many of these chemical modifications, such as phosphorylation, are found in unstructured, or intrinsically disordered, regions of proteins. For these myofilament assoiciated proteins with intrinsic disorder (MAPIDs), it has been difficult to determine how their disordered regions influence the function of the intact protein or the myofilament as a whole. Given that cardiac dysfunction can be accompanied by dramatic shifts in post-translational modifications (PTMs) of myofilament proteins, assessment of these impacts in intrinsically disordered regions is important. We hypothesized that regulation of the actin-binding myofilament protein LIM protein 1, ABLIM1, through its IDRs occurs because PTMs, namely phosphorylation, alter their conformation ensembles. The change in conformations thereby toggles their availability for binding protein partners. To evaluate this hypothesis, we used molecular dynamics to simulate ABLIM1 and thereby determine its conformation ensemble before and after phosphorylation. In accordance with published phosphorylation data in GSK3β knockout models, our results indicate that local changes in the physicochemical properties of ABLIM1's IDRs via phosphorylation can influence its global ensemble properties, with the potential to impact its interaction with myofilament targets like titin. These findings provide important molecular-level insights into a mechanism of regulating cardiomyocyte contraction.

2 Introduction

The sarcomere is the main contractile element of cardiac muscle (Fig. 1). Its tens of proteins are tightly coupled to the myofilament, where they are directly responsible for generating force in response to elevated intracellular Ca^{2+}. Although the structure and function of many sarcomere proteins have been elucidated, MAPIDs [1] are among those that remain poorly understood. Much of this challenge stems from the scant availability of biophysical data for the unstructured regions. The mechanosensitive ABLIM1 protein is an example of a MAPID serving as a key mechanosensitive regulator of muscle contractility [2].

Actin-binding LIM protein 1, the protein encoded by the ABLIM1 gene, is one of more than 60 proteins that contain LIM domains; these proteins serve pivotal functions in the regulation of developmental pathways and the modulation of cell behavior in response to mechanical stimuli [4]. This is done by facilitating protein-protein interactions with auxiliary proteins. Thus, the LIM domains of the ABLIM1 N-terminus have potential to mediate interactions between actin filaments and cytoplasmic targets (Fig. 2). ABLIM1 protein (88 kD) is known to traverse the actin cytoskeleton [5]. Recent evidence suggests that it also establishes a connection between the Z-disk binding domains of titin, which is believed to contribute to the regulation of length-dependent activation (LDA) in cardiomyocytes [3].

ABLIM1 comprises four LIM domains linked to a villin headpiece by a largely intrinsically disordered region. Thus, like many other sarcomere proteins, ABLIM1 intrinsically disordered region (IDR)s are subject to post-translational modifications, which suggests their importance in the rapid regulation of contraction [1]. However, their contributions to myofilament function have not been fully resolved. An IDR linker in a plant actin-binding LIM protein was shown to facilitate self-aggregation, thus influencing F-actin remodeling [6]. Therefore, we anticipated that IDRs in ABLIM1 may play similar roles in regulating important actin-dependent functions in mammals.

ABLIM1 is known to be highly phosphorylated [5, 7], according to the PhosphoSitePlus database [8]. Although the C-terminal half of ABLIM1 is rife with potential sites for post-translational modification (PTM), several phosphorylation sites have been identified in its N-terminal segment. Two of these sites are found between the LIM2 and LIM3 domains (see magenta region in Fig. 3). A study [3] discovered that the state of phosphorylation of ABLIM affects its interactions with the Z1Z2 domain of titin, which coincide with changes in contractility.

GSK3β as a crucial kinase is responsible for phosphorylating ABLIM1 and maintaining strong force generation at stretched sarcomere lengths (length dependent activation, LDA) in healthy cardiac tissue (see Fig. 1). Its knockout in a mouse model was shown to reduce the phosphorylation of ABLIM1 at sites S354, S494, and S496 (see Table S1), with additional phosphorylated protein fragments remaining unchanged. A study by Stachowski *et al*[3] identified that in normal cardiac function, increased GSK3β activity sustains high levels of ABLIM1 phosphorylation, negligible titin/ABLIM1 interactions, and pronounced LDA. In contrast, a decrease in GSK3β activity typical of heart failure (HF)[3, 9] results in lower levels of phosphorylated ABLIM1, increased titin/ABLIM1 binding, and reduced LDA. Therefore, we hypothesized that the phosphorylation status of ABLIM1 impacts the ability of its LIM domains to access titin in the myofibril, where it can hinder LDA.

In this investigation, our objective was to identify how phosphorylation affects the properties of ABLIM1 in binding the Z1Z2 domains of titin. To investigate these properties, we constructed

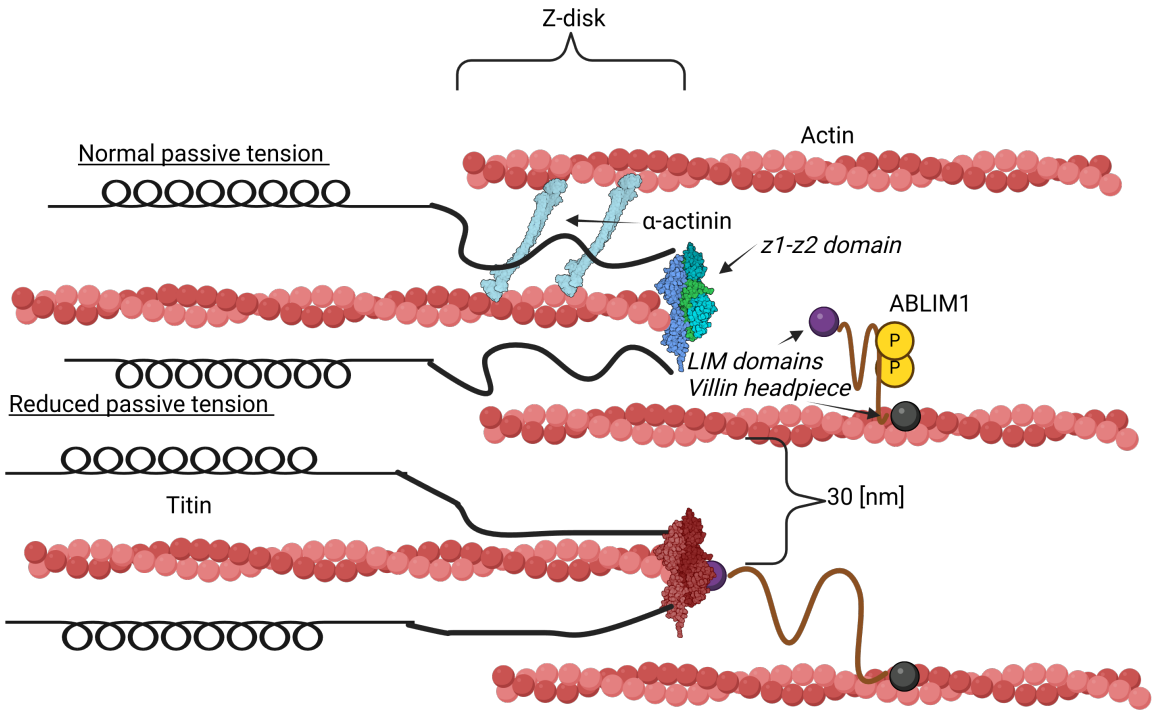

Figure 1: **Schematic of ABLIM1 interacting with titin.** This study investigates how reduced phosphorylation of ABLIM1 could affect its binding to the Z1Z2 domain of titin in the cardiac sarcomere. The C-terminus of ABLIM1 is assumed to be anchored by its villin headpiece domain (gray), while the N-terminal LIM domain region (purple sphere) can potentially interact with the titin z1-z2 domains (blue and light blue). ABLIM1 is a target for GSK3β phosphorylation and impacts passive tension in the myofilament [3]. The scheme was created using Biorender (www.biorender.com).

a molecular model of ABLIM1 by combining simulations of all-atom protein structures and coarse-grain representations. All-atom simulations were performed to determine the secondary structure and key interactions that stabilize the individual LIM domains. Based on these properties, we constructed a coarse-grained model of the N-terminal domain of ABLIM1 (residues M1-S450). The coarse-grained simulations allowed us to determine the statistical properties of the ABLIM1 conformation ensemble, including the openness of the folded LIM domain regions (I97-E343) and the disordered domains (residues M1-V96 and E344-S450). The ensemble properties were used to parameterize a Flory polymer physics model to determine the availability of ABLIM1's LIM domains to bind titin's Z1Z2 domain in the myofilament. Together, these simulations provide important insights into how the structure and dynamics of ABLIM1 could influence LDA, while more broadly elucidating mechanosensitive signaling of myofilament associated protein with intrinsic disorder (MAPID)s as a whole.

3 Materials and methods

3.1 Sequences and structures

The FASTA sequences for ABLIM1 and 2 (human) were obtained from Uniprot with access ID O14639 and Q6H8Q1, respectively. The structure derived from nucular magnetic resonance (NMR)for ABLIM2 LIM domain 2 was obtained from the protein databank (PDB ID: 1V6G, unpublished). This structure was used as a basis for atomistic simulations of ABLIM1's LIM2 domain, given its nearly identical sequence (Fig. 3). An AlphaFold [10] predicted structure of the full-length ABLIM1 protein (human) was downloaded from Uniprot with the access ID O14639.

3.2 Sequence analyses

The ELM database was used to query the ABLIM1 sequence for potential short linear interaction motifs (SLIMs), which are sequences associated with the formation of protein-protein interactionss and are often subject to PTMs. The ABLIM1 FASTA sequence (from Uniprot O14639) was provided as input. The BLASTp [11] sequence alignment algorithm was used to align all LIM domains with one another to ensure sequence identity. Each LIM domain (ABLIM2 LIM2 and ABLIM1 LIMs 1-4) was treated as an independent sequence to align with all other amino acid sequences of the LIM domain.

3.3 Phosphorylation sites

Tandemmass spec (MS/MS) was used by Stachowski *et al* [3] to identify phosphorylated fragments from control and GSK3β KO cardiac ventricular myocyte tissue from mouse. In that study, phosphorylation was detected at ABLIM1 sites S215, S216, S354, S396, S397, S399, Y401, S407, S411, S466, S470, T473, S475, T477, S479, S494, T495, S496, S499, T586, S658, S670, S671, S752, T753, and 1858 (see Table S5). Only sites S354, S494, and S496 were found to be significantly different between samples ($p \leq 0.05$), with each site having a roughly 2-fold reduction in the GSK3β KO tissue (Table S1).

The human sequence is 82% identical to that of the mouse, including a gap where the mouse S354 phosphorylation is found. Therefore, we modeled the equivalent positions of S452 and S454 in the human sequence (see the equivalent residues in Table S5). The protein sequences of the two species are identical in this region. Since the mouse S354 site region adjacent to LIM4 is not found in humans, we instead modeled phosphorylation of the MSSSPKET sequence found between LIM domains 2 and 3, and specifically S216, which is conserved in both species. We selected S216 because the MSSSP at site S216 (see the GSK3β label for ABLIM1 LIM2 in Fig. 3) is a common recognition motif for GSK3β and other kinases per ELM [12]. This site has been identified as a phosphorylation target in humans (PhosphoSitePlus database [8]) [13]. In addition to phosphorylation of the region identified by Stachowski *et al* [3], phosphorylation of S215/S216 has been detected in stem cells and tumors/cancers [14, 15]; an MLCK-null endothelial cell model was found to reduce S216 phosphorylation [16]

3.4 Atomistic molecular dynamics simulations

We performed atomistic MD simulations of the isolated LIM2 domain of ABLIM1, the isolated LIM2 domain of ABLIM2, the LIM2-LIM3 domains of ABLIM1, the phosphorylated LIM2 domain of ABLIM2 (S146D), and the phosphorylated LIM2-LIM3 domains of ABLIM1 (S216D). The starting structures for these atomistic simulations were the resolved LIM2 domain structure of ABLIM2 (PDB 1V6G) or the AlphaFold-predicted full-length structure of ABLIM1. The missing Zn^{2+} cations in the AlphaFold predicted structure were added by first aligning PDB 1V6G to each individual ABLIM1 LIM domain and then copying and pasting Zn^{2+} cations into the AlphaFold predicted structure. The structure was then dissolved in a TIP3P water box with a 12 Å margin and filled with 0.15 M NaCl salts. The CHARMM36m [17] force field was used to describe the system. The prepared system was first subjected to the minimization of energy of a maximum of 50,000 steps of the steepest descent algorithm (although the minimization would end early when the system reached the desired maximum force of $<1.0 \times 10^3$ kJ/mol nm^2), followed by a heating stage during which the system was heated to 310 K over 2 ns in the NVT ensemble. During minimization and heating, restraints were introduced onto the protein backbone atoms with a force constant of 1 kJ/mol nm^2.To maintain the coordination between Zn^{2+} and coordinating residues, harmonic restraints between each Zn^{2+} and the side chains of the coordinating residues of each zinc finger were introduced in ABLIM. A force constant of 1 kJ/mol nm^2 was introduced for minimization, increased to 10 kJ/mol nm^2 in the NVT equilibration step, and finally reached 100 kJ/mol nm^2 for the final equilibration step and throughout production. A time step of 2 fs was employed in most MD simulations except for equilibration, where a 1 fs time step was needed for simulation stability. The cutoff for nonbonded vdW interactions was set at 1.1 nm.Electrostatic interactions are handled using the reaction field method, with a dielectric constant of 15 within the cutoff distance and infinite beyond. The integration of Newtonian equations of motion used the velocity Verlet algorithm. The LINCS algorithm [18] is used for constraint calculations and the velocity-rescaling thermostat and the Parrinello-Rahman barostat are used. The velocity-rescaling thermostat has a friction coefficient of 1 ps^{-1}. The Parrinello-Rahman barostat in GROMACS simulations uses a compressibility constant of 3.0×10^4 1/bar. The selection of Langevin over velocity-rescaling methods is driven by two factors: (1) the preservation of the canonical ensemble and (2) ensuring the velocity distribution maintains the correct Gaussian distribution. As for the

barostat, Berendsen's equation of motion is employed to govern the evolution of the computational box's volume and shape. Atomistic MD simulations were performed using the GROMACS2024 package[19].

3.5 Martini coarse-grained MD simulations

To get better sampling efficiency for large ABLIM constructs, we performed coarse-grained MD using the Martini3 [20] model. The coarse graining of the atomistic structure in the CG structure was performed using the martinize.py script, and the DSSP [21] program was used to detect the secondary structure of the atomistic structure. The CG structure was then solvated with a standard Martini water model using the pre-equilibrated waters downloaded from the Martini website. Elastic network constraints were applied to individual LIM domains with force constants of 500 kJ/mol nm^2 and the lower and upper elastic bond cutoffs were 0.5 and 0.9 nm, respectively. For systems containing purely IDRs, no elastic network constraints were applied. Constraints were imposed between Zn^{2+} ions and the side chain beads of the coordinating residues of the CG models using the same procedure as the atomistic simulations. The system was first energy minimized for 40,000 steps using the steepest descent algorithm and then heated to 300 K in the NVT ensemble over 1 ns. The equilibrated system was subject to a 2000 ns production MD in NPT ensemble at 300 K using a 20 fs time step. Temperature and pressure control were achieved via the Parrinello-Rahman V scale barostat, respectively. CG simulations were performed using the Gromacs2024 package [19].

3.6 Continuum

A scaling relationship for intrinsically-disordered proteins was used to describe the geometric properties of IDRs within ABLIM1. This relationship takes the form of an analytic Flory random coil model [22]:

$$D = R_0 N^{\nu}, \tag{1}$$

where D shows the chain dimensions, R_0 is a prefactor in spatial distance units, and N^{ν} is the number of monomers raised by the apparent Flory scaling exponent. This equation has been found by others to recapitulate the geometric characteristics of proteins with IDRs [22, 23], such as for computing their effective concentrations via $N^{-3\nu}$ [24]. This was done so that we could determine the likelihood that ABLIM1 would form a protein-protein interaction with partners such as titin, based on the protein's ability to span two adjacent actin filaments. We used a similar approach to explain the binding of TnI to TnC [25]. In this paper, we compute the R_g and end-to-end distance, r_e, which scale as Eq. 1 for the Flory model, in part based on fits to data from Alston et al. and Hofmann et al. [22, 23]. That is, we first determined the critical scaling factor ν from the values R_g determined from our molecular dynamics simulations using a modified form of Eq. 1 (Eq. S1); after this, we estimated the coefficient a_0 for $\langle r_e \rangle = a_o N^{\nu}$, which best fits the simulation-predicted $\langle r_e \rangle$ for the given ν value. Using the $\langle r_e \rangle$ determined from Eq. 1, we evaluated the probability of end-to-end distances using [22]:

$$P(r) = 4\pi r^2 \left(\frac{3}{2\pi \langle r_e^2 \rangle} \right)^{3/2} \exp\left(-\frac{3r^2}{2\langle r_e^2 \rangle} \right) \tag{2}$$

3.7 Data availability

All code written in support of this publication is publicly available at https://bitbucket.org/pkhlab/pkh-lab-analyses. Simulation input files and generated data are available upon request.

4 Results

4.1 Primary sequence suggests disorder that is impacted by phosphorylation

4.1.1 ABLIM1 contains globular domains

We first describe the overall structure of ABLIM1 and focus on the folded LIM domains. ABLIM1 consists of a few folded domains, namely four LIM domains (see Fig. 2) and one villin headpiece. Each LIM domain is stabilized by two bound Zn^{2+} ions, comprising four β-sheets (Fig. 2C). The LIM domains exhibit 20-30% sequence identity (see Fig. 3 and Fig. S1), with highly conserved cysteine and histidine residues that coordinate Zn^{2+}. Conserved glycines may confer more conformational variability to the LIM domains, given their less restrictive ϕ and ψ angles.

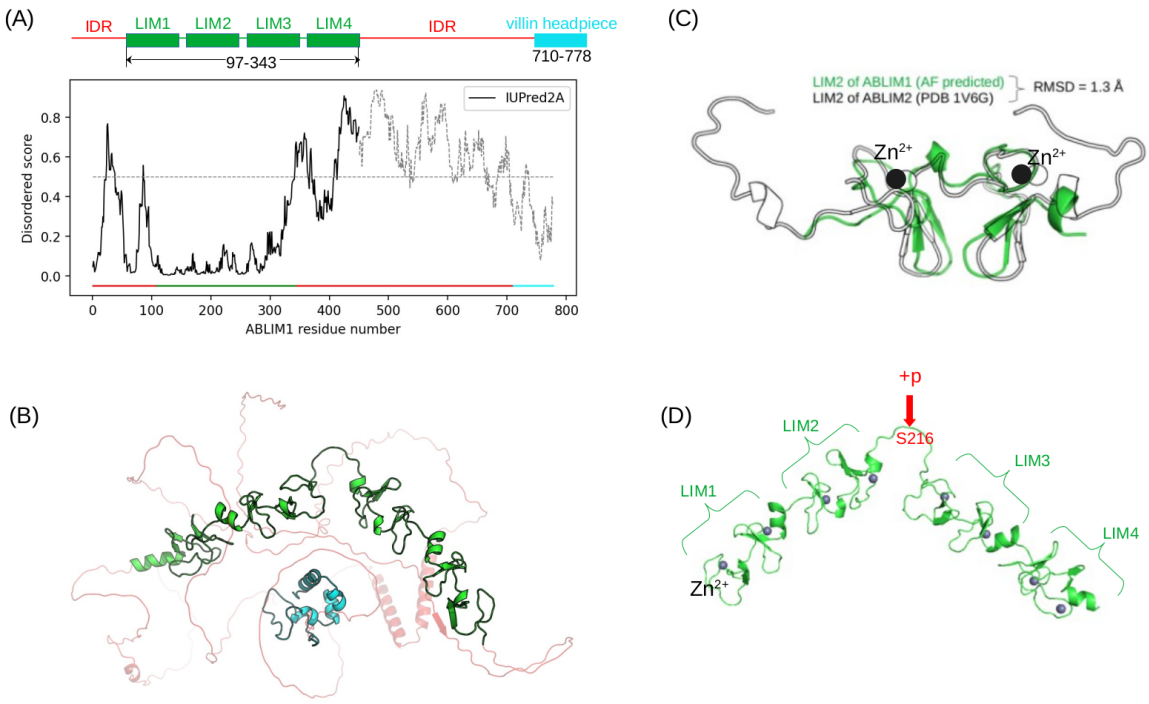

Figure 2: A) Domain organization of human ABLIM1 protein. The disordered score of the ABLIM1 protein predicted by the IUPred2A algorithm [26]. In this study, we considered residues 1-450 of the ABLIM1 protein, and this construct consists of four tandem LIM domains flanked by two intrinsically disordered tails. B) The AlphaFold predicted structure of the entire ABLIM1 protein. C) Overlay of the LIM2 domain predicted by AF of ABLIM1 onto the experimentally resolved LIM2 domain of ABLIM2, in order to justify the use of the ABLIM1 structure predicted by AF as the starting structure for subsequent simulations. D) Zoomed in view of the four LIM domains of ABLIM1, and we consider the phosphorylation of S216 between the LIM2 and LIM3 domains.

4.1.2 ABLIM1 has intrinsic disorder

Several tools predict that many regions of the ABLIM1 sequence are intrinsically disordered. To illustrate this disorder, we show predictions from IUPred2A [26] in Fig. 2A and similar results from in Fig. S4. This analysis reveals that almost 30% of the sequence is disordered, primarily within its N-terminus (M1-V96) as well as the segment spanning LIM4 and the villin headpiece (Q338-M696). Exceptions include folded regions within I97-E343, where its four LIM domains are located, and the C-terminus beginning with position 710, where its villin headpiece is found.

To gain insight into the topology of intrinsically disordered regions, we used the qualitative phase diagram from the Pappu laboratory [27], which relates the positive and negative fractional charge (f_p/f_n) to a polymer's topology, like swollen coils. We first used PONDR-VLXT [28, 29] to predict IDR fragments in the ABLIM1 protein. Our analysis revealed several predicted IDR regions distributed in the ABLIM1 sequence, with most concentrated in the C-terminal half of the protein. This IDR distribution is consistent with the disordered scores predicted by IUPred2A as shown in Fig. 2A.

To understand how the conformational states of these IDRs would change after phosphorylation, we consulted the PhosphoSitePlus database [8] to collect all reported phosphorylation sites that fall within the predicted IDRs. As shown in Fig. 4B, the IDRs of ABLIM1 are enriched with phosphorylation sites. Upon plotting these IDRs into the Pappu diagram using their fraction of positive/negative charge fraction as coordinates, we found that these IDRs are largely concentrated around the cusp between conformational phases, namely around the molten globules and chimeras. We then updated the f_n values based on the number of phosphorylation sites we identified from PhosphoSitePlus, which shifted nearly half of the IDRs upward along the y-axis. Hence, based on the change in fractional charge, phosphorylation may shift several of the IDRs toward more extended configurations and potentially even swollen coil conformations (Fig. 4C).

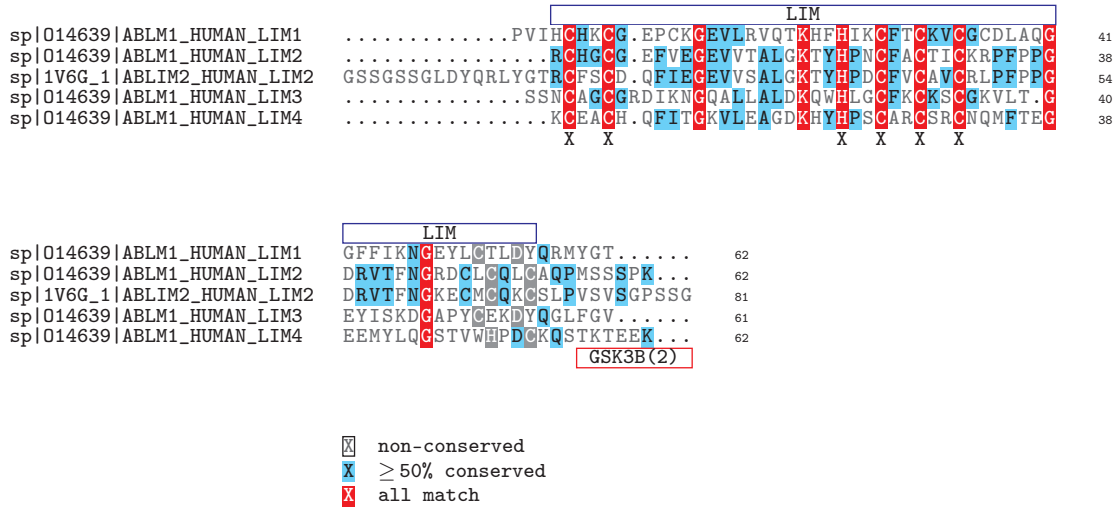

Figure 3: **ABLIM1 and ABLIM2 LIM2 sequence alignments.** A multiple sequence alignment compared the sequence structures of each ABLIM1 LIM to one another, as well as to our reference sequence, ABLIM2 LIM2. Of the red boxes where all sequences align, letters 'C' and 'H', representing Cysteine and Histidine respectively, make up the residues that bind zinc ions in the zinc-fingers of each LIM domain. Conservation between domains is summarized in Fig. S1 Generated from ClustalW [30]. An X below the alignment denotes coordination residues that are aligned in all sequences while a gray highlight denotes coordination residues not perfectly aligned.

ABLIM phosphorylation via GSK3β and its impact on disorder Phosphorylation and other PTMs that alter sequence charges can shift conformation ensembles between different topologies [27]. For ABLIM, this has the potential to modify its structure or its interaction partners [1]. We recomputed the fractional charge density using equation $f = N_{p,n}/N_{total}$, where $N_{p,n}$ is the number of R/K or D/E residues, to account for phosphorylation at three sites: S216, a putative site based on high-throughput hits [3], and two sites S450 and S452 in the disordered C-terminal region (see Fig. 4 B). This shifted sequences along the negatively charged axis (see red dots in Fig. 4C). For all three sites before phosphorylation, the IDRs that harbor them are located close to the transition zone between the molten globules and the chimeras. After being phosphorylated, all three sites make their IDRs' conformation more molten (Fig. 4C). We anticipate that these changes are sufficient to alter the relative orientations of the LIM domains with respect to one another, as well as the effective length of the linker between the LIM domains and the villin headpiece.

4.2 Single LIM demonstrates little impact of phosphorylation

The sequence analyses in the previous section suggest that ABLIM1 exhibits significant intrinsic disorder, prompting us to perform molecular dynamics simulations to characterize the structure and dynamics. To begin, we utilized the atomic resolution structure available for the LIM2 domain of ABLIM2 (PDB 1V6G, unpublished structure) and the AlphaFold predicted structure for ABLIM1, as ABLIM1 does not yet have a crystallographically-determined structure available. The LIM2 domains of ABLIM1 and ABLIM2 share 67 percent sequence identity (85 percent sequence positives) according to a BLAST protein multiple sequence alignment [11] of the LIM domains (see Fig. 3). Therefore, we anticipated that the ABLIM2 structure should be a reliable surrogate for ABLIM1, given their high sequence similarity. A comparison of the structures is shown in Fig. 2.

We then performed all-atom molecular dynamics simulations using ABLIM2 LIM domain 2 (Fig. 3). The binding of Zn^{2+} ions, which are important for stabilizing the LIM domains [31], was examined. For ABLIM2, Zn^{2+} ions are stabilized through cysteine, histidine, and aspartic acid residues positioned via beta sheet folds (Zinc-Finger 1: [C18, C21, H38, C41], Zinc-Finger 2: [C44, C47, C66, C69]). Consequently, we simulated the ABLIM1 fragment comprising LIM domains 2 and 3. The resulting data show that these interactions are maintained throughout the simulation by visual inspection for ABLIM1 as well, confirming the reliability of the atomistic model. Namely, the distances between the bonds to zinc are approximately 2.5 Å and are moderately higher than the value found for the crystal structure of LIM2 (2.3 Å).

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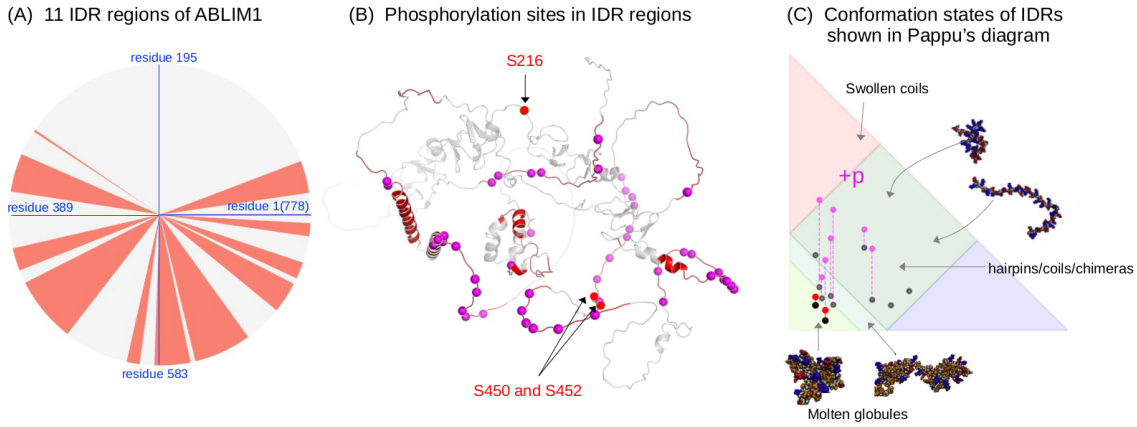

Figure 4: A) Predicted IDR regions (colored red) in the ABLIM1 protein by using the PONDR-VLXT [28, 29] algorithm. The folded domains are colored white. B) Location of ABLIM1 phosphorylation sites collected from the PhosphorusPlus database[8], and only the phosphorylation sites located in the predicted IDRs are shown as purple spheres. The three phosphorylation sites S216, S450, and S452 that we focus on in the present study are shown as red spheres. C) Predicted topologies for native (black / yellow) IDR and phosphorylated (magenta / red) IDR based on the Pappu diagram [27]. Figures are adapted from [1].

4.2.1 LIM domains are moderately labile

We report the corresponding root mean squared fluctuations (RMSF) in Fig. 6A for the ABLIM1 and ABLIM2 structures to assess the flexibility of the ABLIM structures. The smallest RMSF values are around the Zn^{2+}-binding sites, consistent with the protein's contacts with zinc ions and beta sheets remaining stable throughout the simulation. This suggests that the folded structure of the protein is relatively immobile in this region. The radius of gyration (B) is centered relatively tightly about 17 Å, evidencing a compact and well-folded structure. The calculations of R_g for ABLIM1 include LIM domains 2 and 3, therefore the sizes are larger relative to the isolated LIM2 of ABLIM2. We note that the distances between the two Zn ions assume values close to 22 Å, which aligns two of the beta sheets within the core of the protein. This configuration may be achieved through a weak hydrogen bond (approximately 4.5 Å between residues D92 and K132 seen in ABLIM2 LIM2 (see Fig. 6D-E). The relative openness of this region between the two 1/2 LIM domains may indicate that the two sections could move independently of each other to bind targets. This is supported by our observation that the distribution of Zn^{2+} distance values spans 17 to 19 Å, suggesting the protein is relatively mobile on the nanosecond timescales we simulated.

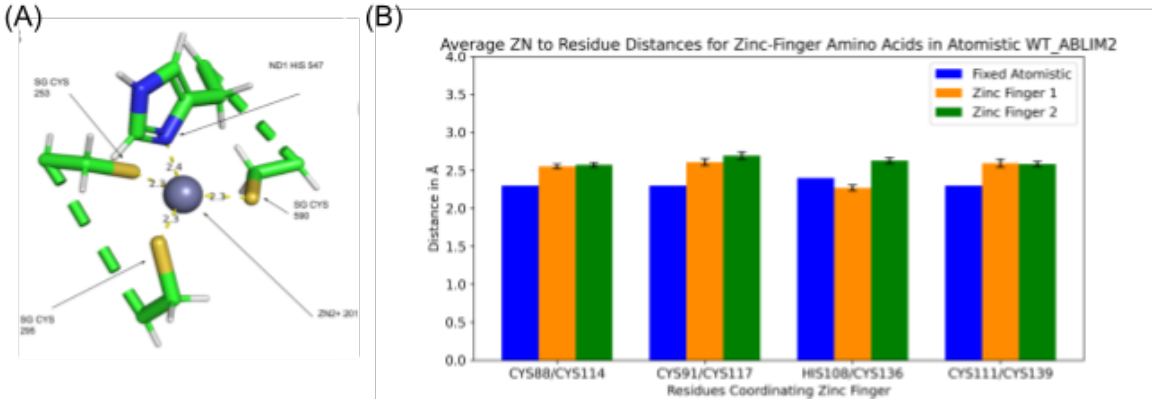

Figure 5: **Zinc cation coordination.** A) Atomistic representation of ABLIM2 LIM2 Zn^{2+} coordination structure with B) Bar chart of Zn^{2+}/coordinating residue (C88, C91, H108, C111, C114, C117, C136, C139) distances computed from molecular dynamics simulations. The error bars represent the standard error of the mean distances in all atomistic simulations.

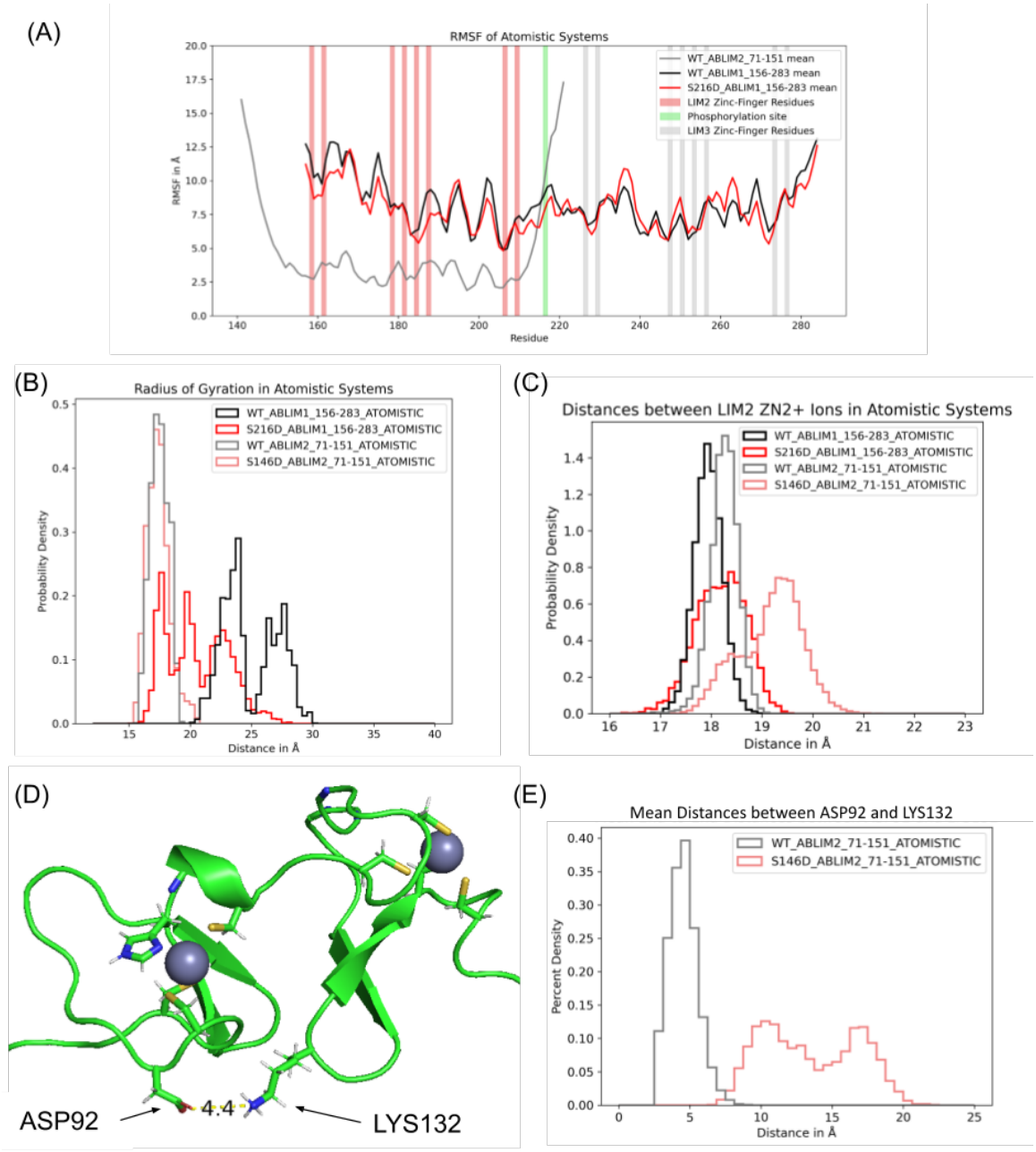

Figure 6: **Molecular dynamics simulations of single LIM2 domain.** A) RMSF comparison of atomistic systems ABLIM2 LIM2 and WT/S216D ABLIM1 LIM2-LIM3. B) Radius of gyration. C) Zn^{2+}/Zn^{2+} distance showing the 1/2 LIM proximity. D) The atomistic structure of the ABLIM2 LIM domain 2, highlighting the interaction between ASP22 and LYS62 in the wild-type simulation model. E) Distance between charged elements of ASP22 and LYS62 in wild-type and S76D phosphorylated ABLIM2 simulations.

4.2.2 Phosphorylation has moderate impact on ABLIM1 LIM2 structure/dynamics

We next performed simulations of the S216D phosphomimetic to understand the structure and dynamics of ABLIM1 in its physiological, phosphorylated states relative to the (unphosphorylated) WT version. We found that phosphorylation at S216D did not significantly impact the RMSF trends relative to the WT (Fig. 6A), whereas the radii of gyration decreased somewhat for ABLIM1 (Fig. 6B) With respect to the distances between the Zn^{2+}atoms, phosphorylation tended to shift towards larger values, with the smaller changes observed for the ABLIM1 construct relative to ABLIM2 (Fig. 6C). This increase in distance suggests an opening of the 1/2 LIM domains relative to WT.

4.3 LIM domain multimers are impacted by phosphorylation

In several reports [32–34], it has been observed that more than two LIM domains are usually required for LIM domain-containing proteins to bind strained actin. As an exception, testin requires a single LIM domain to bind strained actin in cells [35]. Other protein-protein interactions involving LIM domain proteins are typically mediated either by their LIM domains or by additional functional domains, such as PDZ domains [4, 36]. We therefore expanded our ABLIM1 model to include all four LIM domains connected via unstructured regions, in the event multiple domains could be used for binding Z1Z2. Since these were unstructured, we anticipated that the LIM domains could have considerable rotational flexibility that might be insufficiently sampled by conventional atomistic simulations. Therefore, we resorted to coarse-grained Martini models to enhance conformational sampling by using larger integration time steps. Thus, we created CG Martini models of the ABLIM1 LIM domains from its atomistic equivalent (see Fig. 7A). Constraints were placed between the ions and the residues with which they coordinate; secondary structure assignments were made on the basis of results from the atomistic simulations. After equilibration and 2500 ns of simulation, the coarse-grained representations of the LIM domains remained similar to those of the atomistic data (see Fig. 7).

We report in Fig. 7B the structure of the coarse-grained representation's cation binding domain, which shows coordination similar to that in the atomistic equivalents. We report these distances in panel C, but this time using the Cα atom of each side chain of the atomistic reference for comparison. The CG model of ABLIM maintains coordination distances similar to those in the atomistic equivalents. The beads of the CG models encompass multiple atoms, so the centers are likely not exactly matching the side-chain distances reported in atomistic models, which explains the greater distances in CG structures. Additionally, the CG models show a weakening of the secondary structure, which slightly increases the distances between coordinating residue side-chain beads and the zinc ions they coordinated. In addition, the RMSF shown in Fig. 7 D shows lower values near the folded LIM domains and especially near the location of the zinc finger residues, similar to the atomistic data. This suggests that our model is a faithful representation of the atomistic reference with regard to cation coordination.

Next, we examined the radii of gyration (R_g) of the WT and phosphorylated Martini models (see Fig. 7E). $R_g$for CG are considerably smaller than the atomistic simulations, which we attribute to the different masses and positions of atomistic Cα versus backbone beads, since the structures appear similar by visual inspection (see also panel B structures). We next describe the Zn^{2+}-Zn^{2+} distances Fig. 7 F), for which ABLIM2 LIM2 exhibited moderately smaller Zn^{2+}-Zn^{2+} distances (approximately 15 Å) than WT (approximately 17Å). In comparison, their distances in LIM2 from ABLIM1 are a few Å larger than those of ABLIM2. The ABLIM1 LIM2 region (WT_ABLIM1_156-218, shown in Fig. 7F in pale blue) showed the most similar LIM2 Zn^{2+}-Zn^{2+} distances to ABLIM2 LIM2, indicating that the presence of other LIM domains may impact the openness of a LIM domain. Furthermore, phosphorylation appears to increase this distance in all models compared to their respective WT counterparts, with the phosphorylated extended model that includes the IDRs on either end of the LIM domains (M1-V96 & E343-S450) showing the greatest increase in LIM2 Zn^{2+}-Zn^{2+} distance. Despite the differences between the properties of the atomistic and CG structures, an overlay of the domains shows considerable similarity (Fig. 7).

4.3.1 ABLIM1 intrinsic disorder affords diverse conformations of 4x LIM domains

We extended the four LIM domain construct to include flanking regions of roughly 100 amino acids on either side. This was done to determine if the presence of the disordered flanking regions would impact ABLIM1 structure. Consistent with atomistic data (Fig. 6), phosphorylation did not appreciably impact the root mean square fluctuation (RMSF) values, except for a moderate reduction of lability in the ABLIM1 disordered N-terminus (see Fig. 8A). The R_g of the wild-type (WT) construct is approximately 25 Å, which shifted to around 28 Å upon phosphorylation. For comparison, the disordered N and C-terminal regions (WT 1-96 and WT E343-S450) assume radii of gyration (R_g) of approximately 24 Å and 16 Å respectively, versus the region containing LIM

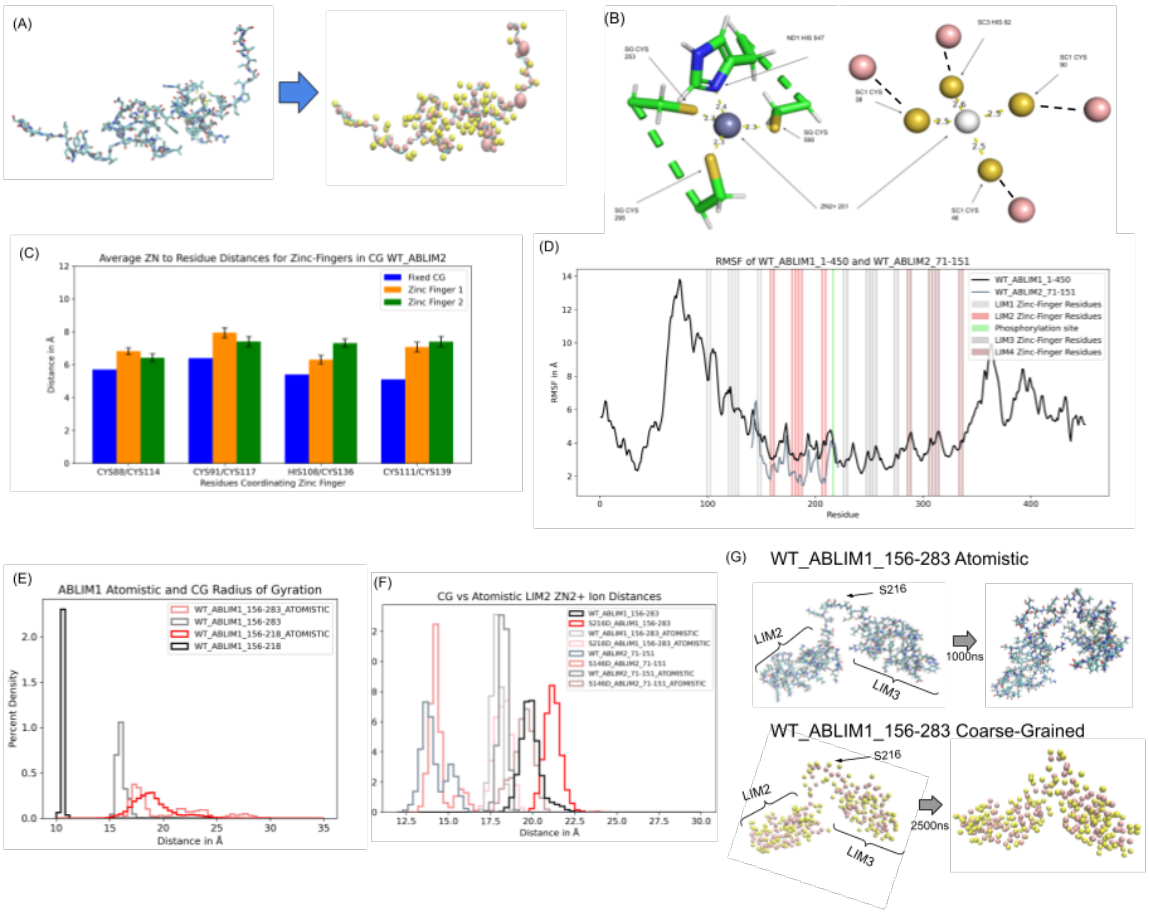

Figure 7: **Coarse-graining.** A) Mapping atomistic structure into Martini coarse-grained model. B) Structure comparison of Zn^{2+} coordination in atomistic vs CG representations. C) Distance measurements based on B). D) RMSF of coarse-grained extended WT ABLIM1 compared to ABLIM2 LIM2 isolate. E) R_g between atomistic and CG. F) LIM2 Zinc-to-Zinc distances across systems. G) Comparison of LIM2-LIM3 Atomistic and CG constructs over the course of simulation.

domains that spans I97-E343 that was centered around 23 Å. To demonstrate the differences in radii of gyration, we provide snapshots of the WT and S216D structures in Fig. 8C, that show that the WT forms a more compact configuration. Hence, phosphorylation appeared to 'straighten' the alignment of the LIM3 and LIM4 domains, leading to distances of roughly 50 Å from S216 to site E343 for the S216D construct, versus 40 Å for the WT (Fig. 8D). We anticipated that this straightening may play a role in the binding of ABLIM1 to other target proteins. This straightening is paralleled by an increase in hydration (Fig. 8E).

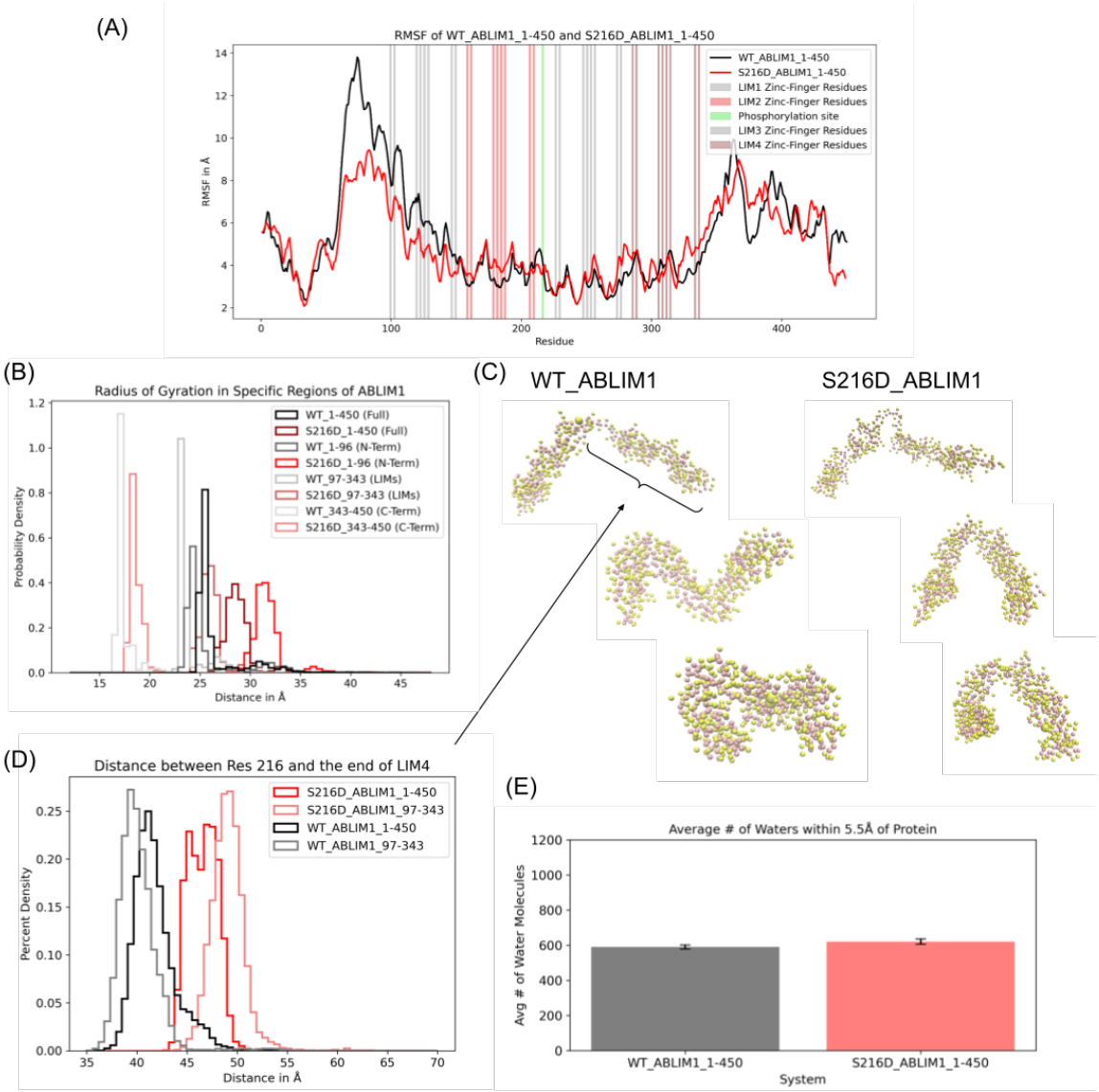

Figure 8: **Extended CG ABLIM1 Systems.** A) RMSF of Extended WT and phosphorylated ABLIM1. B) Radii of gyration of specific subsections of the extended simulations. C) Visualization of WT vs Phosphorylated CG ABLIM1 structures as production simulations progressed. D) Assessment of compression between phosphorylation site and the end of LIM4 across all extended CG simulations. E) Comparison of water molecule accessibility to protein CG beads.

4.3.2 ABLIM1 phosphorylation impacts its IDR conformation ensemble

We next constructed additional models with two phosphomimetics (S450D and S452D) in the C-terminal disordered region, to determine if phosphorylation has a consistent impact on R_g for the longer sequences of ABLIM1 relative to the LIM1-4 construct. Simulations were then performed with the double S/T to D phosphomimetic variants. The results revealed that the double phosphomimetic impacted the radius of gyration of the isolated C-term disordered simulations, apparently narrowing the range of conformations assumed by ABLIM1, as shown in Fig. 9B. Additionally, local differences were seen in the system, indicating that the double phosphomimetic exhibited less rigidity in the structure and enabled collapse of the structure (Fig. 9A).

Altogether, these data demonstrate that the WT remains fairly extended, whereas the N-terminal portion of the IDR, where the phosphomimetics are located, begins to contract. Ultimately, phosphorylation promotes a shortening of the IDR end-to-end distance, as shown in Fig. 9C. Evidently, the collapse of the chain near the double phosphorylation sites imposes restrictions on the range of conformations the IDR can assume, thus impacting its end-to-end distance. Hence, these data suggest opposing effects of phosphorylation on different chain sizes, with increases generally observed for the LIM domain-containing region with S216D, versus a decrease observed for phosphorylation of sites S450 and S452 within the C-terminal IDR.

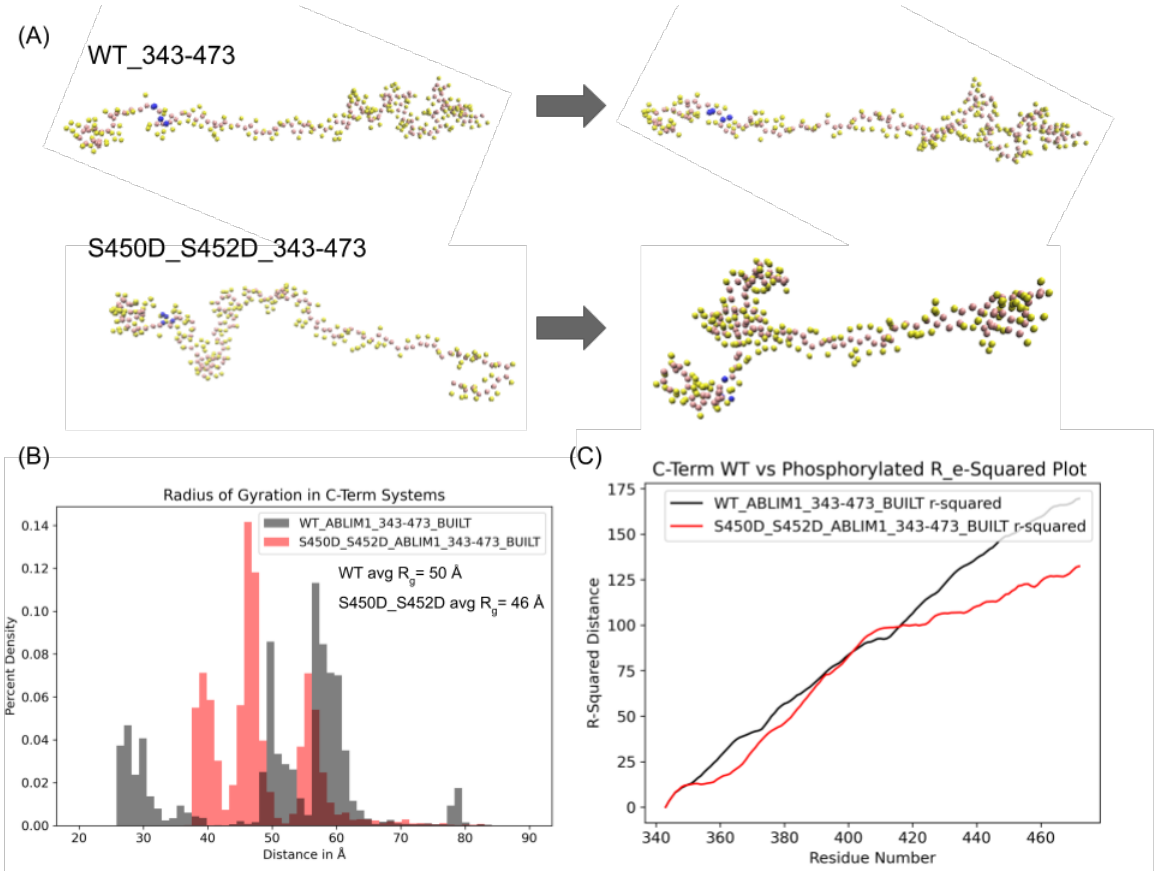

Figure 9: **C-Terminus IDR in CG ABLIM1 simulations** A) Comparisons of the WT and double phosphomimetic (S450D, S452D) structures through production simulation. B) Radius of gyration of the WT and double phosphomimetic simulations. C) End-to-end distance calculations anchored at residue E343 across both models.

To understand the physical basis of opposing trends, we evaluated the fractional charge density of amino acid sequences near phosphorylation sites, as done previously in Fig. 4C. For site S216, the phosphorylatable residue is flanked by the sequence motif AQPMSSSPKETTF. We selected this number of residues given that the Debye length, within which electrostatic screening effects are minimal, is roughly 1 nm at typical cellular ionic strengths [37]. The corresponding fractions of positively (f_p) and negatively charged (f_n) residues in the WT are 0.08 and 0.08 respectively (Table 1), which counterbalance (e.g. net charge density $|f_p\text{-}f_n| = 0$). With S216D, f_n increases

Case	+p	f_p	f_n	$\lvert f_p - f_n \rvert$	% $\langle r_e \rangle$	LIM angle
AQPMSSSPKETTF	0	0.08	0.08	0	reduced	NA
(LIM2-LIM3)	+	0.08	0.15	0.07	extended	NA
RMIHRSTSQGSIN	0	0.15	0	0.15	extended	NA
(LIM4-villin)	++	0.15	0.15	0	extended	NA
WT (vivo)	++	0.148	0.14	0.008	139	collapsed
GSK3β KO (vivo)	+	0.148	0.13	0.018	140	open**
WT (vitro)	0	0.148	0	0.148	187	open
+Gsk (vitro)	++	0.148	>=0.14	<= 0.008	140	collapsed

Table 1: **ABLIM1 fragments and their respective charge properties** ** 216 site unchanged in Stachowski *et al*MS data [3]. % From Fig. 11

to 0.15, reflecting an overall increase in the net charge density. When there is a net charge due to unequal f_p and f_n, disordered peptides tend to have extended conformations induced by self-repulsion [38], hence explaining the straightening of the LIM domains we observed earlier. This phenomenon is also observed for charged brush polymers that tend to swell at low ionic strength versus collapse at high salt when electrostatic screening is greatest [39].

We applied a similar approach to examine the set of amino acids at sites S450 and S452, selecting a sequence incorporating both residues, RMIHRSTSQGSIN. The WT form in this case had a net charge density, $f_p - f_n$, of 0.15, which should exhibit self-repulsion. This net charge is neutralized when the two serines are mutated to aspartic acids. Hence, we expect that the neutralized sequence would contract somewhat relative to the WT, which is consistent with our simulation data for the C-terminal fragment (see Fig. 9C).

4.4 Effects of phosphorylation of S216 on the binding of ABMLI1 to Z1Z2 protein

Several lines of evidence suggest that ABLIM1 binds titin [3]. Co-immunoprecipitation data from Stachowski et al. support binding in vivo, while in vitro experiments further confirmed that binding occurs between ABLIM1 and titin's N-terminal Z1Z2 fragment. Moreover, they also showed that the binding is phosphorylation-dependent, given that GSK-3β activity attenuates ABLIM1-Z1Z2 binding [3]. Building on these findings, our simulations have so far demonstrated that phosphorylation (S216D) opens the four LIM domain constructs relative to the WT case using CG simulations. We confirmed this observation using atomistic simulations of a four LIM domain ABLIM1 construct (see Sect. S1.3.2).

We therefore examined the impact of phosphorylation on ABLIM1/Z1Z2 binding, via rigid-body docking. To this end, we selected representative conformations of ABLIM1 for both WT and S216D cases, and performed ClusPro docking of these conformations to the Z1Z2 protein. This strategy was partially justified by the fact that the Z1Z1 domain is known to exist in an extended conformation in solution [40]. For each ABLIM1 conformation, we considered all poses generated by docking, of which in Fig. 10 are binding poses for the WT S1 state (the compact ABLIM1) and S216D S3 state (the extended ABLIM1 conformations). Interestingly, ABLIM1 in both cases tends to bind to the N-terminus of Z1Z2. We speculate that such binding poses are reasonable since the N-terminus of intact titin is a target for protein-protein interactions [41]. Among the docking poses identified, we found several for which a β-strand from ABLIM1 interacts with another from Z1. The beta-strand stacking is similar to the beta-sheet formed at the interface in the Z1Z2 with telethonin (TCAP) when bound as a complex (PDB 1YA5 [41], see Fig. 12B). We further performed MMGBSA calculations on these ABLIM1-Z1Z2 binding poses to evaluate their stability, and found that the poses exhibit favorable binding free energies ($\Delta G \approx -40$ kcal/mol, see Fig. 10), for all poses and in a phosphorylation-independent manner.

4.5 Tethered ABLIM may interact with titin in a phosphorylation dependent manner

Our simulations and analyses of WT and phosphorylated ABLIM constructs suggest that the charge introduced by phosphate groups impacts IDR compactness. Therefore, we sought to investigate how the complete ABLIM1 might interact with titin within an intact myofibril. To this end, we employed a Flory scaling model for polymers (Eq. 1) to predict the geometric properties of the IDR spanning bridging LIM4 and the villin headpiece, namely radii of gyration and end-to-end distance. Since simulating the complete structure is not feasible, we resorted to simulations of smaller IDR

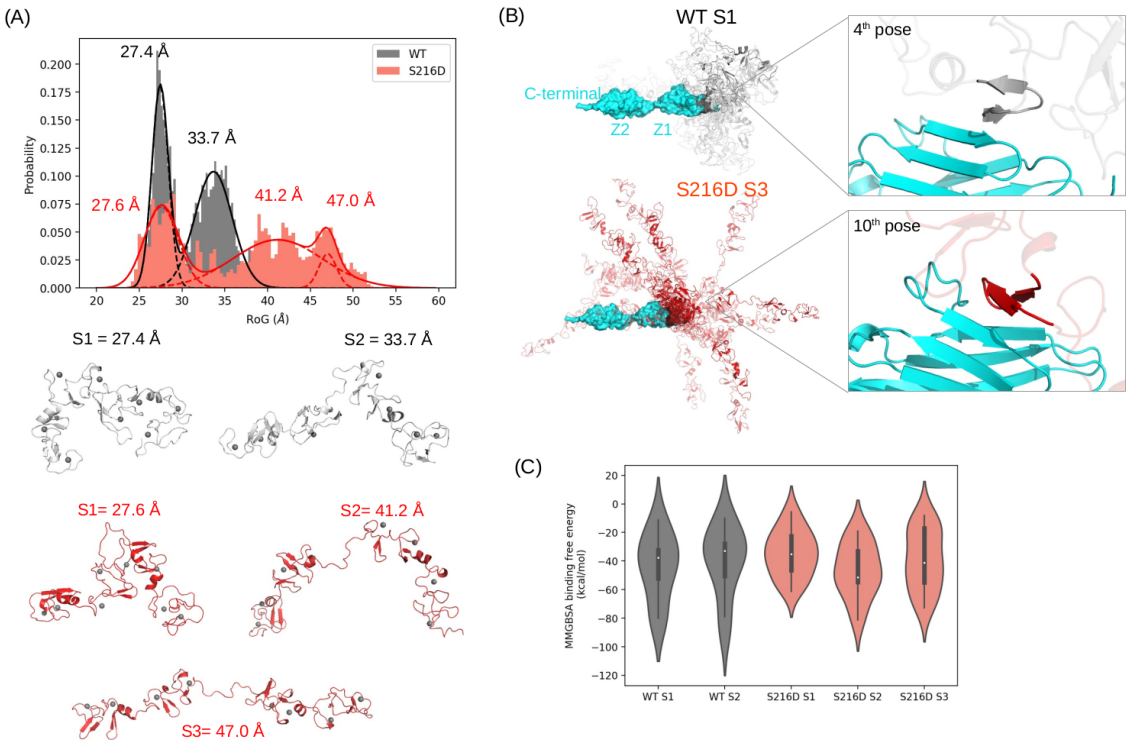

Figure 10: A) Distributions of R_g of four LIM domain constructs obtained from 300 ns atomistic MD simulations (see Fig. S5). The probability density is fitted to Gaussian function to identify major states, and the representative conformations of the identified states are shown below. B) Rigid docking of Z1Z2 structure (PDB 1YA5) to the representative WT and S216D ABLIM1 structures using the ClusPro webserver [42]. ClusPro generated multiple docking poses, and we showed these poses for the WT S1 state and the S216D S3 state, and also showed representative poses in which ABLIM1 forms β-strand interactions with the Z1 domain. C) MMGBSA-calculated binding free energy between ABMLI1 and Z1Z2 based on the ClusPro generated poses.

ABLIM constructs with and without phosphorylation to predict their radius of gyration (R_g) as a function of length. This approach allowed us to determine the scale factor ν, with which we can scale the radii of gyration to the full length of the ABLIM C-terminal IDR.

4.5.1 ABLIM length is sufficient to overlap with titin at typical actin lattice spacings

We assumed that villin binds to a region on actin directly adjacent to the terminus of an actin from a neighboring sarcomere (see Fig. 1). This binding location is consistent with the idea that villin binds actin [43]. The tethering of the C-terminus to actin would leave the N-terminal portion of ABLIM free to rotate and bind to the Z1Z2 dimer formed by paired titins. We next compared our sequence properties to those in Hofmann 2012 [23], where they reported data on the relationship between the radius of gyration (R_g) and the number of segments (amino acids) for folded and unfolded proteins. In Fig. 11A, we compiled R_g data from Hofmann *et al* [23] and our own simulations. Their study fit a form of Eq. 1 to describe this relationship for folded (orange) and unfolded proteins (blue), where the latter exhibited a larger R_g. The fits for the folded and unfolded proteins were $\nu = 0.34$ and $\nu = 0.58$, respectively [23].

To benchmark our results with the disordered region of ABLIM1, we extracted R_g estimates from our molecular dynamics simulation data. For the WT fragment spanning residues 343-473, the average radius of gyration ($\langle R_g \rangle$) of 50 Å for the 131 amino acid sequence (see Fig. 9) corresponds to $\nu = 0.66$ in Eq. 1. Although this value deviates from the 36 Å estimate based on the Hofmann et al. fit for unfolded proteins, they also reported a larger than expected R_g =30 Å for a small intrinsically disordered protein ProTα. In that case, $\nu = 0.65$ was obtained, which more closely matches our result. For our molecular simulations of the phosphorylated fragment that yielded a

$\langle R_g \rangle$ of 46 Å, we obtained a moderately smaller scale factor of $\nu = 0.64$. This decrease is attributed to the two S to D mutations neutralizing the positive charge density of the WT, mitigating swelling due to self-repulsion. Using our estimates for ν based on the simulated fragments, we predicted the corresponding $\langle r_e \rangle$ values for the full (366 amino acid) C-terminal sequence as 93 and 84 Å for WT and phosphorylated forms, respectively.

To relate the geometries of the ABLIM1 fragments to their ability to interact with Z1Z2 on neighboring actin filaments, we use the probability distribution $P(r)$ from Eq. 2. This relationship determines the likelihood that a fragment assumes a distance comparable to the actin filament spacing. We first compute $\langle r_e \rangle$ for the intact ABLIM1 C-terminus using predictions from our molecular simulations of shorter fragments. For this, we report in Fig. S3 the $\langle r_e \rangle$ values for the short WT and phosphorylated ABLIM1 C-terminal fragments, which were found to be 170 Å and 130 Å respectively from Fig. 9D. Using Eq. 1 again, but this time fixing ν to the values determined from the R_g fits, we solved for a_o using the $\langle r_e \rangle$ values from our simulation data. Our fit with the fixed ν values yielded $a_0 = 67$ Å for linear scaling of the end-to-end distance versus the number of residues in Fig. S3. The fitted parameters provided reasonable estimates of the $\langle r_e \rangle$ for our simulated fragments, though they under- and overestimated the values to an acceptable degree. Extrapolated fits to the Flory equation Eq. 1 for the 366 amino acid C-terminus resulted in $\langle r_e \rangle$ values of 311 and 276 Å, respectively.

We then evaluated how the average $\langle r_e \rangle$influenced the chain distributions of the wild-type (WT) fragment and its phosphorylated counterparts. These analyses yielded probability distributions for each end-to-end distance, as shown in Fig. 11. To obtain these results, we substituted the estimated average end-to-end distance ($\langle r_e \rangle$=170 Å) for the WT fragment into equation Eq. 2, yielding a maximum at approximately r_e=120 Å.Based on $\langle r_e \rangle$ values of 311 and 276 Å for the full-length C-terminal cases, we observed that $P(r)$ maxima was right-shifted toward larger lengths of roughly R_e =225 Å for the phosphorylated case versus about 250 Å for the WT.

Lastly, we investigated the properties of the ABLIM protein when bound by its villin domain to an actin filament, relative to the inter-actin filament spacing (see schematic in Fig. 1). Namely, we estimated the end-to-end distance from ABLIM's bound villin domain to its LIM domains to assess the LIM domains' likelihood of interacting with an adjacent actin filament capped with titin Z1Z2 domains. The actin lattice spacing at the Z-band was estimated to be approximately 30.4 nm, based on Irving et al [44], which is marked in Fig. 11B by a blue circle. The P(r) data in Fig. 11B suggest a marginally higher probability for the wild-type (WT) C-terminal region versus the phosphorylated condition to assume an R_e value matching the filament spacing. At this distance, the WT ABLIM is more likely to interact with a Z1Z2 dimer on an adjacent actin relative to its phosphorylated counterpart; by extension, the WT (unphosphorylated) case may have a greater potential to interfere with the Z1Z2 domains that anchor titin to actin. Now assume ABLIM is no longer perpendicular to actin but rather anchored at an angle akin to α-actinin (see Fig. 1); in this scenario, larger R_e values would be needed to bridge adjacent filaments, which results in the WT being increasingly favored over the phosphorylated ABLIM, as illustrated by the shaded region in Fig. 11B.

5 Discussion

5.1 Main points

In this computational study, we examined the myofilament protein ABLIM1 and its interactions with titin at the Z1Z2 domain. Our findings suggest that ABLIM1 LIM domains are compatible with binding titin, and that phosphorylation can influence the conformation distribution of ABLIM1 relative to the WT (unmodified) protein. Furthermore, intact ABLIM1 is capable of spanning typical actin-actin spacings at the z-disk, and its span is sensitive to the phosphorylation state. These findings have significant implications for mechanosignal transduction in cardiac myocytes, particularly in the context of failing hearts where reduced ABLIM1 phosphorylation has been observed [3]. These findings strengthen the support for LIM domains in mediating diverse mechanosensitive functions [2].

5.2 ABLIM1 binding partners

We elucidated the binding properties of ABLIM1 through analysis of the STRING database. Our search of the database revealed that ABLIM1 binds to other sarcomere proteins, including titin, β-actin, and LIM-nebulette, with varying degrees of confidence [45]. This finding is consistent with previous research indicating that ABLIM proteins are generally associated with binding actin, often through their villin-type "headpiece" domain common to tens of cytoskeletal proteins [46]. Additionally, LIM domains, such as those present in ABLIM1, have been suggested to act as

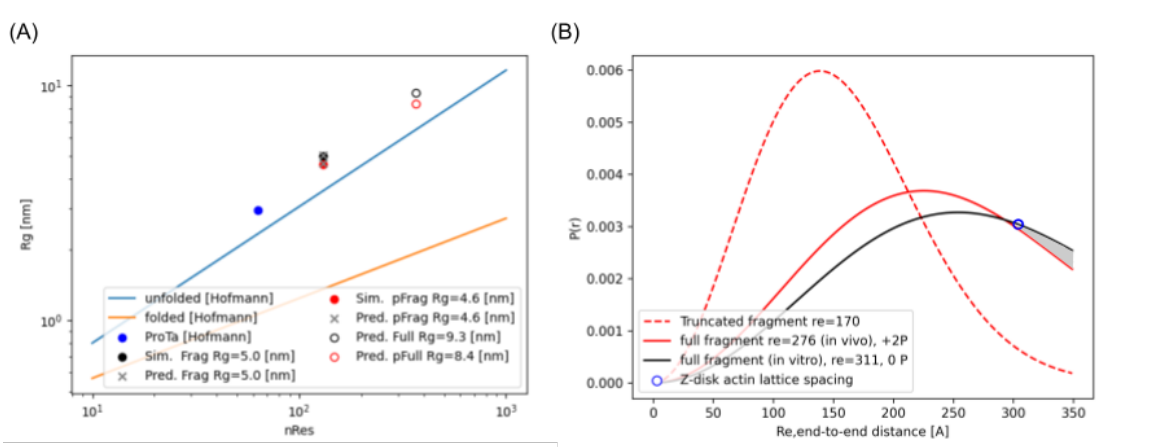

Figure 11: A) Radius of gyration, R_g, versus number of residues (nRes), based on data from Hofmann *et al* [23] and from the molecular dynamics simulations of the truncated ABLIM 343-473 fragment in Fig. 9. Fits to the data are extrapolated to the full length (366 amino acid) fragment using parameters in Table S2. B) Probability distribution of end-to-end distances, based on the average R_e estimated from panel A. An experimental estimate of the actin-actin spacing is marked in blue [44].

protein-binding modules [47] and may recognize different actin conformations, particularly when actin is stressed. Recent molecular dynamics simulations have provided a mechanism by which LIM domains can bind strained actin conformations, including the recognition of two binding sites exposed at the cracked interface [48].

Intriguingly, we identified potential associations of ABLIM1 with KCNJ12 and CLCN1 by STRING analysis. KCNJ12 codes for an ATP-dependent, inward rectifying potassium channel (Kir2.2), and CLCN1 is a gene for a chloride channel. ABLIM1 has been previously identified as an actin-binding LIM protein associated with Kir2.2 in brain proteins [49]. Therefore, the expression of Kir2.2 in the heart [50] could exhibit similar interactions. A previous study indicated that CLCN1 and ABLIM1 are spliced by the same protein MBNL1 [51], the evidence for coexpression and association is lacking. The potential association between ABLIM1 and these ion channels may imply a role for ABLIM1 in modulating cell excitability, providing a link between mechanics and excitation at the z-disk, although further investigation is needed to confirm this hypothesis.

The binding of titin through its N-terminal Z1Z2 domains has been observed [3], although the specific region responsible for this interaction remains unknown. Our data suggest that LIM domains have the capacity to bind Z1Z2 directly, as individual LIM domains can bind to the Z1Z2 fragment of titin as shown via our docking simulations and MMBPSA calculations. In fact, some of the predicted binding poses align a LIM domain beta strand with those of Z1Z2, similar to the resolved Z1Z1-telethonin complex (PDB 1YA5) where intermolecular beta strands interact tightly as antiparallel sheets [41] (Fig. 12). This binding mode is also reported for LMO4 and LDB1 (1RUT) [32], where beta strands from LIM domains align antiparallel with those from the target protein. The telethonin/Z1Z2 complex suggests that telethonin dimerizes Z1Z2 domains from two titin strands, bridging the beta sheets between a Z1Z2 pair (Fig. 12). In this capacity, ABLIM1 could compete with, or compromise, the binding of telethonin to Z1Z2. Accordingly, telethonin mutations are already established in hypertrophic and dilated cardiomyopathies [52]. This raises the possibility that disruption of TCAP binding to titin by ABLIM1 could contribute to cardiac dysfunction.

We show that phosphorylation of ABLIM1 may play a crucial role in determining its conformation ensemble. Specifically, we speculated that phosphorylation primarily affects LIM availability to Z1Z2 by controlling the extension of the linker that connects the LIM domain and the villin headpiece. We propose that this sets the local concentration of the LIM domains near the titin N-terminus (Fig. 12A). Hence, this proposed model suggests that villin headpiece association with actin could enable the LIM domains to bind to the Z1Z2 domain, with the potential to compete with or otherwise disrupt telethonin/Z1Z2 interactions. Our docking results surprisingly indicated that phosphorylation between the LIM domains does not have a significant impact on Z1Z2 interactions, contradicting previous in vitro assay findings [3]. However, computational limitations precluded us from docking larger constructs, for which multi-site phosphorylation

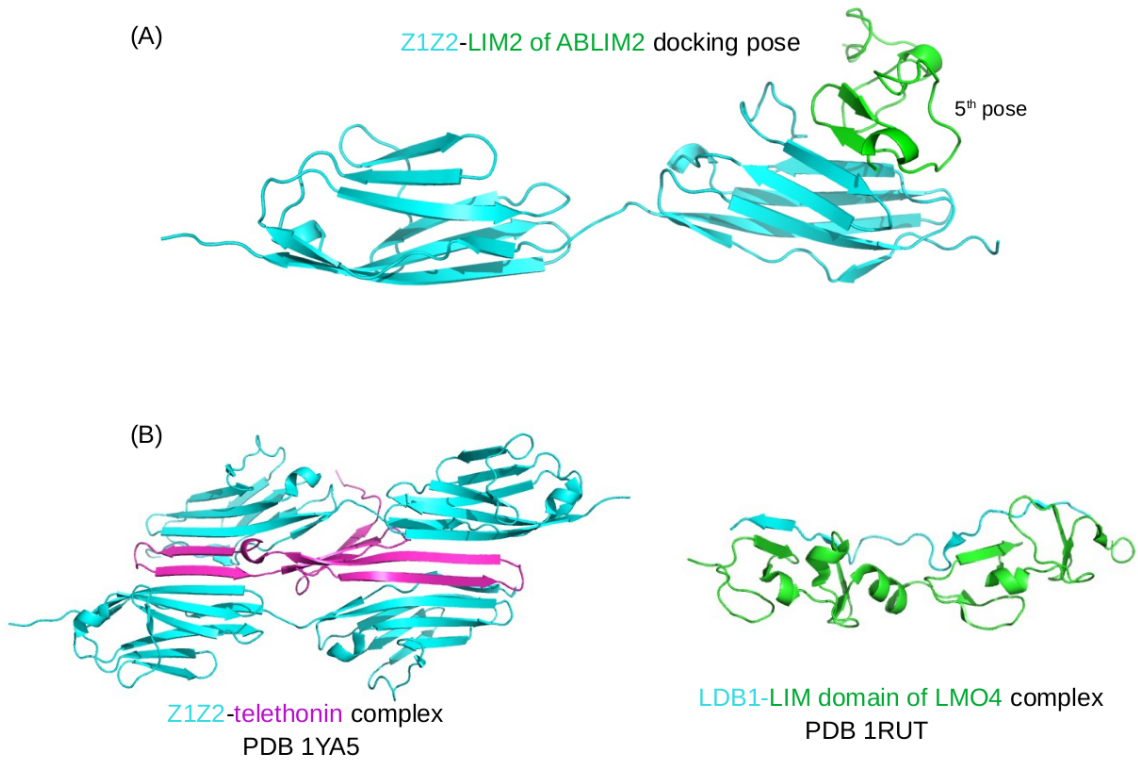

Figure 12: β-strand interaction is likely a conserved binding pattern for LIM domain to bind its target. A) Docking pose between LIM2 domain of ABLIM2 with Z1Z2. B) Reported binding mode between Z1Z2 and telethonin [41], and between LIM domain protein LMO4 and its target LDB1 [32].

could in principle disrupt its interaction with titin. It is also possible that Z1Z2 association with ABLIM1 may also be controlled by the specific pattern of phosphorylation within the ABLIM1 disordered C-terminus. The ELM database suggests that ABLIM1 has numerous potential GSK3β phosphorylation sites, of which several were found to be phosphorylated by mass spectrometry [3]. In addition, a study on ABLIM1 recruitment to cortical actin found that phosphomimetics of S214 and S431 were sufficient for ABLIM1 to colocalize with the cell membrane [7], evidencing that sites both within and outside of the LIM-domain containing region have functional phenotypes. Changes in ABLIM phosphorylation could also impact LIM/actin interactions among other LIM domain targets, and thus influence localization in vivo. Therefore, it is important to quantify a full range of potential phosphorylation sites in human ABLIM1 to appreciate the phosphorylation- and GSK3β-dependence of titin association.

5.3 Consequences in vivo

Based on our ABLIM simulation data, we aimed to relate the interfilament spacing in the sarcomere to the chains' end-to-end distance. Our calculations revealed that the LIM domains of the full-length protein would likely be found roughly 84 Å from the C-terminal villin headpiece when phosphorylated versus 93 when it is not . Hence, the ABLIM LIM/Z1Z2 interaction would be most likely when the disordered domain spanning the N-terminal LIMs and C-terminal villin is not phosphorylated. In principle, if ABLIM1 were tethered to actin by the villin headpiece, the LIM domains could interact with the Z1Z2 titin domains on an adjacent thin filament, given interfilament distances of approximately 30 nm reported in [44]. Moreover, as the sarcomere lattice contracts under isovolumetric stretching [54], the likelihood of interaction would further increase. Such a mechanism is analogous to the role of phosphorylation in toggling interactions between the N-terminal extension of MyBPC and actin, where the protein is tethered to the thick filament by its C-terminal domains [55].

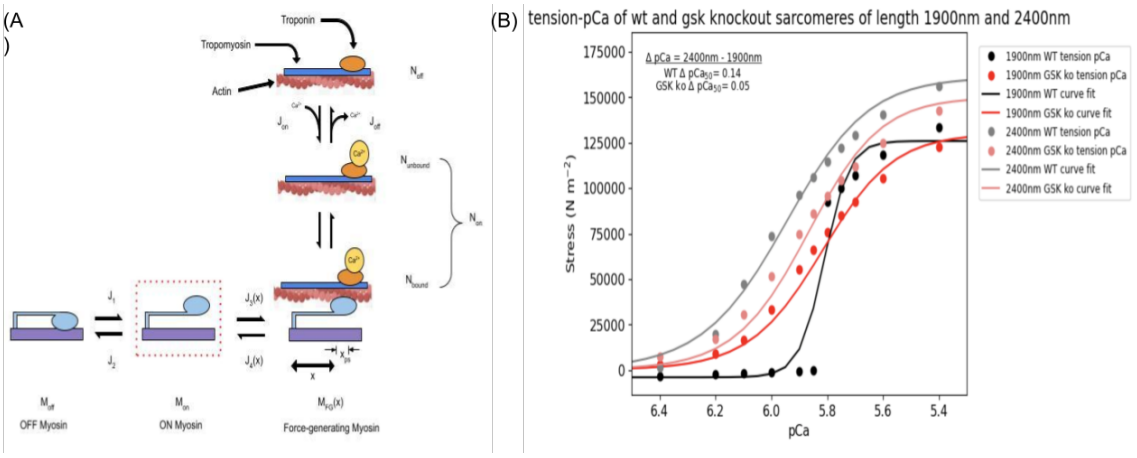

Figure 13: **Force generation in a cardiac sarcomere.** A) A kinetic model of force generation in myofibrils that assumes off, on, and cross-bridge generating states for myosin [53]. We assume changes in passive force due to altered titin/actin interactions impact the transition rate between myosin off and on states. B) Predictions of stress (force/area) for isometric contraction at two sarcomere lengths, based on the model in panel A.

5.4 Length-Dependent Activation (LDA)

Phosphorylation's ability to modulate interactions with Z1Z2 could, potentially, influence myofilament mechanics. We believe the most immediate impact would be reflected in the length-dependent activation of the sarcomere, which describes how more force is generated at greater sarcomere extensions. This phenomenon is a fundamental part of the Frank-Starling effect, where fewer equivalents of calcium are needed to achieve equivalent numbers of cross-bridges relative to when the sarcomere is at its resting length. One recognized contribution to LDA is passive tension arising from titin, which helps restore the filaments to their equilibrium length when stretched [53].

It has been suggested this passive tension enhances the recruitment of myosin in the 'off state' to the 'on state'. This state is primed for myosin to form force-generating cross-bridges with the thin filament [53]. We postulate that some of this passive tension is due to titin being secured to actin termini via dimerization of their Z1Z2 domains via telethonin, which is supported in Pinotsis *et al*[56]. In turn, factors that attenuate this anchoring are expected to decrease LDA, as has already been argued for titin treatments that disrupt passive tension [57].

Consistent with this idea, recent studies [9, 58] suggest that phosphorylation during heart failure decreases passive tension. In addition, GSK3β phosphorylation was shown to reduce ABLIM1 binding to the titin Z1Z2 domain, suggesting a tightly regulated balance between achieving an extended ABLIM conformation to promote titin/ABLIM interactions and directly modulating binding to Z1Z2, possibly through direct interactions of the LIM domain. Along these lines, telethonin deficiency leads to animals being less adaptive to stress due to reduced fractional shortening [59].

To illustrate this concept of reduced passive tension due to disrupted Z1Z2 interactions, we used MyoSim [53] to simulate the maximum force generated within a cardiac sarcomere at fixed lengths and calcium concentrations. In their model, the recruitment of myosin from its bound state on the thick filament to an off-state ready for cross-bridge formation is given by

$$J_1 = (k_1 + Hk_{MLCP})M(1 + k_{force}F) \tag{3}$$

$$F = F_{active} + F_{passive} \tag{4}$$

$$F_{passive} = k_p(L - L_0), \tag{5}$$

where k_1 is a rate constant, H=1 as the myosin RLCs are all phosphorylated, k_{MLCP} and k_{force} are constants, M is the proportion of myosin heads in the off state, F is the total of the F_{active} and $F_{passive}$ forces, where k_p is the stiffness of the passive elastic element, L is the sarcomere length, and L_0 is the sarcomere length at which the passive force is zero (see Fig. 13A). Using this model and parameters in Table S3, we varied the sarcomere lengths from 1.9 μm to 2.4 μm over Ca concentrations ranging from below 0.100 uM to 100 uM to estimate steady-state isometric forces at resting and saturated conditions, respectively. In Fig. 13B we present the simulated contractile force as a stress (F/A), with each normalized to their maximum force at saturating

Ca^{2+}. We report that the predictions for stretched sarcomere of length 2.4 μm reached greater stress compared to resting 1.9 μm length at every calcium concentration (Fig. 13B). Using the definition of the pCa_{50} as the Ca^{2+} concentration at which half-maximal force is obtained, we report values of 5.81 and 5.95 for the slack and stretched configurations, which corresponds to a left-shift of ΔpCa_{50}=0.14. This leftward shift represents an increase in apparent calcium affinity, which together with the increased maximal stress observed at long sarcomere lengths, affirms the Frank-Starling effect. In effect, fewer calcium equivalents were required by the stretched sarcomere to achieve similar levels of stress generated for the resting sarcomere.

To reflect disrupted passive stiffness attributed to titin akin to the reduced activity of GSK3β, we reduced k_p and L_0 for our GSK3β knockout model configuration to match the experimental trends reported by Stachoswki *et al* (Table S3). For this configuration, we saw a comparable maximum stress for the resting sarcomere lengths, consistent with data from Stachowski *et al*, when coupled with a change in the k_1 rate constant from 1 to 2, although our results show a loss of cooperativity evidenced by the smaller slope of the stress/pCa curve. The similar level of stress despite a weaker passive force term is due to our assumption that the resting sarcomere length was shortened. We based our assumption on the similar treatment for titin mutants in [53]. We found that the GSK3β knockout simulations predicted a smaller increase in maximal force at the extended sarcomere length compared to WT. Correspondingly, the ΔpCa50 values were reduced by two thirds to 0.05. In other words, reducing the passive tension in our model was sufficient to reflect the loss of LDA reported by Stachowski *et al*, despite some quantitative differences in cooperativity, for instance, which could be attributed to the simplicity of the kinetic scheme we used.

5.5 Modulation of IDR properties

The intrinsically disordered regions within ABLIM1 are important in regulating myofilament function. One attribute is its ability to exist as an ensemble of conformations, which allows it to interact with multiple components of the myofilament, including actin and myosin, and modulate their activities in response to changing conditions, including pH and ionic strength[1]. This is because of the rugged energy landscape of ABLIM1 that enables it to sample a wide range of potential functional states. This property is particularly advantageous in the context of muscle contraction, where ABLIM1 can rapidly adapt to changing conditions to maintain optimal contractility.

PTMs provide a basis for many proteins to modulate the accessibility of binding sites and surfaces important for recognizing protein targets [60]. Phosphorylation in particular alters the charge distribution of ABLIM1, shifting its conformational ensemble and influencing its interactions with other proteins, as demonstrated in our study. Supporting this are data suggesting that mutations of S214A and S431A in ABLIM1 have been shown to disrupt cancer migration [7], potentially by disrupting its interactions with the actin cytoskeleton. Along these lines, we previously identified [1] 92 PTM sites in the PhosphoSitePlus, database, of which the majority were phosphorylation. Also identified were acetylation and ubiquitination. Similar to PTMs, mutations in IDR have the potential to impact conformational ensemble or target binding. It is not surprising that many mutations are found in disordered regions of MAPIDs. Tens of missense variants have been identified in ABLIM1 on GnomAD [61], though they remain uncharacterized (data not shown); to our knowledge, a pathological variant has not been identified.

5.6 ABLIM1 has numerous SLIMs encoding for kinases

Our previous analysis of ABLIM1 [1] revealed a large number of phosphorylation-based post-translational modifications; many of which were in its intrinsically disordered regions, suggestive of a complex regulatory mechanism. Co-immunoprecipitation (co-IP) experiments have identified numerous targets of ABLIM1, including the titin Z1Z2 domain [3]. To expand on these hits, we queried the ELM webserver [62] for short linear interaction motif (SLIM)s in ABLIM1 and cross-referenced them with phosphorylated fragments identified in mouse data from Stachowski Doll et al. [3]. The ELM results indicate that ABLIM1 harbors dozens of potential SLIMs, many of which are localized to its N-terminal half at the MSSSP segment (Table S4). Notably, the MSSSP sequence is a potential target for several proteins, including GSK3β, cyclin-dependent kinase, casein kinase 2, polo-like kinase 1, and phosphoinositide-dependent protein kinase 1 (e.g., mitogen-activated protein kinases). Beyond this region, GSK phosphorylation motif sites are found throughout the ABLIM1 sequence. In line with these findings, knocking out GSK3B resulted in decreased, but not completely negated ABLIM1 phosphorylation, suggesting that reduced activity of other kinases like CDK could lead to further reductions. At a minimum, these data are highly suggestive of ABLIM1 being under multiple modes of regulatory control by GSK3B and potentially other kinases.

5.7 Limitations

We acknowledge key limitations and assumptions that could motivate future investigations. Firstly, the uncertainty surrounding the interaction between LIM domains and Z1Z2 domains makes it challenging to validate our predicted docking poses. Additionally, performing rigid docking may obscure the actual binding mode that would result from proteins relaxing upon binding, which could lead to inaccurate predictions. Furthermore, although we suggest that ABLIM1 can bind to Z1Z2 and previous studies have established a link between GSK3B KO and decreased passive tension [3], we have not firmly established a direct link between ABLIM1 binding at the Z1Z2 domain and its subsequent impact on passive tension. Resolving the number of myosin heads available for recruitment via methods like small angle x-ray scattering may help [44].

6 Conclusions

Our study's key results reveal significant insights into the role of ABLIM1 in the sarcomere. Notably, the LIM domains of ABLIM1 were found to be capable of binding titin Z1Z2, and its intrinsically disordered chain properties were shown to be dependent on phosphorylation. Importantly, the protein likely spans the lattice spacing in the sarcomere z-disk, with some sensitivity to phosphorylation as well. These findings have broad implications for our understanding of heart failure (HF). For instance, the decrease in phosphorylation during HF [9, 58] suggests that post-translational modification (PTM) control of LIM-containing proteins may play a critical role in disease progression. Together with the observed decrease in length-dependent activation in HF versus wild-type conditions from Stachowski et al., this highlights the importance of phosphorylation in tuning ABLIM1's functional contribution to cardiac contractility.

7 Acknowledgements

Research reported in this publication was supported by the Maximizing Investigators' Research Award (MIRA) (R35) from the National Institute of General Medical Sciences (NIGMS) of the National Institutes of Health (NIH) under grant number GM148284. This work used PSC Bridges from the Advanced Cyberinfrastructure Coordination Ecosystem: Services & Support (ACCESS) program, which is supported by National Science Foundation grants #2138259, #2138286, #2138307, #2137603, and #2138296. We are grateful for Stefano Sala's careful reading of the manuscript.

Supplementary Information (SI):

A hypothesis for how Actin-Binding LIM Protein 1 modulates titin in cardiac muscle

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S1 Supplement

S1.1 Supplemental Tables

Site	**Fold change**	Modeled
215/216	---	S76 in isolated LIM
354	0.516 (p=0.042)	Not in human
494	0.627 (p=0.043)	In human (450, 452)
496	0.630 (p=0.045)	

Table S1: Phosphorylation sites from [3] (mouse)

Description	Value
b	3.4 for a.a [63]
actin/actin separation	30.4 nm [44]
N_{1-97}	97
$N_{343-473}$	130
$N_{343-710}$	367

Table S2: **Summary of parameters and distances**

Parameter	**WT**	GSK3β knockout
int_passive_k_linear (k_p)	14	7
int_passive_hsl_slack (L_0)	1265	1000
k_1	1	2

Table S3: **Parameters used for simulations of isometric force generation**.Based on the kinetic model from [53]. All other parameters assumed the default values.

SLIM	# Occur	Fragment
CDK	3	MSSSPK
CK2	9	MSSSPKE
GSK3	28	MSSSPKET
PLK	3	KETTFSS
ProDKin	12	MSSSPKE

Table S4: Table of short linear interaction motifs serving as kinase targets, as suggested in the ELM database [64] for human ABLIM1. # occur refers to the number of predicted motifs in the sequence, inclusive of the MSSSP sequence.

Mouse fragment	site(s)	Human site(s)	Kinase?
DCLCQLCAQPMSS(p)SPK	215	215	GSK3 (human)
DCLCQLAQPMSSS(p)PK	216	216	GSK3 (human)
S(p)SSDFFYPK	354	N/A	
TS(p)SESIYSRPGSSIPGSPGHTIYAK	396	352	GSK3
TSS(p)ESIYSRPGSSIPGSPGHTIYAK	397	353	GSK3
TSSES(p)IYSRPGSSIPGSPGHTIYAK	399	355	GSK3
TSSESIY(p)SRPGSSIPGSPGHTIYAK	401	357	GSK3
TSSESIYSRPGSS(p)IPGSPGHTIYAK	407	363	GSK3
TSSESIYSRPGSSIPGS(p)PGHTIYAK	411	367	GSK3
QS(p)LGES(p)PRTLSPTPSAEGYQDVR	466,470	422, 426	GSK3
T(p)LSPTPSAEGYQDVR	473	429	GSK3
TLS(p)PTPSAEGYQDVR	475	431	GSK3
TLS(p)PTPS(p)SESIYSRPGSSIPGSPGHTIYAK	475,479	431, 435	GSK3
TLS(p)PT(p)PSAEGYQDVR	475,477	431,433	GSK3
S(p)TSQGSINSPVYSR	494	450	GSK3
STS(p)QGSINSPVYSR	496	452	GSK3
ST(p)SQGS(p)INSPVYSR	499,495	455,451	GSK3
NSPLPYRPDSRPLT(p)PTYAQAPK	586	503	GSK3
IETDHWPGPPS(p)LAAVGTDPR	658	574	
S(p)SGREEDEEELLR	670	586	CK2 (human)
SS(p)GREEDEEELLR	671	587	CK2 (human)
NGLHRPVS(p)TDFAQYNSYGDISGGVR	752	669	
NGLHRPVST(p)DFAQYNSYGDISGGVR	753	670	

Table S5: Tabulation of phosphorylated fragments identified in [3], compared to the homologous positions in human ABLIM1. Sites annotated as GSK3B phosphorylation sites by ELM are marked as such.

Parameter	**Value**	**Meaning**	**Ref**
b	0.38 [nm]	bond length	[23]
l_p	0.4 [nm]	persistence length	[23]
λ_B	0.7 [nm]	Bjerrum length for $\epsilon_r = 80$	
κ	1.0 [nm]	Inverse Debye length	
f_-	--	fraction of negative charge	
f_+	--	fraction of positive charge	
v_0	0.6	excluded volume chain	[23]

Table S6: Parameters used in the polymer physics model.

Case	Sites	Sequence	f_p	f_n	rep/attr
ABLM1	210-222	AQPMSSSPKETTF	0.07	0.07	neutral
ABLM1	210-222	AQPMdSSPKETTF	0.07	0.14	repulsive
MYBPC3	c0c1	RSAFRRTSLAGAGRRTSDSHED	0.23	0.14	repulsive
MYBPC3	c0c1	RDAFRRTSLAGAGRRTSDSHED	0.23	0.18	less repulsive

Table S7: Data table for sites, sequences, and values of f_p and f_n

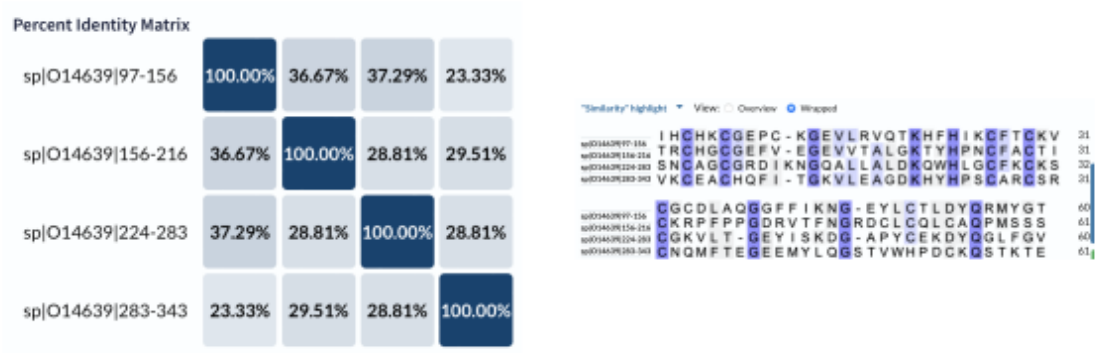


Figure S1: Conservation between LIM domains in ABLIM 1.

S1.2 Supplemental Figures

S1.3 Supplemental Results

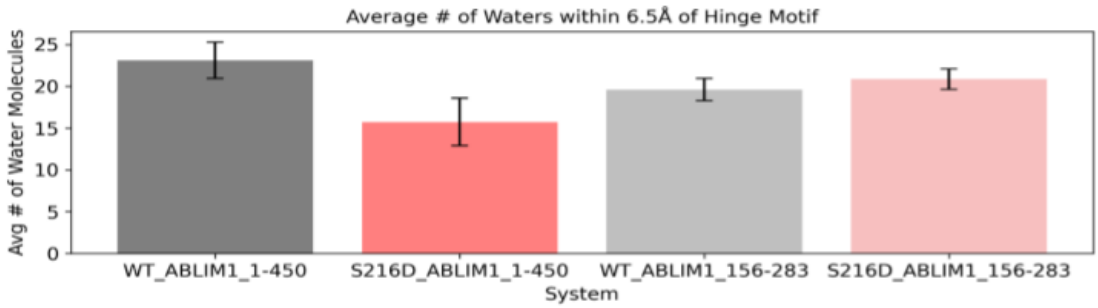
S1.3.1 Disorder

We additionally used the globprot web interface [65] to predict intrinsically-disordered regions for ABLIM1 (ACCESSION code O14639), based on the Russell-Linding statistic [65]. The predictions for the folded LIM domains and villin head piece showing in Fig. S4 are consistent with IUPRED 2 A predictions in the main text. The disordered regions are more prevalent in the sequence spanning 336 to 743, consistent with our other results.

S1.3.2 Atomistic MD of the four LIM domain construct with and without phosphorylation at S216

In order to explore the effects of phosphorylation at S216 on the conformations of the folded LIM domains, we performed atomistic MD simulations on the wild-type (WT) system, comprising residues 97-343 of ABLLIM1, and on the phosphorylated system, where S216 was mutated to D216 to mimic the negative charges introduced by phosphorylation (Fig. S5A). MD simulations were carried out using the Amber20 package [66], with the protein described by the ff19SB force field [67] and solvated in a 10 Å margin OPC water box [68], containing 0.15 M KCl salts. The simulation protocol included energy minimization, heating, equilibration, and a 300 ns production run, with the detailed protocol reported in our previous study [69]. During the MD simulations, the coordination between the Zn^{2+} ions and their coordinating residues was maintained using harmonic restraints with a force constant of 20 kcal/mol/Å^2. Since the simulations were initiated from the AlphaFold-predicted structure, we observed that during the 300 ns production run, both the WT and S216D systems underwent significant conformational changes and became stable by the end of the simulation, with RMSDs of approximately 20 Å compared to the initial structure.

To compare the conformational ensembles between WT and S216D, we calculated the radius of gyration (R_g) for both systems (Fig. S5B). We found that the S216D system experienced significant expansion and collapse in its conformation, as evidenced by an increasing and then decreasing



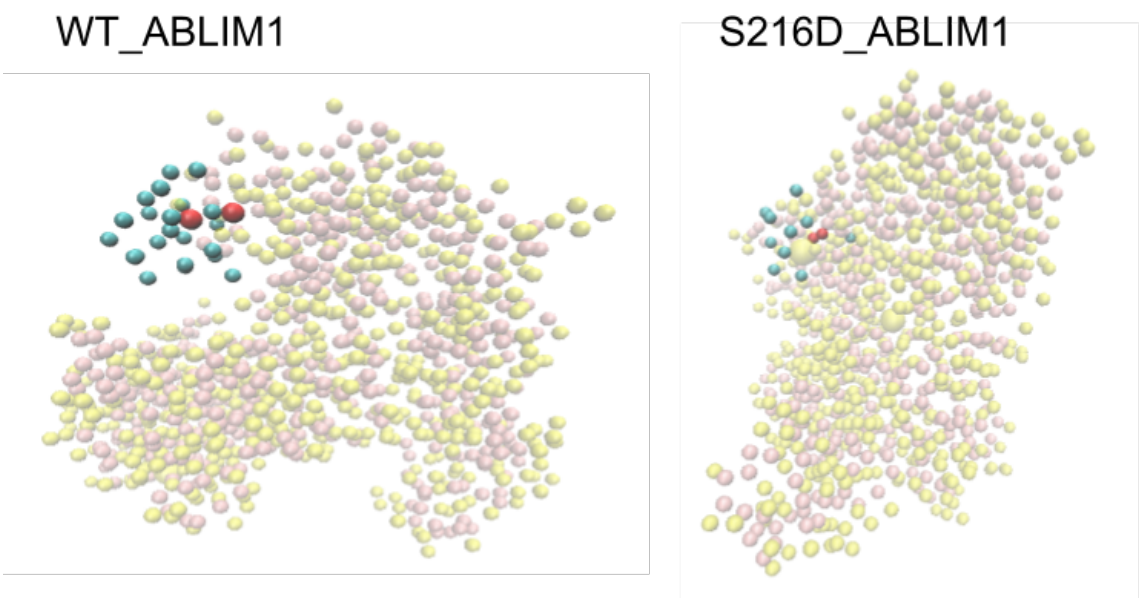


Figure S2: Average number of water molecules within 6.5Åof the hinge motif (Res 212-220) in coarse-grained ABLIM1 models

R_g curve, whereas the WT system showed a relatively stable R_gÀs a result, the $R_g$distribution for S216D spanned a wider range (25–50 Å) compared to the WT system (25–40 Å). These findings from the atomistic MD simulations confirm the observations made in our coarse-grained (CG) simulations. Phosphorylation at S216, located in the linker region that connects the LIM2 and LIM3 domains, can indeed affect the conformation of the entire folded region of ABLLIM1, promoting a more open conformation.

S1.3.3 Fractional charge and self-repulation

The Flory ideal chain model predicts that the radius of gyration scales as a function of ν[23]

$$R_g = \sqrt{\frac{2\xi b}{(2\nu+1)(2\nu+2)}} N^{\nu} \tag{S1}$$

$$\nu = \nu_0 + \nu^* \tag{S2}$$

Deviations from ideal Flory scaling of polymer properties have been attributed to imbalances in the fraction of positively versus negatively charged amino acids [23].

Attractive versus repulsive corrections to scaling coefficient ν can be estimated using

$$\nu^* = \frac{4\pi\lambda_B (f-g)^2}{\kappa^2} - \frac{\pi\lambda_B^2 (f+g)^2}{\kappa}, \tag{S3}$$

for which we define its parameters in Table S6. Per Hofmann supp, $\nu^* > 0$ pertains to net repulsion (unfolding that increases the effective volume) while $\nu < 0$ corresponds to net attraction (folding).

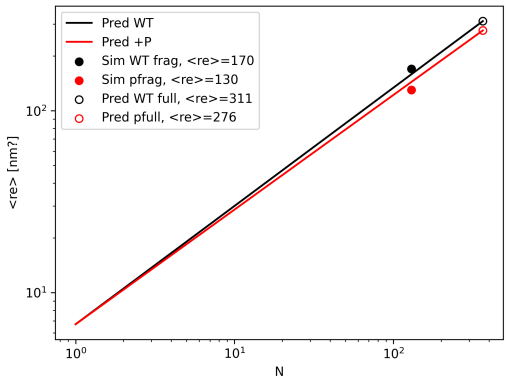


Figure S3: Predictions of $\langle r_e \rangle$ with respect to number of amino acids (N), based on fitting to fragment simulation data using Eq. 1. Here, $a_0 \approx 6.7$Å

As an example for the effects of fractional charge density, phosphorylation of ABLM1 in the LIM2-LIM3 loop increases the fractional negative charges, which potentially extends the disordered region. In contrast, the C0C1 region in MYBPC3 has a higher fractional density of positive residues relative to negative, which we expect to extend the disordered region. Its phosphorylation would decrease the difference in charge density and potentially contract the chain. Indeed, phosphorylation has been shown to reduce MYBPC's interaction with the thin filament, suggesting that the structure contracts [70]. This is supported by findings from the Warshaw lab that phosphorylated MYBPC3 has a shorter contour length than the wild-type [71].

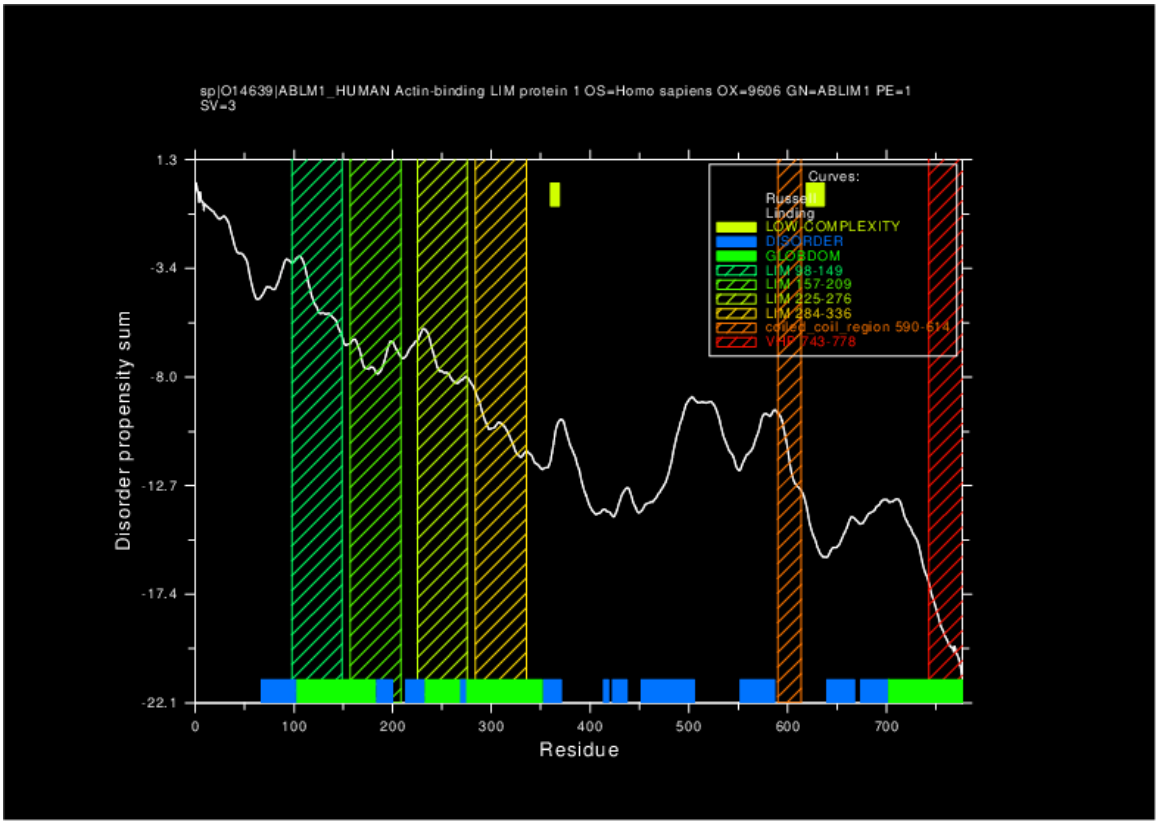


Figure S4: Predictions of disorder in ABLIM1 using the globprot interface [65].

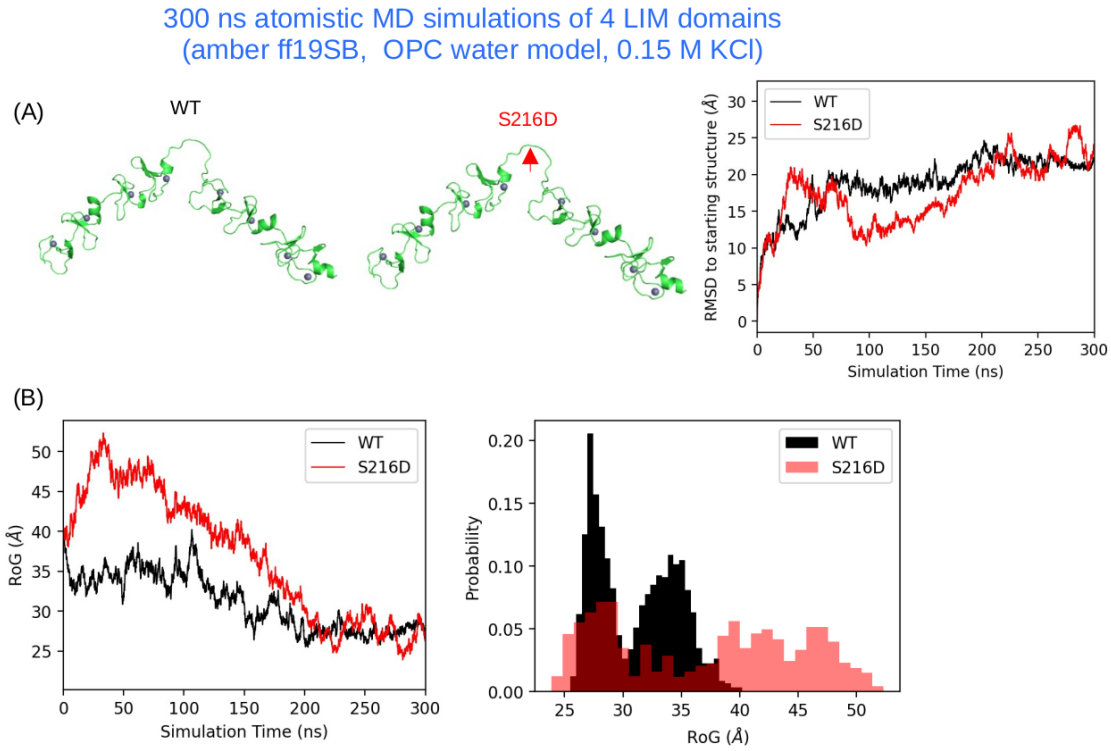


Figure S5: Atomistic MD runs of WT and phosphorylated ABLIM1 four LIM domain constructs. A) The ABLIM1 structure of residues 97-343 predicted by AlphaFold was used as starting structure of MD simulations. The location of S216 in between LIM2 and LIM3 domains was is indicated by a red arrow. The Zn^{2+} cations are depicted as gray spheres. The time-dependent RMSD relative to the starting structure is plotted. B) Time-dependent RoG of the two systems as well as the RoG distributions are plotted.

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