



# Dynamic structure of the full-length scaffolding protein NHERF1 influences signaling complex assembly

Received for publication, February 27, 2019, and in revised form, June 5, 2019. Published, Papers in Press, June 6, 2019, DOI 10.1074/jbc.RA119.008218

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Edited by Wolfgang Peti

The Na<sup>+</sup>/H<sup>+</sup> exchange regulatory cofactor 1 (NHERF1) protein modulates the assembly and intracellular trafficking of several transmembrane G protein-coupled receptors (GPCRs) and ion transport proteins with the membrane-cytoskeleton adapter protein ezrin. Here, we applied solution NMR and small-angle neutron scattering (SANS) to structurally characterize full-length NHERF1 and disease-associated variants that are implicated in impaired phosphate homeostasis. Using NMR, we mapped the modular architecture of NHERF1, which is composed of two structurally-independent PDZ domains that are connected by a flexible, disordered linker. We observed that the ultra-long and disordered C-terminal tail of NHERF1 has a type 1 PDZ-binding motif that interacts weakly with the proximal, second PDZ domain to form a dynamically autoinhibited structure. Using ensemble-optimized analysis of SANS data, we extracted the molecular size distribution of structures from the extensive conformational space sampled by the flexible chain. Our results revealed that NHERF1 is a diffuse ensemble of variable PDZ domain configurations and a disordered C-terminal tail. The joint NMR/SANS data analyses of three disease variants (L110V, R153Q, and E225K) revealed significant differences in the local PDZ domain structures and in the global conformations compared with the WT protein. Furthermore, we show that the substitutions affect the affinity and kinetics of NHERF1 binding to ezrin and to a C-terminal peptide from G protein-coupled receptor kinase 6A (GRK6A). These findings provide important insight into the modulation of the intrinsic flexibility of NHERF1 by disease-associated point mutations that alter the dynamic assembly of signaling complexes.

Signal transduction in the biological milieu is a dynamic exchange of protein-protein interactions (1, 2), coordinated by a diverse family of scaffolding proteins (2–4). Structural mod-

ularity of the scaffolds is fine-tuned for linking and transporting the different binding partners to the supramolecular signaling complexes. Well-known scaffold modules include Src homology 3, Src homology 2, PTB, WW, and the more abundant PDZ domains, which are ubiquitous for recruiting diverse protein targets (3, 4). As mediators of protein-protein interactions, PDZ domains have been shown to possess remarkable specificity for C-terminal binding motifs as well as internal peptide sequences of proteins (3). PDZ domains have emerged as key organizers of protein complexes at the plasma membrane, cytoplasmic tails of membrane proteins, and ion channels to promote their transport and localization to the cell surface for signaling (5).

Full-length NHERF1 includes tandem PDZ domains, PDZ1 and PDZ2, and a C-terminal ezrin-binding domain (EBD)<sup>4</sup> juxtaposed with a PDZ-binding type 1 motif (Fig. 1). The EBD is a specific target of the FERM domain from ezrin (ezFERM), which disrupts the autoinhibition between the PDZ2 domain and the C-terminal tail in NHERF1 (6). Binding of ezrin with NHERF1 allosterically increases the PDZ domain affinity for ligands, such as the transmembrane receptors and ion channels (7, 8). Examples of transmembrane protein complexes that are regulated by the NHERF1-ezrin linkers include the transmembrane sodium-hydrogen exchanger 3 (NHE3) complexes, cystic fibrosis transmembrane (9), the parathyroid hormone receptor (10), and the CHIP-based protein quality control machinery (11).

Previously, we employed small-angle X-ray and neutron scattering, SAXS and SANS, respectively, to investigate the global conformational switch triggered in full-length NHERF1 by association with ezFERM (7). The study revealed a mesoscopic movement of the PDZ domains upon switching between the autoinhibited “closed” structure ( $R_g = 41$  Å,  $D_{max} = 140$  Å) and the target-accessible “open” conformation ( $R_g = 51$  Å,  $D_{max} = 175$  Å) (7, 12, 13). However, the earlier results lacked the resolution required to correlate the ensemble-dependent dynamics of the modular structure with the extent of order in

This work was supported by National Science Foundation Grant MCB-1817684 (to Z. B.) and National Institutes of Health Grant 1R01DK105811 (to P. A. F.). The authors declare that they have no conflicts of interest with the contents of this article. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

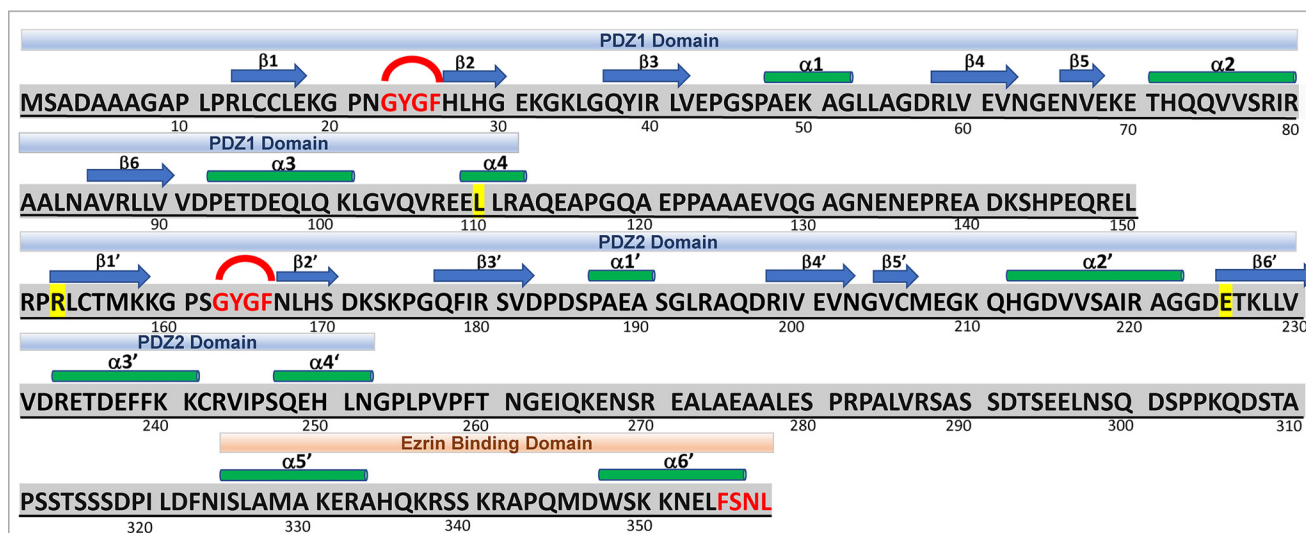
This article contains Figs. S1–S7 and Tables S1 and S2.

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<sup>4</sup> The abbreviations used are: EBD, ezrin-binding domain; CB loop, carboxylate-binding loop; EB, ezrin binding; FERM, 4.1-ezrin/radixin/moesin; CT, C-terminal; NHERF1, Na<sup>+</sup>/H<sup>+</sup> exchange regulatory cofactor 1; SAXS, small-angle X-ray scattering; SANS, small-angle neutron scattering; SPR, surface plasmon resonance; TROSY, transverse relaxation optimized spectroscopy; PTH, parathyroid hormone; MC, Monte Carlo; TAD, torsion angle dynamics; RCI, random coil index; CSD, chemical shift difference.



**Figure 1.** Amino acid sequence (residues 1–358) of full-length human NHERF1 protein annotated with the secondary structure in the extended PDZ1 (residues 11–112) and PDZ2 (residues 150–260) domains and the C-terminal ezrin-binding domain (residues 329–358). The color-coded secondary structure elements highlight the  $\alpha$ -helices (green),  $\beta$ -strands (blue), COO<sup>−</sup>-binding loop (red), and the C-terminal type 1 PDZ-binding motif (red). The two longer fragments of NHERF1 discussed in the text include PDZ2CT domains (residues 150–358) and CT domain (residues 260–358), respectively.

the ultra-long spacers. The interdomain linkers constitute nearly 30% of the NHERF1 sequence and are remarkably well-conserved (>90%) across different species (10) but possess low structural propensity (Fig. 1).

Traditional NMR has been highly successful in characterizing flexible scaffolding proteins with ordered domains randomized by unstructured linkers (14, 15). The isolated PDZ1 and PDZ2 domains from NHERF1 possess novel helical extensions that stabilize the structure and allosterically modulate peptide affinity (16, 17). Here, multidimensional solution NMR combined with SANS experiments were used to study the complete structural and dynamic characteristics of the intact protein. Our results reveal full-length NHERF1 cannot be represented by a single conformation. Instead, it is a dynamic ensemble of variable PDZ domain configurations linked by highly-flexible regions.

Naturally occurring mutations in the human *NHERF1* gene have been implicated in impaired renal phosphate transport with increased risk of nephrolithiasis, bone demineralization (18), and cancer (19). Gene sequencing of afflicted patients identified at least three loss-of-function mutations (L110V, R153Q, and E225K) in NHERF1 (18). In the isolated PDZ1 (L110V) and PDZ2 (R153Q) domains, we have shown the mutations modulate the target affinity by lowering the thermodynamic stability of the protein (16, 17). In this study, we investigated the mutations in the context of full-length NHERF1 to elucidate their simultaneous impact on the intramolecular autoinhibition of the PDZ2 domain and target affinity. Using NMR, we mapped the local perturbation in each PDZ domain and, combined with ensemble analysis of SANS data, demonstrated the effect of the mutations on the global structure and function.

Ezrin is indispensable for releasing autoinhibition, but phosphorylation plays an equally critical role in modulating the cellular activity of NHERF1 through its ability to oligomerize (20) and associate with various binding partners (10, 21, 22). In

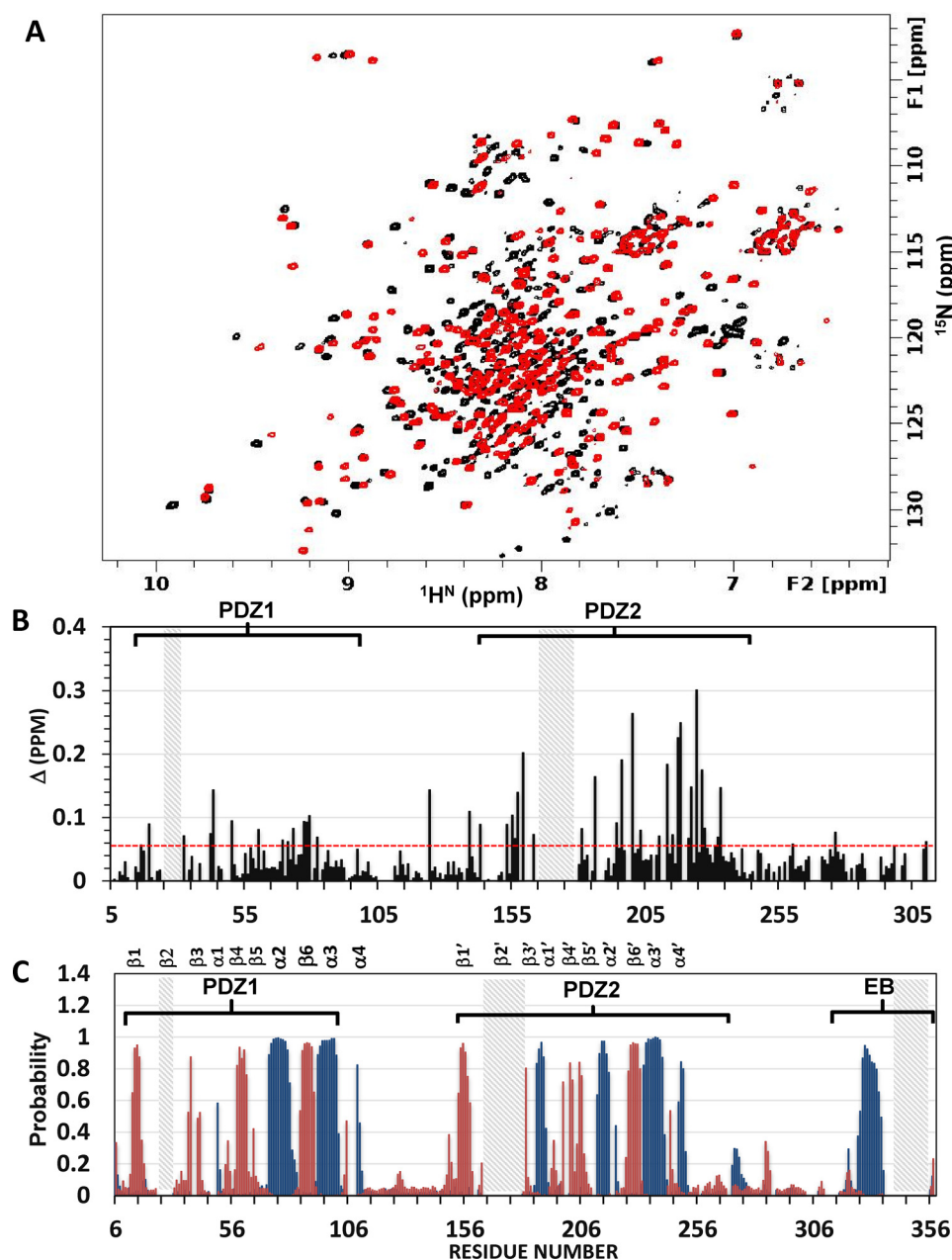
humans, NHERF1 is reversibly phosphorylated at Ser-290 by a multiprotein kinase cascade involving GRK6A, which in turn regulates PTH-sensitive, NPT2A (sodium-dependent phosphate transport protein 2A)-mediated phosphate uptake (23, 24). Although GRK6A has much higher affinity for the N-terminal PDZ1 domain, it is through interactions with the partially masked PDZ2 domain that NHERF1 is phosphorylated in the C-terminal hinge region (20). We have further evaluated the extent to which the structural differences affect disease mutant interactions with ezrin and G protein-coupled receptor kinase A (GRK6A). We used SPR to measure the binding affinity and the kinetics of the association of each of the three mutants with ezFERM and a C-terminal peptide from GRK6A. Collectively, the results provide a structural and dynamic framework for understanding the internal mechanics of WT and NHERF1 variants in key functional states.

## Results

### NMR structural analysis of full-length NHERF1

Using structural information provided by NMR chemical shift analysis, we confirmed the boundaries of the structured domains, the nature of interdomain contacts, and the structural propensities of the linker regions in full-length NHERF1. The initial characterization focused on the autoinhibited and open state triggered by association of NHERF1(wt) with the FERM domain of ezrin (ezFERM). Despite the relatively high-molecular mass of NHERF1 (~39 kDa) and its complex with ezFERM (~79 kDa), the high quality of the 2D <sup>15</sup>N-TROSY spectra (Fig. 2A) enabled us to successfully assign ~76% of the backbone resonances of the 358-residue construct, using <sup>2</sup>H/<sup>13</sup>C/<sup>15</sup>N-labeled samples and TROSY-based triple resonance experiments.

In NHERF1(wt), the “on-off” association of PDZ2 with the C-terminal residues results in extensive broadening of backbone amide resonances in both PDZ2 ( $\alpha$ 2 and  $\beta$ 2– $\beta$ 3) and EB (residues 337–358) domains due to coalescence of resonances



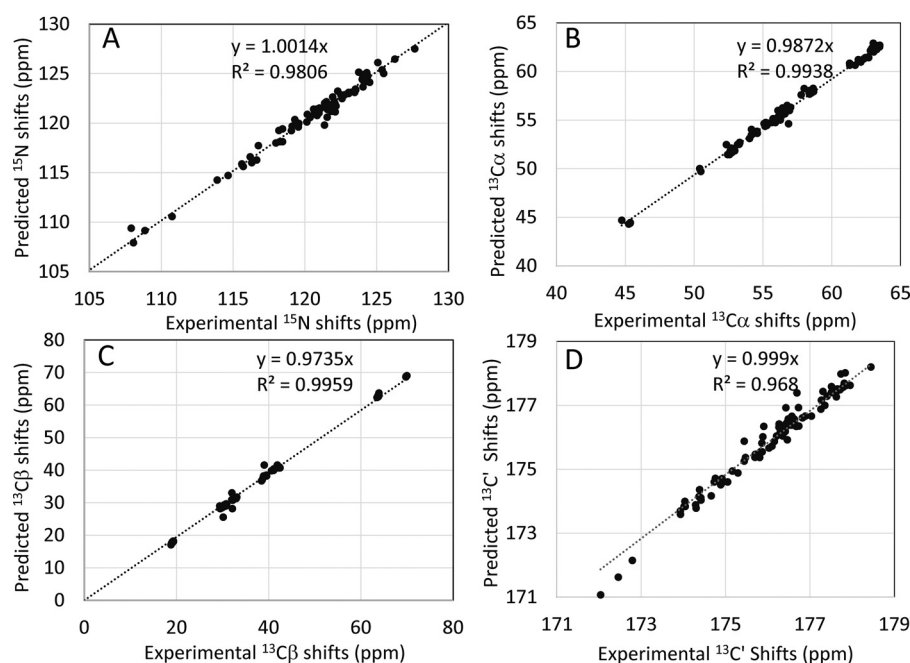
**Figure 2.** A, overlay of 2D  $^{15}\text{N}$ -TROSY spectra of full-length  $^2\text{H}/^{13}\text{C}/^{15}\text{N}$ -labeled NHERF1 bound to unlabeled ezrin (black) and the free-state (red). B, bar plot of weighted amide proton ( $^1\text{H}^{\text{N}}$ ) and nitrogen ( $^{15}\text{N}$ ) chemical shift difference between the bound and free protein versus residue number. The red line shows the mean  $\pm$  S.D. for CSD (0.062 ppm). C, secondary structure prediction of NHERF1 based on chemical shift index calculated in TALOS+ (25). Residues in  $\beta$ -sheet (red) and  $\alpha$ -helices (blue) are indicated by different colors. The gray box indicates the exchanged broadened residues in the peptide-binding site at the  $\beta$ 2-strand from PDZ1 and PDZ2 domain, respectively, and the C-terminal EB domain.

on intermediate time scales. In the ezFERM-bound state, the conformational exchange in the PDZ2 domain is quenched, and some of the largest chemical shift changes mapped to residues in the ligand-binding site (Fig. 2B). Unexpectedly, we also observed line-broadening in the  $\beta$ 2 strand (residues 25–31) in the PDZ1 ligand-binding site. Like the PDZ2 domain, we recovered the intensity of the lost signals in PDZ1 upon ezFERM binding. Collectively, these changes are consistent with transient autoinhibitory interactions involving the PDZ2 domain and to a lesser extent the PDZ1 domain.

The secondary structure predictions obtained from the analysis of the backbone chemical shifts ( $\text{C}\alpha$ ,  $\text{C}\beta$ ,  $\text{C}'$ ,  $\text{N}$ , and  $\text{H}^{\text{N}}$ ) of

NHERF1 in the autoinhibited state using TALOS+ (25) are displayed in Fig. 2C. The secondary structure profile is identical to the  $\alpha\beta$  fold of the isolated PDZ domains (16, 17), which is preserved upon ezFERM-binding in the open state (Fig. S1). The random coil index (RCI) from TALOS+ analysis indicates that the linker regions, connecting PDZ1–PDZ2 domains (residues 112–146) and between PDZ2–EB domains (residues 252–324), have disordered backbones (Fig. S1). To confirm the RCI predictions, we compared the experimental chemical shifts against the random coil values incorporated in the POTENCI database used for identifying intrinsically-disordered proteins (26). The excellent agreement between the predicted random





**Figure 3. Correlation plots of intrinsically disordered protein chemical shifts predicted by POTENCI (26) and the corresponding experimental shifts for residues in the linker between PDZ1-PDZ2 domain (residues 113–146) and the C-terminal region (residues 252–323). A, amide nitrogen ( $^{15}\text{N}$ ); B,  $\alpha$ -carbon ( $^{13}\text{C}_\alpha$ ); C,  $\beta$ -carbon ( $^{13}\text{C}_\beta$ ); and D, carbonyl carbon ( $^{13}\text{C}'$ ) shifts, respectively.**

coil shifts of the linker residues and the corresponding experimental values confirmed that these regions are intrinsically disordered and completely flexible (Fig. 3). The unusually long (residues 262–324) and disordered C-terminal tail lends credence to the possibility that the EBD could interact with both PDZ domains, albeit with different affinities.

### Dynamic intramolecular autoregulation in NHERF1

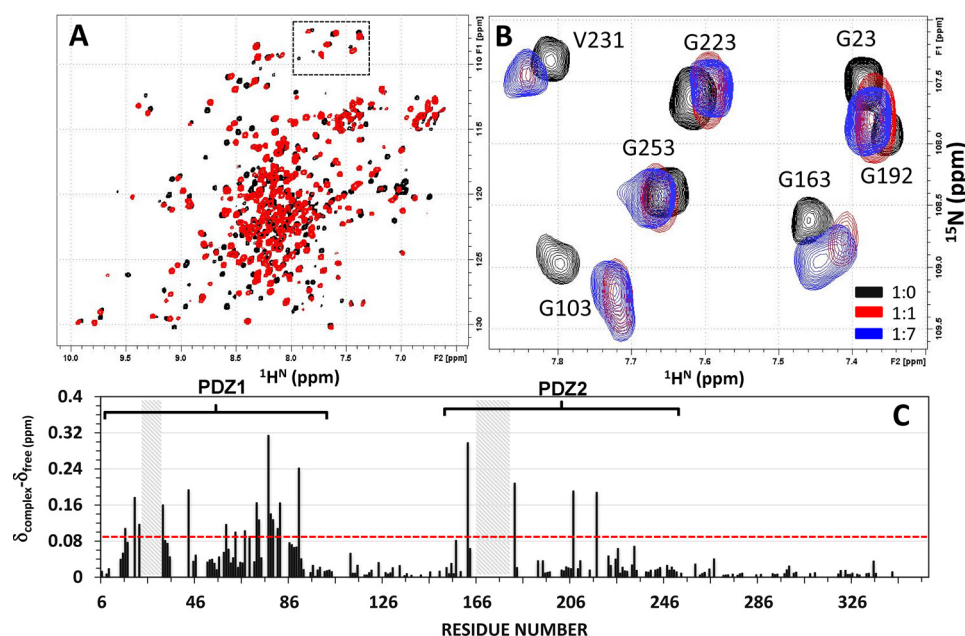
In the isolated PDZ1 domain, the residues in the ligand-binding site can be observed in the 2D  $^{15}\text{N}$  HSQC spectrum (17). Hence, the logical origin of the observed loss-of-signal in PDZ1 from full-length NHERF1 is either a *weak* intra- or intermolecular interaction with an internal binding motif or the C-terminal sequence (–FSNL). Because we recovered the lost signal intensity upon the EB domain binding to ezFERM, we can disqualify purported interactions involving an internal segment in the linker regions. Instead, the most probable cause is a weak intramolecular interaction with the C-terminal type 1 motif (–SXL), which is effectively independent of the protein concentration ( $>40\ \mu\text{M}$ ). The C-terminal motif without a positively-charged side chain at the penultimate position ( $X = \text{Arg}^+$ ) is not optimized for high-affinity binding to the PDZ1 domain (17, 27). Nevertheless, we expect the weak millimolar affinity could increase by the local concentration effect.

Thus, in solution, monomeric NHERF1 can adopt at least two inactive closed conformations and a fully open state when bound to ezFERM. NHERF1 has been shown to dimerize at concentrations greater than  $140\ \mu\text{M}$  that are physiologically ( $<10\ \mu\text{M}$ ) irrelevant (13, 22, 28). To estimate the contribution of the different structural states of NHERF1 to any experimental measurement, we applied a quantitative relationship between intra- and intermolecular binding constants developed originally for polymer chains of variable length in systems of similar complexity (29–31), as shown in Equation 1,

$$K_i' = C_{\text{eff}} \times K_a^i, f_{\text{bound}} = \frac{K_i'}{(1 + \sum K_i')}, f_{\text{free}} = \frac{1}{(1 + \sum K_i')} \quad (\text{Eq. 1})$$

where  $K_a^i$  is the  $i$ th bimolecular association constant;  $C_{\text{eff}}$  is the local concentration calculated from the end-to-end distance probability distribution (Fig. S2); and  $K_i'$  is the effective association constant. Based on the bimolecular affinity ( $K_d \sim 93\ \mu\text{M}$ ) between the isolated PDZ2 domain and a C-terminal peptide (32), we expect at least  $\sim 77\%$  monomer at the protein concentrations ( $\sim 140\ \mu\text{M}$ ) required for the NMR studies. Using the worm-chain model, the probability of the end-to-end distance of the 91-residue linker between PDZ2 and EB domain maximizes at  $\sim 37\ \text{\AA}$ . In this distance range, free NHERF1 is a mixed population of closed (76%) and open (24%) conformations as predicted by the intramolecular association constant  $K'$  and effective local concentration,  $C_{\text{eff}}$  (Equation 1 and Fig. S2). Assuming a slightly longer end-to-end distance of the linker ( $\sim 60\ \text{\AA}$ ) between the PDZ1-EB domains based on model structures, the effective local concentration is lower, resulting in a much smaller fraction of the closed PDZ1 conformer ( $<5\%$ ).

The significant population of the open conformer of NHERF1 ( $\sim 24\%$ ) has important biological ramifications for access to the target binding site at both PDZ domains when ezrin is dormant. Ezrin in the inactive state is autoinhibited, masking the NHERF1-binding site that is only exposed by a conformational change triggered by phosphorylation and phosphatidylinositol 4,5-bisphosphate binding (33, 34). To illustrate the effect of the interconverting NHERF1 populations on binding site access, we used a 20-residue C-terminal peptide derived from GRK6A (Fig. 4) to simultaneously monitor the chemical shift perturbation in each PDZ domain at increasing peptide concentrations in the absence of ezFERM. The GRK6A peptide



**Figure 4.** A, overlay of 2D  $^{15}\text{N}$ -TROSY spectra of NHERF1 in the free (black) and GRK6A peptide-bound (1:7 ratio) state (red) at 900 MHz at 15 °C. B, boxed inset from 2D  $^{15}\text{N}$ -TROSY overlay of three different titration points with NHERF1 and GRK6A peptide ratios indicated in the legend. The selected region shows the effect of peptide binding on the N-terminal Gly-23/Gly-163 from the CB loop (Fig. 1), which is not exchange-broadened in the apo-state of the protein. C, weighted average of amide CSD of NHERF1 bound to GRK6A peptide (1:7 ratio) peptide at 15 °C. The dashed horizontal line at 0.8 ppm (mean  $\pm$  S.D.) indicates the threshold for significant chemical shift perturbation.

has much higher binding affinity for the isolated PDZ1 compared with the PDZ2 domain from NHERF1 (23). Accordingly, the N-terminal PDZ1 domain was readily saturated at a 1:1 protein-to-peptide ratio. In the PDZ2 domain, binding was inhibited but not abrogated, supporting limited access permitted by the dynamic C-terminal interactions (Fig. 4B). Therefore, an important outcome of partially open states is different ligands have some access to both PDZ domains instead of relying on the complete release of autoinhibition by ezFERM binding. The dynamic mechanism offers a plausible explanation for why the PDZ2 domain is essential for phosphorylating Ser-290 in the C-terminal domain of WT NHERF1 (23, 24).

#### Effects of disease mutations on local structure of NHERF1

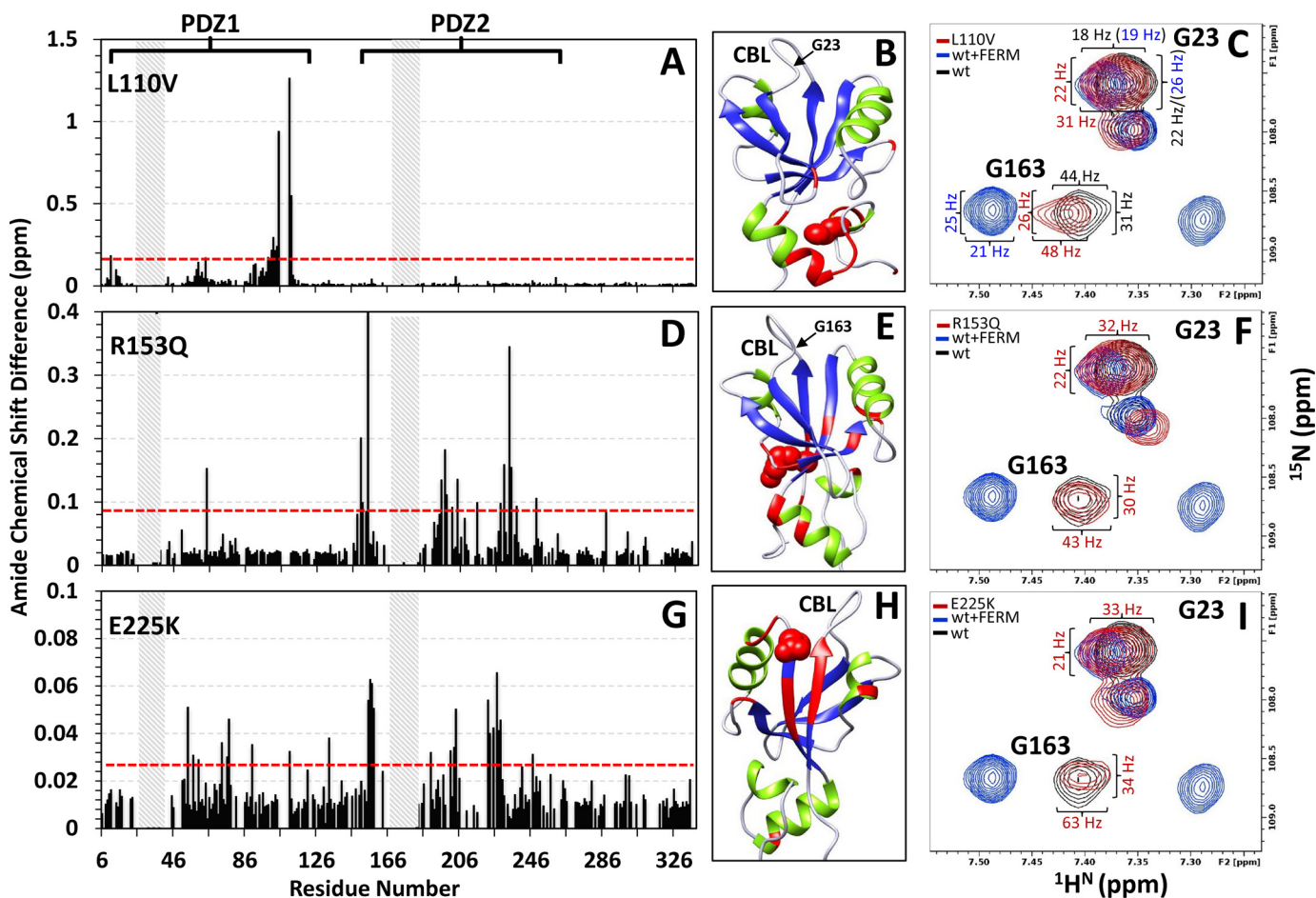
To map the structural differences between NHERF1(wt) and the disease-associated variants (L110V, R153Q, and E225K), we obtained sequence-specific resonance assignments of each protein. The corresponding amide ( $^1\text{H}/^{15}\text{N}$ ) chemical shift differences (CSD) compared with the WT protein are plotted in Fig. 5. In the histogram plots, we observe distinct clusters of residues with significant CSD in the PDZ1 (Fig. 5, A and B) and PDZ2 domains (Fig. 5, D, E, G, and H) that correlate directly with the location of the mutations in the sequence. The structural integrity of the PDZ domains was confirmed by analyzing the backbone resonances in TALOS+, which did not disclose any unexpected loss of secondary structure (Fig. S3). The canonical fold, consisting of a six-stranded  $\beta$ -sheet and four  $\alpha$ -helices, is preserved in all three mutants (Fig. S3).

In the L110V mutant, the structural perturbation is localized mainly in the C-terminal helical extension of the PDZ1 domain and the N terminus of the linker (Fig. 5, A and B). Based on the PDZ2 domain structure (16, 35), R153Q mutation is expected to disrupt favorable electrostatic interactions between the side

chain of Arg-153  $\text{N}^{\text{H}}+$  ( $\beta$ 1) and the negatively charged  $\text{COO}^-$  groups from Asp-197 ( $\beta$ 4) and Asp-232 ( $\beta$ 6). As a consequence, any rearrangement in the side-chain packing results in chemical shift changes across strands of the  $\beta$ -sheet structure (Fig. 5E). When compared with the WT protein, the E225K mutation results in very small amide chemical shift changes along the backbone ( $<0.06$  ppm) suggesting limited structural perturbation (Fig. 5G). However, the location of the charge reversal mutation near the CB loop (facing out) is likely to have a direct effect on the CB loop interactions with the carboxylate group (Fig. 5H).

Based on the extent of structural changes observed within the PDZ domains, we were interested in elucidating how these effects propagate to the binding site and mediate intramolecular interactions. Specifically, the two mutations in the PDZ2 domain are likely to influence the conformational switch between the closed and open states. The most suitable NMR probes to follow the changes in the intramolecular switch would be the chemical shifts of residues in the EB domain or those in the carboxylate-binding loop ( $^{-163}\text{GYGF}^{166}$ ). Because neither mutation had a detectable effect on the intermediate exchange phenomenon that bleaches out most of the NMR resonances from the residues in the binding site, we focused instead on Gly-23 from PDZ1 and Gly-163 from the PDZ2 domain (Fig. 1). The two Gly residues represent the sole NMR reporters within the binding loop that offers critical structural and dynamic information on interactions with ligands.

The effect of the binding loop configurations on the two NMR probes (Gly-23/Gly-163) is shown in the overlay of the WT (close/open), ezFERM bound (open), and the mutant NHERF1 proteins (Fig. 5, C, F, and I). The release of WT PDZ2 autoinhibition triggered by ezFERM binding is clearly captured



**Figure 5. Chemical shift perturbation analysis of NHERF1 mutants compared with the WT protein.** The histograms display the weighted average of amide ( $^1\text{H}/^{15}\text{N}$ ) chemical shift difference as a function of residue number from data acquired at 900 MHz and 15 °C. The panels display the data for three different mutants of full-length NHERF1. A, L110V (0.16 ppm); D, R153Q (0.087 ppm); and G, E225K (0.026 ppm). The red dashed line indicates the mean  $\pm$  S.D. with values greater than the threshold mapped on the NMR structure of the isolated PDZ1 (2MOT) (B), and PDZ2 (2KJD) domain (E–H) structures. C, F, and I, overlay of 2D  $^{15}\text{N}$  TROSY spectrum of ezFERM-bound NHERF1(wt) (blue), free NHERF1(wt) (black), and variants (red), which are indicated in the panel legends, to show the changes in Gly-23/Gly-163 from CB loop in the two PDZ domains. The corresponding line width (Hz) at half-height of the Gly cross-peaks are similarly color-coded along F2 ( $^1\text{H}^{\text{N}}$ ) and F1 ( $^{15}\text{N}$ ) dimensions, respectively.

by a shifted Gly-163 amide cross-peak (blue contours) in the NHERF1(wt) 2D  $^{15}\text{N}$ -TROSY spectrum. In contrast, Gly-23 in the PDZ1 domain remains unaffected by the C-terminal conformational changes. Compared with the WT protein (black contours), none of the mutations display a significant chemical shift change at Gly-163 (red contours), which would be consistent with the fully open state analogous to the ezFERM-bound protein. Instead, we observed differential  $^1\text{H}^{\text{N}}$  line-broadening that reflects a dynamic shift in the exchange phenomenon in the CB loop in both the PDZ domains. The elevated  $^1\text{H}^{\text{N}}$  linewidth of Gly-163 in E225K ( $\sim 63$  Hz) compared with L110V/R153Q mutants ( $\sim 45.5 \pm 2.5$  Hz) and the WT protein ( $\sim 44$  Hz) suggests this mutation near the CB loop witnesses an unmediated effect of the C-terminal interactions (Fig. 5H). In the fully open ezFERM-bound state of NHERF1(wt), the much sharper  $^1\text{H}^{\text{N}}$  line widths ( $\sim 21$  Hz) indicate the lack of conformational exchange in the unbound CB loop from the PDZ2 domain. The overall trend at Gly-23 suggests increased  $^1\text{H}^{\text{N}}$  line-broadening in the mutants ( $\sim 32 \pm 1$  Hz) compared with the autoinhibited ( $\sim 22$  Hz) and open state ( $\sim 26$  Hz). It is very likely that the altered dynamics at Gly-23 in the PDZ1 domain indicate a subtle shift in the population between the different

autoinhibited configurations in the variants. It is reasonable to assume that the exchange rate itself is unchanged because the mutations are structurally remote and cannot directly mediate the interactions at the PDZ1 CB loop. In summary, the NMR results evince the mutations fail to deactivate the conformational switch completely, and the CB loop in the PDZ2 domain is interconverting between a variable fraction of C-terminal “bound” and “free” states, respectively (16, 32).

To further explore ligand access to both PDZ domains in the mutants, we also compared the CB loop Gly-23/Gly-163 chemical shifts in the presence of a peptide from GRK6A (Fig. S4). As evinced by the conspicuous chemical shift changes in Gly-23, all three mutants bind the peptide in the PDZ1 domain like the WT protein at 1:1 protein-to-peptide ratio (Fig. 4B). In the PDZ2 domain, the broad Gly-163 peak suggests it is not saturated even at a 1:4 ratio (Fig. S4, D and F). Thus, we have established that the mutations have a subdued impact on the structural mechanism of intramolecular autoinhibition. Because of adverse NMR line shapes, any shift in the open and closed populations could not be reliably quantified. Therefore, we decided to pursue a different approach using SANS data to study the



**Table 1**

Summary of ensemble averaged structural and dynamic parameters from SANS data analysis of NHERF1 in GAJOE

|                         | $C$   | $I(0)$ (1/cm)   | $R_g$ | $D_{\max}$ | $R_{\text{flex, selected}}$ | $R_\sigma$ | $\chi^2$ |
|-------------------------|-------|-----------------|-------|------------|-----------------------------|------------|----------|
|                         | mg/ml |                 | Å     | Å          | %                           | %          |          |
| NHERF1(WT) <sup>a</sup> |       |                 | 40.4  | 135        |                             |            |          |
| NHERF1(WT) <sup>b</sup> | 1.0   | 0.1565 ± 0.0040 | 39.2  | 134.4      | 83                          | 0.9        | 0.68     |
| L110V <sup>b</sup>      | 0.95  | 0.1437 ± 0.0043 | 39.7  | 134.8      | 78                          | 0.76       | 0.75     |
| R153Q <sup>b</sup>      | 1.13  | 0.1682 ± 0.0044 | 39.5  | 124.4      | 69                          | 0.57       | 0.73     |
| E225K <sup>b</sup>      | 1.11  | 0.1674 ± 0.0041 | 35.5  | 121.2      | 72                          | 0.65       | 0.76     |

<sup>a</sup>  $R_g/D_{\max}$  values are from SEC-SAXS data reported previously (40).<sup>b</sup>  $R_g/D_{\max}$  and flexibility parameters calculated from optimized ensemble obtained by fitting SANS data in GAJOE. Starting ensemble composed of random structures yields  $R_{\text{flex}} = 85.5\%$ .

conformational properties of WT and mutant NHERF1 protein as a dynamic ensemble in solution.

### Global conformational changes in WT and mutant NHERF1 from SANS

The SANS experiments on the WT and variants of <sup>d</sup>NHERF1 (deuterated) were performed at low protein concentrations (~25 μM), where it is predominantly monomeric (Table 1 and Fig. 6, A and B) (13). The corresponding  $P(r)$  distribution functions are alike reinforcing the structural similarities between the WT protein and the mutants (Fig. 6C).

To tease out the conformational differences between the NHERF1 variants, we performed an ensemble analysis of the SANS data using the program EOM (36, 37) by generating an ensemble pool consisting of the major closed and open conformations. Several programs are available for fitting solution scattering data to large ensembles of multidomain proteins (36, 38, 39). However, an inherent limitation of the existing software is the inability to sample the configurational space of internal loops with restrained termini. Therefore, to sample the closed conformation of NHERF1, we used rigid-body Monte Carlo (MC) simulation of the PDZ domain motion by allowing the linkers to break during the random spatial search in XPLOR-NIH (14). The linkers were rejoined, and the covalent geometry was fixed before performing simulated annealing in torsion angle space (TAD). A more detailed description of the protocol used to generate the ensemble pool of the closed and open conformations of NHERF1 is provided under “Experimental procedures.” As seen in Fig. 6, D and E, the width of the starting ensemble occupies a significant volume of the conformational space using a combination of MC and TAD in Xplor-NIH. The results of the ensemble-averaged analysis of the SANS data in the program GAJOE from EOM (36, 37) are summarized in Fig. 6 and Fig. S5. The quality of the ensemble-averaged fit of the calculated scattering intensities to the experimental SANS data ( $\chi^2 < 0.8$ ) was quite good (Table 1).

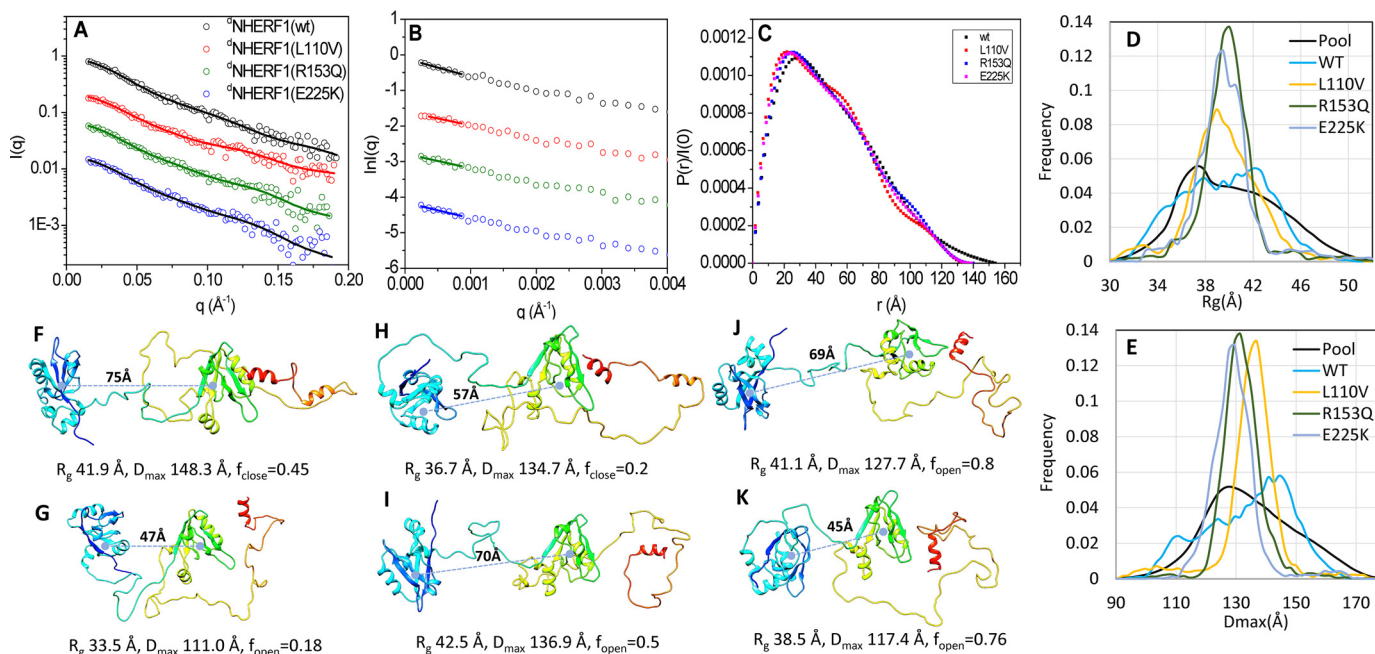
The overall molecular size distribution profile of the WT protein that fits the SANS data are consistent with the SEC-SAXS data (Table 1) of monomeric NHERF1 reported in our previous studies (40). The close agreement between the  $R_g$  values confirms deuteration does not affect the conformation of NHERF1. From the overlays in Fig. 6, D and E, the difference in the ensemble properties of the three mutants compared with the WT protein is quite significant. In Fig. 6, F–K, representative structures from the “optimized ensemble” from GAJOE (36) are displayed along with dimensions and contributions from pool fractions.  $R_{\text{flex}}$  is the metric used to describe the flex-

ibility of the selected ( $R_{\text{flex, selected}}$ ) ensemble compared with that of the random starting pool. It can vary from 100% (flexible) to a perfectly rigid system (0%). Likewise, the ratio of the variance of the selected/starting ensemble distribution,  $R_\sigma < 1$ , indicates flexibility. As summarized in Table 1, the relatively high  $R_{\text{flex, selected}} = 83\%$  and  $R_\sigma = 0.90$  values reflect the broad distribution of a highly-flexible system sampling simultaneous partially open and closed structures in solution. There is a significant fluctuation in the distance between the two PDZ domains, which is proportional to the presence of compact ( $R_g \sim 47$  Å) and more extended chains ( $R_g \sim 75$  Å). Because of the length of the ultra-long and flexible linkers, the pool fraction was uncorrelated with the  $D_{\max}$  values or state of the intramolecular autoinhibition (Fig. 6, F–K). Likewise, the ensemble populations bear limited correlation with the theoretically predicted ratio of open and closed states. Thus, the apparent randomness of the rotational and translational motion of the linked PDZ domains suggests purely Brownian dynamics is at play in the absence of persistent interactions to restrict the domain motion (8, 14, 33). This conclusion is well-supported by the NMR data where the two PDZ domains are structurally independent and flexibly tethered by intrinsically disordered linkers.

By NMR, we demonstrated the overall  $\beta$ -sheet fold in the mutated PDZ domains is preserved, and thus we can assume the backbone trace is also similar to the WT protein. Because our goal was to evaluate general trends in the  $R_g$  and  $D_{\max}$  profiles for the mutants, we fitted the experimental SANS data using the same random ensemble pool as NHERF1(wt) in GAJOE. In the overlay of the  $R_g$  and  $D_{\max}$  distribution profiles, the L110V mutation in the PDZ1 domain clearly behaves differently from the other two mutations located in the PDZ2 domain (Fig. 6 and Table 1). The higher  $D_{\max}$  values in L110V mutant can be rationalized by structural changes at the junction between the extended PDZ1 structure and the disordered linker (Fig. 5A). The mutation in the dynamic C-terminal  $3_{10}$ -helix (17) could modulate the elasticity of the linker changing the effective distance between the PDZ domains.

Compared with WT protein, the mutated PDZ2 domains (R153Q/E225K) favor narrow matching  $R_g$  and  $D_{\max}$  distribution profiles. This trend is also reflected in the reduced  $R_{\text{flex}}$  (~71%) and  $R_\sigma$  (~0.61) values (Table 1). The major fraction (~80%) of the structures in the unbiased ensemble selected by GAJOE to fit the experimental data appears to favor randomly oriented C-terminal tails. In the E225K mutant, the average separation between the PDZ domains in the dominant conformer shrinks dramatically (~45 Å) from NHERF1(wt)

## Structure of wildtype NHERF1 and disease variants



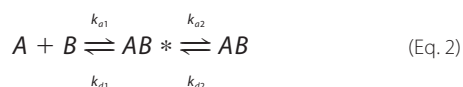
**Figure 6. Ensemble analysis of SANS data of WT and mutant NHERF1 protein structures using GAJOE/EOM.** A,  $I(q)$  versus  $q$  experimental data. The scale of scattering intensity is arbitrary to display data for all mutants. B, Guinier plot calculated from  $I(q)$  versus  $q$  experimental data. C,  $P(r)$  functions that are normalized by forward scattering intensity  $I(0)$  of the different mutants. Overlay of  $R_g$  (D), and  $D_{\max}$  (E) frequency distribution of starting ensemble (black) and best-fitted ensemble pools of different NHERF1 proteins. The displayed structures represent the major fractions from the optimized ensemble selected by GAJOE. F and G, NHERF1(wt); H and I, L110V; J, R153Q; K, E225K. The legend in each panel includes  $R_g$ ,  $D_{\max}$ , distance between the center-of-mass of the PDZ1 and PDZ2 domains, fraction of the conformer selected from the two starting pools.

(~75 Å) (Fig. 6, F and K). There is some evidence to suggest the unstructured C-terminal tail has a propensity to collapse when released from interactions with the PDZ2 domain (40). Thus, it is possible the compact ensemble reflects the population is shifting either in favor of partially open states with collapsed chains or alternative weak interactions at the PDZ1 domain as evidenced by the NMR analysis.

### Binding of ezFERM to NHERF1 mutants

To understand the impact of the disease mutations on the biochemical functions of full-length NHERF1, we have used SPR to analyze the binding affinity and kinetics with ezFERM and the 22-residue peptide from the C-terminal tail of GRK6A that possesses a type 1 PDZ-binding motif (23).

In Fig. 7A, the equilibrium binding curves of NHERF1 or mutants to ezFERM can best be fit by a 1:1 binding model with low  $\chi^2$  values (<5.0). Overall, NHERF1(wt) and the disease mutants have comparable equilibrium dissociation constants (Table S1) in the 13–43 nM range, with some variation among the mutants. We have shown previously that the SPR sensorgrams with ezrin (Fig. S6) are better fit by a two-step kinetic model (40) involving a fast and slow process (Equation 2), instead of a single 1:1 state or the bivalent binding model.



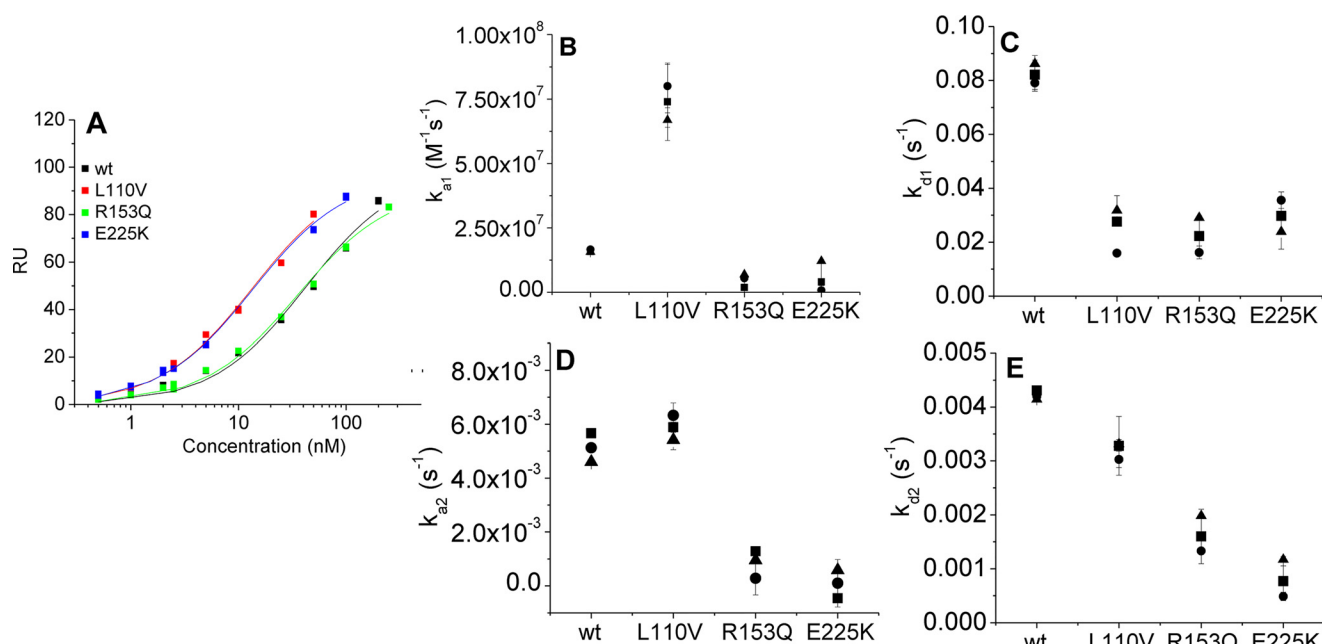
In Equation 2, A refers to ezFERM and B to NHERF1 or a mutant;  $k_{a1}/k_{d1}$  refer to the association/dissociation rate of the

fast binding event, and  $k_{a2}/k_{d2}$  refer to the corresponding rate constants for the slow-binding event.

In NHERF1(wt), the fast-binding mode has an association rate constant,  $k_{a1} = 1.58 \times 10^7 \text{ M}^{-1} \text{ s}^{-1}$ , similar to values reported earlier (42). In the L110V mutant, the association rate  $k_{a1}$  is higher than WT and other mutants by an order of magnitude (Fig. 7B). The fast association is correlated with the increased separation between the PDZ and EB domains (Fig. 6E), thereby making the EB domain associated with the PDZ2 domain more accessible to ezFERM. The off-rate  $k_{d1}$  shows small variation but is not greater than an order of magnitude across the different proteins.

The slower association rate  $k_{a2}$  is about 2–3 orders of magnitude smaller than  $k_{a1}$  for the WT protein with a monotonic decrease in the mutants (Fig. 7C). We attribute the slower kinetic process to conformational changes in the C-terminal tail of NHERF1 upon docking with ezFERM accompanied by a weak-binding interaction (16, 40, 43). This two-step kinetic model is well-supported by the published X-ray structure of the 38-residue EB domain (amino acids 321–358) from NHERF1 bound to the moesin FERM domain (43). The X-ray structure revealed a high-affinity C-terminal  $\alpha$ -helix (residues 348–358) bound to the F3 subdomain of FERM linked to a second N-terminal helix (residues 325–334) that interacts weakly with the F2 subdomain of FERM (44). The monotonic decrease in the  $k_{a2}$  values in the mutants could very well be due to increased disorder in the EB domain because of a shift in the population between the closed and open states (16).

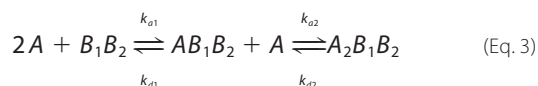




**Figure 7. Affinity and kinetics of NHERF1 (wt) and mutants binding to ezFERM.** A, equilibrium curves of NHERF1 (wt) and mutants binding to ezFERM fitted with a 1:1 binding model, see Table S1 for  $K_d$  values. Y-axis values reported in SPR resonance units (RU). Displayed univariate scatter plots obtained from three repeat SPR measurements: B and D, two-state kinetic association rate constants ( $k_{a1}$  and  $k_{a2}$ ); C and E, dissociation rate constants ( $k_{d1}$  and  $k_{d2}$ ). Different symbols with Y-error bars have been used for each measurement.

### Binding of GRK6A peptide to NHERF1 mutants

The equilibrium-binding curves of NHERF1 (wt) or mutants to GRK6A peptide were best fit with a bivalent model. This model also makes the most physical sense, given the tandem PDZ-binding sites. The bivalent kinetic model that is used to fit SPR sensorgrams is shown in Equation 3,



where A is the GRK6A peptide;  $B_1$  and  $B_2$  refer to PDZ1 and PDZ2 domains in NHERF1;  $k_{a1}/k_{a2}$  are bivalent association rate constants; and  $k_{d1}/k_{d2}$  are the bivalent dissociation rate constants.

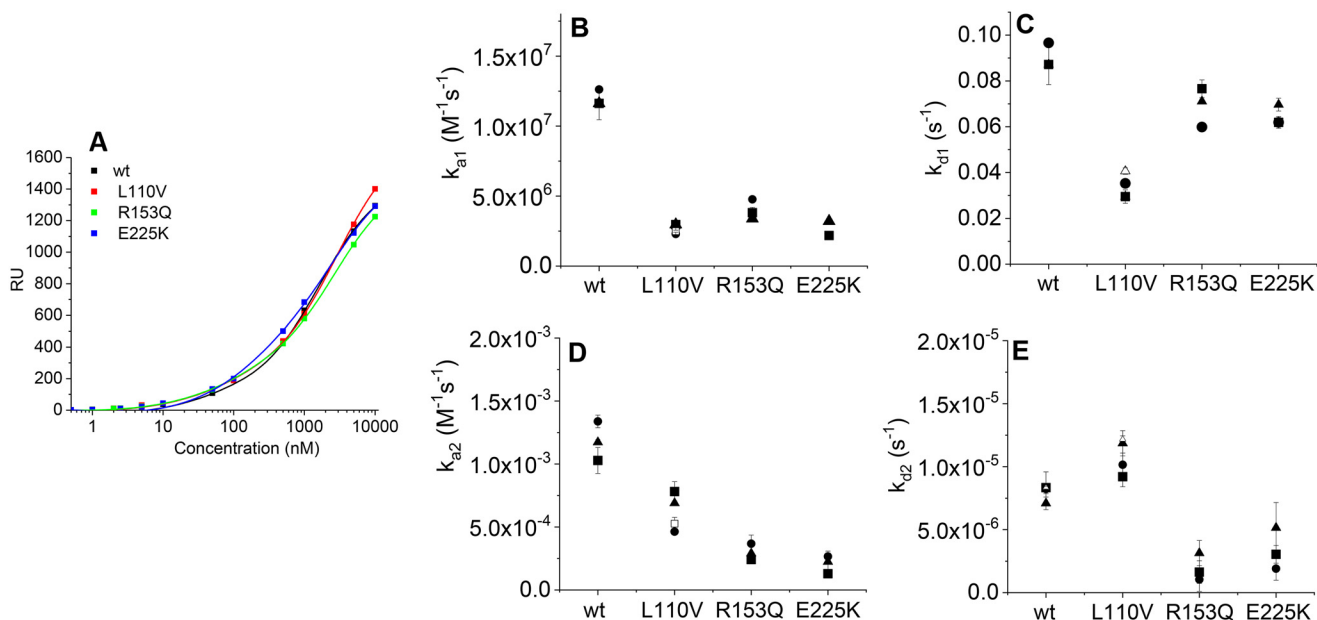
In NHERF1 (wt) we obtain effective dissociation constants  $K_{d1} \sim 160$  nM and  $K_{d2} \sim 4000$  nM by fitting the data with the bivalent binding model. As shown by NMR, the difference in affinity reflects the competition of the GRK6A peptide to displace the C-terminal residues from the PDZ2-binding site. The equilibrium  $K_{d1}$  values show very little variation among the mutants (Fig. 8A and Table S2), with L110V and R153Q mutants possessing slightly higher affinity than E225K and NHERF1 (wt). The  $K_{d2}$  values are nearly constant. Overall, the equilibrium dissociation constants are consistent with what we expect from the peptide sequence analysis. The intrinsic affinity of the GRK6A peptide for the WT PDZ1 domain should be higher than the PDZ2 domain (-PTRL) because of the positively charged Arg<sup>+</sup> located at the penultimate site (-1) (15).

The kinetic measurements confirmed both NHERF1 (wt) PDZ domains bind the GRK6A peptide but with significantly different association rate constants. The fast association ( $k_{a1} \sim 1.2 \times 10^7 \text{ M}^{-1} \text{ s}^{-1}$ ) value for NHERF1 (wt) is typical of a diffusion-limited process (17, 45, 46). Increased accessibility of the

PDZ1 ligand-binding site in NHERF1 irrespective of the state of autoinhibition results in at least 3 orders of higher association rate than the PDZ2 domain (Fig. 8, B and D). As shown in Fig. 8B, all three mutations retard the association rate constant by an order of magnitude compared with NHERF1 (wt) at the PDZ1 domain. The  $k_{d1}$  values of R153Q and E225K are comparable with the WT protein but that of L110V is apparently slower than NHERF1 (wt). In the PDZ2 domain, the R153Q and E225K mutations result in slower  $k_{a2}$  and  $k_{d2}$  values, which deviate from NHERF1 (wt). The slower kinetics primarily reflect autoinhibition and structural changes within the PDZ2-binding site that impede the formation of the complex with GRK6A and interfere with phosphorylation.

### Discussion

The modular structure of NHERF1 is highly advantageous for its scaffolding function in assembling and trafficking of cellular complexes. The flexibility of the modular architecture offers a powerful mechanism to permute a single chain configuration into an ensemble of structures with minimum entropic barrier (47, 48). As a prototypical scaffold we established that NHERF1 exists as a continuum of structures that can coordinate the spatial and temporal location of the PDZ1 and PDZ2 domains with respect to each other. The function of the intact protein can no longer be described by a binary switch shuttling exclusively between a closed and open conformation. Instead, it can be viewed in solution as a diffuse ensemble of different PDZ and EB domain configurations. This dynamic description contrasts with structurally similar multi-PDZ domain proteins (49) that have limited mobility, where short linkers result in correlated motion of the domains. In NHERF1, we observe a range of interdomain distances (40–80 Å) and random alignment within the conformational space populated



**Figure 8. Affinity and kinetics of NHERF1 (wt) and mutants binding to GRK6A peptide.** A, equilibrium curves of NHERF1 (wt) and mutants binding to GRK6A peptide from SPR are fitted by a two-site binding model, see Table S2 for  $K_d$  values. Y-axis values reported in SPR resonance units (RU). Displayed univariate scatter plots obtained from three repeat SPR measurements: B and D, bivalent association rate constants ( $k_{a1}$  and  $k_{a2}$ ); C and E, dissociation rate constants ( $k_{d1}$  and  $k_{d2}$ ). Different symbols with Y-error bars have been used for each measurement.

by the ensemble that would support nearly independent movement of the PDZ domains despite being linked.

The length and number of linkers is a common evolutionary strategy used to modify the conformational space accessible to modular proteins (50). By NMR we confirmed nearly 30% of the NHERF1 chain is disordered, which agrees with the amino acid compositional bias in the linker and the C-terminal region. For example, the linker region between the PDZ domains is dominated by disorder-promoting residues like Pro (20%) and charge-rich Glu (20%) (51, 52). However, the C-terminal tail is relatively rich in Ser (20%) with tunable flexibility by phosphorylation (53–55). Because NHERF1 is primarily involved in cross-linking ezrin bound to the actin cytoskeleton and plasma membrane proteins, the ability to sample an unusually large conformational space has an innate advantage for capturing targets and bridging the different components of the signaling pathways.

The length and overall flexibility of the autoinhibitory C-terminal tail carrying the PDZ-binding motif is vital for modulating the strength of the intramolecular interaction with the PDZ2 domain. Based on the structural models used to fit the SANS data, the effective chain length corresponding to 91 residues ( $\sim 40$  Å) appears to be within a range suitable for modest intramolecular affinity required to inhibit the PDZ2 domain-binding site. Concurrently, the transient interactions at the PDZ2 domain in the dynamic closed state of NHERF1 (32) does not preclude rapid exchange between the myriad of binding partners during cell signaling.

One of major goals of this study was to probe the structural basis of impaired activity in naturally occurring NHERF1 mutations. What makes these disease mutations intriguing is the fact that none are physically located in the peptide-binding site and yet mediate interactions with binding partners. Using biophysical and structural tools, we investigated in detail the complex

relationship between the mutated PDZ domains, the ensemble dynamics of the intact scaffold, and autoinhibition. By NMR, we were able to delineate the local structural changes triggered within the individual PDZ domains and to evaluate their impact on the ensemble of global conformations in the intact scaffold by SANS. Complementary equilibrium and kinetic SPR measurements revealed the local changes in the PDZ domains influence the efficiency of substrate recognition by altering the rate of association/dissociation.

The disease mutations can detune NHERF1 function by at least two mechanisms: either the altered structure of the mutant PDZ domains modulates the binding affinity to specific substrates (56), or the dynamic interaction between the PDZ2 and EB domain is impaired. Thus, one might expect mutations in the PDZ1 domain will primarily affect target binding, whereas those located in the PDZ2 domain have a dual impact on autoinhibition and binding affinity.

Therefore, it comes as no surprise that the binding affinity between ezFERM and the remote C-terminal EB domain shows marginal differences between the different mutations located in the PDZ domains and the WT protein. However, the kinetic measurements yield more interesting differences. The L110V mutant illustrates the effect of structural changes in the PDZ1 domain are not isolated and can mediate remotely the kinetics of EB domain docking in ezFERM. The two mutations, R153Q and E225K, in the PDZ2 domain present a very different conundrum. The intramolecular association even if perceptibly weakened in the mutants does not facilitate association with the EB domain. Instead, we observe the rate of association is much slower and that presents a potential kinetic bottleneck when anchoring NHERF1 at the membrane. A plausible explanation could be the EB domain is simply more disordered in the mutants when it is partially disengaged from PDZ2 (16). Thus, a higher entropic barrier must be overcome for binding induced

folding of the C-terminal helical structure in the presence of ezFERM.

The magnitude of structural alterations in the mutated PDZ domains has a marginal impact on association between GRK6A peptide with NHERF1 and is in sharp contrast to Npt2a where the interactions are debilitated (56). The two-step binding model with GRK6A involves a high-affinity PDZ1-binding step overlapped with a much weaker association in the autoinhibited PDZ2 site. The structural rearrangement triggered by L110V and R153Q mutations results in a 3-fold decrease in the high-affinity binding constant (nanomolar) for the GRK6A peptide but remains unchanged in the E225K mutant. The weak binding step driven by the release of PDZ2 autoinhibition is uniformly depressed in the mutants but not eliminated. The complementary kinetic experiments from SPR revealed the rates of association and dissociation are significantly slower compared with the WT protein at both PDZ sites. The systematic retardation of the  $k_{on}$  rates in the mutants suggests an alternative kinetic mechanism interferes with cellular activity.

From these key observations, we infer that the NHERF1 mutations could not only undermine interactions in some cases (56) but also deregulate time-dependent cellular events within signaling cascades as we have shown in this study. Notwithstanding the subtle differences in the intrinsic activity, all three NHERF1 mutants abolished PTH-sensitive  $P_i$  uptake resulting in comparable and severe phenotypes in patients (18). There is some evidence to suggest the pathogenic mechanism for heterozygous loss-of-function NHERF1 mutations identified in renal and skeletal phenotypes (56, 57), and certain types of breast cancer (58) could be accounted for by haploinsufficiency, wherein a single functional copy of a gene is insufficient to maintain normal function. Additional clinical and biochemical studies on other biological targets are necessary to generalize the conclusions from this study and the direction of future efforts. By combining different structural and biophysical techniques, we present unique insight into molecular mechanisms by which the disease mutations can alter the function of a flexible scaffold like NHERF1 to assemble signaling complexes.

## Experimental procedures

### Protein expression

The recombinant proteins corresponding to full-length NHERF1 (residues 11–358) and the mutants (L110V, R153Q, and E229K) were expressed in *Escherichia coli* BL21 (DE3) cells (Novagen, Inc.) and purified according to published methods (13). For uniform enrichment of the protein with  $^{15}\text{N}/^{13}\text{C}$  isotopes, BL21 (DE3) cells were grown in M9-minimal medium containing  $^{15}\text{NH}_4\text{Cl}$  (Cambridge Isotope Laboratories) and  $[^{13}\text{C}_6]\text{glucose}$  as sole nitrogen and carbon sources, respectively. Deuterated proteins were produced by *E. coli* grown in M9-minimal medium containing 99%  $\text{D}_2\text{O}$  and protonated glucose. Typical NMR samples include 140  $\mu\text{M}$   $^2\text{H}/^{13}\text{C}/^{15}\text{N}$ -labeled NHERF1 dissolved in 20 mM sodium phosphate, pH 7.5, 150 mM NaCl, 0.5 mM DTT, 0.5 mM EDTA, 90%  $\text{H}_2\text{O}$ , 10%  $\text{D}_2\text{O}$ . A 1:1 complex of  $^2\text{H}/^{15}\text{N}/^{13}\text{C}$ -labeled NHERF1 and unlabeled FERM domain from ezrin was prepared under identical buffer conditions as described previously (13). The 22-residue C-terminal peptide from GRK6A with an N-terminal biotin tag was custom synthesized (Genscript, NJ).

### NMR spectroscopy

The NMR data were acquired on Bruker AVANCE series of spectrometers equipped with z-axis gradient TCI/TXI Cryo-Probes<sup>TM</sup> at a sample temperature of 15 °C and  $B_0$  field strengths of 800 and 900 MHz, respectively. The multidimensional datasets were processed in Topspin 2.1 from Bruker Biospin and analyzed using CARA1.5 (59). The backbone resonances of  $^2\text{H}/^{13}\text{C}/^{15}\text{N}$ -labeled NHERF1 in the presence and absence of the ezFERM domain and the three NHERF1 mutants were assigned by combining the information of the isolated fragments PDZ1 (BMRB 18824) + PDZ2CT (BMRB 16638) supported by a complete suite of TROSY-based triple resonance experiments to assign the spacer between the PDZ domains.

Two-dimensional line-shape analysis was done in Topspin 3.5 by processing the data with gaussian window function (LB (line broadening) = −2 Hz, GB (gaussian maximum position) = 0.2) followed by deconvolution.

### SANS experiments

SANS data were collected using the EQ-SANS instrument (60), which is a TOF SANS instrument located at the Spallation Neutron Source (SNS) of Oak Ridge National Laboratory. A single instrument configuration with a 4-m sample-to-detector distance was employed. The instrument choppers ran at 60 Hz and were set to provide a minimum wavelength of 2.5 Å. The beam was defined with a 25-mm diameter source aperture and a 10-mm diameter sample aperture. The configuration spans a  $q$ -range from  $\sim 0.01$  to  $\sim 0.40$  Å<sup>−1</sup> (where  $q = 4\pi\sin(\theta)/\lambda$ ,  $2\theta$  is the scattering angle, and  $\lambda$  is the wavelength of the neutron), which probes the length scales required to see the complex and facilitates subtraction of the solvent background from the scattering signal from the samples. The SANS experiments were performed at 10 °C. The software Mantid was used to reduce the data from the samples and the associated solvent backgrounds using standard procedures that correct for incident flux spectrum, sample transmission, and detector sensitivity, as well as the detector dark current (61). The final  $I(q)$  versus  $q$  plots were obtained by azimuthally averaging the data after subtracting the solvent scattering. The reduced scattering data were subjected to consecutive Guinier analysis at  $qR_g < 1.13$  (Fig. 6B). The length distribution function  $P(r)$  in Fig. 6C was generated using the program GNOM (62).

### Ensemble analysis of SANS data

The initial structure of the full-length NHERF1 closed structure was built in MDA (Multi-Domain Alignment) Chimera 1.11 (63) by joining the PDZ1 and PDZ2CT template structures we determined previously by solution NMR (16, 17). A representative ensemble of the two major states was generated in XPLOR-NIH 2.47 by adapting established protocols for SAXS refinement of multidomain proteins detailed elsewhere (64, 65). Briefly, PDZ1 and PDZ2 domains are treated as rigid bodies that can translate and rotate freely within a sphere radius of 40–80 Å during the MC search (“randomizeDomainPos”) by



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breaking the linkers. This step is followed by rejoining the linkers and a quick round of simulated annealing with TAD (1000 to 25 K) in the linkers followed by energy minimization. For the closed structure, the coordinates of PDZ2 and EB domains are grouped and treated as a single rigid body, but in the open state, the EB domain can move freely in space with respect to the two PDZ domains. A van der Waals repulsion term is used to prevent atomic clashes during the MC search and structures that violated the term were rejected during the Powell energy minimization step. To prevent overlap of backbone atoms, the final ensemble of ~20 K structures was generated in multiple steps by randomizing the domain positions of seed structures selected from the previous iteration. All the calculations were performed using either an in-house multicore cluster or the Virtual Cluster NMRBox at University of Connecticut Health Center. The SANS scattering intensity curves were calculated for each conformer in the two ensemble pools corresponding to the open and closed states in CRYSON (41). Using a genetic clustering algorithm GAJOE from EOM 2.0 (36), the weighted average of the SANS curves for a subset of conformers from the randomized ensemble was fitted to the experimental data by minimizing  $\chi^2$ . Both the ensemble size (maximum 20 conformers) and the pool fractions (open and closed states) were allowed to vary during the optimization process (100 rounds of genetic clustering). The program uses the optimized ensemble (to extract the average flexibility of the selected conformers,  $R_g$ , and maximum length ( $D_{\max}$ ) distributions) displayed in Fig. 6. The overlay of the experimental and theoretical scattering intensity of the ensemble is shown in Fig. S5.

### Surface plasmon resonance experiments

SPR experiments were performed on an X100 instrument (GE Healthcare). To immobilize GRK6Act22, the Biacore CM5 Biosensor chips was activated by *N*-hydroxysuccinimide and *N*-ethyl-*N'*-[3-(diethylamino) propyl] carbodiimide (GE Healthcare). The ligand, GRK6Act22, dissolved at 5  $\mu$ g/ml in 10 mM sodium acetate, pH 4.9, was injected to coat the activated sensor chip surface. Free ligand was washed away, and uncoated sites were blocked by 1 M ethanolamine, pH 8.5. The control flow cell was activated and blocked without ligand injection. The biotinylated GRK6Act22 ligand was immobilized on SA streptavidin sensor chip (GE Healthcare) using the manufacturer's protocol until the desired response target was reached. The analytes, NHERF1(wt) or variants, were dissolved in HBS-EP buffer containing 10 mM HEPES buffer, pH 7.4, 3 mM EDTA, and 0.005% surfactant polysorbate 20 and different NaCl concentrations, respectively. The analytes were injected over the ezFERM-coated surfaces at 30  $\mu$ l/min for 180 s at increasing concentrations. The dissociation time is 800 s. At the end of the injection-dissociation cycle, the sensor chip was regenerated with 4.0 M  $\text{MgCl}_2$ , 50 mM triethylamine (pH 9.15), and HBS-EP buffer. The SPR experiments were performed at 15 °C. The response curves were obtained by subtracting the background signal, generated from a control cell injected with the same analyte but without ligand coating of the hydrogel matrix to remove the effects of bulk refractive index and non-specific binding. The data were further corrected by subtracting the signal generated from buffer alone. Background-corrected

response curves were fit to the nonlinear equation one-site or two-site binding model in the BIA evaluation software. To obtain the kinetic association and dissociation rate constants, the SPR response curves (Figs. S6 and S7) were fitted using kinetic binding models provided by the BIAEvaluation Software.

**Author contributions**—S. B., P. A. F., and Z. B. conceptualization; S. B., C. B. S., W. T. H., and Z. B. formal analysis; S. B. and Z. B. writing-original draft; S. B., C. B. S., W. T. H., P. A. F., and Z. B. writing-review and editing; P. A. F. and Z. B. funding acquisition.

**Acknowledgments**—The data collected at New York Structural Biology Center was made possible by ORIP/National Institutes of Health Facility Improvement Grants CO6RR015495 and S10OD016432 (800 MHz). The 900 MHz NMR spectrometers were purchased with funds from National Institutes of Health Grant P41GM066354, the Keck Foundation, New York State Assembly, the United States Department of Defense, and National Institutes of Health Grant 2G12 RR003060 from the NCRR to City College of New York. This study made use of NMRbox: National Center for Biomolecular NMR Data Processing and Analysis, a Biomedical Technology Research Resource (BTRR), supported by National Institutes of Health Grant P41GM111135 from NIGMS. A portion of the research conducted at ORNL's Spallation Neutron Source was sponsored by the Scientific User Facilities Division, Office of Basic Energy Sciences, United States Department of Energy. We thank Carrie Gao for technical support during the SANS experiments.

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**Dynamic structure of the full-length scaffolding protein NHERF1 influences signaling complex assembly**

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*J. Biol. Chem.* 2019, 294:11297-11310.

doi: 10.1074/jbc.RA119.008218 originally published online June 6, 2019

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Access the most updated version of this article at doi: [10.1074/jbc.RA119.008218](https://doi.org/10.1074/jbc.RA119.008218)

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