ALS-linked protein disulfide isomerase variants cause motor dysfunction

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Abstract

Disturbance of endoplasmic reticulum (ER) proteostasis is a common feature of amyotrophic lateral sclerosis (ALS). Protein disulfide isomerases (PDIs) are ER foldases identified as possible ALS biomarkers, as well as neuroprotective factors. However, no functional studies have addressed their impact on the disease process. Here, we functionally characterized four ALS-linked mutations recently identified in two major PDI genes, PDIA1 and PDIA3/ERP57. Phenotypic screening in zebrafish revealed that the expression of these PDI variants induce motor defects associated with a disruption of motoneuron connectivity. Similarly, the expression of mutant PDIs impaired dendritic outgrowth in motoneuron cell culture models. Cellular and biochemical studies identified distinct molecular defects underlying the pathogenicity of these PDI mutants. Finally, targeting ERP57 in the nervous system led to severe motor dysfunction in mice associated with a loss of neuromuscular synapses. This study identifies ER proteostasis imbalance as a risk factor for ALS, driving initial stages of the disease.

Keywords amyotrophic lateral sclerosis; ERP57; PDIA1; protein disulfide isomerase

Subject Categories Molecular Biology of Disease; Neuroscience

DOI 10.15252/embj.201592224 | Received 6 June 2015 | Revised 27 December 2015 | Accepted 5 January 2016 | Published online 11 February 2016

The EMBO Journal (2016) 35: 845–865

See also: N Maharjan & S Saxena (April 2016)

Introduction

Amyotrophic lateral sclerosis (ALS) is a fatal neurodegenerative disorder affecting motoneurons in the brain and spinal cord (Peters et al., 2015). The progressive degeneration of motoneurons leads to loss of motor control resulting in paralysis and death. Approximately 10% of ALS cases are familial (fALS), caused by rare variants in multiple genes (Leblond et al., 2014), while the majority is considered sporadic (sALS). Repeat expansion in the intronic region of C9orf72 and mutations in the gene encoding cytosolic superoxide dismutase...
dismutase 1 (SOD1) are the most frequent genetic causes of fALS, accounting for around 50% of fALS cases (Ferraiuolo et al., 2011), whereas mutations in TAR DNA-binding protein (TARDBP, also known as TDP43) and fused-in-sarcoma/translated-in-liposarcoma (FUS/TLS) genes represent about 10% of fALS cases (Ferraiuolo et al., 2011). Although the etiology of ALS remains poorly understood, abnormal aggregation and altered proteostasis is a common feature of ALS (Turner et al., 2013; Hetz & Mollereau, 2014). As a major compartment for protein folding and quality control, disruption of normal endoplasmic reticulum (ER) function leads to the accumulation of misfolded proteins causing a condition known as ER stress (Walter & Ron, 2011). ER proteostasis disturbance is increasingly recognized as a major driver of neurodegenerative diseases and is also indicated as a common feature of sALS and fALS (Roussel et al., 2013; Hetz & Mollereau, 2014). ER stress engages the unfolded protein response (UPR), an adaptive response that orchestrates the recovery of homeostasis and the induction of apoptosis to eliminate irreversibly damaged cells (Hetz, 2012). Recent evidence indicates that ER stress is a salient pathological feature of iPSC-derived ALS motoneurons (Kiskinis et al., 2014), and one of the earliest events detected before any denervation is observed (Saxena et al., 2009), underlying the differential neuronal vulnerability of motoneurons. Similarly, alteration in the expression of UPR genes was recently reported as a salient feature of ALS patients carrying C9orf72 mutations (Prudencio et al., 2015). Importantly, accumulating studies using genetic or pharmacological manipulation of the UPR have demonstrated a functional role of the pathway in mouse models of ALS (Hetz et al., 2013; Oakes & Papa, 2015), highlighting the therapeutic potential for disease treatment.

Proteomic analysis of spinal cord tissue of ALS mouse models uncovered major changes in the levels of two ER stress-inducible foldases of the protein disulfide isomerase (PDI) family, known as PDIA1 (also referred to as PD or P4H) and ERp57 (also known as PDIA3 or Grp58) (Atkin et al., 2006). This finding was then confirmed in spinal cord tissue (Llave et al., 2007; Atkin et al., 2008) and cerebrospinal fluid (Atkin et al., 2008) of sALS patients. Furthermore, the upregulation of PDIA1 and ERp57 protein levels was also identified as the best hits in a proteomic screening for biomarkers in patient blood, suggesting that monitoring these PDIs may be used as indicators for diagnosis and disease progression (Nardo et al., 2011). Protein inclusions containing SOD1, TDP-43, and Fus co-localize in the ER, where they catalyze the formation (oxidation), breakage (reduction), and rearrangement (isomerization) of disulfide bonds of proteins that traffic through the secretory pathway (Ellgaard & Ruddock, 2005; Rutkevich & Williams, 2011). Intramolecular and intermolecular disulfide bonds have important consequences for the structure and function of proteins (Feige & Hendershot, 2011), mediating in many cases the generation of protein aggregates in brain diseases (Andreu et al., 2012). In addition to their function as foldases, PDIs can also act as molecular chaperones for unfolded/misfolded proteins at the ER (Hatahet & Ruddock, 2009). PD family members are built by modules of thioredoxin-like catalytic a domains and non-catalytic b domains. The catalytic a domain contains the CXXC active-site motifs that react with thiols of substrate proteins (Appenzeller-Herzog et al., 2010). The non-catalytic b domains are responsible for substrate recruitment and provide interaction sites for cofactors (Hatahet & Ruddock, 2009; Appenzeller-Herzog et al., 2010). PDIA1 was shown to have a central role in oxidative protein folding, since its deletion in mammalian cells results in delayed disulfide bond formation (Rutkevich et al., 2010). ERp57 is a component of the calnexin (CNX) and calreticulin (CRT) cycle, where it is responsible, in complex with CNX and/or CRT, for the folding of glycosylated and disulfide bond-containing proteins (Rutkevich & Williams, 2011). Unexpectedly, PDIA1 and ERp57 may be involved in pro-apoptotic mechanisms in the context of Alzheimer’s and Huntington’s disease models (Hofstrom et al., 2010). Importantly, increasing reports suggest relevant roles of PDI family members beyond assisting protein folding, including cell signaling, protein quality control, redox control, apoptosis, and cell signaling (Turano et al., 2011).

Although PDIs are emerging as relevant factors in neurodegenerative diseases including ALS, studies addressing the biological relevance of these foldases to the nervous system are lacking. Here, we characterize in detail the impact of ALS-linked PDI variants on motoneuron function using cellular, biochemical and in vivo approaches; in addition, we define for the first time the function of ERp57 in the nervous system. Our results reveal distinct consequences of these mutations to the structure and function of PDIA1 and ERp57, triggering detrimental effects to motoneuron function and connectivity. This study suggests that alterations in PDI biology are a risk factor to develop ALS.

**Results**

**ALS-linked PDI mutants disrupt motoneuron connectivity and function in zebrafish**

We recently identified missense variants in PDIA1 and ERp57 in ALS cases, where we highlight p.D292N and p.R300H which are located in the b' domain of PDIA1, and p.D217N and p.Q481K in ERp57, which map to the b' domain and the catalytic a' domain, respectively (Fig 1A). To assess the possible pathological effects of these PDI variants on an in vivo setting, we used zebrafish, a validated model for dissecting mechanisms of neurodegeneration in ALS (Kabash et al., 2010; Patten et al., 2014). In zebrafish, we were unable to
observe any phenotype caused by PDIA1\textsuperscript{D292N}, probably due to the extremely low level of expression of this mutant in the model at the protein level (Fig 1B and Appendix Table S1). While the majority of embryos expressing wild-type PDIA1 or ERp57 appeared normal in overall morphology at 24 h post-fertilization (hpf), a large fraction of embryos expressing PDIA1\textsuperscript{R300H}, ERp57\textsuperscript{D217N}, and ERp57\textsuperscript{Q481K} showed a striking shortening of the axis and tail curvature (Appendix Table S1; and Fig 1C and D, see arrows), both features previously observed in various zebrafish models of ALS (see examples in Armstrong & Drapeau, 2013; Kabashi et al., 2011, 2009). To directly assess the possible effects of ALS-linked mutant expression on motoneuron function, we analyzed motoneuron morphology in animals selected with overall normal appearance using transgenic zebrafish embryos expressing Kaede (a photoactivatable fluorescent protein) in motoneurons under the control of the elav/HuC promoter (Sato et al., 2006). Expression of PDIA1\textsuperscript{R300H}, ERp57\textsuperscript{D217N}, and ERp57\textsuperscript{Q481K} did not disrupt the normal spatial organization and number of motoneurons. However, these variants impaired axonal morphology, producing motor axons with abnormal shape, involving a reduction in the length and increased branching (Fig 1C–F). Furthermore, analysis of pre-synaptic (SV2) and post-synaptic (α-bungarotoxin) markers within neuromuscular junctions (NMJ) of myotomes revealed disrupted synapse formation in embryos expressing PDIA1\textsuperscript{R300H} and ERp57\textsuperscript{Q481K} (Fig EV1, see arrows).

We then monitored the possible effects of ALS-linked PDI variants on the motor performance of zebrafish. Consistent with the
alterations observed in motoneuron connectivity, expression of ERp57Q481K and, to a lesser extent, PDIA1R300H induced motor behavioral defects at 48 hpf, as revealed by an increase in the number of stimuli necessary to trigger a touch-evoked escape response (Fig 1G). In addition, a reduction in the speed of the escape response was observed in these experiments when ERp57Q481K and PDIA1R300H were expressed (Fig 1G). These results indicate that expression of the ALS-linked mutants PDIA1R300H and ERp57Q481K disrupted motoneuron connectivity and function in zebrafish, the phenotype resembled those described in other ALS studies in this vertebrate model (see examples in Babin et al, 2014; Kabashi et al, 2011, 2009).

Expression of PDI variants impairs neuronal outgrowth

To gain insights into the molecular mechanism involved in ALS-linked PDI mutant pathogenesis, we expressed these variants in different motoneuron cell culture systems. First, we transiently transfected the murine motoneuron cell line NSC34 with wild-type PDIs or the four PDI variants alone. We calibrated the system to obtain low overexpression levels compared with endogenous levels of PDIA1 or ERp57 (Fig 2A). Based on our studies with disrupted neuronal branching in vivo, we induced differentiation for 24 h by serum starvation followed by the morphological analysis of GFP-positive cells. Unexpectedly, expression of wild-type PDIA1 and ERp57 resulted in marked enhancement of neurite outgrowth (Fig 2B). This effect was lost when PDIA1 or ERp57 mutants were expressed (Fig 2B), suggesting that these mutations abolish the neurite-extending function of the wild-type proteins. In addition, expression of PDI mutants reduced the percentage of NSC34 cells with neurites (Fig 2C). However, no neurotoxicity of mutant PDIs was observed when NSC34 cell viability was analyzed (Appendix Fig S1A).

We then generated primary motoneurons cultures derived from the spinal cord of rat embryos followed by morphological analysis. In these experiments, motoneurons expressing wild-type PDIA1 or ERp57 showed a robust enhancement of dendritic outgrowth, whereas mutant PDIs completely lost this activity, showing a decrease in the length of dendritic branches when compared with wild-type PDIA1 and ERp57 (Fig 2D). These effects were recapitulated when we quantified the length of primary, secondary and tertiary neurites (Appendix Fig S1B). Again, no neuronal death was detected in these assays upon transient expression of mutant PDIs (Appendix Fig S1C).

We then addressed the possible impact of ALS-linked PDI mutants on neurite outgrowth in human motoneurons derived from the human embryonic stem cell line HuESC 3 H9::GFP, by expressing PDI variants using lentiviral-mediated transduction (Appendix Fig S1D). We confirmed our findings in human motoneurons, observing that these mutants also reduced the ability of PDIs to enhance neurite outgrowth (Fig 2E). These observations are consistent with recent findings indicating that a major phenotype of ALS-derived human motoneurons carrying well-described genetic mutations is the reduction of dendritic branching (Matus et al, 2014).

Based on the observation of increased neurite outgrowth in cells overexpressing the wild-type form of PDIA1 or Erp57, we then monitored the contribution of the endogenous proteins to the process. To this end, we stably transduced NSC34 cells with lentiviruses expressing shRNAs against PDIA1 and ERp57 mRNAs (Appendix Fig S1E). Remarkably, we observed a significant reduction in the number of cells bearing neurites after differentiation (Fig 2F). Together, our results suggest that Erp57 and PDIA1 have an important function in enhancing neuronal outgrowth and that the ALS-linked PDI variants characterized here adversely affect dendritic extension and connectivity.

ALS-linked PDI mutants do not affect the susceptibility of cells to ER stress

PDIs represent an important group of ER stress-responsive genes that are thought to contribute to the recovery of proteostasis downstream of the UPR. To explore the possible impact of ALS-linked PDIs identified here to the physiology of the ER, we first analyzed their subcellular distribution. NSC34 cells were co-transfected with V5-tagged PDI variants together with a KDEL-RFP construct to assess their subcellular distribution. In addition to showing a normal co-localization with the ER marker, mutant PDIA1 or Erp57 did not alter the morphology of this organelle (Appendix Fig S2).

We next analyzed whether the expression of ALS-linked PDIs alters the susceptibility of cells to ER stress. NSC34 cells expressing mutant or wild-type PDIA1 and ERp57 were treated with the ER stress agent tunicamycin (an inhibitor of N-glycosylation). The expression of the UPR mediators XBP1 and ATF4, or the upregulation of the ER chaperone BiP, was not enhanced in cells expressing ALS-linked PDIs compared to the wild-type forms (Fig EV2A). We also monitored the viability of cells undergoing ER stress. Treatment of cells with different doses of thapsigargin (an inhibitor of the SERCA pump) leads to equivalent percentages of cell death in cells expressing wild-type or mutant PDIs as monitored by propidium iodide staining (Fig EV2B). Similar results were obtained when cells were treated with tunicamycin (Fig EV2C). These results are consistent with our recent findings indicating that Erp57 does not affect the susceptibility of cells to undergo ER stress (Torres et al, 2015). Finally, to monitor the physiological status of the ER with an additional parameter, we determined the rate of secretion of two proteins that are synthetized through the secretory pathway. NSC34 cells were co-transfected with a BDNF-GFP expression construct together with our PDI variants. Western blot analysis of the supernatant of cells after 18 or 42 h of transfection indicated no alterations in the rate of BDNF-GFP secretion (Fig EV2D). Similar results were obtained when we measured the levels of progranulin in the cell culture media using ELISA, where only PDIA1R300H showed a minor reduction in progranulin secretion (Fig EV2E). Taken together, these results suggest that the expression of ALS-linked PDIs do not trigger clear alterations to the homeostasis of the ER.

ALS-linked PDIA1 mutants have altered enzymatic activity

To define the possible molecular defects underlying the pathogenicity of the ALS-linked PDI variants, we undertook several cellular and biochemical approaches to assess key aspects of PDI biology. To investigate the effects of the mutations on the functionality of the PDIs, we expressed the four PDI mutants in NSC34 cells. In absence of reducing agents, we observed the appearance of protein complexes after Western blot analysis, reflecting increased mixed disulfide bond formation for PDIA1D292N, ERp57D217N, and ERp57Q481K compared to the respective wild-type proteins (Figs 3A
and 4A). As controls, we included previously reported substrate-trapping mutants in which one cysteine (Cys) in each active site was exchanged to alanine (PDIA1Cys or ERp57Cys) (Jessop et al., 2009). These results suggest that mutant PDIs form altered disulfide-dependent complexes with an increased number of substrates or binding partners.

Figure 2. Motoneuron morphology upon expression of ALS-linked PDI variants.

A NSC34 cells were transiently transfected with expression vectors for V5-tagged wild-type and mutant PDIs. After 48 h, overexpressed PDI variants were assessed under reducing conditions in an 8% SDS-PAGE. An antibody detects total PDIA1 (endogenous mouse PDIA1 and exogenous human V5-tagged PDIA1) (first panel). A second antibody detects only human PDIA1, therefore only V5-tagged PDIA1 appears (second panel). A mouse- and human-specific antibodies were used to detect total ERp57 (third panel). Anti-V5 was used to detect the exogenous PDI variants. Anti-β-actin was used as a loading control.

B, C NSC34 cells were transiently transfected with the indicated PDI constructs together with a GFP expression plasmid. Cells were then differentiated for 24 h in Neurobasal medium containing B27 supplement to induce cell differentiation. Increased neurite outgrowth is indicated with white arrow heads. (B) Quantification of the average primary neurite lengths was performed, all cells from three independent experiments were compiled. A minimum of 100 cells per experiment were analyzed. In addition, (C) the percentage of cells with neurites was quantified in the three independent experiments (right panel).

D Primary rat ventral spinal cord neurons were prepared and after 4 days in vitro (DIV) transfected with GFP alone or together with the indicated PDI constructs. Cells were fixed at 10 DIV and SMI32 staining was performed to identify motoneurons. Images were taken and the total outgrowth of GFP- and SMI32-positive cells was quantified. Results are compiled from three independent experiments.

E Human motoneurons were differentiated from the human embryonic stem cell (ESC) HuESC 3 HB9-GFP line. Differentiated neurons were transduced with lentivirus expressing GFP alone or together with PDI-expressing plasmids. Transduced cells were cultured for another 10 days. To identify motoneurons after lentiviral transduction, immunocytochemistry analyses were performed. Quantification of neurite outgrowth in the different experimental conditions of GFP- and HB9-positive neurons was obtained. Neurite number and assessment of the length of each neurite were performed in a similar manner as for primary rat motoneurons (see Materials and Methods). Four independent experiments were performed.

F NSC34 cell lines stably knocked down for PDIA1 or ERp57 were differentiated for 24 h in Neurobasal medium containing B27 supplement to induce cell differentiation. The percentage of cells with neurites was quantified in the three independent experiments. A minimum of 100 cells per experiment were analyzed.

Data information: Statistical analyses were performed using one-way ANOVA and Bonferroni’s post hoc tests. Mean ± SEM with only statistically significant P-values are shown: *P ≤ 0.05; **P ≤ 0.01; ***P ≤ 0.001. Scale bars represent 25 µm (B, D and E).

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Published online: February 11, 2016

Figure 3. Effects of ALS-linked mutations in PDIA1 on the structure and enzymatic activity.

A PDI mutants form abnormal disulfide-dependent protein complexes. NSC34 cells were transiently transfected with expression vectors for V5-tagged wild-type and mutant PDIA1. After 48 h, differential disulfide-dependent interactions/aggregations of overexpressed PDI variants was assessed under reducing (+DTT) and non-reducing (−DTT) conditions in an 8% SDS-PAGE. Anti-V5 was used for detection in Western blot.

B Analysis of the PDIA1 structure to model the effects of the R300H mutation. The close association between Arg300 located to the β′ domain of PDIA1 with Trp396 located to the α′ domain adjacent to the active-site motif CGHC (designated as AS1 in yellow) is shown in comparison with the mutated version of PDIA1R300H, highlighting the same residues. A potential stabilization of the interaction between the β′ and α′ domain is shown that may be caused by the interaction of the imidazole rings of mutated His300 with Trp396.

C ALS-linked PDIA1 variants were generated as recombinant proteins and then analyzed by circular dichroism (CD). Averages for CD spectroscopic scans of PDIA1VVT and mutants are shown.

D Averages for CD spectroscopic thermal denaturation of recombinant PDIA1VVT and mutants.

E Representative electrophoresis analysis of proteinase K-treated recombinant PDIA1 variants. Mass spectrometer analysis of proteinase K-digested samples from total sample and from in-gel trypsin-digested protein samples (arrows indicate band 1 and band 2) indicated differences in the removal of the x-linker region. Bottom panel: ratios of band 1 to band 2 were quantified in four independent experiments.

F Representative fluorescence spectra of recombinant PDIA1 β′α′ fragments and the equivalent ALS-linked mutants (n = 6). Ratios from the two peak areas and change compared to PDIA1 β′α′VVT. Both mutants analyzed show a significant shift in peak position compared to wild type, but in opposite directions, suggesting that PDIA1Δ1229N shifts equilibrium toward the capped version (x-region over the binding pocket) and the PDIA1Δ1300H mutant toward the uncapped version (Nguyen et al, 2008).

G The activity of recombinant PDIA1 was measured in vitro using a BPTI refolding assay following by mass spectrometry analysis. The percentages of different BPTI species was calculated (6H, fully reduced; 15, one disulfide bond; 25, two disulfide bonds; 35, three disulfide bonds) at time point 2.5 min in four independent experiments.

H Measurement of H2O2 levels at the ER lumen of living cells. Left panel: reduced PDIs can be oxidized by ERO1Lα, which then transfers electrons to molecular oxygen (O2) to generate hydrogen peroxide as product from PDI activity. Right panel: NSC34 cells were transiently co-transfected with ER luminal HyPer sensor and indicated PDIs. After 48 h, the 490/420 nm fluorescence ratio was recorded for 2 min under basal conditions. Means and SEM derived from all cells per condition (n = 55–74) monitored in four independent experiments are shown.

I HEK293T cells were transfected with expression vectors for V5-tagged wild-type and mutant PDIA1, as well as empty vector. After 48 h, V5-tagged proteins were immunoprecipitated and eluted with V5 peptide. The interaction with endogenous ERO1Lα was analyzed by Western blot. The inputs and elutions are shown as control. Right panel: quantification of the degree of interaction is presented.

Data information: Statistical analyses were performed using Student’s t-test in (F, G and I) or one-way ANOVA and Bonferroni’s post hoc tests in (H). Mean ± SEM with P-values: n.s., P > 0.05; *P ≤ 0.05; **P ≤ 0.01; ***P ≤ 0.001.

Source data are available online for this figure.

We previously analyzed the available structure of the PDIA1 bb′α′ fragment (Wang et al, 2012) and concluded that the substitution of Arg300 in PDIA1 to histidine may result in a bb′α′ interdomain rearrangement (Gonzalez-Perez et al, 2015), which could interfere with the redox-dependent substrate binding of PDIA1 (Fig 3B). This mutation may generate an abnormal interaction between Trp396 and the imidazole ring of His300, impacting the accessibility to the substrate binding site as well as the active site (adjacent to Trp396) (Fig 3B). The PDIA1Δ1229N mutation is located in the substrate binding β′ domain of PDIA1, and, remarkably, a mutation of this
Published online: February 11, 2016

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The EMBO Journal

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2016 The EMBO Journal
Vol 35 | No 8 | 2016 851

Figure 4. ALS-linked mutations in ERp57 lead to altered interactions with calnexin and calreticulin.
A PDI mutants form abnormal disulfide-dependent protein complexes. NSC34 cells were transiently transfected with expression vectors for V5-tagged wild-type and mutant ERp57. After 48 h, differential disulfide-dependent interactions/aggregations of overexpressed PDI variants was assessed under reducing (+DTT) and non-reducing (−DTT) conditions in an 8% SDS–PAGE. Anti-V5 was used for detection in Western blot.
B ALS-linked ERp57 variants were generated as recombinant proteins and then analyzed by circular dichroism (CD). Averages for CD spectroscopic scans of recombinant ERp57WT and mutants are shown. C A thermal denaturation curve of ERp57WT and mutants was performed. D Representative electrophoresis of proteinase K-treated ERp57 recombinant proteins. E Surface plasmon resonance analysis was performed to monitor the affinity of recombinant ERp57 for recombinant CRT P domain. Kd values are expressed as percentage of ERp57WT. Values are derived from four independent experiments. For absolute Kd values, please see Appendix Table S2. F HEK293T cells were transfected with expression vectors for V5-tagged wild-type and mutant ERp57, as well as empty vector. After 48 h, V5-tagged proteins were immunoprecipitated and eluted with V5 peptide. The interaction with endogenous calnexin (CNX) and calreticulin (CRT) was analyzed by Western blot. The inputs and elutions are shown. Right panel: quantification of the degree of interaction is presented. G The gain of an N-glycosylation site of ERp57 was predicted after the analysis of the protein sequence since the change of Asp217 to an Asn creates the NxT/S consensus sequence. Neuro2a cells were transfected with expression vectors for V5-tagged wild-type and mutant ERp57, as well as empty vector and treated with 1 μg/ml tunicamycin (Tm) for 20 h to inhibit N-glycosylation. Alternatively, protein extracts were digested with PNGase F and the possible removal of the N-glycosylation was analyzed by Western blot using anti-V5 antibody.

Data information: Statistical analyses were performed using Student’s t-test in (E) and (F). Mean ± SEM with P-values: *P ≤ 0.05; **P ≤ 0.001. Source data are available online for this figure.

aminic acid was already shown to affect the accessibility to the substrate binding site and a’ and b’ interdomain flexibility (Nguyen et al., 2008). To better define possible structural changes in PDI1 mutants, we generated recombinant proteins for in vitro characterization. As determined by far UV circular dichroism, thermal denaturation, and protease resistance assays, we conclude that none of the mutant proteins showed gross structural defects (Fig 3C and D). Minor but significant differences were observed in the proteolytic pattern of the PDI1 mutants compared with PDI1WT, with both showing altered variation in cleavage around the x-linker region that lies between the b’ and a’ domains (Fig 3E). In particular, differences were observed in the ratio of the two major degradation products formed (band 1 and 2) (Fig 3E, bottom panel). Mass spectrometry analysis of these bands indicated that PDI1 mutations resulted in altered variation in cleavage around the x-linker region that lies between the b’ and a’ domains (Fig 3F). The x-linker can adopt multiple conformations which determine the accessibility of substrates to the primary substrate binding site in the b’ domain (Nguyen et al., 2008). Fluorescence analysis of single tryptophan of isolated b’ constructs showed that PDI1D292N mutation results in a significant shift in the equilibrium toward the capped state, where the x-region blocks access to the binding pocket, while the PDI1E300H mutation has the opposite effect (Fig 3F).

To determine the consequences of the mutations on the activity of PDI1, an oxidative refolding assay was performed using the classical substrate bovine pancreatic trypsin inhibitor (BPTI) (Karala et al., 2009). PDI1E300H showed significantly greater amounts of fully reduced BPTI (indicated as 6H) and lower amounts of native
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ALS-associated Erp57 variants display altered interactions with CNX and CRT

As part of the CNX-CRT cycle, Erp57 is responsible for disulfide bond formation of a subset of glycosylated proteins (Maattanen et al., 2010). Structural analysis of the available Erp57 structure suggests that the ALS-linked mutation D217N results in a loss of a negative charge in the proximity of a domain containing the positively charged residues K214, R274, and R282 known to facilitate binding of the negatively charged P domain of CNX or CRT (Pollock et al., 2004; Silvennoinen et al., 2004; Kozlov et al., 2006; Dong et al., 2009). The Q481K mutation may also influence the binding to CNX based on its location as previously suggested (Pollock et al., 2004). Like PDA1 mutants, recombinant Erp57 variants did not show any significant alteration in their structure as measured by far UV circular dichroism, thermal denaturation, and protease resistance assays (Fig 4B–D). Based on the predicted physicochemical changes of Erp57 upon mutation, we used surface plasmon resonance analysis to measure the direct binding to the CRT P domain. We observed a significant increase in affinity of both Erp57=D217N and Erp57=Q481K for the P domain of CRT (Fig 4E and Appendix Table S2). To confirm these findings in living cells, we performed immunoprecipitation experiments using HEK293T cells. We found that Erp57=D217N displays a strong increase in the binding to endogenous CRT and CNX, whereas Erp57=Q481K displayed only a slight increase in the binding to both lectins (Fig 4F).

Of note, we also observed a shift in the electrophoretic pattern of Erp57=D217N when expressed in zebrafish, as well as in NSC34 cells, but not with the recombinant protein. Analysis of the sequence surrounding this mutation site revealed that the change of Asp217 to Asn creates a putative artificial N-linked glycosylation site (NKT), a phenomenon previously described for pathogenic gene variants in other diseases (Vogt et al., 2007). Consistent with this prediction, treatment of cells with tunicamycin, an inhibitor of N-linked glycosylation, reversed the electrophoretic shift observed upon Erp57=D217N expression (Fig 4G). Similar results were observed by digesting cell extracts with PNGase F to remove N-linked glycosylations (Fig 4G).

Together, these biochemical studies identified distinct structural and functional defects of these ALS-linked PDI mutants, which are likely to impact the function of these foldases.

Deletion of Erp57 in the CNS results in impaired motor performance

The function of PDIs in the physiology of the nervous system remains largely unexplored. Since ALS patients presented mutations in PDI genes in one allele and our in vitro studies suggest a loss of function according to our differentiation assays, we determined whether PDI haploinsufficiency could have an impact in the motor function of the nervous system. Therefore, we generated a conditional knockout mouse for Erp57 using the loxP and Cre recombinase system under the control of the neuronal progenitor promoter Nestin (referred to as Erp57=Kes−/− mice). We were able to obtain viable animals, indicating that Erp57 deficiency in the brain bypassed the embryonic lethality observed in full knockout animals. Analysis of Erp57 expression levels in spinal cord tissue and brain indicated a complete deletion of Erp57, whereas heterozygous animals (Erp57=Kes+/−) presented a 50% reduction in the protein levels (Fig 5A). Targeting Erp57 in the nervous system led to a retardation of growth as measured by the progression of body weight gain (Fig 5B). In addition, a substantial reduction in the rate of Erp57=Kes−/− animals born was detected, as compared to the expected Mendelian proportions (Table 1).

We then analyzed several behavioral parameters normally affected in ALS models to measure coordination and the motor activity. Remarkably, Erp57 haploinsufficiency (Erp57=Kes−/−) led to a significant decline in rotator performance compared to littermate Erp57=Kes−/− mice, which was further exacerbated in Erp57=Kes−/− mice (Fig 5C). This effect was stable over time (Appendix Fig S3A). Analysis of motor strength and coordination using the hanging test also revealed clear deficits in Erp57 knockout mice and intermediate phenotypes in heterozygous animals (Fig 5D and Videos EV1, EV2 and EV3). Unexpectedly, a subgroup of Erp57=Kes−/− animals died prematurely; where nine out of 19 animals died before 150 days of age (Fig 5E). Thus, loss of Erp57 function in the central nervous system results in motor dysfunction and premature death, suggesting a functional role of this PDI in neurons.

We then performed histological analysis of spinal cord tissue of Erp57=Kes−/− mice. Immunofluorescence analysis of the distribution of neurons in the spinal cords of the Erp57=Kes−/− and Erp57=Kes−/− mice revealed no obvious changes in the ventral horn neuron densities after NeuN staining (Fig 5F). These results were confirmed by quantitative stereological analysis of spinal cord tissue after Nissl or choline acetyltransferase (ChAT) staining (Fig 5G). In addition, no signs of astrogliosis were detected in the spinal cord of Erp57=Kes−/− mice using GFAP staining (Fig 5F). Similarly, visualization of Purkinje cell distribution in the cerebellum indicated normal neuronal counts (Appendix Fig S3B). In contrast to the phenotype described to CNX knockout animals (Kraus et al., 2010), no changes in spinal cord myelination were found in Erp57=Kes−/− animals (Fig 5H). Thus, Erp57 deficiency results in motor problems in the absence of evident signs of motoneuron cell death, suggesting the occurrence of altered neuronal dysfunction rather than a neurotoxic effect.

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Our studies in zebrafish suggested that PDI mutants have adverse effect on neuromuscular connectivity but not on overall motorneuron survival. To assess the impact of ERp57 deficiency on motorneuron function in vivo, we performed electromyography (EMG) measurements. Fifty percent of ERp57 Nes+/- mice tested displayed fibrillations and positive sharp waves, indicating impaired motor function. These findings suggest that ERp57 deficiency contributes to motor dysfunction and premature death, potentially through its role in maintaining neuromuscular connectivity and motorneuron health.
waves (Fig 6A), suggesting a loss of integrity of NMJs. As a positive control for this test, a symptomatic SOD1G86R transgenic mouse was monitored (Appendix Table S3). The loss of neuromuscular synapses is one of the first signs of ALS, leading to progressive loss of motor control. Based on the functional impairment to the motor capacities of ERp57 mice, we extensively analyzed NMJs in the diaphragm, one the relevant muscles that loses the innervation in ALS (Dupuis et al, 2009; Perez-Garcia & Burden, 2012; Liu et al, 2013). The analysis of NMJ distribution in ERp57-deficient mice revealed a narrower band of acetylcholine receptor (AChR) clusters along the length of the diaphragm compared to wild-type control animals (Fig 6B, upper panel). Quantification of the number of bins revealed a significant reduction in ERp57Nes+/− animals (Fig 6B, bottom panel). Three-dimensional reconstructions of NMJs indicated that ERp57 deficiency resulted in abnormal postsynaptic morphologies and reduced muscle innervation (Fig 6C). Remarkably, ERp57-deficient animals displayed either incomplete or aberrantly distributed NMJs, while the number of fully innervated normal pretzel-like NMJs was strongly diminished (Fig 6C and D). Detailed quantitative analyses of postsynaptic NMJ morphologies indicated a significant increase of altered NMJs in ERp57Nes+/− and ERp57Nes−/− diaphragms, we observed a clear accumulation of dismantled NMJs in both genotypes (Fig 6D). Consistent with these results, quantifications of the area and perimeter of NMJs indicated a significant reduction of both parameters in ERp57Nes+/− and ERp57Nes−/− animals (Fig 6E). These

Table 1. Generation rate of ERp57 wild-type, heterozygous, and conditional knockout of indicated mouse crossings.

<table>
<thead>
<tr>
<th>Crossings</th>
<th>Pups</th>
<th>ERp57WT/WT</th>
<th>ERp57Nes+/−</th>
<th>ERp57Nes−/−</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>ERp57WT/WT×ERp57WT/WT</td>
<td>Observed No. 134</td>
<td>24</td>
<td>8</td>
<td>166</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Observed % 80.7</td>
<td>14.5</td>
<td>4.8</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Expected % 100</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>ERp57WT/WT×ERp57Nes+/−</td>
<td>Observed No. 82</td>
<td>27</td>
<td>13</td>
<td>122</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Observed % 67</td>
<td>27</td>
<td>13</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Expected % 100</td>
<td>50</td>
<td>25</td>
<td>75</td>
<td></td>
</tr>
<tr>
<td>ERp57WT/WT×ERp57Nes−/−</td>
<td>Observed No. 80</td>
<td>25</td>
<td>12.5</td>
<td>100</td>
<td></td>
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<tr>
<td></td>
<td>Observed % 100</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td></td>
</tr>
</tbody>
</table>

Figure 6. ERp57 deficiency results in loss of neuromuscular connectivity.

A Representative EMG recordings of ERp57WT (n = 16), ERp57Nes−/− (n = 12) and ERp57Nes−/− (n = 5) mice is presented. The presence of positive sharp waves (PSW) in ERp57Nes−/− and ERp57Nes−/− mice indicated muscle denervation.

B Analysis of NMJ and muscle morphologies were performed in ERp57WT (n = 5), ERp57Nes−/− (n = 5) and ERp57Nes−/− (n = 4) mice. Quantifications of endplate width, measuring the most ventral region of the diaphragms every 134 μm considering both sides of the innervation profile. Twenty to forty measurements per diaphragm were obtained per animal.

C Whole-mounted diaphragms from ERp57WT and ERp57Nes−/− mice were co-stained with anti-neurofilament (red) and β-BTX to reveal the postsynaptic densities (green). Three-dimensional reconstructions (lower panel) of higher magnification are shown. ERp57WT NMJs are fully innervated pretzel-like, whereas ERp57Nes−/− NMJs display less complex postsynaptic densities and an incomplete or aberrantly distributed innervation pattern (Videos EV4–EV7).

D Representative 3D reconstructions of z-stacks showing the five categories in which NMJ morphologies were grouped: pretzel, fragmented, O-shaped, C-shaped, and dismantled NMJs. Histogram of the distribution frequency of > 200 different NMJ per animal is shown.

E Quantitative morphometry of > 60 NMJs in the different genotypes analyzed.

Data information: For statistical analysis, one-way ANOVA with Bonferroni post hoc test was performed in (B, D, and E). Mean ± SEM with P-values: *P ≤ 0.05; **P ≤ 0.01; ***P ≤ 0.001.
results indicate that the motor defects observed in ERp57 conditional knockout mice are associated with a drastic perturbation of neuromuscular connectivity.

Based on the altered NMJs in ERp57-deficient mice, we then analyzed the possible consequences in muscle physiology. We confirmed that the expression levels of ERp57 in the muscle of ERp57Nes/-/- mice were not affected (Fig 7A). By assessing the overall integrity of the muscle, no gross changes were found in muscle morphology (Fig 7B, top panel), skeletal muscle fibrosis (Fig 7B, middle panel), or degeneration/regeneration cycles (Fig 7B, lower panel). Since the functional and structural properties of skeletal muscle depend on motor axon innervation, we assessed muscle morphology in Tibialis anterior sections stained for NADH-TR activity to identify oxidative myofibers (Fig 7B). NADH-TR positive (slow twitch) and negative (fast twitch) myofibers were quantified as percentage of total for each genotype. This analysis revealed an altered distribution of oxidative myofibers in ERp57-deficient animals (Fig 7C). Furthermore, the mean diameter of slow- and fast-twitch muscle fibers was reduced in ERp57Nes/-/- animals (Fig 7C). In summary, these results indicate that ERp57 deficiency in the nervous system leads to a profound impairment of motor control, possibly caused by disrupting neuromuscular synapses, and as a consequence, altered muscle physiology. The global phenotype of ERp57Nes/-/- animals may resemble an early symptomatic stage of ALS and other neuromuscular disorders.

**Targeting ERp57 in the nervous system alters the expression of SV2 synaptic protein**

Sporadic ALS cases are associated with the accumulation of abnormal protein aggregates containing proteins that are also mutated in a small percentage of familial cases including TDP43 and SOD1 (Turner et al, 2013). To assess whether the loss of ERp57 has any consequences on wild-type SOD1 and TDP43, we monitored their expression levels and aggregation status in the brain cortex of ERp57-deficient animals. We did not observe any clear aggregation...
of these proteins using Western blot analysis or a filter trap assay (Appendix Fig S4A–D). As positive controls, protein extracts from mutant SOD1G93A or TDP43A315T transgenic mice were used to visualize protein aggregates. Similarly, no changes in SOD1 or TDP43 levels were observed in the spinal cord of these animals (Appendix Fig S4E).

Overall our results suggest that ERp57 deficiency in the nervous system triggers motor defects associated with alterations to the neuromuscular junctions, indicating detrimental consequences at the functional level rather than a neurotoxic mechanism. Synaptic proteins and receptors are generally folded at the ER and traffic through the secretory pathway to reach their final destination. Many of them are disulfide bonded, glycosylated, or both and therefore represent potential substrates of ERp57. We analyzed the expression of a panel of synapse-located proteins in the brain cortex of ERp57-deficient animals including synaptic vesicle protein SV2, the presynaptic marker synaptophysin, and postsynaptic marker PSD95, as well as NMDA receptor 2A (NMDAR2A). Remarkably, from this screening, a significant decrease in the levels of SV2 was observed in both ERp57Nes+/− and ERp57Nes−/− animals (Fig 8A and B). In addition, we observed the accumulation of high molecular weight species of SV2 (Fig 8A and B), suggesting the occurrence of abnormal aggregation similar to the phenotype observed for well-characterized ERp57 substrates (Jessop et al., 2009). These alterations were not evident in the spinal cord of ERp57-deficient animals, possibly because the expression levels and isoforms detected in this tissue were lower than in brain cortex (Appendix Fig S5). These results indicate that ERp57 alters the expression of SV2, an essential protein mediating synapse function in the nervous system.

Discussion

The upregulation in the levels of PDI family members is a salient feature of ALS, as well as other neurodegenerative diseases including Alzheimer’s, Parkinson’s, and Creutzfeldt-Jacob disease (reviewed in Andreu et al., 2012). Therefore, PDI family members are emerging as relevant stress-response genes in diverse neurological disorders; however, little is known about how PDIs contribute to these pathologies. Since PDIs participate in many processes including protein folding, ER-associated degradation (ERAD), protein quality control, redox homeostasis, cell signaling, and apoptosis (Grek & Townsend, 2014), disruption of their function may affect hundreds of substrates. Here, we have uncovered an unanticipated function of PDIs in motor control and neuromuscular connectivity. Using a series of complementary approaches, we describe a novel pathological mechanism of ALS where PDI malfunction appears to correlate with a striking alteration in the morphology of NMJs, possibly contributing to the abnormal motor control observed in ERp57 conditional knockout mice. Our findings are in agreement with recent studies in prion and Alzheimer’s disease models suggesting that chronic disturbances to ER function could trigger a reduced synthesis of synaptic proteins, leading to cognitive and motor impairment rather than neuronal loss (Moreno et al., 2012; Ma et al., 2013). We speculate that perturbations to the PDI folding network operate as a probable ALS risk factor, consistent with the view that altered ER proteostasis can drive neuronal dysfunction and degeneration during the disease (Roussel et al., 2013; Hetz & Mollereau, 2014).

For several reasons, it is likely that the ALS-linked PDI variants studied here trigger neuronal dysfunction through a subtle progressive adverse impact on motoneuron function. First, to differing degrees, the PDI variants reported here induced motoneuron pathology in zebrafish, analogous to that induced by mutant SOD1, FUS, TDP43, and C9orf72 in this vertebrate model (Kabashi et al., 2009, 2011; Armstrong & Drapeau, 2013; Lee et al., 2013; Babin et al., 2014). Second, the four PDI variants analyzed were clearly adverse for motoneurons in vitro, disturbing dendritic elongation and morphology, which may affect neuronal connectivity,
although they were not overtly neurotoxic to the cultured motoneurons. This is in agreement with recent studies of iPSC-derived ALS motoneurons expressing different genetic mutations in which morphological alterations, rather than neurotoxicity, are a major and consistent phenotype (Chen et al., 2014; Kiskinis et al., 2014). Importantly, we provide evidence indicating that the expression of wild-type PDIΔ1 and Erp57 contribute to the process of neuronal outgrowth. We speculate that PDIs regulate to some degree the composition and structure of synapses through their folding and quality control function at the ER. Additionally, other mechanisms may be relevant including the modulation of cytoskeleton dynamics, since Erp57 has a relevant activity on regulating ER calcium release (Li & Camacho, 2004). Furthermore, our results are reminiscent of findings with mutant SOD1 transgenes, which in many neuronal culture systems do not elicit a lethal phenotype, yet impair neuronal functionality. Third, loss of Erp57 in mice triggers motor dysfunction without motor neuron loss, possibly by altering neuromuscular synapses. While the mechanism for this striking phenotype remains unclear, our data suggest that altered morphology of the NMJ may contribute to the motor dysfunction. We are currently performing proteomic studies to identify PDI substrates altered after expression of ALS-linked PDI variants. We speculate that functional disturbances of PDIs may be involved in the initial stages of ALS where neuromuscular alterations rather than motoneuron loss (late event in the disease and most models) drive the appearance of disease signs. Importantly, ER proteostasis impairment is the earliest defects observed in SOD1 mutant mice before denervation occurs (Saxena et al., 2009) and recent studies have associated these alterations to the abnormal hyperexcitability observed in ALS motoneurons (Kiskinis et al., 2014). Besides, changes in neuronal functionality observed here may also relate to the non-motor symptoms observed in a subgroup of ALS patients (Ling et al., 2013). Fourth, the variants were all heterozygous missense changes, arguing either that they exert a dominant influence or that the mutant PDI proteins lead to haploinsufficiency, consistent with our functional studies in Erp57 conditional knockout mice and cell culture models. Homozygosis may also result in early embryonic lethality as observed in Erp57 knockout animals (Garbi et al, 2006). Based on genetic analyses to date, and our biological studies, we consider these PDI mutants as risk factors or modifiers of phenotype rather than causant variants; they may contribute to disease by both gain- and loss-of-function mechanisms.

A few knockout mouse models for PDIs have been described to date, including Erp57, Erp29, Erdj5, PDIΔ1, and Agr2 (Garbi et al., 2006; Park et al., 2009; Hosoda et al., 2010; Nemere et al., 2010; Hahm et al., 2013; Hirsch et al., 2014). Nevertheless, in none of these studies, CNS-related phenotypes were reported so far when the expression of PDIs was targeted in vivo. Recently, however, we reported the generation of the transgenic mouse model overexpressing Erp57 in the CNS. We found that while the overexpression of Erp57 has no effect on the survival of dopaminergic neurons, it enhances peripheral nerve regeneration suggesting a differential role in neuronal vulnerability (Castillo et al., 2015). In agreement with the current study, recent findings suggest that motoneurons are selectively vulnerable to perturbations of ER function. A recent study indicates that the differential expression of the BiP cofactor SIL1 underlies the differential vulnerability of the affected motoneuron population in ALS (Filezac de L’Etang et al., 2015). Loss of one copy of SIL1 accelerated experimental ALS enhancing ER stress, whereas its overexpression provided robust neuroprotection (Filezac de L’Etang et al., 2015). Furthermore, mutations in SIL1 result in spontaneous degeneration in mice (Zhao et al., 2005) and cause Marinesco-Sjögren syndrome. Interestingly, deletion of one CRT allele in the context of mutant SOD1 transgenic mice led to exacerbated muscle weakness and denervation, accelerating the progression of the disease (Bernard-Marissal et al., 2014). Consistent with our results, motoneuron dysfunction in this model did not involve increased motoneuron loss, suggesting also a role of CRT in early ALS phases involving muscle denervation (Bernard-Marissal et al., 2015). On the other hand, CNX deficiency leads to motor defects due to alterations in the structure of myelin sheets in the spinal cord (Kraus et al., 2010). Finally heterozygous mutation in BiP in mice leads to the development of serious motor problems during aging, associated with the selective degeneration of motoneurons and proteostasis alterations including the spontaneous accumulation of SOD1 aggregates (Jin et al., 2014). Together with our findings, these data suggest that the perturbations to the ER proteostasis network may contribute to early events in ALS associated with impaired neuromuscular function. Since the capacity of the ER to buffer fluctuations of proteostasis decline with age (Douglas & Dillin, 2010; Mardones et al., 2015), it may be feasible that PDI variants have more drastic effects in neuronal connectivity during aging and, together with other ALS risk factors, may translate into an irreversible damage to motoneuron function and the manifestation of the disease. As noted above, we have identified two fundamental consequences of the mutations in PDIΔ1 and Erp57: (i) a disturbance of the primary foldase function, as indicated by our biochemical and cellular characterization, and (ii) structural and functional changes to the neuromuscular synapse. The alterations in the levels and aggregation state of the synaptic protein SV2 in the brain cortex of Erp57 knockout animals lead us to speculate that persistent subtle changes in synaptic proteostasis may cause in the long term a progressive disturbance of neuronal connectivity. In agreement with this hypothesis, we previously observed a reduction of the steady-state levels of the prion protein (PrP) in the brain of Erp57 knockout mice (Torres et al., 2015). Although only a minority of ALS cases are genetically associated with PDI variants, we would argue based on studies depicting altered PDI expression in sALS (Matus et al., 2013b) that dysfunction of the PDI foldase network is a relevant factor in ALS. Interestingly, the mutations studied here in PDIs do not cause ER stress and do not affect SOD1 or TDP43 aggregation, suggesting that we uncovered a novel mechanism of ALS pathogenesis. Thus, our findings provide a proof of concept for one possible mechanism underlying the etiology of ALS involving alterations to the ER proteostasis machinery. Hence, PDIs are novel elements in ALS pathogenesis that may ultimately represent an important pathway for future therapeutic intervention.

Materials and Methods

Cell media and antibiotics were obtained from Life Technologies (Maryland, USA). Fetal calf serum was obtained from Atlanta Biologicals. Hoechst was purchased from Molecular Probes. All...
transfections were performed using the Effectene reagent (Qiagen). PNGase F was obtained from New England Biolabs; tunicamycin and thapsigargin were obtained from Sigma. DNA was purified with Qiagen kits.

**DNA constructs**

The pcDNA3.1/V5 plasmids carrying genes for PDIA1\(^{WT}\), PDIA1\(^{Cys}\), ERp57\(^{WT}\), and ERp57\(^{Cys}\) were described before (Jessop et al., 2007, 2009). Site-directed mutagenesis following manufacturer’s instructions was performed to create ALS mutant constructs (Stratagene cat. No. 200517-5). All mutated constructs were verified by DNA sequencing. The plasmid for HyPerER\(_{lum}\) was previously described (Enyedi et al., 2010). Mature PDIA1 and ERp57, PDIA1 b’x and calreticulin P domain (residues 206–305) constructs were previously cloned into a pET23-based expression vector, which incorporates an N-terminal His-tag to the cloned gene. Site-directed mutagenesis was performed according to instructions of the PluTM Turbo DNA polymerase kit (Stratagene, La Jolla, CA, USA), and the resulting constructs were checked by DNA sequencing.

**Cell culture assays**

NSC34 cells were grown in Dulbecco’s modified Eagle’s medium–high glucose (DMEM; Gibco), supplemented with 10% fetal bovine serum (FBS), 100 units/ml penicillin, and 0.1 mg/ml streptomycin (Invitrogen) at 37°C under 5% CO\(_2\). Routinely, cells were transfected with Effectene transfection reagent (Qiagen) using the recombinant helper-free CAPO4 transfection protocol to reduce cell toxicity (Jiang & Chen, 2006; Sepulveda et al., 2010). Briefly, after 1 h of incubation at 5% CO\(_2\), the cells were incubated for 20 min with transfection medium pre-equilibrated in a 10% CO\(_2\) incubator to dissolve the DNA-CAPO4 precipitates and then returned to a 5% CO\(_2\) incubator. At 10 DIV, cells were fixed in 4% paraformaldehyde and immunostained with an antibody against MAP2 (1:400; Santa Cruz Biotechnology) to visualize all neurons (interneurons as well as motoneurons), and SMI-32 antibody (1:1,000 Convance) to identify motoneurons (Nagai et al., 2007; Fritz et al., 2013) (also see antibody list in the Appendix). Dendritic number and assessment of the length of each dendrite was performed as described previously (Sepulveda et al., 2010). Viability assays were performed as described in Fritz et al. (2013).

The human embryonic stem cell line (ESC) HuESC 3 Hb9::GFP line, where the coding sequence of GFP is under the control of Hb9 promoter restriction fragment, was described previously (Di Giorgio et al., 2008). Cells were differentiated as described in Di Giorgio et al. (2008) with the sole modification that ES cells were grown under feeder-free conditions. Two days after plating differentiated neurons were transduced with lentivirus pseudotyped with VSVG envelope expressing PDIA1\(^{WT}\), PDIA1\(^{D292N}\), PDIA1\(^{R300H}\), ERp57\(^{WT}\), ERp57\(^{D217N}\), or ERp57\(^{Q481K}\) using a CaPO4 transfection protocol to reduce cell toxicity (Jiang & Chen, 2006; Sepulveda et al., 2010). Briefly, after 1 h of incubation at 5% CO\(_2\), the cells were incubated for 20 min with transfection medium pre-equilibrated in a 10% CO\(_2\) incubator to dissolve the DNA-CAPO4 precipitates and then returned to a 5% CO\(_2\) incubator. At 10 DIV, cells were fixed in 4% paraformaldehyde and immunostained with an antibody against MAP2 (1:400; Santa Cruz Biotechnology) to visualize all neurons (interneurons as well as motoneurons), and SMI-32 antibody (1:1,000 Convance) to identify motoneurons (Nagai et al., 2007; Fritz et al., 2013) (also see antibody list in the Appendix). Dendritic number and assessment of the length of each dendrite was performed as described previously (Sepulveda et al., 2010). Viability assays were performed as described in Fritz et al. (2013).

**Morphological analysis of motoneurons**

Ventral spinal cord neurons were transfected with the bicistronic pCDH plasmid coding for GFP and either PDIA1\(^{WT}\), PDIA1\(^{D292N}\), PDIA1\(^{R300H}\), ERp57\(^{WT}\), ERp57\(^{D217N}\), or ERp57\(^{Q481K}\) using a CaPO4 transfection protocol to reduce cell toxicity (Jiang & Chen, 2006; Sepulveda et al., 2010). Briefly, after 1 h of incubation at 5% CO\(_2\), the cells were incubated for 20 min with transfection medium pre-equilibrated in a 10% CO\(_2\) incubator to dissolve the DNA-CAPO4 precipitates and then returned to a 5% CO\(_2\) incubator. At 10 DIV, cells were fixed in 4% paraformaldehyde and immunostained with an antibody against MAP2 (1:400; Santa Cruz Biotechnology) to visualize all neurons (interneurons as well as motoneurons), and SMI-32 antibody (1:1,000 Convance) to identify motoneurons (Nagai et al., 2007; Fritz et al., 2013) (also see antibody list in the Appendix). Dendritic number and assessment of the length of each dendrite was performed as described previously (Sepulveda et al., 2010). Viability assays were performed as described in Fritz et al. (2013). The human embryonic stem cell line (ESC) HuESC 3 Hb9::GFP line, where the coding sequence of GFP is under the control of Hb9 promoter restriction fragment, was described previously (Di Giorgio et al., 2008). Cells were differentiated as described in Di Giorgio et al. (2008) with the sole modification that ES cells were grown under feeder-free conditions. Two days after plating differentiated neurons were transduced with lentivirus pseudotyped with VSVG envelope expressing PDIA1\(^{WT}\), PDIA1\(^{D292N}\), PDIA1\(^{R300H}\), ERp57\(^{WT}\), ERp57\(^{D217N}\), and ERp57\(^{Q481K}\), respectively, with a MOI of 10 viral particles per neuron, after transduction cells were cultured for another 10 days. To identify motor neurons after lentiviral transduction, immunocytochemistry analyses were performed as described in Lopez-Gonzalez et al. (2009). Briefly, cells were washed three times with phosphate-buffered saline (PBS) and fixed with 4% paraformaldehyde for 20 min at room temperature. Cultures were washed three times with PBS and blocked by incubation with 10% bovine serum albumin (BSA)/0.3% Triton X-100 in PBS for 45 min. The following primary antibodies were used at the indicated dilutions in 10% BSA/PBS: rabbit anti-GFP 1:500 (Molecular Probes) and goat anti-choline acetyltransferase antibody (ChAT) 1:200 (Millipore), the secondary antibodies coupled with Alexa 488 or Alexa 568 (1:500; Molecular Probes), and nuclei were stained with DAPI (Vector Labs). Quantification of axonal growth in the different experimental conditions of GFP- and ChAT-positive neurons was obtained using a Nikon TE2000-E2 microscope with a Yokogawa CSU10b spinning disk confocal scan head and custom laser launch, NEOs AOTP and relay optics (Solamere Technology Group, Salt Lake City, Utah).
Multiwavelength confocal z-series were acquired with a Nikon 20X Plan fluor oil objective (NA = 1.0) and a QImaging Rolera MGi camera using the standard digitizer. The final pixel size was 0.5388 μm/pixel, the z step was 0.3 μm, and the exposure time was 1 s per image. Metamorph Software controlled the microscope hardware and image acquisition. Dendritic number and assessment of the length of each dendrite were performed in the same manner as described above for primary rat motoneurons.

Immunoprecipitation

Immunoprecipitations (IP) were performed as previously described (Hetz et al., 2006). 293T cells were transfected using Effectene; after 48 h, cells were collected and washed once with 1 ml PBS, pH 7.4. Cells were resuspended in 500 μl NP-40 buffer (0.2% NP-40, 50 mM Tris/HCl pH 7.5, 150 mM NaCl, and protease inhibitor cocktail (Roche)) and incubated at 4 °C overnight. After vortexing for 20 s, cell lysates were centrifuged at 10,000 rpm for 5 min at 4 °C. The supernatant was incubated with anti-V5 antibody beads (V5 tagged Protein Purification Kit, MBL International) on a rotor wheel for 4 h at 4 °C. Then, beads were washed three times with NP-40 buffer, increasing to 500 mM NaCl in the final wash. Protein complexes were eluted by adding V5 peptide (V5 tagged Protein Purification Kit, MBL International) for 30 min at room temperature. Input and eluates were analyzed by Western blot.

Biochemical blot analysis

Protein expression in NSC34 or N2a cells was performed as described previously (Hetz et al., 2009). Cells were lysed and homogenized by sonication in NP-40 buffer (50 mM Tris (pH 8.0), 150 mM NaCl, and 1% NP-40 containing a protease inhibitor cocktail from Roche (Basel, Switzerland)). Zebrafish embryos were lysed and homogenized in RIPA buffer (20 mM Tris (pH 8.0), 150 mM NaCl, 0.1% SDS, 0.5% DOC, and 0.5% Triton X-100 containing a protease inhibitor cocktail from Roche, Basel, Switzerland)). Murine cortex, spinal cord and muscle tissue were lysed and homogenized by sonication in NP-40 buffer (10 mM Tris (pH 8.0), 100 mM NaCl, 1 mM EDTA, and 1% NP-40 containing a protease inhibitor cocktail from Roche (Basel, Switzerland)) and phosphatase inhibitor cocktails 2 and 3 (Sigma-Aldrich). The following antibodies (see antibody list in the Appendix) and dilutions were used for Western blot: mouse anti-V5 1:5,000 (Invitrogen), rabbit anti-ER/O1 1:2,000 (Novus Biologicals), mouse anti-PDIA1 (1D3) 1:3,000 (Enzo), rabbit anti-PDIA1 (H-160) 1:1,000 (Santa Cruz), rabbit anti-ERp57 1:3,000 (Santa Cruz), rabbit anti-NM-DM2A 1:1,000 (Convance), mouse anti-synaptophysin 1:500 (Millipore), rabbit anti-PdS95 1:5,000 (Millipore), mouse anti-SV2 1:500 (Developmental Studies Hybridoma Bank), sheep anti-SOD1 1:3,000 (Calbiochem), rabbit anti-TDP43 1:2,000 (Proteintech), rabbit anti-β-actin-HRP conjugate 1:2,000 (Cell Signaling), goat anti-actin 1:1,000 (Santa Cruz), and rabbit anti-HSP90 1:3,000 (Santa Cruz). As secondary antibodies goat anti-rabbit HRP conjugate 1:3,000 (Invitrogen), rabbit anti-mouse HRP conjugate 1:3,000 (Invitrogen), donkey anti-sheep HRP conjugate 1:3,000 (Sigma-Aldrich), or rabbit anti-goat HRP conjugate 1:3,000 (Invitrogen) were used.

PNGase F treatment was performed according to the manufacturer’s instructions. Briefly, 20 μg of N2a cell extract was digested for 2 h at 37 °C. Protein samples were prepared using standard procedures. Five micrograms was loaded onto 10% PAA-minigels and subsequently Western blotted. V5-tagged proteins were detected with mouse anti-V5 (1:15,000). BDNF detection in cell supernatant was performed by transiently co-transfecting N2a cells with BDNF-GFP (Haubensak et al., 1998) and PDIs. Cells were grown in normal culture containing 10% FBS. About 200 μl of media was collected after 18 and 30 h after gently swirling. Media were centrifuged at 11,000 g for 5 min to remove cell debris. Typically, 40 μl of media was run in the SDS–PAGE without any concentration step. BDNF-GFP was detected after Western blot using anti-GFP (1:3,000). Protein extracts were also analyzed by filter trap was performed as recently reported (Torres et al., 2015). RNA purification and real-time PCR were performed as previously described (Lisbona et al., 2009) using the following primers: actin forward 5’-TACCACCATGTAACCAGCA-3’, actin reverse 5’-CTCAG GAGGAGCAATGATCTTGAT-3’, erp57 forward 5’-GACGGCTTTGCCCC TGAGTATG-3’, and erp57 reverse 5’-GTTGCGCATGCATCCACC-3’.

Analysis of zebrafish axonal motoneuron morphology and detection of NMJ

Wild-type Tubingen and transgenic Tg(Huc:Kaede) (Sato et al., 2006) zebrafish (Danio rerio) strains were maintained, crossed, injected, raised, and staged as described (Sato et al., 2006). Animal experimentation protocols were approved by the Bioethics Committee of the Faculty of Medicine at the University of Chile. For in vitro synthesis of capped RNA with the T7 mMESSAGE mMACHINE system (Ambion), pcDNA3.1/V5-based constructs (version of the human PDIA1WT, PDIA1R300H, PDIA1D292N, ERp57WT, ERp57D217N, and ERp57Q418K) were linearized with StuI. For overexpression experiments, zebrafish embryos were microinjected at one-cell stage with sense mRNA diluted in water, using a Picospritzer III (general valve) pressure ejector. After testing different doses, the final mRNA concentrations used were 80 pg/embryo for PDIA1 (PDIA1WT, PDIA1R300H, and PDIA1D292N), and 30 pg/embryo for ERp57 (ERp57WT, ERp57D217N, and ERp57Q418K) (Appendix Table S1). Global expression phenotypes were analyzed at 60–70% epiboly and 24 hpf in an SMZ-1000 Nikon stereomicroscope.

For analysis of axonal projections of motoneurons, microinjected Tg(Huc::Kaede) zebrafish embryos with PDI mutants and wild-type controls mRNA were anesthetized with tricaine (Sigma-Aldrich) at 36 hpf, and mounted in agarose for spinning disk confocal microscopic observation and photography. Image acquisition was performed with Velocity software (PerkinElmer). Axonal projections of motoneurons at a defined location in the spinal cord were determined as previously described (Kabashi et al., 2009, 2011). Analysis of Z-stacks by confocal microscopy was performed in three to four traced axonal projections per embryo. The axonal lengths of the labeled axon from the spinal cord were traced to their first branching point using ImageJ software. These values were averaged for each of the embryos analyzed (6–10 zebrafish per condition). For immunostaining, mRNA-injected embryos were fixed at 72 hpf in 4% paraformaldehyde/PBS overnight at 4 °C and washed three times in PBS for 10 min. After 20 min of 2.5% trypsin treatment, embryos were immunoassayed using mouse anti-SV2 (1:200; Development Studies Hybridoma Bank), followed by incubation with Alexa 568-conjugated goat anti-mouse antibody (1:200; Molecular Probes),...
and Alexa 488-conjugated α-bungarotoxin (1:100; Molecular Probes) according to established protocols (Wang et al., 2008). Fluorescent images of fixed embryos were taken using a Fluoview1000 Spectral confocal microscope (Olympus®) and Plan-Apochromat 20x and 40x/1.0 W lenses. Images were processed with ImageJ (http://rsbweb.nih.gov/ij/), Velocity (Improvement), and Adobe Photoshop CS3 (Adobe) softwares.

Touch-evoked responses were assessed on a 1.5–zoom stereomicroscope (Kyoto Optical) as described previously (Kabashi et al., 2009, 2011). Briefly, in order to induce escape-swimming response, embryos at 48 hpf were stimulated lightly by touching them at the level of the tail using a gel-loading tip, their responses recorded with a VL-Z7U digital video camera (Sharp) at 30 frames/s.

Recombinant proteins and biochemical characterization

Proteins were expressed in E. coli strain BL21 (DE3) pLysS or pLysS-RARE grown in autoinduction media. His-tagged proteins were purified by immobilized metal affinity chromatography and ion exchange chromatography as described previously (Lappi et al., 2004). Purified proteins were checked for authenticity by mass spectrometry, and the concentrations were calculated based on their calculated molar extinction coefficients. Far UV CD spectra of proteins and thermal denaturation were performed with Chirascan Plus CD Spectrometer (Applied Photophysics, UK). Protein concentration was 100 µg/ml, and the measurements were carried out in 20 mM phosphate buffer pH 7.3 with five repeats over 195–250 nm using a cell with a path length of 10 mm, a spectral bandwidth of 1 nm, and a time constant of 0.5 s. Thermal denaturation was done with temperature range from 22 to 92°C with smooth temperature ramp of 1°C/min using TC125 temperature controller (Quantum Northwest, Liberty Lake, WA, USA). All spectra were corrected for the blank spectra with no protein added, and the thermal denaturation was analyzed calculating the change in spectra at 220 nm.

SPR measurements were performed with Biacore T200 (GE Healthcare, Uppsala, Sweden). CRT P domain in 10 mM acetate pH 4.5 was immobilized onto CM5 chip (GE Healthcare) using amine coupling according to manufacturer’s instructions. The immobilization level was approximately 1,000 RU. The binding of ERp57 wild type and mutants was analyzed in 20 mM phosphate buffer pH 7.3 with concentration range from 0 to 1 µM of protein, at flow rate 30 µl/min and contact time 120 s at 25°C. Washing for 10 min with running buffer was enough for regeneration. Limited proteolysis was carried out in 20 mM phosphate buffer pH 7.3 in the presence of 10 mM β-mercaptoethanol. About 10 µM protein was incubated with or without 10 µg/ml protease K (Roche, Indianapolis, IN, USA) for 30 min at 25°C (for ERp57) or at 4°C (for PDIA1). The reaction was stopped with 5 mM PMSF (Sigma-Aldrich, St. Louis, MO, USA). Protein fragments were separated on SDS–PAGE. Desired peptide fragments were cut out from the gel and analyzed by mass spectrometry after in-gel trypsin digestion. In addition, total sample mixtures were analyzed by mass spectrometry. Fluorescence spectra were measured on FluoroMax-4 (HORIBA Instruments, Edison, NJ, USA) with 1 µM PDIA1 b’x wild type and 20 mM phosphate buffer pH 7.3. Shifts in fluorescence ratios (331–337 nm/352–358 nm) were calculated as described previously (Nguyen et al., 2008).

BPTI was purified as described previously (Nguyen et al., 2008). Pure reduced BPTI was lyophilized and resuspended into 10 mM HCl pH 2.0 to prevent oxidative refolding. The BPTI refolding was carried out as described previously (Karala et al., 2009) with the exception that the reaction was stopped by the addition of 50 mM NEM. Samples were diluted 1:10 in 0.1% TFA and analyzed by ESI-mass spectrometry (Synapt G2, Waters, Milford, MA, USA) coupled to ACQUITY UPLC machinery (Waters) with BEH300 C4 1.7 µm 2.1 × 10 mm UPLC column for desalting and protein separation prior mass spectrometric analysis. UPLC was performed using 0.4 ml/min flow with 0.1% formic acid and 3% to 40% acetonitrile gradient over 15 min.

Generation of conditional ERp57 knockout mice

The ERp57 flox mice were previously described where exons 2 and 3 were flanked with two loxp sites (Garbi et al., 2006) and were kindly provided by Dr. Günther Hämmerling (German Cancer Research Center, Heidelberg, Germany). Mice expressing Cre recombinase under the control of the nestin promoter were obtained from The Jackson Laboratory (B6.Cg-Tg(Nes-cre)1Kln/J, 003771). To generate mice deficient in ERp57 in the central nervous system (CNS), ERp57 flox mice were crossed with Nestin-Cre transgenic mice as we described before (Hetz et al., 2008), and generated offspring carrying the floxed or knockout allele in heterozygous or homozygous form designated as follows: ERp57WT (wild type), ERp57Nes+/- (heterozygous), and ERp57Nes−/− (conditional knockout). All experiments and animal care follows the Institutional Review Board’s Animal Care of the University of Chile (CBA # 0305 FMUCH). The following primers were used for genotyping of mice: erp57 floxed allele, forward 5’-CGCCAGCCTTCATCTTAGTG-3’; erp57 floxed reverse 5’-CAGAGATCCTGCCTCTG-3’, Cre forward 5’-GC GTCTCGACGATAAAACTATC-3’, and Cre reverse 5’-GTGAAA CGACATGGCTGTCATCT-3’.

Beginning at 24 days of age, mice were evaluated weekly by three criteria for the onset of motor neuron defects and disease symptoms: (i) weight, (ii) rotarod performance, and (iii) hanging test. Rotarod test was performed as previously described (Vidal et al., 2012). In brief, mice were placed into a rod rotating (Model LE8500, Panlab SL) at a constant speed of 4 rpm. The time until mice fell from the rod was measured until 120 s. Mice were first trained three times per day for five consecutive days. The hanging test was described previously (Klein et al., 2011).

Electromyography (EMG)

Animals were anesthetized with avertin and placed in a prone position on a thermal pad at 37°C for the examination. EMG recordings using a Cardinal Synergy electromyography (EMG) machine were obtained with a 30G needle using a gain of 50 µV/division and a band pass filter with low and high cutoff frequency settings of 20 and 10,000 Hz, respectively. Potentials were recorded from several sites of the hindlimb muscles with a concentric needle electrode (30G). A ground self-adhesive gelled surface electrode was placed over the tail. The recording electrode was inserted into the tibialis anterior (TA) or gastrocnemius/soleus muscles, and spontaneous electrical activity was recorded for 90 s. The procedure took 15–20 min per mouse, after which the mice were euthanized.
Immunohistochemistry

Histological analysis was performed as previously described (Valenzuela et al., 2012). Mice were anesthetized deeply with 33 μl/g of 10 mg/ml avertin in 0.1 M saline phosphate buffer (PBS) and perfused transcardially with 4% paraformaldehyde. Spinal cords were collected and transversely sectioned (20-μm-thick slices) using a cryostat microtome (Leica, Nussloch, Germany). Sections were immunostained using the antibodies NeuN 1:600 (MAB377, Millipore Bioscience Research Reagents) and GFAP 1:1,000 (N1506, Dako). Tissue sections were viewed with an Olympus IX71 microscope, and images were captured using a QImaging QICAM Fast 1394 camera. Neuronal numbers were assessed by counting NeuN-positive cells in the ventral horn.

In addition, calbindin staining was performed in cerebellum sections using standard methods. Tissue was incubated with anti-calbindin 1:200 (Cell Signaling) for 16 h at 4°C and developed with an anti-rabbit IgG (Vectastain) and DAB (Sigma Chemical Company) using instruction of the manufacturer. Tissue sections were viewed with a Nikon Eclipse 80i microscope, and images were captured using a Nikon DS-Fi1 camera.

Skeletal muscle staining

Whole-mounted diaphragms were dissected out and fixed in 4% PFA for 1 h at 4°C. Samples were first permeabilized in 0.5% Triton X-100 and treated with 0.1 M glycine, pH 7.4, for 15 min and then blocked in 2% BSA and 0.5% horse serum, for 12–16 h. Muscles were incubated with a rabbit anti-neurofilament antibody (Abcam, Cambridge, UK) (1:1,000), for 12–16 h and then with a Cy3-conjugated donkey anti-rabbit antibody (Jackson Immuno Research, West Grove, PA) (1:300) plus Alexa488-conjugated α-bungarotoxin (α-BTX) (Invitrogen, Carlsbad, CA) (1:1,000) for 12–16 h. Sections were flat mounted between two coverslips and imaged. Tibialis anterior muscles were removed, mounted in OCT (Sakura Finetek, Torrance, CA, USA), and quickly frozen in liquid nitrogen-cooled isopentane. Cryosections (20 μm) were fixed with 4% paraformaldehyde for 20 min at room temperature and subsequently processed. Muscle fiber morphology was analyzed with conventional hematoxylin/chromotrope staining, whereas fibrosis was analyzed by staining collagen depositions with a 1% Bismarck Brown aqueous solution for 12 min. Samples were mounted in Entellan medium (Merck, Darmstadt, Germany). To analyze muscle regeneration, cold methanol-fixed cryosections were stained with 1 μg/ml Alexa488-conjugated wheat germ agglutinin (Invitrogen) and 0.3 μM DAPI. Cryosections were also stained with a NAHD reduced solution (Tris–buffer, pH 7.4, NAHD reduced, nitro-blue tetrazolium) (Sigma, St. Louis, MO, USA) for 45 min, and fibers were classified into slow twitch (dark blue), intermediate (blue), and fast twitch (light blue). The identity and diameter of > 100 fibers per type were determined using ImageJ software and are expressed as the percentage of the total.

NMJ analyses

For endplate band quantification, fluorescent images of α-BTX-stained right hemidiaphragms were captured with a Nikon Eclipse 80i fluorescent microscope, and AChR cluster distribution was analyzed. The endplate bandwidth of 20–40 bins per animal, obtained every 134 μm at the central region of each hemidiaphragm was measured with ImageJ. To analyze postsynaptic morphologies, z-stack pictures were imaged at 1-μm intervals with a Zeiss LSM 780 confocal microscope at the CMA Bio-Bio facility, University of Concepcion, Chile. Maximal intensity projections images were reconstructed in 3D using ImageJ software and analyzed to determine the proportion of the different NMJ morphologies, grouped into “pretzels”, normal shapes with continuous stripes, “fragmented”, where pretzels are separated into > 4 fragments, “O” or “C” shaped, less complex postsynaptic densities with no internal stripes, and “dismantled”, structures with a shrunked shape. The morphology of > 200 NMJs was manually determined and expressed as the percentage of the total. The area and perimeter of > 60 AChR densities per animal were automatically determined in a 60 μm² ROI for each postsynaptic structure using ImageJ software. Representative 3D videos where acquired with Imaris Scene Viewer 7.6.4 software (Bitplane, Zurich, Switzerland).

Protein sequence and structural analysis

Structural analysis was performed using the SWISSMODEL server (http://swissmodel.expasy.org/) and Chimera1.6.1 imaging software. The PDB structure 3uem (Wang et al., 2012) was used as a template to model PDIA1 mutants, whereas for ERp57 mutants, the PDB structure 3f8u (Dong et al., 2009) was used.

Statistical analysis

For statistical analysis GraphPad Prism Software version 5.01 was used. All graphs show mean with SEM. Significance was calculated using Student’s t-test, one-way ANOVA, or two-way ANOVA with Bonferroni’s post hoc test.

Expanded View for this article is available online.

Acknowledgements

We thank Dr. Miklos Geiszt (Semmelweis University, Hungary) for providing HyPer-ER vectors and Dr. Neil Bulleid (University of Glasgow, Scotland) for providing PDIA1-VS and ERp57-VS plasmids. We thank Dr. Günter Hammerling (German Cancer Research Center, Germany) for kindly providing the floxed Erp57 mice. We thank Silke Escobar, Javiera Ponce, Claudia Molina, Alvaro Diaz, and Ulrich Bergmann for technical assistance. This work was primarily funded by the Frick Foundation, Muscular Dystrophy Association 382453 in addition to ALS Therapy Alliance 2014–F-059, Millennium Institute No. P09-015-F, CONICYT-USA2013-0003 (to C.H.) and Ring Initiative ACT1109 grants (to C.H. and P.H.) and FONDAP 15150012 (to C.H., S.M., RLV) and FONDECYT no. 3110067 and 1150608 (to D.B.M.), and FONDECYT no. P15150012 (to R.L.V.). We also received support from the Michael J Fox Foundation for Parkinson’s Research, COPEC-UC Foundation, FONDEF no. DI111007 and FONDECYT no. 1140549, Office of Naval Research-Global (ONR-G) N62909-16-1-2003 and ALSR Therapeutic Idea Award AL1500551 (to C.H.), FONDECYT no. 1110324 (to A.C.); ALS Therapy Alliance and NIH (NS057593-07) (to F.B.G.), CONICYT Doctoral Fellowship (to M.T., A.D., J.O., V.P., and V.V.), CONICYT
ALS-linked PDI variants cause motor dysfunction

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Published online: February 11, 2016

The EMBO Journal

24110099 (to F.J.B.); FONDECYT 1130321 and MINREB Millennium Nucleus RC120003 (to J.P.H.). FONDECYT no. 1110433 (to P.H.). R.H.B. is supported by ALS Therapy Alliance, Project ALS, P2ALS, the Angel Fund, the Pierre L. de Bourgknecht ALS Research Foundation, the Al-Athel ALS Research Foundation, the ALS Family Charitable Foundation and NIH/NINDS 1R01NS050557. P.G.-P. was supported by the Alfonso Martin Escudero Foundation (Madrid). M.J.S. and L.W.R. were supported by Biocenter Oulu, Finland.

Author contributions
PG-P discovered and cloned PDI variants into expression vector. M.J.S and L.W.R performed in vitro structural and biochemical studies. UW performed immunoprecipitation experiments. UW, AS, and RA performed HyperER experiments. SM and NM performed PDI knockdown experiment. RLV and UW performed colocalization studies. SA performed ELISA. AC, KP, RA, and UW performed mitochondrial and muscle protein analyses. PH and SF-C performed spinal cord stereology. UW, DBM, and PR performed cortex, spinal cord, and muscle protein analysis. PH and SF-C performed spinal cord stereology. JS and MC performed EMG measurements. UW managed and collected all data and conducted statistical analysis. UW, CH, RHB, BvZ, F-BG, MLC, LWR, and JPH designed and supervised the experiments. UW and CH wrote the manuscript. RHB, BvZ, F-BG, MLC, LWR, and JPH revised and edited the manuscript.

Conflict of interest
The authors declare that they have no conflict of interest.

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