Structural basis for ligand capture and release by the endocytic receptor ApoER2

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Abstract

Apolipoprotein E receptor 2 (ApoER2) is a close homologue of low-density lipoprotein receptor (LDLR) that mediates the endocytosis of ligands, including LDL particles. LDLR family members have been presumed to explore a large conformational space to capture ligands in the extended conformation at the cell surface. Ligands are subsequently released through a pH-titrated structural transition to a self-docked, contracted-closed conformation. In addition to lipoprotein uptake, ApoER2 is implicated in signal transduction during brain development through capture of the extracellular protein reelin. From crystallographic analysis, we determine that the full-length ApoER2 ectodomain adopts an intermediate contracted-open conformation when complexed with the signal-competent reelin fragment, and we identify a previously unappreciated auxiliary low-affinity binding interface. Based on mutational analyses, we propose that the pH shift during endocytosis weakens the affinity of the auxiliary interface and destabilizes the ligand–receptor complex. Furthermore, this study elucidates that the contracted-open conformation of ligand-bound ApoER2 at neutral pH resembles the contracted-closed conformation of ligand-unbound LDLR at acidic pH in a manner suggestive of being primed for ligand release even prior to internalization.

Keywords: ApoER2; endocytic receptor; LDLR family; ligand uptake; reelin

Subject Categories: Membrane & Intracellular Transport; Signal Transduction; Structural Biology

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Introduction

Low-density lipoprotein receptor (LDLR) binds LDL particles at the cell surface, and the complex internalizes through endocytosis [1]. After internalization, the LDL particles dissociate from LDLR in the early endosome and are delivered to the lysosome where they are degraded. Meanwhile, LDLR is recycled back to the cell surface for further uptake of LDL. Since LDLR plays a pivotal role in the clearance of LDL from blood plasma, deletion or defects of LDLR increase LDL levels, causing familial hypercholesterolemia (FH) [2,3]. LDLR is a type I membrane protein, and its ectodomain contains an N-terminal tandem repeat of seven LDLR type-A (LA1–7) modules followed by an epidermal growth factor precursor homology (EGFPH) domain [4,5]. The EGFPH domain consists of two EGF-like modules (EGF-A and EGF-B), a YWTD-propeller homology (EGFPH) domain [4,5]. The EGFPH domain consists of two EGF-like modules (EGF-A and EGF-B), a YWTD-propeller homology (EGFPH) domain [4,5]. Each LA module generally assumes a compact disulfide-knotted structure containing a Ca2+-coordinated acidic residue cluster and an aromatic residue, constituting a putative ligand-binding site [8–14]. Although the LA modules always occur as a set of multiple repeats in LDLR and its homologues, ligand recognition is often mediated by particular subset of the module repeat segment [15]. Several crystal structures of the LA module from LDLR family members have been determined in complex with non-LDL ligands, such as receptor-associated protein (RAP) and virus coat protein [16,17], conforming to a canonical ligand recognition mode: LA modules commonly accommodate a Lys side chain of the ligand into a pocket surrounded by the conserved acidic cluster and the aromatic residue. LA modules presumably recognize LDL and other lipoproteins through a similar mechanism given that the major components of lipoproteins, apoB and apoE, have an abundance of basic residues [16,18].

Dissection of this potential mechanism requires a structure-based understanding of the interaction between LDLR and its ligands at the cell surface. A moderate-resolution structure of the full-length LDLR ectodomain has been previously determined by X-ray crystallography [19]. The structure showed a hairpin-like self-docked conformation, in which linearly arranged LA1–7 modules are contracted by EGF modules and cover the top face of theYWTD-propeller domain. Since the ectodomain was crystallized under slightly acidic conditions at pH 5.3, this conformation was thought to reflect the binding-inactive state of the receptor (hereafter defined as a contracted-closed conformation) in the endosomal compartment. The structure of the same LDLR ectodomain has also been determined in complex with protein...
convertase subtilisin/kexin type 9 (PCSK9) under neutral conditions of pH 7.0 [20]. PCSK9 is known to serve as a regulatory protein of LDLR to promote its degradation [21,22]. In contrast to the contracted-closed LDLR structure under acidic conditions, the LDLR ectodomain bound by PCSK9 exhibited an extended conformation. Because the LA modules are liberated from theYWTD domain due to a swing motion of EGF modules at neutral pH in this extended, or extended-open, conformation, it has been presumed that the ectodomain becomes more flexible to explore a large conformational space and capture its binding partners. The structural analysis raised the possibility that PCSK9, unlike other LDLR ligands, binds with the EGF-A module of LDLR to prevent EGF modules from arranging as observed in the contracted-closed conformation [20]. The detailed molecular mechanism of the ligand release, however, still remains elusive, as no physiological ligand-complex structures are available for the entire ectodomain of LDLR or for its closely related homologues. Unfortunately, crystallization of the LDLR:LDL complex for structural analysis is expected to be extremely difficult due to the fact that the chemical composition of the LDL particle is inhomogeneous. Structural analysis of LDL bound to LDLR by cryo-electron microscopy has suggested that theYWTD domain interacts with LDL, but the conformation of the entire ectodomain remains unresolved [23].

Invoked by the dilemma described above, we hypothesized that an informative model of LDLR function could be developed by determining a functionally relevant structure of an LDLR family member in a ligand-bound complex that is more amenable to crystallographic analyses. Among the variety of LDLR family members, apolipoprotein E receptor 2 (ApoER2) shows significant similarities to LDLR in both domain organization and function [24,25]. The ectodomain of ApoER2 consists of the same set of structural modules in the same order as LDLR although splicing variants containing different numbers of the LA repeats in the ligand-binding domain are identified for ApoER2 [26,27]. Moreover, ApoER2 mediates the uptake of apoE-containing lipoproteins via endocytosis [27]. In addition to lipoprotein uptake, ApoER2 binds the extracellular protein reelin to mediate the signal transduction that regulates cortical layer formation during brain development [28]. Reelin is a gigantic glycoprotein that contains a characteristic concatenation of eight repeats termed “reelin repeats” [29]. It has been established that the fifth and sixth reelin repeats (R56) comprise the signaling-competent fragment and interact with ApoER2 primarily using the first LA module (LA1) [30]. X-ray crystallographic analysis demonstrated that LA1 of ApoER2 captures a Lys residue on reelin with a conserved acidic–aromatic pocket [31], indicating that reelin is recognized by ApoER2 via the canonical ligand-binding mechanism of the LDLR family. Hence, we chose the ApoER2–reelin pair as a model to explore the structural mechanism of ligand recognition by the LDLR family members.

In this study, we determined the crystal structure of the ApoER2 ectodomain in complex with the reelin R56 fragment and found that the receptor assumes a contracted-open conformation by engaging the ligand through multiple binding interfaces. The resulting structure, combined with surface plasmon resonance analysis under neutral and acidic pH, provides important clues for understanding the mechanism by which LDLR family members release ligands in the endosomal compartment.

Results

Quantitative binding analysis between ApoER2 ectodomain and reelin R56

To quantify the affinity of the ApoER2 and reelin R56 binding interaction, we first performed surface plasmon resonance (SPR) analysis using the entire ectodomain fragment of the human ApoER2 splicing variant lacking LA4-6. It is known that this ApoER2 variant is expressed in human brain tissue [32] and that the same variant serves as the receptor for reelin in mouse [33,34]. The ApoER2 ectodomain (ApoER2 ECD) fragment was immobilized on the sensor chip, and the reelin R56 fragment was injected over the sensor chip surface. The dissociation constant between ApoER2 ECD and reelin R56 was estimated to be $1.2 \times 10^{-8}$ M at pH 7.5 by steady-state analysis (Fig 1A, Table 1).

In addition, SPR measurements performed at pH 5.5 resulted in a drastic increase in the dissociation constant (Fig 1B, Table 1). Our results indicate that the binding affinity of the reelin R56 fragment for ApoER2 decreases after endocytosis, similarly to that of the LDL particle for LDLR. In our previous work, we performed an analogous experiment using only the LA1 module of ApoER2. There we found the dissociation constant between LA1 and reelin R56 at neutral pH to be $7.3 \times 10^{-8}$ M, a fivefold in comparison with the full-length ApoER2 ECD in this work. It was also observed that R56 dissociates from the full-length ApoER2 ECD relatively slowly compared with the partial fragments, as was consistent with our preliminary analysis [30]. As shown in Fig 1A, the response curve of the ApoER2 ECD-R56 interaction in the present analysis drops gradually after the end of injection. In contrast, it has been observed in our previous work that the curve drops almost directly to baseline in case of the partial fragments including the LA1 fragment [31]. We therefore expected that the ApoER2 ECD possesses auxiliary low-affinity binding interfaces except for LA1, which would contribute to the stabilization of the ligand complex.

Figure 1. Steady-state analysis of SPR data #1: Estimation of dissociation constants and exploration of binding interfaces.

A, B Estimation of dissociation constants at (A) pH 7.5 and (B) pH 5.5. A representative result from triplicate SPR measurements is plotted for each condition. To obtain overlaid sensograms, serially diluted reelin R56 fragments were injected over a sensor chip surface with ApoER2 ECD fragments immobilized through biotin–streptavidin interactions (inset). Equilibrium response ($R_{\text{eq}}$) values were plotted against the concentration of injected R56 to calculate the dissociation constants ($K_{\text{d}}$). The $K_{\text{d}}$ value for each condition is listed as the mean of triplicates with the standard deviation in Table 1.

C–F Introduction of salt bridge-disrupting mutations to LA modules: (C) D68N in LA1, (D) E107Q in LA2, (E) E150Q in LA3, and (F) E191Q in LA7.

Source data are available online for this figure.
Figure 1.

A) Reelin R56 WT vs ApoER2 ECD WT: pH 7.5

B) Reelin R56 WT vs ApoER2 ECD WT: pH 5.5

C) Reelin R56 WT vs ApoER2 ECD D68N/LA1: pH 7.5

D) Reelin R56 WT vs ApoER2 ECD E107Q/LA2: pH 7.5

E) Reelin R56 WT vs ApoER2 ECD E150Q/LA3: pH 7.5

F) Reelin R56 WT vs ApoER2 ECD E191Q/LA7: pH 7.5
Identification of a low-affinity binding interface within the ApoER2 LA modules

To explore the binding sites in regions other than the LA1 module, we next designed a series of ApoER2 ECD derivatives to perturb the affinity of candidate interfaces. For each mutation, a specific acidic residue was mutated to disrupt potential salt bridges in the putative ligand-binding interface of the respective LA module (LA1: D68N, LA2: E107Q, LA3: E150Q, and LA7: E191Q, respectively; Fig EV1). The mutated acidic residues are not involved in the coordination of calcium ions unlike other acidic residues in the cluster. Therefore, the introduced mutations are thought to partially weaken the binding affinity for basic residues, while maintaining the structural integrity of the respective LA modules. Consistent with previous binding and structural analyses, the mutation in LA1 drastically reduced the binding affinity for R56 ($K_D > 2.8 \times 10^{-6}$ M; Fig 1C, Table 1). In addition, the LA2 mutant also showed a threefold reduction in affinity ($K_D = 3.8 \times 10^{-8}$ M; Fig 1D, Table 1), whereas the affinities of the LA3 and LA7 mutants were in the same range as that of the wild type (Fig 1E and F, Table 1). These results strongly indicate that the LA2 module is involved in the complex formation.

Structure determination of the entire ApoER2 ectodomain in complex with reelin R56

To elucidate the details of the complex formation, we then determined the X-ray crystal structure of the entire ApoER2 ECD in complex with the reelin R56 fragment (Fig 2). Co-crystals were obtained under neutral conditions of pH 7.5 using constructs of the two proteins expressed in mammalian cells. The R56 fragment was selenomethionylated for single-wavelength anomalous diffraction (SAD) phasing. The initial model for the complex was built against an electron density map at 3.2 Å resolution. The crystal contains two nearly identical complexes in the asymmetric unit. The electron density for R56 is relatively clear, producing a model consistent with a crystal structure determined for unbound reelin R56 [30]. R5 and R6 are composed of two homologous subrepeats (subrepeats A and B) and an intervening EGF-like module, respectively, and are arranged side by side. Interestingly, the overall structure of ApoER2 ECD seems similar to the contracted-closed conformation of LDLR crystallized under the acidic conditions [19]. The interface between R56 and LA1 (referred to as Interface-1) is also almost identical to that observed in the crystallographic analysis of the R56:LA1 complex (Fig 3A) [31]. In the present structure, the N-terminal LA modules are folded back toward the YWTD propeller domain, but they form no direct contacts between them.

The model of ApoER2 contains some ambiguity in the region between LA2 and EGF-A due to disorder (Fig 2A and B). We could not observe significant electron densities for LA3 and LA7, whereas density for EGF-A was weak but still clear enough to build a reliable model using the NMR structure of LDLR EGF-AB unit as a reference (PDB code: 1HJ7) [35]. Although we expect the LA2 module to interact with R56 based on the SPR analysis, LA2 appears to be highly mobile. The electron density corresponding to LA2 was undoubtedly present in the region following the C-terminus of LA1, but it was impossible to confidently trace the backbone of LA2 in the electron density map.

Assignment of the LA2 model by constrained real space fragment search

To assign a reliable model of LA2 against the weak electron density, we separately determined a high-resolution structure of a partial fragment containing LA2 and fitted it into the electron density of the complex crystal as a rigid body. For this purpose, the LA12 fragment was produced in E. coli and crystallized after refolding in redox buffer. The resulting LA12 structure determined at 1.9 Å resolution showed an extended arrangement where the respective ligand-binding surfaces of the two LA modules were pointed in opposite directions (Fig 2C). In fact, the LA2 model did not overlap with the observed weak electron densities when we aligned the LA12 structure onto the LA1 module in the complex. The relative orientation of LA1 and LA2 seems to be restricted by the hydrogen-bonding network in the inter-module linker and by the intimate interactions with symmetry neighbors in the crystal. In general, the inter-LA arrangement is presumed to be flexible among the LDLR family members. In LDLR, for instance, the LA3-LA4 arrangement in the contracted-closed ectodomain structure under the acidic conditions [19] is significantly different from that in the LA34 fragment in complex with RAP [16]. We therefore postulated that LA12 in the

| Analyte (reelin R56) | Ligand (ApoER2 ECD) | pH  | Ca** conc. | $K_D$ (M)* | P-value |
|---------------------|---------------------|-----|------------|------------|---------|
| Wild type           | Wild type           | 7.5 | 2 mM       | ($1.2 \pm 0.1) \times 10^{-6}$ |         |
|                     |                     | 5.5 | 2 mM       | ($4.1 \pm 0.3) \times 10^{-7}$ |         |
| Wild type           | D68N/LA1            | 7.5 | 2 mM       | ($2.8 \pm 0.1) \times 10^{-6}$ | 0.0061c |
| Wild type           | E107Q/LA2           | 7.5 | 2 mM       | ($3.8 \pm 0.2) \times 10^{-8}$ | 0.0002c |
| Wild type           | E150Q/LA3           | 7.5 | 2 mM       | ($1.0 \pm 0.0) \times 10^{-8}$ |         |
| Wild type           | E191Q/LA4           | 7.5 | 2 mM       | ($1.1 \pm 0.0) \times 10^{-8}$ |         |

*Each $K_D$ value represents the mean of triplicate SPR measurements with standard deviation. Processing of the sensorgram and curve fitting of affinity analysis were performed separately in the triplicate experiments, and the three obtained $K_D$ values were used to calculate the mean, standard deviation, and P-value.  

**The actual $K_D$ value should be higher than the reported value since the highest concentration of the analyte in the SPR measurement was lower than the estimated $K_D$ value.  

The difference of the $K_D$ value compared with that calculated for the interaction between reelin R56 wild type versus ApoER2 ECD wild type at pH 7.5 is statistically significant with the indicated P-value, which is calculated by the unpaired two-tailed t-test.

Table 1. Summary of SPR analysis #1: Estimation of dissociation constants and exploration of binding interfaces.
ApoER2 complex also rearranges by a hinge motion at the inter-module linker, thereby suitably placing LA2 for interaction with R56. We fitted the LA2 model by a constrained real space fragment search (Fig 2D). This procedure searched the position and orientation of the LA2 model, which maximized electron density values at atomic positions, while constraining the distance between LA1 and LA2. As a result, similar solutions were obtained for both of the two complexes in the asymmetric unit of the crystal, where LA2 is located close to the bottom face of reelin R5B. (Hereafter, the interface between LA2 and reelin R5B is referred to as Interface-2.)

This interaction mode is consistent with the canonical ligand-binding mode as observed in other LA–ligand pairs including Interface-1 of the ApoER2 ECD:reelin R56 complex. Importantly, the acidic residue cluster on the ligand-binding surface of LA2 is oriented to the side chain of K2194 on reelin R5B despite the lack of imposed distance restraints between them during the constrained real space search. Although several other solutions showed high scores in the search, most of them placed the LA2 model in similar positions and orientations to those in the top solution (Fig EV2A and B).
Figure 3. Three binding interfaces between ApoER2 ECD and reelin R56.

A Close-up view of Interface-1. The R6A subrepeat of reelin R56 and ApoER2 LA1 are shown in green and magenta, respectively. The side chains of the residues constituting the binding interface are shown as stick models while the calcium ion is indicated as an orange sphere. Crystal structure of reelin R56 in complex with LA1 (white: PDB code: 3A7Q) superposed onto R6A. Relative arrangement of R6A and LA1 is essentially consistent between the ApoER2 ECD-R56 and LA1-R56 complexes.

B Close-up view of Interface-2. In addition to K2193, R2193 on reelin R5B (cyan) seems to be involved in the interaction with ApoER2 LA2 (magenta). LA2 possesses two histidine residues, H96 and H99, close to the acidic cluster coordinating a calcium ion (orange sphere).

C Close-up view of Interface-3. The ribbon models of EGF-A (dark blue), EGF-B (light blue) and reelin R5A (green) are shown with transparent surface. The appendage-like loop of R5A is highlighted in red. Interface-3 is maintained through shape complementarity between the appendage-like loop and the concaved surface of EGF-AB. As highlighted with the stick model, both of EGF-A and EGF-B provide for the residues coordinating a calcium ion (orange sphere).

D Comparison of conformation in the appendage-like loop region. The conformation of the loop is significantly different between the three available crystal structures, unbound R56 (cyan), in complex with ApoER2 LA1 (magenta), and in complex with ApoER2 ECD (green), whereas the base of the loop is fixed by a disulfide bond (stick model) and a calcium ion (orange sphere). The loop region between S1986 and D1994 is highlighted in dark color while the rest part of R5A is shown in light color in each reelin R5A model. The structure of ApoER2 EGF-AB is shown as a blue surface model.

E Sequence alignment of mouse reelin repeats around the appendage-like loop of reelin R5A. The loop between the β3 and β4 strands in R5A is obviously longer in comparison with the seven other reelin repeats. The region highlighted in red was substituted to a G3 linker, and the mutant was subjected to SPR analysis (see Fig.4). The conserved cysteine pair that forms a disulfide bond is indicated in orange. The secondary structure of R5A was displayed below the alignment.
Examination of the interaction between reelin R5B and ApoER2 LA2

To examine the reliability of the model assignment and the contribution of Interface-2 to the complex stabilization, we introduced mutations to the binding site identified on reelin R5B. Based on the structural model, it seems that R2193, in addition to K2194, contributes to the specific interaction with the acidic residue cluster (Fig 3B). Supporting this conclusion, involvement of an analogous secondary basic residue has been frequently observed in the interaction of other LA-ligand pairs as well [16]. To abolish the putative interaction with LA2, the reelin R56 double-mutant R2193A/K2194A was constructed and subjected to SPR analysis. Consequently, this mutant showed a 10-fold drop in the binding affinity for the ApoER2 ECD wild type ($K_D = 1.6 \times 10^{-7}$ M; Fig 4A, Table 2). Obviously, the response curve dropped rapidly after the end of injection, indicating a faster dissociation of the R56 mutant compared with the wild type. This mutational effect is more likely explained by a change in interface affinity than by a change in tertiary conformation as the R2193A/K2194A R56 fragment and wild type R56 have similar hydrodynamic properties and thermal stabilities in analytical gel filtration and a thermal shift assay, respectively (Fig EV3).

Unique among the four LA modules in this ApoER2 splicing variant, LA2 contains two histidine residues (His-96 and His-99) on the binding surface (Figs 3B and EV1B). Protocation of histidine side chains under acidic conditions would be expected to disrupt the interaction with R2193 and K2194 on R5B due to electrostatic repulsion. We therefore constructed two ApoER2 ECD mutants, H96K/H99K and H96A/H99A, to test whether these two histidine residues act as a pH sensor. The H96K/H99K mutant mimics the protonated state of the histidine residues under acidic conditions while H96A/H99A abolishes electrostatic repulsion due to protocation. In fact, the dissociation constant between ApoER2 ECD and reelin R56 increased to $4.5 \times 10^{-6}$ M by the mutation H96K/H99K under neutral pH conditions (Fig 4B, Table 2) while the reduction in the dissociation constant was observed for H96A/H99A under the same condition ($8.0 \times 10^{-9}$ M; Fig 4D, Table 2). Furthermore, the H96A/H99A mutation stabilized the interaction even under acidic pH conditions ($K_D = 1.2 \times 10^{-7}$ M; Fig 4E, Table 2) whereas the dissociation constant for H96K/H99K ($K_D = 4.9 \times 10^{-7}$ M; Fig 4C, Table 2) was comparable to that for the ApoER2 ECD wild type under neutral pH conditions as described above ($K_D = 4.1 \times 10^{-7}$ M; Table 1).

Dissecting the contribution to affinity from structural elements in the interface between reelin R5A and ApoER2 EGF-AB

Further inspection of the complex structure revealed an intimate intermolecular interaction between R5A and EGF-AB (referred to as Interface-3). A prominent feature of the interface on R5A is an appendage-like loop region (Cys-1983 to Asp-1994) formed between the β3 and β4 strands (Fig 3C). The loop fits into the concaved surface formed between EGF-A and EGF-B. A characteristic pair of cysteines is present to form a disulfide bond in all of the reelin repeats (Fig 3E), and Cys-1983 forms a disulfide bond with Cys-2030 in R5. Asp-1994 is located just upstream of the calcium-binding site, which is also a characteristic structural element of the subrepeats. Interestingly, the insertion between the β3 and β4 strands in R5A is exceptionally long compared to those in the other subrepeats A (Fig 3E). In addition, the conformation of this β3–β4 loop differs between the three crystal structures of R56 that we have determined so far [30,31] (Fig 3D). In the structure of R56 alone, the loop region compactly packs against the surface of R5A. In the R56:LA1 complex, the loop appears to protrude out from R5A in an extended conformation. This conformation is consistent with the electron density in the present complex structure, although the model was not unambiguously assigned in this region due to disorder. While binding to EGF-AB may stabilize an alternate conformation of the loop, we were surprised to learn that it does not greatly contribute to affinity of the interface. In fact, the binding affinity did not change significantly when the appendage loop (Pro-1984 to Glu-1993) was replaced with a flexible linker composed of three repeats of glycine and serine ($K_D = 1.3 \times 10^{-8}$ M; Fig 4F, Table 2). It is possible that this negligible contribution is the result of an enthalpy–entropy tradeoff in the ordering of the loop in the wild-type interface.

Another minimal perturbation considering the central position of calcium ions in Interface-3, we hypothesized that this interface should also be sensitive to calcium depletion during endocytosis. EGF-A and EGF-B are classified as the calcium-binding EGF, and the calcium ion bound to EGF-B is located at the center of concaved surface. Although the influence of calcium depletion has not been studied for ApoER2, we hypothesized that eliminating calcium from our binding experiments would have a particularly strong effect on Interface-3. It has been reported for LDLR that the corresponding calcium ion dissociates from EGF-B under low calcium conditions even at neutral pH [36], while calcium ions seem to be more tightly bound to the LA modules under the same condition [37,38]. Therefore, we presumed from considerations of...
Figure 4.

A. Reelin R56 R2193A/K2194A vs ApoER2 ECD WT: pH 7.5

B. Reelin R56 WT vs ApoER2 ECD H96K/H99K: pH 7.5

C. Reelin R56 WT vs ApoER2 ECD H96K/H99K: pH 5.5

D. Reelin R56 WT vs ApoER2 ECD H96A/H99A: pH 7.5

E. Reelin R56 WT vs ApoER2 ECD H96A/H99A: pH 5.5

F. Reelin R56 GS3 linker vs ApoER2 ECD WT: pH 7.5

G. Reelin R56 WT vs ApoER2 ECD WT: pH 7.5, Ca²⁺ 3 μM
conserved sequence and function that the ApoER2 EGF-B domain is also likely to release the calcium ion under low calcium conditions, resulting in a considerable conformational change of the concaved surface. Nevertheless, the dissociation constant slightly increased from $1.2 \times 10^{-8}$ M to $3.3 \times 10^{-8}$ M (Fig 4G, Table 2) when the calcium concentration was lowered from 2 mM to 3 μM in the SPR analysis. Although the influence of calcium depletion would not be limited to a structural change of the concaved surface, the above result is consistent with our conclusion from mutation of the appendage loop that the contribution of Interface-3 to complex stabilization is marginal.

### Discussion

In the present study, we have discovered that the LA2 module of ApoER2 provides an auxiliary binding interface for the reelin R56 fragment, supplementing the known high-affinity interface in LA1. In the crystallographic analysis, we located the LA2 module near the bottom face of reelin R5B, where the putative ligand-binding surface of LA2 recognizes two basic residues on R5B (R2193 and K2194) by the ligand-binding mechanism canonical to the LA module. In accordance with this, we observed through SPR analysis that the introduction of a salt bridge-disrupting mutation (E107Q) to LA2 slightly destabilized the complex by a roughly threefold change in $K_d$. Furthermore, the more severe R2193A/K2194A double mutation in R56 exhibited a significant 10-fold further increase in the dissociation constant of the complex as compared with the R56 wild type interaction.

Based on additional mutational analyses, we presume Interface-2 also plays a pivotal role in the ligand release process during endocytosis due to pH-sensitive histidines that are unique to Interface-2 among the interfaces between R56 and ApoER2. Our SPR analysis has shown that the binding affinity of the entire ApoER2 ECD:reelin R56 complex affinity is adversely affected by an acidic pH shift. Substitution of the two histidines to lysines destabilized the complex even under the neutral pH conditions whereas the substitution to alanines reduced the sensitivity to pH shift and stabilized the complex at acidic pH. The side chains of these two histidines are likely deprotonated in the crystal structure of ApoER2 ECD:reelin R56 complex that was obtained at pH 7.5, enabling LA2 to interact with the positively charged surface of R5B.

Another important finding from the present structure determination is that the ectodomain of ApoER2 does not assume the extended conformation when it binds with reelin R56 under neutral pH conditions (Fig 5). This contradicts the general expectation that the extended conformation is necessarily the binding-active conformation in LDLR homologues. With respect to the position of the EGF-AB, the conformation of reelin R56 complexed ApoER2 is rather similar to the contracted-closed conformation of unbound LDLR under acidic conditions (Fig 5A and D). In our structure, the EGF-AB unit protrudes from the side of blades 5 and 6 of the YWTD β-propeller (Fig 5B and E), whereas EGF-AB of the LDLR:PCSK9 complex is located on the side of blades 1 and 2 in the extended conformation under neutral pH conditions (Fig 5C and F). These observations conform to the notion that the receptor in the open conformation where the LA modules are liberated from the YWTD domain is flexible due to the mobility of the EGF-AB unit, and indicate the presence of metastable conformation that is neither extended nor contracted-closed. We therefore defined the structure of the ApoER2 ectodomain with reelin R56 as a contracted-open conformation where the LA modules are open to the ligand but are positioned close to the top face of the YWTD domain. It seems that the formation of the contracted-open conformation is permitted by the presence of Interface-3 between EGF-AB and R6A. Without this interaction, the LA1 and LA2 modules, which, respectively, interact with basic residues of reelin R56 in a specific manner, cannot be located in proximity to the top face of YWTD. It was presumed that the receptor on the cell surface can explore a large conformational space, without interactions between the LA modules and YWTD domain, to capture the ligand. Our results, however, raised the possibility that ApoER2 has a preference for the contracted-open conformation after it binds with the ligand although the structure of ApoER2 ectodomain will be influenced to some degree by crystal lattice forces. The structural unit containing a YWTD flanked by two EGF modules (EGF-YWTD-EGF) occurs widely in the LDLR family members other than the LDLR close homologues. Interestingly, the N-terminal (incoming) EGF is located either between the blades 1 and 2, or between the blades 5 and 6 in all of the known crystal structures containing the EGF-YWTD-EGF unit, whereas the
C-terminal (exiting) EGF is always located between the blades 3 and 4 (Fig EV4). We therefore presume that the arrangement of EGF-B unit against YWTD in the present ApoER2 structure is not a randomly chosen state out of numerous conformations, but reflects one of the two distinct metastable conformations of this receptor.

The structural features of the ApoER2 ECD:reelin R56 complex are also consistent with a common mechanism between ApoER2 and LDLR for the final process of ligand release. It has been reported in the crystallographic analysis of the full-length LDLR ectodomain that the contracted-closed conformation is mediated by the intramolecular interactions between the top face of the YWTD domain and the LA repeats, where the interaction via the LA4 module is dominant (Fig 6A and B). In LDLR, LA4 interacts with the side chain of K560 in the YWTD domain in a similar manner to the canonical ligand-binding mode of the LA modules. The YWTD domain contains two histidines (H562 and H586) close to K560, and the protonation of these residues is thought to enhance the affinity between LA4 and YWTD under acidic conditions. In the above-discussed Interface-2 of the ApoER2 ECD:reelin R56 complex, the protonation of histidine residues in LA2 was expected to destabilize the interactions with the basic residues of R5B. In contrast, the protonated histidine residues of YWTD should stabilize the interactions with the LA4 module as they can form salt bridges with the acidic residues of LA4. In fact, it is also known that histidine mutations, such as H562Y, cause FH, likely because it reduces the release activity of LDL [39,40], suggesting the importance of the contracted-closed conformation for ligand release through a competitive inhibition mechanism. The corresponding lysine and two histidine residues are conserved on the top face of the ApoER2 YWTD domain and can constitute a putative intramolecular binding
interface (Fig 6C and D). Among the four LA modules in ApoER2, LA1 is the most proximal to this putative interface in the ApoER2 ECD:reelin R56 complex. Hence, there is a possibility that LA1 forms an intramolecular interaction with the putative interface on YWTD when the entire ApoER2:reelin complex is destabilized and LA1 dissociates from the bottom face of R6A after endocytosis. Such a partner exchange for the LA1 module should be the final step in the ligand release process. We postulate here that the reduction in the binding affinity of ApoER2 for reelin R56 under acidic pH is mainly derived from the electrostatic repulsion at Interface-2. Nevertheless, the increase in the dissociation constant under low pH was much larger than that arising from the H96K/H99K mutation on LA2, which mimics the pH-titrated disruption of Interface-2. The intramolecular interaction between LA1 and YWTD under acidic conditions, if it occurs, would sequester LA1 from interaction with reelin R56, decreasing the apparent association constant and the observed affinity. Further studies are required to address the issues of whether or not the contracted-closed conformation is formed through LA1, or any other LA modules, and whether or not it promotes ligand release through a competitive inhibition mechanism in this splicing variant of ApoER2.

The present study again raises the importance of structural change from the extended to the contracted-closed conformation in receptor recycling. It has been hypothesized that the extended conformation observed in the LDLR:PCSK9 complex reflects a “recycling-inhibited” state, in which PCSK9 prevents the receptor from changing to the contracted-closed conformation [20]. The LDLR:PCSK9 complex is maintained by multiple interfaces where the YWTD domain as well as the EGF-A module serves as the binding sites for PCSK9. In fact, it has been shown that disruption of the extended conformation by mutation leads to a reduction in binding affinity for PCSK9, indicating the importance of proper positioning of the respective binding interfaces in the complex. In contrast, our present study revealed that ApoER2 can bind with its ligand, reelin R56, in the contracted-open conformation. Although disordered regions in the electron density demonstrate that the ApoER2 ectodomain remains flexible to a significant degree even after binding with reelin, it is suggested that the ligand binding guides the receptor to
adopt the conformation that can readily change to the contracted-closed conformation after the pH-titrated ligand dissociation. These observations raised the possibility that the ectodomain conformation correlates with the receptor fate in LDLR and its homologues. In other words, a contracted-open conformation leads to receptor recycling and an extended conformation leads to receptor degradation.

In conclusion, we first discovered, based on mutagenesis, the presence of an auxiliary low-affinity binding interface between ApoER2 and the signaling-competent R56 fragment of reelin. Subsequently, we succeeded in determining the crystal structure of the full-length ectodomain of ApoER2 in complex with reelin R56. Our present structure demonstrates that ApoER2 assumes a contracted-open conformation when it binds with its ligand, in contrast to the previously reported extended conformation of LDLR in complex with PCSK9. The contracted-open conformation is maintained by multiple binding interfaces between the receptor and ligand, and the binding affinity of the auxiliary interface seems to be weakened mainly by the pH shift during internalization. Although the structure of unbound ApoER2 has not yet been determined, the conservation of the basic patch on the YWTD domain indicates that ApoER2

![Figure 7. Mechanistic model for receptor recycling and degradation in ApoER2.](EMBO reports 993)

The present structural analysis suggests that ApoER2 in complex with its ligands, such as reelin R56, has a preference for adopting the contracted-open conformation although it should exist in equilibrium between the contracted-open and extended conformations at the cell surface. After the receptor:ligand complex is internalized through endocytosis, the binding affinity decreases due to the pH shift in the endosomal compartment. In such an environment, ApoER2 is also expected to assume a contracted-closed conformation to release the ligand, as LDLR does. Subsequently, the receptor is transported back to the cell surface and recycled. In contrast, the previous crystallographic and mutational analyses have indicated that LDLR in complex with PCSK9 has a preference for the extended conformation. It is also known that the binding affinity for PCSK9 is enhanced under acidic conditions. The LDLR-PCSK9 complex is therefore stabilized after internalization and is transported to the lysosome for degradation.
could be capable of adopting the contracted-closed conformation through intramolecular contacts between the LA modules and YWTD domain after endocytosis. Based on the structural data from the present study, we propose a mechanistic model for the ligand uptake and receptor recycling in ApoER2 (Fig 7). Although the number of LA repeats is different between LDLR and the splicing variant of ApoER2 studied in the current work, our ApoER2 structure in complex with reelin R56 is expected to serve as a structural basis for analyzing the pH-dependent ligand uptake mechanism conserved among the LDLR family members. Profound understanding of the mechanism should also contribute to development of a strategy for regulating LDL uptake and receptor recycling, which would further lead to the development of future therapeutic strategies for FH.

Materials and Methods

Expression of biotinylated ApoER2 ECD for surface plasmon resonance analysis

For immobilization on the sensor chip surface, human ApoER2 ECD was fused to a biotin acceptor sequence (ApoER2 ECD-BAS), and then biotinylated by co-expression with biotin ligase from E. coli (BirA) as described previously [41]. More precisely, the gene for ApoER2 ECD-BAS was cloned into the pSGHV0 vector [42] to produce it with N-terminally fused human growth hormone (hGH) plus an octahistidine (His8) tag and the tobacco etch virus (TEV) protease consensus sequence. The modified BirA construct (sBirA-KDEL) contains the N-terminal signal peptidase of bovine prolactin for translocation and a C-terminal ER retention signal for localization. The mutations to disrupt interface salt bridges were introduced to the LA modules of ApoER2 ECD-BAS according to the QuikChange protocol (Agilent Technologies). The constructed plasmids encoding ApoER2 ECD-BAS and sBirA-KDEL were co-transfected into HEK-293T cells using polyethylene imine (PEI), then cultured for 3–4 days in complete DMEM containing 10% fetal bovine serum and 100 µM D-biotin. The harvested cell culture supernatant was clarified by centrifugation and filtration, neutralized by adding 1.0 M Tris-Cl (pH 8.0) to a final concentration of 10 mM, and then incubated with Ni-NTA agarose beads. After washing beads with 20 mM HEPES-Na (pH 7.5), 300 mM NaCl, the proteins were eluted with 20 mM Tris-Cl (pH 8.0), 300 mM NaCl, and 20 mM imidazole. N-terminally hexahistidine-tagged TEV protease (His6-TEV) was added to the elution fraction to cleave off the N-terminal hGH-His8 portion, and then the fraction was dialyzed against 20 mM HEPES-Na (pH 7.5) and 150 mM NaCl. The fractions containing reelin R56 were pooled and concentrated by ultrafiltration. In addition, the double mutation R2193A/K2194A was introduced into the reelin R56 construct using the QuikChange protocol while the appendage loop-replaced mutant was constructed by an inverse PCR strategy. These mutants were also expressed and purified according to the same protocol as that for the wild type.

Surface plasmon resonance analysis

Surface plasmon resonance was performed with a Biacore 2000 instrument (GE Healthcare) at 25°C in 20 mM HEPES-Na (pH 7.5), 150 mM NaCl, 2 mM CaCl2, and 0.005% (wt./vol.) Surfactant P20. Biotinylated ApoER2 ECD-BAS fragments were diluted in running buffer, and then immobilized as the ligand on a Sensor Chip SA up to an average of 550 resonance units (RU), according to the manufacturer’s protocol. Sensorgrams were collected by injecting various concentrations of wild type or mutant reelin R56 fragments as the analytes. For regeneration, the sensor chip was washed with 20 mM HEPES-Na (pH7.5), 1 M NaCl, and 20 mM EDTA after each run. The sensorgrams were corrected for bulk refractive index errors using a mock flow cell containing only pre-coupled SA. Dissociation constants (Kd) were calculated using BLAevaluation with affinity analysis. The binding response after 120 sec injection at a flow rate of 30 µl/min was recorded as the response at equilibrium (Req). The R_eq value was plotted against the concentration of analyte (C) and subjected to least-square fitting to the following equation: 

\[ R_{eq} = K_d \times C \times R_{max} / (1 + K_A \times C) \]

where K_A = 1 / K_0 and R_max is the theoretical maximum binding response. Under low pH conditions, measurement was performed using 20 mM MES-Na (pH5.5), 150 mM NaCl, 2 mM CaCl2, and 0.005% (wt./vol.) Surfactant P20. The Kd value in each condition was estimated as the mean of triplicate measurements with the standard deviation. The results of SPR analysis were summarized in Tables 1 and 2.

Expression and purification of ApoER2 ECD for crystallization

To produce the ApoER2 ECD fragment, CHO lec 3.2.8.1 cells [45] were transfected with plasmid encoding ApoER2 ECD fused with hGH plus His8 and a TEV recognition site at the N-terminus (hGH-ApoER2 ECD) [30] and selected for resistance against 1.5 mg/ml G418. The clone with the highest secretion levels was cultured in a roller bottle (Corning). The culture supernatant was collected in a dialysis tube and concentrated with Aquacide II (Merck Millipore). The hGH-ApoER2 ECD was purified from the concentrated culture supernatant with Ni-NTA agarose chromatography. After washing the beads with 20 mM Tris-Cl (pH 8.0), 300 mM NaCl, and 20 mM imidazole, the proteins were eluted with 20 mM Tris-Cl (pH 8.0), 300 mM NaCl, and 250 mM imidazole. The fusion proteins were treated with His6-TEV protease to release the hGH plus His8 tag. TEV protease and hGH-His8 were removed by a second round of Ni-NTA agarose chromatography. The ApoER2 ECD fragment was expressed in HEK293S GnTI-cells [43]. PA-tagged reelin R56 was purified from culture supernatant using NZ-1-immobilized Sepharose as described previously [44]. The C-terminal PA tag was removed by TEV protease treatment, and the reelin R56 fragment was further purified by gel filtration on HiLoad 16/60 Superdex 200 prep grade (GE Healthcare) equilibrated with 20 mM HEPES-Na (pH 7.5) and 150 mM NaCl. The fractions containing reelin R56 were pooled and concentrated by ultrafiltration. In addition, the double mutation R2193A/K2194A was introduced into the reelin R56 construct using the QuikChange protocol while the appendage loop-replaced mutant was constructed by an inverse PCR strategy. These mutants were also expressed and purified according to the same protocol as that for the wild type.

Expression and purification of reelin R56 for surface plasmon resonance analysis

Recombinant mouse reelin R56 protein fused to a TEV protease recognition site and a PA tag at the C-terminus was transiently expressed in HEK293S GnTI-cells [43]. PA-tagged reelin R56 was purified from culture supernatant using NZ-1-immobilized Sepharose as described previously [44]. The C-terminal PA tag was removed by TEV protease treatment, and the reelin R56 fragment was further purified by gel filtration on HiLoad 16/60 Superdex 200 prep grade (GE Healthcare) equilibrated with 20 mM HEPES-Na (pH 7.5) and 150 mM NaCl. The fractions containing reelin R56 were pooled and concentrated by ultrafiltration. In addition, the double mutation R2193A/K2194A was introduced into the reelin R56 construct using the QuikChange protocol while the appendage loop-replaced mutant was constructed by an inverse PCR strategy. These mutants were also expressed and purified according to the same protocol as that for the wild type.
further purified by loading onto anion-exchange chromatography on a MonoQ 5/50GL column (GE Healthcare) equilibrated with 20 mM Tris-Cl (pH 8.0), and 1 mM CaCl₂ and eluting over a linear gradient from 0 to 400 mM NaCl over a 20-column volume at a flow rate of 1 ml/min.

**Preparation of SeMet-substituted reelin R56**

Previous work has described the stable transfectant of CHO lec 3.2.8.1 cells that expresses the reelin R56 fragment fused to an N-terminal signal sequence from mouse nidgen-1 and to a C-terminal TEV protease recognition site [30]. To prepare the selenomethionine-substituted reelin R56, cells in culture flasks were washed with phosphate-buffered saline and incubated with methionine-free alpha-MEM (Cell Science & Technology Institute, Sendai, Japan), supplemented with 5% dialyzed fetal bovine serum (Invitrogen), 50 mg/l l-selenomethionine (SeMet) (Wako Chemical Co.). The media from the first 12–14 h of culture were discarded, and cells were incubated in fresh media supplemented with SeMet for 2–3 days. The SeMet-substituted reelin R56 was purified from the culture supernatants by ammonium sulfate precipitation and Ni-NTA agarose chromatography (QIAGEN). After washing the Ni-NTA agarose column with 20 mM Tris-Cl (pH 8.0), 300 mM NaCl, and 250 mM imidazole, the fractions containing the properly folded fragment were further purified on a Superdex 200 10/300 GL column (GE Healthcare) equilibrated with 20 mM Tris-Cl (pH 7.5), 150 mM NaCl, and 1 mM CaCl₂, at a flow rate of 0.5 ml/min.

**Preparation of the ApoER2 ECD:reelin R56 complex**

Prior to crystallization of the ApoER2 ECD:SeMet-labeled reelin R56 complex, the optimal ratio of each component to form the complex was estimated by gel filtration chromatography. ApoER2 ECD and reelin R56 fragments purified as described above were mixed at various ratios and subjected to a Superdex 200 10/300 GL column equilibrated with 20 mM Tris-Cl (pH 7.5), 150 mM NaCl, and 2 mM CaCl₂. A mixture of reelin R56 and ApoER2 ECD at the ratio providing a single peak corresponding to their complex on the elution profile was used for crystallization. The protein concentration of the complex was estimated to be ~10 mg/ml using the molar extinction coefficients at 280 nm for ApoER2 ECD and reelin R56 [46].

**Preparation of the ApoER2 LA12 fragment**

The LA12 fragment was overexpressed as a glutathione S-transferase (GST) fusion protein in *E. coli* BL21 (DE3) where a His₉ tag and a TEV protease recognition site were incorporated between the GST and LA12 portions. *E. coli* cells were cultured at 37°C for 4 h after induction of protein expression with 1 mM isopropyl-β-D-thio-galactopyranoside and harvested as a pellet by centrifugation. Subsequently, the cells were resuspended and lysed by sonication in a buffer containing 10 mM Tris-Cl (pH 8.0), 300 mM NaCl, and 10 mM imidazole supplemented with 1 mM dithiothreitol. After removing the cell debris, the supernatant of the cell lysate was applied on a Ni-NTA agarose column (GE Healthcare). The bound fusion protein was washed with 10 mM Tris-Cl (pH 8.0), 300 mM NaCl, and 20 mM imidazole, and eluted with 10 mM Tris-Cl (pH 8.0), 300 mM NaCl, and 250 mM imidazole. Elution fractions containing the fusion protein were dialyzed against 20 mM Tris-Cl (pH 8.0) and 300 mM NaCl, and treated with His₉-TEV to cleave off the GST-His₉ portion. The TEV-treated fractions were passed through a Ni-NTA column again, and the LA12 fragment was collected as flow-through. Subsequently, the LA12 fragment was refolded by dialysis at 4°C against 50 mM Tris-Cl (pH 8.0), 10 mM CaCl₂, 2 mM L-cysteine, and 0.5 mM L-cystine according to the protocol reported previously [47]. The refolded LA12 fragment was applied to a MonoQ 5/50GL anion-exchange column (GE Healthcare) equilibrated with 20 mM Tris-Cl (pH 8.0) and 1 mM CaCl₂, and eluted on a linear gradient from 0 to 500 mM NaCl over a 20-column volume at a flow rate of 1.0 ml/min. The fractions containing the proper folded fragment were further purified on a Superdex 200 10/300 GL gel filtration chromatography column (GE Healthcare) by an isocratic elution with 20 mM Tris-Cl (pH 8.0), 150 mM NaCl, and 2 mM CaCl₂ at a flow rate of 0.5 ml/min. The purified LA12 fragment was concentrated by ultrafiltration, and the protein concentration was estimated to be ~5.9 mg/ml according to the same method as described above.

**Crystallization and data collection**

Initial crystallization conditions were searched by random screening where 0.1 μl of the protein solution was mixed with the same volume of precipitant solution using a mosquito® (TTPlabtech), and equilibrated against 100 μl of the precipitant solution in the reservoir. For the ApoER2 ECD:reelin R56 complex, diffraction quality crystals were reproducibly obtained from a solution containing 11–12.5% (wt./vol.) PEG3350, 200–250 mM sodium thiocyanate, and 20 mM HEPES-Na (pH 7.5) after optimization. For the LA12 fragment, a single crystal obtained from the commercial screening kit, Wizard™ I (Emerald BioStructures), was used for data collection. The composition of the reservoir is as follows: 20% (wt./vol.) PEG monomethylther 2000 and 100 mM Tris-Cl (pH 7.0). Prior to data collection, the crystals were soaked in cryoprotectant prepared by mixing the reservoir and ethylene glycol at a volume ratio of 4:1, and flash frozen in liquid nitrogen. For the complex, X-ray diffraction data were collected at Photon Factory (PF) BL-5A with an ADSC Quantum 315r CCD detector using the inverse beam mode to ensure the quality of anomalous signal. For the LA12 fragment, data collection was performed at PF BL-17A using an ADSC Quantum 315r CCD detector. The diffraction images were processed with XDS [48]. The diffraction intensities were then scaled and converted to structure factors with AIMLESS [49] and TRUNCATE [50] in the CCP4 program suite [51,52]. The data collection statistics are summarized in Table 3.

**Structure determination of the ApoER2 LA12 fragment**

The crystal structure of the LA12 fragment was solved by molecular replacement method using the program MOLREP [53]. Both of the LA1 and LA2 modules were successfully assigned by using the
**Table 3. Data collection and refinement statistics in X-ray crystallographic analysis.**

| Molecular entities          | Reelin R56: ApoER2 ECD | ApoER2 LA12 |
|-----------------------------|------------------------|-------------|
| Data collection             |                        |             |
| Space group                 | A6                    | P2₁,2₁,2₁   |
| Cell dimensions             |                        |             |
| a, b, c (Å)                 | 205.95, 205.95, 169.84 | 31.16, 41.78, 55.06 |
| α, β, γ (°)                 | 90, 90, 120           | 90, 90, 90  |
| No. of monomers or complexes/ a.s.u. | 2                | 1           |
| X-ray source                | PF/BL-5A              | PF/BL-17A   |
| Wavelength (Å)              | 0.97/0.94             | 1.00/0.000  |
| Resolution limits (Å)       | 49.5–3.2 (3.28–3.20)  | 41.8–1.9 (1.94–1.90) |
| No. of unique reflections   | 67,441 (4,551)        | 6,043 (372) |
| Completeness (%)            | 100 (100)             | 99.9 (100)  |
| Redundancy                  | 14.8 (14.6)           | 5.2 (5.3)   |
| <l, r>/<l>/<r>/<l>           | 16.4 (2.6)            | 9.5 (2.9)   |
| Rmerge a                   | 0.139 (1.051)         | 0.086 (0.855) |
| CC<sub>1/2</sub>            | 0.997 (0.873)         | 0.995 (0.711) |
| Refinement                  |                        |             |
| Resolution limits (Å)       | 49.5–3.2 (3.28–3.20)  | 33.3–1.9 (1.95–1.90) |
| Rwork b                    | 0.200 (0.260)         | 0.210 (0.315) |
| Rfree c                    | 0.255 (0.310)         | 0.247 (0.282) |
| No. of non-H atoms          | 18,892                | 668         |
| Protein/sugar/solvent       | 18,822 / 70 / 0       | 633 / 0 / 35 |
| Averaged temperature factors (Å) | 99.77             | 37.06       |
| Protein/sugar/solvent       | 99.80 / 92.74 / -     | 37.05 / - / 43.00 |
| RMSD from ideality          |                        |             |
| Bond length (Å)/ bond angle (°) | 0.006 / 1.18 | 0.012 / 1.67 |
| Ramachandran plot (MolProbity) | 89.8 / 0.30         | 98.7 / 0    |

Values in parentheses are for highest resolution shell.

aR<sub>merge</sub> = ΣΣ<sub>i</sub>/<hi>/<hi> − <hi>/ΣΣ<sub>i</sub>/<hi>, where <hi>/<hi> is the r<sub>th</sub> measurement.

bR<sub>work</sub> is the crystallographic R-factor (R<sub>crys</sub>) for the working set used for the refinement. R<sub>crys</sub> = ΣΣ<sub>i</sub>||F<sub>obs</sub>(<hi>)/F<sub>cals</sub>(<hi>)||ΣΣ<sub>i</sub>||F<sub>obs</sub>(<hi>)||, where F<sub>obs</sub>(<hi>) and F<sub>cals</sub>(<hi>) are the observed and calculated structure factors.

cR<sub>free</sub> is R<sub>crys</sub> calculated for the test set consisting of 5% of reflections excluded from the refinement.

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**ApoER2 LA1 structure (PDB code: 3A7Q) as the search model.**

Manual model fitting and refinement were performed using the programs COOT [54] and REFMACS5 [55], respectively. After several rounds of refinement, the crystallographic R-factor and free R-factor were reduced to 20.96 and 23.96%, respectively, at 1.9 Å resolution. The quality of the final model was validated using the program MolProbity [56]. 97.5% of the 79 amino acid residues in the model were located in the favored region, and no residues were assigned as the outliers.

**Structure determination of the ApoER2 ECD: reelin R56 complex**

The crystal structure of the ApoER2 ECD: reelin R56 complex was solved by the Se-SAD method. We identified the positions of Se atoms with the program HKL2MAP [57] coupled with SHELX/C [58], and the phases were calculated and improved with SHARP/ autoSHARP [59,60]. Initial models for the respective modules were built by using the known structures. For the reelin R56 and ApoER2 LA1 pair, the crystal structure of their complex (PDB code: 3A7Q) was used as the initial model and fitted into the electron density. For the ApoER2 EGFPH domain, the structure of the full-length LDLR ectodomain (PDB code: 1N7D) and the partial models (PDB codes: 1UQ and 1H17) were used as the reference. Among the remaining three LA modules of ApoER2, LA3 and 7 were not modeled at all due to disorder. Although electron density for putative LA2 modules was weak, we were able to assign a plausible model using a procedure termed as constrained local real space search, as described in the next section. Manual model fitting and refinement were performed essentially as described above. The crystallographic R-factor and free R-factor were finally reduced to 18.46 and 25.60%, respectively, at 3.2 Å resolution. Among the 2,377 residues in the model, 89.6% were located in the favored region and only 0.3% were assigned as outliers.

**Model assignment of the LA2 fragment by the constrained local real space search**

In contrast to LA3 and LA7, electron density of putative LA2 module was definitely observed in the vicinity of LA1 module. However, due to weak density, any attempt to model LA2 module was failed including manual chain tracing and real space fragment search. Then, we performed the constrained local real space fragment search. The starting coordinates of LA2 were manually determined by locating high-resolution LA2 model at the center of the electron density blob of 2mF<sub>o</sub>–DF<sub>c</sub> map (Fig 2D). As LA2 is covalently linked to LA1 with a loop consisting of four residues, any candidates with the distance between the terminal residues larger than 3.7 × 5 Å were rejected. The candidates were evaluated by a scoring function S which evaluates electron density values at atomic coordinates; S(Δx, Δy, Δz, α, β, γ) = Σr ρ(r(Δx, Δy, Δz)) + Σr ρ(Δx(Δx, Δy, Δz)), where ρ(r) is the linearly interpolated electron density value at r, R is the rotation matrix, and Σr(Δx(Δy, Δz)) is the translation vector. The sampling intervals for rotation and translation were 15° and 1 Å, respectively. The translation search was limited within ± 5 Å for each direction. This procedure was implemented as a C++ program using the Clipper library [61]. After rejecting any candidates that clashed with atoms of other domains, the candidate with the highest score S was selected as the solution (Fig EV2A and B). This procedure was independently applied to two copies of LA2 in the asymmetric unit, and consistent solutions were obtained. The linker between LA1 and LA2 was manually built using COOT. The whole model was subjected to restrained refinement using REFMACS5 with external structural restraints using high-resolution LA2 structure and a jelly-body refinement scheme [62]. The external structural restraints were prepared using ProSMART [63]. The real space correlation coefficient (RSQC) was evaluated for LA2 with 2mF<sub>o</sub>–DF<sub>c</sub> map using phenix.get_cc_mtz_pdb [64]. The local...
RSCC after the refinement for two copies of LA2 was 0.677 and 0.649, respectively.

Analytical gel filtration

Analytical gel filtration was performed with an AKTApurifier instrument (GE Healthcare). 10 μg of purified wild type or mutant reelin R56 was applied to a Superdex 200 Increase 10/200 GL column (GE Healthcare) equilibrated with 20 mM HEPES-Na (pH 7.5), 150 mM NaCl, and 2 mM CaCl₂. The theoretical molecular weight (Mw) was calculated using ExPasy ProtParam tool [65], and the estimated Mw was calculated using Gel Filtration Standard (Bio-Rad) supplemented with ferritin protein as a standard.

Thermal shift assay

Thermal shift assay was performed with a CFX96 Touch Real-Time PCR Detection System (Bio-Rad). For each wild type and mutant sample, 4 μl of 100 ng/μl reelin R56 was dispensed in 0.2-ml tubes and diluted with 15 μl of 20 mM HEPES-Na (pH 7.5), 150 mM NaCl, and 2 mM CaCl₂. Subsequently, the measurement was started immediately after adding 1 μl of 150-fold diluted SYPRO Orange (Invitrogen) to the diluted protein solution. During the experiment, the temperature was increased from 25 to 85°C in 60 steps with a ramp rate of 0.1°C/s at each step.

Accession numbers

The atomic coordinates and structure factors of the ApoER2 ECD: reelin R56 complex and the ApoER2 LA12 fragment have been deposited in the Protein Data Bank with accession numbers of 5B4X and 5B4Y, respectively.

Expanded View for this article is available online.

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Author contributions

JT and TN designed the study. HH, NY, and ST contributed the protein production and crystallization. HH, NY, and TN performed the crystallographic analysis. KY and MY developed the protocol of the constrained local real space search. HH performed the SPR measurements and analyzed the results. HH, NY, KY, JT, and TN wrote the manuscript.

Conflict of interest

The authors declare that they have no conflict of interest.

References

1. Brown MS, Goldstein JL (1986) A receptor-mediated pathway for cholesterol homeostasis. Science 232: 34–47
2. Brown MS, Goldstein JL (1974) Expression of the familial hypercholesterolemia gene in heterozygotes: mechanism for a dominant disorder in man. Science 185: 61–63
3. Usifo E, Leigh SE, Whitall RA, Lench N, Taylor A, Yeats C, Orengo CA, Martin AC, Celli J, Humphries SE (2012) Low-density lipoprotein receptor gene familial hypercholesterolemia variant database: update and pathologic assessment. Ann Hum Genet 76: 387–401
4. Yamamoto T, Davis CG, Brown MS, Schneider WJ, Casey ML, Goldstein JL, Russell DW (1984) The human LDL receptor: a cysteine-rich protein with multiple Alu sequences in its mRNA. Cell 39: 27–38
5. Sudhof TC, Goldstein JL, Brown MS, Russell DW (1985) The LDL receptor gene: a mosaic of exons shared with different proteins. Science 228: 815–822
6. Jeon H, Blacklow SC (2005) Structure and physiologic function of the low-density lipoprotein receptor. Annu Rev Biochem 74: 535–562
7. Springer TA (1998) An extracellular beta-propeller module predicted in lipoprotein and scavenger receptors, tyrosine kinases, epidermal growth factor precursor, and extracellular matrix components. J Mol Biol 283: 837–862
8. Fass D, Blacklow S, Kim PS, Berger JM (1997) Molecular basis of familial hypercholesterolemia from structure of LDL receptor module. Nature 388: 691–693
9. North CL, Blacklow SC (2000) Solution structure of the sixth LDL-A module of the LDL receptor. Biochemistry 39: 2564–2571
10. Daly NL, Scanlon MJ, Djordjevic JT, Kroon PA, Smith R (1995) Three-dimensional structure of a cysteine-rich repeat from the low-density lipoprotein receptor. Proc Natl Acad Sci USA 92: 6334–6338
11. Daly NL, Djordjevic JT, Kroon PA, Smith R (1995) Three-dimensional structure of the second cysteine-rich repeat from the human low-density lipoprotein receptor. Biochemistry 34: 14474–14481
12. Clayton D, Breereton IM, Kroon PA, Smith R (2000) Three-dimensional NMR structure of the sixth ligand-binding module of the human LDL receptor: comparison of two adjacent modules with different ligand binding specificities. FEBS Lett 479: 118–122
13. Kurniawan ND, Atkins AR, Bieri S, Brown CJ, Brereton IM, Kroon PA, Smith R (2000) NMR structure of a concatemer of the first and second ligand-binding modules of the human low-density lipoprotein receptor. Protein Sci 9: 1282–1293
14. Huang W, Dolmer K, Gettins PG (1999) NMR solution structure of complement-like repeat C8R from the low density lipoprotein receptor-related protein. J Biol Chem 274: 14130–14136
15. Russell DW, Brown MS, Goldstein JL (1989) Different combinations of cysteine-rich repeats mediate binding of low density lipoprotein receptor to two different proteins. J Biol Chem 264: 21682–21688
16. Fisher C, Beglova N, Blacklow SC (2006) Structure of an LDLR-RAP complex reveals a general mode for ligand recognition by lipoprotein receptors. Mol Cell 22: 277–283
17. Verdaguer N, Fita I, Reithmayer M, Moser R, Blaas D (2004) X-ray structure of a minor group human rhinovirus bound to a fragment of its cellular receptor protein. Nat Struct Mol Biol 11: 429–434
18. Zaiou M, Arnold K5, Newhouse YM, Innerarity TL, Weisgraber KH, Segall ML, Phillips MC, Lund-Katz S (2000) Apolipoprotein E-low density lipoprotein receptor interaction. Influences of basic residue and amphipathic alpha-helix organization in the ligand. J Lipid Res 41: 1087–1095
19. Rudenko G, Henry L, Henderson K, Ichtchenko K, Brown MS, Goldstein JL, Deisenhofer J (2002) Structure of the LDL receptor extracellular domain at endothosomal pH. Science 298: 2353–2358
20. Lo Surdo P, Bottomley MJ, Calzetta A, Settembre EC, Cirillo A, Pandit S, Ni YG, Hubbard B, Sitlani A, Carfi A (2011) Mechanistic implications for LDL receptor degradation from the PCSK9/LDLR structure at neutral pH. EMBO Rep 12: 1300–1305
21. Li J, Tumanut C, Cavigan JA, Huang WJ, Hampton EN, Tumanut R, Suen KF, Trauger JW, Spraggion G, Lesley SA et al (2007) Secreted PCSK9 promotes LDL receptor degradation independently of proteolytic activity. Biochem J 406: 203–207
22. McNutt MC, Lagace TA, Horton JD (2007) Catalytic activity is not required for secreted PCSK9 to reduce low density lipoprotein receptors in HepG2 cells. J Biol Chem 282: 20799–20803
23. Ren G, Rudenko G, Ludtke SJ, Deisenhofer J, Chiu W, Pownall HJ (2010) Model of human low-density lipoprotein and bound receptor based on cryoEM. Nat Rev Mol Cell Biol 11: 1059–1064
24. Willnow TE, Nykjaer A, Herz J (1999) Lipoprotein receptors: new roles for ancient proteins. Nat Cell Biol 1: E157–E162
25. Schneider WJ, Nimpf J (2003) LDL receptor relatives at the crossroad of endocytosis and signaling. Cell Mol Life Sci 60: 892–903
26. Brandes C, Novak S, Stockinger W, Herz J, Schneider WJ, Nimpf J (1997) Avian and murine LRBB and human apolipoprotein E receptor 2: differentially spliced products from corresponding genes. Genomics 42: 185–191
27. Kim DH, Iijima H, Goto K, Sakai J, Ishii H, Kim HJ, Suzuki H, Kondo H, Saeki S, Yamamoto T (1996) Human apolipoprotein E receptor 2. A novel lipoprotein receptor of the low density lipoprotein receptor family predominantly expressed in brain. J Biol Chem 271: 8373–8380
28. Tissier F, Coffinet AM (2003) Reelin and brain development. Nat Rev Neurosci 4: 496–505
29. D’Arcangelo G, Miao GG, Chen SC, Soares HD, Morgan JJ, Curran T (1999) A protein related to extracellular matrix proteins deleted in the mouse mutator reeler. Nature 374: 719–723
30. Yasui N, Nogi T, Kitao T, Nakano Y, Hattori M, Takagi J (2007) Structure of a receptor-binding fragment of reelin and mutational analysis reveal a recognition mechanism similar to endocytic receptors. Proc Natl Acad Sci USA 104: 9988–9993
31. Yasui N, Nogi T, Takagi J (2010) Structural basis for specific recognition of reelin by its receptors. Structure 18: 320–331
32. Kim DH, Magoori K, Inoue TR, Mao CC, Kim HJ, Suzuki H, Fujita T, Endo Y, Saeki S, Yamamoto TT (1997) Exon/intron organization, chromosome localization, alternative splicing, and transcription units of the human apolipoprotein E receptor 2 gene. J Biol Chem 272: 8498–8504
33. Brandes C, Kahr L, Stockinger W, Hiesberger T, Schneider WJ, Nimpf J (2001) Alternative splicing in the ligand binding domain of mouse ApoE receptor-2 produces receptor variants binding reelin but not alpha 2-macroglobulin. J Biol Chem 276: 22160–22169
34. Hibi T, Mizutani M, Baba A, Hattori M (2009) Splicing variations in the ligand-binding domain of ApoER2 results in functional differences in the binding properties to Reelin. Neurosci Res 63: 251–258
35. Saha S, Boyd J, Werner JM, Knott V, Handford PA, Campbell ID, Downing AK (2001) Solution structure of the LDL receptor EGF-AB pair: a paradigm for the assembly of tandem calcium binding EGF domains. Structure 9: 451–456
36. Malby S, Pickering R, Saha S, Smallridge R, Linse S, Downing AK (2001) The first epidermal growth factor-like domain of the low-density lipoprotein receptor contains a noncanonical calcium binding site. Biochemistry 40: 2555–2563
37. Arias-Moreno X, Velazquez-Campoy A, Rodriguez JC, Pocovi M, Sancho J (2008) Mechanism of low density lipoprotein (LDL) release in the endosome: implications of the stability and Ca2+ affinity of the fifth binding module of the LDL receptor. J Biol Chem 283: 22670–22679
38. North CL, Blacklow SC (1999) Structural independence of ligand-binding modules five and six of the LDL receptor. Biochemistry 38: 3926–3935
39. Hopkins PN, Wu LL, Stephenson SH, Xion Y, Katsumata H, Nobe Y, Nakajima T, Hirayama T, Emi M, Williams RR (1999) A novel LDLR mutation, H190Y, in a Utah kindred with familial hypercholesterolemia. J Hum Genet 44: 364–367
40. Beglova N, Jeon H, Fisher C, Blacklow SC (2004) Cooperation between fixed and low pH-inducible interfaces controls lipoprotein release by the LDL receptor. Mol Cell 16: 281–292
41. Yasui N, Kitago Y, Beppu A, Kohno T, Morishita S, Gomi H, Nagae M, Hattori M, Takagi J (2011) Functional importance of covalent homodimer of reelin protein linked via its central region. J Biol Chem 286: 35247–35256
42. Leahy DJ, Dann CE III, Longo P, Perman B, Ramyar KX (2000) A mammalian expression vector for expression and purification of secreted proteins for structural studies. Protein Expr Purif 20: 500–506
43. Reeves PJ, Callewaert N, Contreras R, Khorana HG (2002) Structure and function in rhodopsin: high-level expression of rhodopsin with restricted and homogeneous N-glycosylation by a tetracycline-inducible N-acetylglucosaminyltransferase I-negative HEK293S stable mammalian cell line. Proc Natl Acad Sci USA 99: 13419–13424
44. Fujiy Y, Kaneko M, Neyazaki M, Nogi T, Kato Y, Takagi J (2014) PA tag: a versatile protein tagging system using a super high affinity antibody against a dodecapeptide derived from human podoplanin. Protein Expr Purif 95: 240–247
45. Stanley P (1989) Chinese hamster ovary cell mutants with multiple glycosylation defects for production of glycoproteins with minimal carbohydrate heterogeneity. Mol Cell Biol 9: 377–383
46. Gill SC, von Hippel PH (1989) Calculation of protein extinction coefficients from amino acid sequence data. Anal Biochem 182: 319–326
47. Fisher C, Abdul-Aiziz D, Blacklow SC (2004) A two-module region of the low-density lipoprotein receptor sufficient for formation of complexes with apolipoprotein E ligands. Biochemistry 43: 1037–1044
48. Kabsch W (2010) Xds. Acta Crystallogr D Biol Crystallogr 66: 125–132
49. Evans PR, Murshudov GN (2013) How good are my data and what is the resolution? Acta Crystallogr D Biol Crystallogr 69: 1204–1214
50. French S, Wilson K (1978) On the treatment of negative intensity observations. Acta Crystallogr A 34: 517–525
51. Winn MD, Ballard CC, Cowtan KD, Dodson EJ, Emsley P, Evans PR, Keegan RM, Krissinel EB, Leslie AG, McCoy A et al (2011) Overview of the CCP4 suite and current developments. Acta Crystallogr D Biol Crystallogr 67: 235–242
52. Collaborative Computational Project, Number 4 (1994) The CCP4 suite: programs for protein crystallography. Acta Crystallogr D Biol Crystallogr 50, 760–763
53. Vagin A, Teplyakov A (1997) MOLREP: an automated program for molecular replacement. J Appl Cryst 30: 1022–1025
54. Emsley P, Lohkamp B, Scott WG, Cowtan K (2010) Features and development of Coot. Acta Crystallogr D Biol Crystallogr 66: 486–501
55. Murshudov GN, Vagin AA, Dodson EJ (1997) Refinement of macromolecular structures by the maximum-likelihood method. Acta Crystallogr D Biol Crystallogr 53: 240–255
56. Chen VB, Arendall WB 3rd, Headd JJ, Keedy DA, Immormino RM, Kapral GJ, Murray LW, Richardson JS, Richardson DC (2010) MolProbity: all-atom structure validation for macromolecular crystallography. Acta Crystallogr D Biol Crystallogr 66: 12–21
57. Pape T, Schneider TR (2004) HKL2MAP: a graphical user interface for phasing with SHELX programs. J Appl Cryst 37: 843–844
58. Schneider TR, Sheldrick GM (2002) Substructure solution with SHELXD. Acta Crystallogr D Biol Crystallogr 58: 1772–1779
59. Bricogne G, Vonrhein C, Flensburg C, Schiltz M, Paciorek W (2003) Generation, representation and flow of phase information in structure determination: recent developments in and around SHARP 2.0. Acta Crystallogr D Biol Crystallogr 59: 2023–2030
60. Vonrhein C, Blanc E, Roversi P, Bricogne G (2007) Automated structure solution with autoSHARP. Methods Mol Biol 364: 215–230
61. Cowtan KD (2003) The Clipper C++ libraries for X-ray crystallography. iUCr Comput Comm Newslett 2: 4–9
62. Nicholls RA, Long F, Murshudov GN (2012) Low-resolution refinement tools in REFMACS. Acta Crystallogr D Biol Crystallogr 68: 404–417
63. Nicholls RA, Fischer M, McNicholas S, Murshudov GN (2014) Conformation-independent structural comparison of macromolecules with ProSMART. Acta Crystallogr D Biol Crystallogr 70: 2487–2499
64. Adams PD, Afonine PV, Bunkóczi G, Chen VB, Davis IW, Echols N, Headd JJ, Hung LW, Kapral GJ, Grosse-Kunstleve RW et al (2010) PHENIX: a comprehensive Python-based system for macromolecular structure solution. Acta Crystallogr D Biol Crystallogr 66: 213–221
65. Gasteiger E, Hoogland C, Gattiker A, Duvaud S, Wilkins MR, Appel RD, Bairoch A (2005) The proteomics protocols handbook. New York: Humana Press: 571–607

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