

MULTIPLE ROLES FOR THE MAJOR HISTOCOMPATIBILITY COMPLEX CLASS I- RELATED RECEPTOR FcRn

Victor Ghetie and E. Sally Ward

*Center for Immunology and Cancer Immunobiology Center, University of Texas
Southwestern Medical Center, Dallas, Texas 75235-8576; e-mail:
sally@skylab.swmed.edu*

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■ **Abstract** Multiple functions have recently been identified for the neonatal Fc receptor FcRn. In addition, a human homolog of the rodent forms of FcRn has been identified and characterized. This major histocompatibility complex class I-related receptor plays a role in the passive delivery of immunoglobulin (Ig)Gs from mother to young and the regulation of serum IgG levels. In addition, FcRn expression in tissues such as liver, mammary gland, and adult intestine suggests that it may modulate IgG transport at these sites. These diverse functions are apparently brought about by the ability of FcRn to bind IgGs and transport them within and across cells. However, the molecular details as to how FcRn traffics within cells have yet to be fully understood, although *in vitro* systems have been developed for this purpose. The molecular nature of the FcRn-IgG interaction has been studied extensively and encompasses residues located at the CH2-CH3 domain interface of the Fc region of IgG. These Fc amino acids are highly conserved in rodents and man and interact with residues primarily located on the $\alpha 2$ domain of FcRn. Thus, it is now possible to engineer IgGs with altered affinities for FcRn, and this has relevance to the modulation of IgG serum half-life and maternofetal IgG transport for therapeutic applications.

INTRODUCTION

The neonatal Fc receptor FcRn was first identified in rodents as the receptor that transfers maternal gammaglobulins (IgGs) from mother to young via the neonatal intestine (1-6). However, more recent data have indicated that this receptor not only delivers IgGs across the maternofetal barrier during gestation (7-9), but is also responsible for the maintenance of serum IgG levels (10-13). How does FcRn carry out these apparently diverse functions? It appears that the ability of FcRn to transport IgGs in intact form both within and across cells is exploited in

each of these activities (reviewed in 14). However, the molecular details as to how FcRn functions in distinct cellular environments have yet to be unraveled. Recent developments (15, 16) have resulted in model systems that could provide valuable tools for both cellular and molecular studies directed towards a better understanding of FcRn function. The role of FcRn as an IgG transporter offers novel routes towards the generation of therapeutics for use in situations in which IgG delivery is required (e.g. fetal immunization) or a modulation of IgG levels is desirable (e.g. autoimmunity). Thus, understanding how this protein functions has a multitude of potential applications in the treatment of human disease.

FCRN: THE GENES AND PROTEIN

The gene encoding rat FcRn was first isolated by Simister & Mostov in 1989 (17). Unexpectedly, FcRn was shown to comprise a heterodimer of β 2-microglobulin and a 45- to 53-kDa protein, suggesting that the heavy chain might be a major histocompatibility complex (MHC) class I homolog. The cloning and sequencing of the heavy-chain gene confirmed this possibility (17) and expanded the function of this class of molecules beyond their known role in antigen presentation. All three extracellular and transmembrane domains of FcRn share homology with the corresponding regions of MHC class I molecules, with much less homology between the cytoplasmic domains (17). The divergence in the cytoplasmic regions is consistent with the different functional activities of the two types of proteins.

The X-ray crystallographic structure of the extracellular domains of FcRn confirmed that it is structurally similar to MHC class I molecules (18). Notably, the peptide groove that is occupied by peptide or, in some cases, glycolipid ligand in classical and nonclassical MHC class I molecules (19–22) is occluded in FcRn. This occlusion is primarily caused by the presence of proline at position 165 of the α 2 domain helix, which introduces a kink. However, it is interesting that the introduction of a proline at the corresponding position in the MHC class I molecule H-2D^d does not affect peptide presentation to T cells (23), suggesting that additional structural features of FcRn may result in the closed groove.

More recently the genes encoding both mouse and human FcRn alpha chains have been isolated (24, 25). The rodent and human genes share homology, with mouse and rat FcRn being highly related and the human form more divergent. The identification of human FcRn in human syncytiotrophoblast (25–28) led to the suggestion that it plays a role in the maternofetal transfer of IgGs, which is discussed in more detail below. The isolation and characterization of human FcRn provided an important link between studies of FcRn in rodents and humans.

THE MOLECULAR DETAILS OF THE FcRn- IMMUNOGLOBULIN G INTERACTION

Mapping the Binding Site for FcRn on Immunoglobulin G

A combination of approaches has been used to localize the interaction site for FcRn on IgG. This has involved the analysis of mutated derivatives of human and mouse IgGs/Fc fragments in both *in vivo* and *in vitro* binding studies (9, 29–32). The *in vivo* studies include the analysis of the IgGs or Fc fragments using assays in which FcRn is known to play a role, namely transfer across the neonatal intestine, maternofetal transfer, and serum half-life determination (discussed further below). Activity in these assays almost invariably provides an indication of FcRn affinity (9, 29, 31). The studies have resulted in the identification of several conserved amino acids located at the CH2-CH3 domain interface that play a central role in the interaction of rat or mouse FcRn with human or mouse IgGs. Ile253 and His310 are key players in the interaction (9, 29–31). These residues are highly conserved across species (Table 1), and their location on the three-dimensional structure of human IgG1 (hIgG1)-derived Fc (33) is shown in Figure 1 (see color insert). His436 plays a minor but significant role in the mouse FcRn-IgG interaction (31). The lack of conservation of this amino acid across species (Table 1) is consistent with more limited involvement.

TABLE 1 Variations of IgG sequences in the region involved in the binding of FcRn

		Amino Acid Sequence at Position:														
		252	253	254	255	256	257	307	308	309	310	311	433	434	435	436
mouse	IgG1	Thr	Ile	Thr	Leu	Thr	Pro	Pro	Ile	Met	His	Gln	His	Asn	His	His
	IgG2a	Met	Ile	Ser	Leu	Thr	Pro	Pro	Ile	Gln	His	Gln	His	Asn	His	His
	IgG2b	Met	Ile	Ser	Leu	Thr	Pro	Pro	Ile	Gln	His	Gln	Lys	Asn	Tyr	Tyr
	IgG3	Met	Ile	Ser	Leu	Thr	Pro	Pro	Ile	Gln	His	Gln	His	Asn	His	His
rat	IgG1	Thr	Ile	Thr	Leu	Thr	Pro	Pro	Ile	Leu	His	Gln	His	Asn	His	His
	IgGa	Thr	Ile	Thr	Leu	Thr	Pro	Pro	Ile	Val	His	Arg	His	Asn	His	His
	IgG2b	Leu	Ile	Ser	Gln	Asn	Ala	Pro	Ile	Gln	His	Gln	His	Asn	His	His
	IgG2c	Met	Ile	Thr	Leu	Thr	Pro	His	Ile	Gln	His	Gln	His	Asn	His	His
human	IgG1	Met	Ile	Ser	Arg	Thr	Pro	Thr	Val	Leu	His	Gln	His	Asn	His	Tyr
	IgG2	Met	Ile	Ser	Arg	Thr	Pro	Thr	Val	Val	His	Gln	His	Asn	His	Tyr
	IgG3*	Met	Ile	Ser	Arg	Thr	Pro	Thr	Val	Leu	His	Gln	His	Asn	Arg	Phe
	IgG4	Met	Ile	Ser	Arg	Thr	Pro	Thr	Val	Leu	His	Gln	His	Asn	His	Tyr

*Allotype containing Arg instead of His at Position 435

In functional studies in mice, mutation of His433 to alanine in recombinant Fc fragments derived from both human and mouse IgG1 does not affect the activity of the protein (31, 32), although simultaneous mutation of His433 and Asn434 does have a moderate effect (29). In contrast, mutation of His435 to alanine results in a dramatic loss of function (31, 32). Thus, the effect of the double His433/Asn434 mutation is most likely caused by perturbation of the conformation of the critical residue His435. The spatial location of these amino acids is shown in Figure 1. A more recent study in our laboratory has indicated that the sequence difference of hIgG1 and hIgG3 (G3m,s⁻,t⁻ allotype) at position 435 (His in IgG1; Arg in G3m,s⁻,t⁻ allotype of IgG3) is responsible for the lower activity of IgG3 in FcRn-mediated functions, providing further support for a role for residue 435 in the FcRn interaction (32). In contrast to our *in vivo* and *in vitro* analyses, surface plasmon resonance analyses of chimeric human-mouse IgGs (containing the hIgG4 constant region) in which His435 was mutated to arginine detected no significant effect on the pH dependence of the FcRn-IgG interaction, and, in the same study, His433 was implicated in FcRn binding (30). There is therefore a discrepancy between the relative roles of His433 and His435 in the FcRn (rodent)-IgG interaction, and this is possibly a reflection of the different systems and approaches used. However, the available data unequivocally demonstrate the involvement of IgG histidines in FcRn binding, and Table 1 shows that these histidines are highly conserved in mouse, rat, and human. This provides an explanation for the strict pH dependence (binding at pH 6–6.5; very weak or undetectable binding at pH 7.2) of the FcRn-IgG (or Fc) interaction that is observed by using soluble recombinant FcRn in binding studies (30, 34, 35) and cell-binding assays (3, 4, 6, 36). This mechanism of achieving pH-dependent binding in ranges of pH that are physiologically relevant avoids the need to invoke conformational changes and could be exploited in the engineering of other proteins. Indeed, the crystallographic analysis of rat FcRn at pH 6.5 and pH 8 shows no major conformational differences between the two forms (37). By analogy, other proteins, such as the hemochromatosis protein HFE, bind to the transferrin receptor in a pH-dependent way with binding at slightly basic pH and release at acidic pH, that is, the reverse pH dependence to that seen with FcRn, and this is again mediated by histidines (38).

Further analyses of the activity of rat IgGs in FcRn-mediated functions in mice revealed a role for several additional residues in proximity to the CH2-CH3 domain interface (39). The putative involvement of these amino acids was probed by transplanting the rat IgG sequences (Table 1) onto the corresponding positions in the highly homologous mouse IgG1 Fc region. Analysis of the resulting recombinant Fc fragments demonstrated that amino acids at position 257 and, to a lesser extent, positions 307 and 309 play a role in the FcRn-Fc interaction. The location of residue 257 is shown in Figure 1. The study also excluded the involvement of residues 386 and 387, which are located in an exposed loop in the vicinity of the FcRn interaction site (40). The role of residues 257, 307, and 309 is less marked than that of Ile253, His310, and His435. However, sequence variations at 257,

307, and 309 can be used to explain the different affinities of rat IgGs for FcRn [affinities decreasing in the order IgG2a > IgG1 > IgG2c > IgG2b (39)]. This ranking of affinities is consistent with the binding activities of rat IgGs to isolated neonatal rat brush borders, with the exception of rat IgG2c, which was reported to have undetectable activity (41). It is possible that the discrepancies between the two studies (39, 41) are caused by functional differences between mouse and rat FcRn and/or variations in the sources of the ligands used.

Consistent with the functional data, the 6-Å resolution structure of the rat FcRn-Fc complex indicated that FcRn interacts with Fc residues located at the CH2-CH3 interface (40). Furthermore, fragment B of staphylococcal protein A (SpA), which, from the three-dimensional structure of an SpA (fragment B)-human Fc complex (33), is known to bind to amino acids at this interdomain interface, competes with IgG for binding to FcRn (42). Earlier studies indicated that blockade of the FcRn interaction site on rabbit IgG by SpA (or fragment B) resulted in a dramatic reduction in serum half-life (43), consistent with the more recent data in mice supporting a role for FcRn in serum IgG homeostasis (10-13).

The Conformational Dependence of the FcRn Interaction Site on Immunoglobulin G

It is interesting that analyses of chimeric IgGs comprising mouse variable regions linked to human constant-region domains indicate that amino acids distal to the CH2-CH3 domain interface may also be involved in regulating serum half-life in mice and, by extension, in binding to FcRn (44). It will be of interest to determine the affinities for FcRn of these recombinant IgGs in which the constant-region domains of IgG2 and IgG1 were shuffled with the corresponding regions of IgG3 and IgG4, respectively. The data obtained for these engineered IgGs led to the suggestion that the FcRn interaction can be affected by long-range conformational effects of amino acids that are distal to the FcRn footprint (44). In this respect, critical IgG residues for the FcRn interaction (9, 29-31) are located on three loops that are spatially close but distal in primary amino acid sequence (Figure 1). This suggests that they might be highly dependent on the conformation of the β strands that support them and also on the relative disposition of the CH2 and CH3 domains. Several observations are consistent with this explanation. (a) The effect of mutation (Pro to Ala) at position 257 of a recombinant mouse IgG1-derived Fc fragment on serum half-life is most likely from perturbation of the conformation of the loop encompassing Ile253 (39). This same sequence difference is probably responsible for the shorter serum half-life of rat IgG2b relative to rat IgG1/IgG2a in mice (39). (b) Mutation of Glu333 to Ala results in a significant decrease in serum persistence of a recombinant Fc fragment [mouse IgG1-derived (V Ghetie & ES Ward, unpublished observations)]. This amino acid is located in a β strand in the CH2 domain that is on the 'interior' of the CH2 domain and therefore not suitably positioned for direct interaction with FcRn (33). (c)

Removal of the hinge region by recombinant techniques from an Fc fragment results in a shorter serum half-life (45). The role of the hinge appears to be to constrain the CH2 domains such that the configuration of the FcRn interaction site at the CH2-CH3 domain interface is optimal, rather than through direct FcRn:hinge interactions. This suggestion was validated by replacing the wild-type hinge sequence with a synthetic hinge that has a distinct sequence but allows -S-S-linked homodimerization of the Fc (CH2-CH3) domain monomers. This engineered, disulfide-constrained Fc fragment has the same half-life as an Fc fragment containing the wild-type hinge sequence (45). In this context, the longer and more flexible hinge region of hIgG3 compared with hIgG1 (46) might account, in part at least, for the shorter serum half-lives of IgG3 hinge-containing chimeras compared with those containing IgG2-derived hinge sequences (44).

The data from these mutagenesis studies suggest that the FcRn interaction site on IgG or Fc is highly conformational dependent. This may make it a challenging task to mimic FcRn binding by an IgG-derived peptide, in contrast to the demonstrated ability of a CH2 domain-derived peptide to compete with IgGs for binding to C1q (47). However, the demonstration that an Fc region-derived peptide encompassing residues 308–317 blocks the binding of SpA to IgG (48) suggests that individual strands encompassing key FcRn interaction residues may be effective mimics.

Is There a Relationship Between the FcRn and Fc γ R Interaction Sites on Immunoglobulin G?

Mutagenesis studies from several different laboratories have indicated that residues in the lower hinge region of IgG are important for binding to Fc γ RI, Fc γ RII, and/or Fc γ RIII (49–55). However, each receptor sees this site with a slightly different footprint, and, in addition, there are two other regions that play a role in binding to Fc γ RI (Pro331) and Fc γ RII (Glu318) (50). These regions are spatially close to the lower hinge (33). The available data indicate that Fc γ R binding is also dependent on glycosylation of IgG (56–58) and that even minor alterations in carbohydrate structure can have an effect on this activity (59, 60). Thus, the FcRn interaction site appears to be distinct from the region of IgG involved in Fc γ R binding. Furthermore, at least for some species/isotypes, FcRn binding is not affected by the absence of CH2 domain glycosylation (29, 35).

It is interesting that the recent crystal structures of human Fc γ RIIa (61) and Fc γ RIIb (62) resulted in two interaction models for Fc γ RII-IgG complex formation that are fundamentally different. Fc γ RIIa was solved as a crystallographic dimer in which the binding regions of each monomer were brought into proximity to generate a single IgG interaction site, and the IgG-Fc γ RIIa interaction was postulated to involve the lower hinge region of IgG (61). This model is consistent with data from mutagenesis studies (reviewed in 54). In contrast, Fc γ RIIb was suggested to bind to IgG or Fc in the region encompassing the CH2-CH3 domain interface, with both sites on IgG occupied to form a symmetric 1:2 IgG:Fc γ RIIb

complex (62). The validity of the model proposed for Fc γ RIIa has been investigated by carrying out surface plasmon resonance-binding studies with recombinant, soluble human Fc γ RIIa or mouse Fc γ RI and mouse/hIgGs (M Hogarth, personal communication). For both Fc γ Rs, binding to IgG was not inhibited by either SpA or recombinant soluble FcRn, providing clear evidence that the Fc γ R interaction site does not encompass the CH2-CH3 domain interface. Consistent with this are earlier observations that mutations of IgGs affecting Fc γ R binding do not alter the activity of the IgG in a function that is known to be mediated by FcRn, namely serum persistence (63).

Mapping the Interaction Site for Immunoglobulin G on FcRn

Although the X-ray crystallographic structure of rat Fc-FcRn complexes indicated the potential contacts for Fc on FcRn (40), the resolution was not sufficiently high to unequivocally define the amino acids involved. The binding site of mouse/rat IgG on rat FcRn has therefore been mapped using site-directed mutagenesis followed by analysis of the mutants by *in vitro* binding assays (42, 64). This has resulted in the identification of several α 2 domain and one β 2-microglobulin residue as playing a direct role in the interaction. The α 2 domain residues (Glu117, Glu132, Trp133, Glu135, and Asp137) are reasonably well conserved across species (17, 24, 25), and their location on the rat FcRn structure (18) is shown in Figure 2 (see color insert). The acidic nature of four of these amino acids, together with the role of IgG histidines in binding, suggests that electrostatic forces may play a predominant role in mediating the Fc/IgG-FcRn interaction. Hydrophobic effects may also be involved, and it is plausible that Trp133 interacts with the conserved Ile253 of IgGs (64). Residue 1 (Ile) of β 2-microglobulin, which is conserved in rats, mice, and humans (46), has also been shown to be involved in binding to IgG but to a lesser extent than the α 2 domain residues (64). This amino acid has been proposed to contact IgG via hydrophobic interactions in the vicinity of residue 309 and/or 311. Alternatively, this N-terminal residue may play a role through more indirect effects on Glu117 in the α 2 domain (64). The α 2 domain residues that are involved in binding to IgG are located in close proximity on a region at the end of the α 2 domain helix (18; Figure 2). Residues 84–86 of the α 1 domain are spatially close to this region of FcRn, but, from mutagenesis studies, have been shown not to contact IgG (64). The majority of contacts for IgG on FcRn therefore entail amino acids in the α 2 domain. Furthermore, the interaction of IgG with FcRn occurs in a mode distinct from that reported for T-cell receptor-peptide-MHC class I interactions (65, 66), in which the T-cell receptor footprint spans the surface of the two MHC helices and binds antigenic peptide in a diagonal orientation.

Much evidence from *in vitro* studies has supported a role for FcRn dimerization in high-affinity binding to IgG, resulting in the formation of "lying-down" complexes comprising an FcRn dimer bound to one IgG/Fc molecule (42, 64, 67,

68; Figure 3). First, FcRn dimers mediated via $\alpha 3$ domain contacts have been observed in several different crystal forms of rat FcRn (18, 40). Second, mutation of Gly191, His250, His251, and a loop encompassing residues 219–224 (all $\alpha 3$ domain residues) results in a reduction in the affinity of FcRn for IgG (42, 64). The effects of these mutations have been interpreted to be caused by destabilization of FcRn dimerization and/or loss of contacts to an IgG molecule bound to an adjacent FcRn molecule in a lying-down complex (42, 64, 69). Third, immobilization of FcRn molecules on a biosensor chip favors the formation of the dimeric, high-affinity form of FcRn (68). In addition, oriented coupling of FcRn via exposed, engineered cysteines located at different sites indicates that the ori-

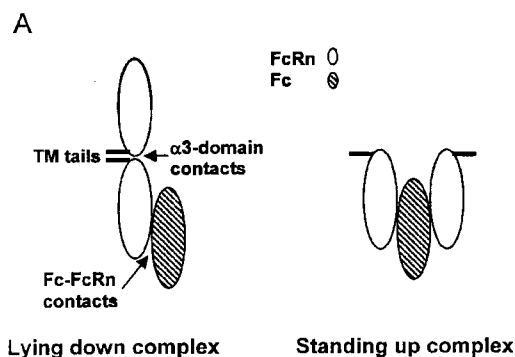
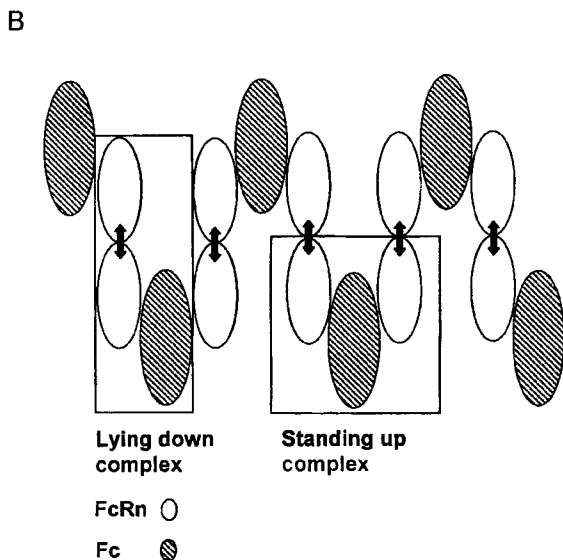


Figure 3 A. Schematic representation of “lying-down” and “standing-up” FcRn-Fc complexes (40). Both complexes comprise a stoichiometry of 1 Fc:2 FcRn molecules, but they show fundamental differences in the configuration of the constituent molecules. Lying-down complexes comprise Fc bound to an FcRn-FcRn dimer, with the dimer mediated primarily via $\alpha 3$ domain contacts and associated carbohydrate (37). In contrast, the standing-up complex comprises a symmetric FcRn-Fc-FcRn configuration. However, in the lying-down complex, additional contacts may be made between the Fc molecule and the secondary, that is, distal, FcRn molecule (64), but for simplicity these are not shown. B. Schematic representation of oligomeric ribbons (82) in which both standing-up and lying-down complexes coexist. For simplicity the transmembrane regions (TM) of FcRn are not shown. The *arrows* indicate the contacts that mediate FcRn dimerization.



entation of FcRn immobilization affects the extent of dimerization and, in turn, the affinity of its interaction with IgG (67).

More recent X-ray crystallographic studies have demonstrated that $\alpha 3$ domain-associated carbohydrate (at Asn225) interacts to form much of the contacts at the FcRn dimer interface via a "carbohydrate handshake" (37). This indicates that, depending on the expression host used to make recombinant FcRn, the type of carbohydrate could affect the stability of FcRn dimerization with consequent effects on affinity measurements of the Fc/IgG-FcRn interaction (37). However, neither the carbohydrate addition site nor Gly191 in the $\alpha 3$ domain is conserved in human FcRn (25), suggesting that, if this FcRn species forms an analogous dimer, then other molecular mechanisms must be involved.

The Stoichiometry of the Fc/Immunoglobulin G-FcRn Interaction

The presence of two potential binding sites for FcRn on IgG suggested that FcRn might bind to ligand in a symmetric 2:1 "standing up" complex (Figure 3A). For rat FcRn-Fc complexation, this possibility was supported by isothermal-titration calorimetry and column-binding assays (70). However, more recent studies have indicated that this symmetric complex may not always be formed (35). Although the need for two functional FcRn interaction sites on a recombinant Fc fragment was observed using *in vivo* studies in mice to assess FcRn function (71), the stoichiometry of the complex formed between recombinant mouse FcRn and mouse Fc was observed to be 1:1 (35). This apparent discrepancy prompted us to propose a model analogous to the situation described as "half-sites reactivity" in enzymology (14, 72, 73). In this model, we predicted that the FcRn interaction sites on IgG might not be equivalent and that, when binding occurs on one side of the Fc region, the affinity of the other site decreases. The segmental flexibility of IgG (74-76) would be consistent with such a model. This is also reminiscent of data obtained for the Fc ϵ RI-IgE interaction, in which a 1:1 complex is observed despite the presence of two potential interaction sites on IgE (77, 78). Furthermore, by fluorescence resonance energy transfer methods, evidence to support a bent configuration for IgE in solution has been obtained (76). In the same study (76), the flexibility of IgG was observed to be greater than that of IgE. Furthermore, for IgE the asymmetry is so extreme that it is not possible to detect the binding of a second Fc ϵ RI molecule to IgE.

An asymmetric model for the FcRn-IgG interaction has recently been supported by modeling studies (69) and equilibrium gel filtration (79) or sedimentation equilibrium analyses (80). The high degree of flexibility of IgG in solution (76) is consistent with the concept that FcRn binding induces asymmetry (69) rather than the asymmetry being preformed before FcRn docking, and Fc distortion after FcRn binding was suggested in the earlier crystallographic analysis of rat Fc with FcRn (40). It has also been reported that the stoichiometry of the IgG-FcRn interaction varies depending on the IgG species/isotype and glycosylation

state of the recombinant FcRn (37, 79). More generally, it is probable that the binding observed in solution with soluble (or biosensor chip-bound) FcRn might not be representative of the physiological situation when FcRn has both trans-membrane regions and a cytoplasmic tail that might mediate direct or indirect interactions via adaptor proteins etc. Thus, although valuable data concerning the IgG-FcRn interaction have been obtained from *in vitro* binding studies with recombinant FcRn, the validity of extrapolating these findings to the *in vivo* situation may be questioned. It is clear, however, that *in vitro* binding affinity of an IgG or Fc for recombinant FcRn almost invariably correlates with the *in vivo* activity in FcRn-mediated functions (31, 81).

A model that incorporates both standing-up FcRn-IgG:FcRn complexes and lying-down IgG-FcRn dimer (through $\alpha 3$ domain contacts) complexes observed in the FcRn-Fc cocrystal has been proposed by Bjorkman and colleagues (82). This embraces data supporting the existence of both types of complex (40, 67, 68) and proposes the formation of oligomeric ribbons (Figure 3B). Such ribbons have been suggested to mediate membrane vesicularization by bridging adjacent membranes (83). Some *in vitro* data support the model (40, 67, 68), but to date the existence of oligomeric ribbons *in vivo* has not been proven owing to obvious technical limitations. However, this model explains the effects of mutations at both the FcRn-Fc interaction site and the FcRn-FcRn dimer interface (42, 64).

MULTIPLE FUNCTIONS FOR FcRn

FcRn: the Neonatal Fc Receptor

FcRn was first identified as the Fc receptor responsible for transferring maternal IgGs from mothers' milk across the intestinal epithelial cells of the neonatal gut of rodents (1–6). In rodents, this is the major route by which IgGs are transferred, whereas, in humans, essentially all IgGs are transferred prenatally across the placenta (see below). Early studies of rodent FcRn, using isolated rat brush border membranes, indicated that FcRn binds to IgG in a pH-dependent way, with binding at pH 6–6.5 and an undetectable interaction at pH 7.2 (3, 4, 6, 36). This result, combined with histochemical analyses, was used to build a picture of how FcRn functions as an IgG transporter (84). IgG binds to the luminal surface of the epithelial cells via FcRn and the FcRn-IgG complexes are taken up by receptor-mediated endocytosis. The complexes are then transcytosed across the cells and delivered via exocytosis at the basolateral surface of the cells. FcRn-IgG dissociation occurs at this site owing to the instability of the interaction at pH 7.4 (3, 4, 6, 36). This model has formed the basis of our current understanding of FcRn function, but variations on this theme need to be invoked when this receptor operates in different cellular environments (discussed below). Several observations indicate that FcRn is the only IgG transporter involved in the delivery of maternal IgGs from mothers' milk. (a) In $\beta 2$ -microglobulin-deficient ($\beta 2m^{-/-}$)

mice that do not express functional FcRn, maternal IgGs are not transferred (8, 85). (b) Analyses of mutated murine IgG1-derived Fc fragments in assays directed towards determining their ability to be transferred across the neonatal gut indicate a direct correlation between binding affinity for FcRn and the activity in inhibiting transfer of wild-type IgG1 (29, 31).

FcRn and the Maternofetal Transfer of Immunoglobulin Gs

The isolation and characterization of rat FcRn from the yolk sac endoderm led to the proposal by Roberts et al (7) that this Fc receptor is involved in the maternofetal transfer of IgGs. Quantitatively, this represents the minor route of IgG delivery from mother to young in rodents. The studies demonstrated that the FcRn-IgG interaction occurred in apical vesicles and not on the yolk sac cell surface (7). In addition, cell surface expression of FcRn could not be detected. This led to the suggestion that FcRn binding to IgG occurs only after nonspecific uptake via fluid-phase pinocytosis by yolk sac. Bound IgG is then transported across the cell and delivered to the basolateral surface, where it is released at the slightly basic pH. Binding in acidic endosomes is consistent with the known pH dependence of the FcRn-IgG interaction. There is therefore an important mechanistic difference between yolk sac and intestinal transfer. This difference may result in yolk sac transfer being less efficient (particularly at low IgG concentrations), because IgGs are not captured by cell surface receptors, but the difference is apparently a necessary tradeoff for the ability of FcRn to bind ligand in a strictly pH-dependent way. Interestingly, *in vitro* assays have shown that the neonatal intestine does not need to be bathed in an acidic medium on the apical surface to carry out transcytosis (86), indicating that, even for this tissue, receptor-mediated cell surface binding of IgG is not a prerequisite for uptake. By analogy with intestinal transfer, in neonates, maternofetal IgG transfer is ablated in $\beta 2m^{-/-}$ mice (8, 85). Furthermore, the efficiency of transfer of different IgG isotypes or mutated Fc fragments in mice correlates with binding affinity for FcRn (9). FcRn therefore appears to be solely responsible for IgG transport.

Maternofetal transfer of IgGs in humans shows some specificity insofar as there is preferential transport of some isotypes over others (see below). In addition, the Fc region of IgG is known to be essential (87; reviewed in 88). The isolation of FcRn cDNA from human syncytiotrophoblast suggested that it is responsible for maternofetal transfer (25), consistent with the criteria that this transfer show some specificity and be mediated through the Fc region. In humans, the different organization of the fetal membranes results in IgG transfer across the syncytiotrophoblast of the chorioallantoic placenta rather than the yolk sac, and it is the major, if not sole, route of IgG delivery to offspring. Human FcRn has subsequently been identified at the protein level in syncytiotrophoblast (26–28) and in one study has been reported to be undetectable on the apical membrane (28). Regardless of whether it is on the apical surface, the consensus

appears to be that, in the apical region of the cells, the majority is located in vesicles that are most likely acidic endosomes. However, it is controversial whether human FcRn is expressed in placental endothelial cells (26–28). If not expressed in this location, how IgGs transfer across this cellular barrier to the fetal circulation remains an open question.

Colocalization studies indicate that FcRn associates with IgG in endosomes in syncytiotrophoblast cells (28). Thus, IgG-FcRn association most likely occurs after IgG uptake in acidic, apical endosomes in an analogous way to that proposed for rodent yolk sac. Consistent with this result, IgG uptake by syncytiotrophoblast is coincident with uptake of a fluid-phase marker (89). In this respect, other proteins such as placental alkaline phosphatase and annexin II have been suggested to play a role in mediating IgG uptake, but recent data argue against this (90; reviewed in 88). Furthermore, the expression of FcγRs in placenta (87, 91, 92) suggested that these may play a role in transferring IgGs. However, this is not supported by the selectivity of binding of these FcRs to different IgG isotypes. For example, FcγRIIb binds preferentially to IgG3 compared with IgG4 (54), but this preference does not impinge on the relative efficiency of maternofetal transfer of these isotypes (see below). The function of placental FcγR expression is most likely in the clearance of immune complexes, particularly on Hofbauer cells, in which all three forms are expressed (87, 91, 92; reviewed in 88).

The relative transfer efficiencies of hIgGs across the placenta remain a controversial issue, with some studies indicating poor transport of IgG2 (93–95) and others showing equivalent passage of all subclasses (96, 97). The discrepancies are most likely caused by the systems used and obvious ethical limitations on experimentation. The use of an *in vitro* perfused placental assay that gives a good indication of the ability of a protein/drug to cross the placenta during pregnancy indicated that the hierarchy of transfer is hIgG4 > hIgG1 > hIgG3 > hIgG2 (98). The development of *in vitro* systems to assess IgG transport across trophoblast cells (15, 99) should provide the opportunity to obtain quantitative data concerning FcRn-mediated transport, and this would have obvious practical implications. However, limitations of such cell systems may be that only one cell type is being investigated, in contrast to the situation during *in vivo* transfer, when several distinct cellular barriers must be traversed.

A Role for FcRn in Immunoglobulin G Homeostasis

Over 30 years ago, Brambell and colleagues proposed that the receptors mediating transfer of maternal IgGs might be related to the protective receptors that regulate serum IgG half-life (100, 101). These receptors were suggested to function by binding and protecting IgGs against lysosomal degradation; that is, they act as salvage receptors. Consistent with this hypothesis, analyses of the binding affinity for murine FcRn of mutated mouse IgG1-derived Fc fragments with reduced serum persistence indicated that the sites of IgG or Fc that binds to FcRn and

regulates serum half-life closely overlap (29, 31, 102). This result prompted us to analyze the serum half-lives of murine IgG1 and IgG1-derived Fc fragments in mice that are $\beta 2m^{-/-}$ and, as a result, do not express functional MHC class I molecules or homologs including FcRn (10). The half-lives of these proteins were abnormally short in these mice (10), and these results have been independently confirmed by others (11, 12). In fact, in $\beta 2m^{-/-}$ mice, the half-life of the wild-type Fc fragment is essentially the same as that of a mutated Fc with no detectable binding affinity for FcRn (10).

The short serum half-lives of IgGs in $\beta 2m^{-/-}$ mice are consistent with observations that, in these mice, the circulating IgG levels are abnormally low despite an apparently normal B-cell compartment (103). The rates of IgG synthesis in these mice are insignificantly different from those in wild-type mice (11). Although we reported differences in IgG synthetic rates between wild-type and $\beta 2m^{-/-}$ mice when using the β phase half-life in the calculation (10), this difference becomes insignificant if the catabolic rate is used (V Ghetie & ES Ward, unpublished data). Consistent with the hypercatabolism that is observed in $\beta 2m^{-/-}$ mice, mice crossed onto a $\beta 2m^{-/-}$ background are also resistant to the IgG-mediated disease, bullous pemphigoid (104). Furthermore, mice crossed onto a $\beta 2m^{-/-}$ background are resistant to the induction of systemic lupus erythematosus after idiotype (16/6Id) immunization (105). This was originally believed to be caused by the lack of classical MHC class I molecules in these mice, but an alternative explanation could be that these mice have abnormally low serum IgG levels. However, recent studies in systemic lupus erythematosus-susceptible mice in which the B cells are engineered to express only surface immunoglobulin have revealed an IgG-independent mechanism for renal and vascular disease (106).

In all studies to date, a good correlation between affinity for FcRn binding and serum half-life has been observed for Fc mutants or IgG variants (29, 31). Significantly, this correlation can be extended to engineered Fc fragments with higher affinity than their parent wild-type molecule. This was carried out by randomly mutating a recombinant murine Fc fragment at three residues located in proximity to the FcRn interaction site (81). These amino acids (Thr252, Thr254, and Thr256) were chosen because they are exposed and not highly conserved across species. The library of mutated fragments was expressed on the surface of bacteriophage and Fc fragments with higher affinity for recombinant mouse FcRn selected (81). One of these Fc fragments with mutations of Thr252, Thr254, and Thr256 to Leu, Ser, and Phe, respectively, had a significantly longer serum half-life than the wild-type Fc. This suggests that it should be possible to combine protein design with selection to generate therapeutic antibodies with increased serum persistence. In this context, a chimeric antibody (mouse variable domains linked to human constant regions) in which the constant region domains were shuffled to generate a hybrid IgG1/IgG4 molecule had a significantly longer half-life in mice than either of the parent IgG1 or IgG4 molecules (44). It will be of interest to unravel the molecular basis of this effect.

Where and How Does Immunoglobulin G Homeostasis Occur?

Much evidence supports the concept that FcRn is ubiquitously expressed in adult tissues (10, 25, 107), in addition to its earlier localization to neonatal gut and yolk sac/placenta. The expression of FcRn in almost every tissue analyzed led us and others to propose that the endothelial cells might be the site at which IgG homeostasis occurs (10, 108). This would be consistent with the close apposition of these cells to the bloodstream and earlier suggestions of Mariani & Strober (109) concerning the site of regulation of serum IgG levels. Distribution studies of murine IgG1, Fc fragments, and anti-FcRn antibodies indicate that the major sites of FcRn function in adult, nonpregnant mice are the skin and muscle, with a lesser involvement of liver and adipose (110). Furthermore, histochemical analyses of mouse muscle and liver indicate that FcRn is expressed in the endothelium of small arterioles and capillaries but cannot be detected in larger vessels such as the central vein and portal vasculature. Functional FcRn can also be isolated from a murine endothelial cell line (110). Interestingly, immunohistochemistry indicates that the steady-state distribution of FcRn in these cells is primarily intracellular, which is reminiscent of the data for rat FcRn expression in yolk sac (7). Analysis of FcRn expression in humans also indicates that it is expressed in endothelial cells (108), and this is consistent with earlier observations that human FcRn is widely expressed throughout adult tissues (25).

A model for how FcRn might function in its role as an IgG homeostat is shown in Figure 4. IgGs are taken up by endothelial cells by nonspecific pinocytosis and then enter acidic endosomes. If the IgGs bind to FcRn, they are salvaged from lysosomal degradation. Paradoxically, the endothelial cells are therefore involved in both the breakdown and salvaging of IgGs. The route by which FcRn takes in salvaging IgGs is far from clear; whether it acts as a recycling or transcytotic receptor or both in its role as the protective receptor is as yet unknown. By analogy with FcRn as an IgG homeostat, it is interesting that, when FcRn is apparently functioning as a transcytotic receptor during maternofetal transfer, significant amounts of IgGs are degraded (3, 111, 112). It is tempting to speculate that FcRn can act in recycling or transcytotic mode (or both), depending on the cell type in which it is expressed. The model (Figure 4) explains how FcRn acts as a homeostat that is finely tuned to regulate serum IgG levels. When IgG levels decrease, more FcRn is available for IgG binding so that an increased amount of IgG is salvaged. Conversely, if serum IgG levels rise, FcRn becomes saturated, and this results in an increase in the proportion of pinocytosed IgGs that are degraded.

A Possible Role for FcRn at Other Sites

In addition to its role in regulating serum IgG levels and transferring maternal IgGs, additional studies have indicated that the transporting function of FcRn is

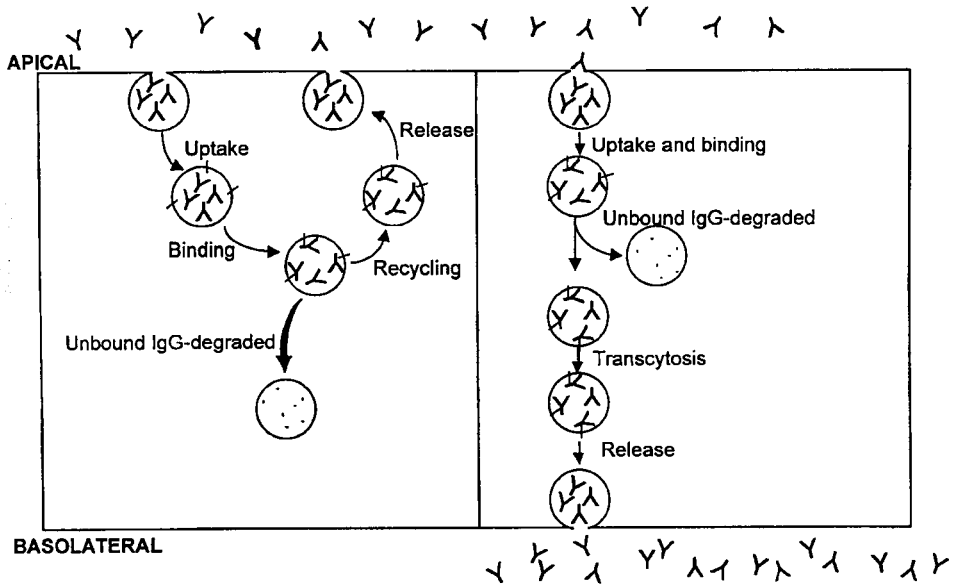


Figure 4 Models for the trafficking of FcRn in its role as an IgG homeostat in endothelial cells. IgGs are initially taken up by nonspecific pinocytosis because the pH of the blood-stream is not permissive for the IgG-FcRn interaction. Pinocytosed IgG molecules (Y) bind to free FcRn (—) in acidified endosomes. IgG that does not bind to FcRn is destined for degradation in lysosomes. The available evidence with in vitro cell lines indicates that FcRn can act as either a transcytotic or recycling receptor, and it is as yet unknown in which mode it operates during IgG homeostasis. However, if FcRn transcytoses IgG molecules across endothelial cells, then bidirectional transcytosis by necessity occurs for the IgG to be returned to the serum. Alternatively, IgG may traffic in one or both directions via transcellular channels (142), in addition to being transcytosed by an FcRn-mediated process. Surface expression of FcRn is not shown on this figure, because the available data indicate that the steady-state distribution in endothelial cells is primarily intracellular (110).

exploited for other purposes. For example, the detection of FcRn in human intestinal epithelial cells (113), and the bidirectional transcytosis of IgG across human intestinal T84 cell monolayers (113a) has led to several suggestions concerning its possible function. (a) It might be involved in the transfer of passive immunity via oral feeding of IgG. (b) FcRn expression at this site might act to detect pathogenic antibody in the lumen of the intestine. (c) By analogy with the transfer of immune complexes by the intestinal cells of the neonatal rodent, human FcRn might serve to deliver antigens to induce either immune activation or tolerance.

(d) By analogy with the cow (114), transfer of IgG into the gut via an FcRn-mediated process might play a role in the clearance of IgGs.

FcRn has also been identified in the adult rodent liver (110, 115; R Junghans, personal communication) and lactating mammary gland (116). For the liver, hepatocytic expression was suggested to play a role in delivering immune complexes from the canalicular space to the Kupffer cells and the bile (115). However, an inverse correlation between binding affinity for FcRn and transfer into bile has been observed for recombinant Fc fragments in mice (110). In addition, no significant differences were observed for serum-to-bile transport of IgGs in wild-type and $\beta 2m^{-/-}$ deficient mice, and all IgG transport could be accounted for by passive transfer (Junghans, personal communication). These observations suggest that the function of FcRn in hepatocytes might be to act as a recycling receptor whereby it salvages IgGs back into the bloodstream. In contrast, lack of binding to FcRn appears to result in an Fc fragment transiting into the bile by an unknown mechanism (110).

By analogy with the activity of FcRn in liver, a similar function has been attributed to FcRn in the murine lactating mammary gland (116). For both Fc fragments and complete IgGs, an inverse correlation between delivery into milk and affinity for FcRn was observed. This unexpected observation led us to propose that this relationship might result in a balance of IgGs in the neonatal serum that reflects the composition in the mother's bloodstream. More specifically, for transfer of maternal IgGs into neonatal serum, an IgG has to pass through two barriers: the mammary gland and the neonatal gut. Censorship by FcRn at both barriers would result in dramatic decreases of the levels of IgG isotypes that bind relatively weakly to FcRn at the expense of higher-affinity binders. Hence, we envisage that the process of transfer may occur in two steps, the first (maternal blood to milk) at which an inverse correlation between affinity and transfer is observed and the second (gut lumen to neonatal blood) at which a direct correlation is observed (Figure 5). This hypothesis would suggest that FcRn operates primarily in recycling mode in the mammary gland and in transcytotic mode in the neonatal gut.

What relevance does this have to humans, in whom maternofetal transfer is the major, if not sole, route of passive IgG delivery? Interestingly, on day 2 postpartum, the levels of IgGs in colostrum range from ~30% (IgG1) to 2% (IgG4) of the levels in the maternal serum (117), suggesting that some maternal IgG transfer to the neonate may occur in the first few days of life. However, the levels of IgG in the colostrum/milk drop precipitously over the next few days post partum, resulting in IgG concentrations that are ~100-fold lower than in serum (117). This suggests that, if FcRn is expressed in the human lactating mammary gland, it may result in IgGs being recycled away from the milk to exclude this Ig class. In contrast, during colostrum production, it may be that FcRn is not as effective in this recycling function. Although ethical considerations make testing of this hypothesis difficult, it may be possible to address using *in vitro* cell lines.

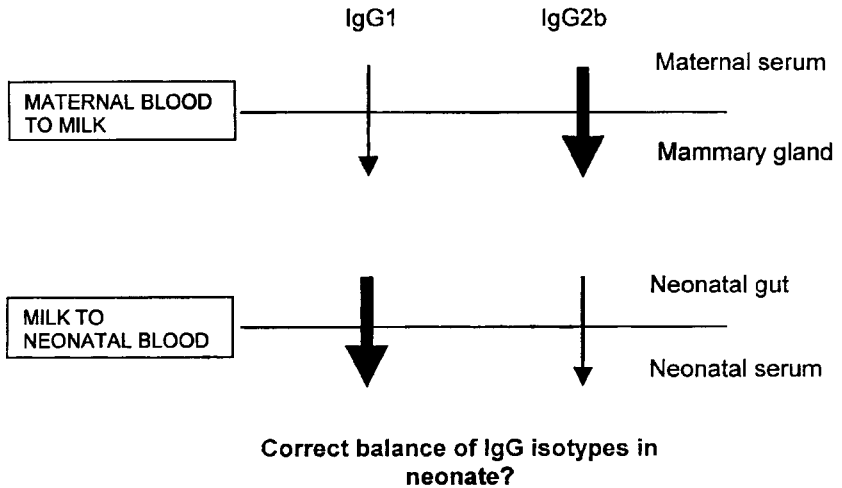


Figure 5 Schematic representation of a model for the transfer of IgGs from the maternal to neonatal bloodstream via mothers' milk, indicating the barriers that must be traversed and their relative transfer efficiencies. In mice, rat IgG1 accumulates in milk less efficiently than rat IgG2b (116), that is, in inverse correlation with affinity for FcRn (39). In contrast, the available data indicate that the transfer of an IgG molecule across the neonatal intestine correlates closely with its affinity for FcRn (29, 31). The outcome of this two-step transfer would be that the IgG subclass ratio in the neonatal serum would closely resemble that in the maternal blood.

ANALYSIS OF THE TRAFFICKING OF FcRn

The analysis of transcytosis of human IgGs across *in vitro* monolayers of *ex vivo* trophoblast cells has been reported (99). More recently this has been extended to the use of the BeWo choriocarcinoma cell line (15). For both systems, IgG transport occurs preferentially in the apical to basolateral direction, rather than the opposite direction. Although preferential binding of IgG to the apical surface of BeWo cells at pH 6.0 indicates that human FcRn is present on the cell membrane, this mode of binding is unlikely to be operative *in vivo*, where the cells are bathed at pH 7.4 [at which only nonspecific binding could be detected (15)]. The data from these analyses are consistent with the proposed model for transcytosis across the rat yolk sac (7) and also with IgG-human colocalization studies in isolated human syncytiotrophoblast (28). Thus, this *in vitro* system should be a valuable tool to study human FcRn function in the placental trophoblast.

To analyze the role of the cytoplasmic tail of FcRn in intracellular sorting, polarized Madin-Darby canine kidney (MDCK) cells have been transfected with Fc γ RIIb-rat FcRn cytoplasmic tail chimeras (16). Several types of constructs were made, but the most informative are the wild type, a variant in which the di-leucine

motif was mutated to di-alanine, and a truncated mutant with essentially no cytoplasmic tail. The di-leucine motif has been shown to mediate basolateral sorting and receptor internalization for many different receptors [e.g. FcγRII (118) and the CD3γ chain of the T-cell receptor (119)]. However, for rat FcRn the di-leucine motif appears to play no role in basolateral sorting, although truncation of almost all of the cytoplasmic tail resulted in reduced transport to the basolateral surface. This suggests that there may be an as yet unidentified motif involved in sorting of the FcγRII-FcRn chimera to the basolateral surface. In contrast to its lack of involvement in basolateral sorting, the di-leucine motif mediates efficient internalization of FcRn (16). It is interesting that receptor internalization was not completely ablated in the di-alanine variant, leading to the suggestion that a casein kinase II phosphorylation site in the cytoplasmic domain (N-terminal to the di-leucine motif) might also regulate the surface expression of rat FcRn. Such casein kinase II sites have been reported to play a role in receptor internalization in other systems (120). In contrast to the di-leucine motif, this site is not conserved in human FcRn (17, 25), suggesting that there may be subtle differences in FcRn trafficking across species.

In MDCK cell transfectants expressing the FcγRIIb-FcRn chimera, transcytosis occurred in both directions but was more efficient in the basolateral-to-apical direction than vice versa (16). Moreover, the apical surface was more active in recycling than the basolateral surface. However, these studies were carried out using anti-FcγRIIb Fab fragments, and whether these biases in transcytosis and recycling are seen with natural ligand remains to be analyzed. The MDCK system has provided much valuable information concerning the trafficking of other receptors (121, 122) and should be useful for the elucidation of the molecular mechanisms involved in FcRn function.

PROSPECTS: DOES FcRn HAVE RELEVANCE IN THE CLINIC?

The apparently diverse roles of FcRn are linked by the ability of FcRn to bind and traffic IgGs within and across cells. The observation that the catabolic rate of IgG is dependent on its plasma concentration (123), known as the concentration-catabolism phenomenon, was until recently without explanation. However, the identification of FcRn as the receptor that regulates serum IgG homeostasis gives a molecular explanation for this phenomenon. This leads to the question of how FcRn expression is regulated, because fluctuations in FcRn levels would in turn affect serum IgG concentrations. To date, little is known about this regulation, but the presence of motifs for two cytokine-inducible factors [nuclear factor (NF)-interleukin (IL)-6 and NF-1] upstream of mouse FcRn (124) suggests that it may be upregulated during the acute phase of an immune response. It is tempting to suggest that dysregulation of FcRn expression may be involved in situations in

which hypercatabolism is observed, such as after burns (125) and in myotonic dystrophy (126). Furthermore, it is possible that some types of IgG deficiencies such as familial idiopathic hypercatabolism (127) may be caused by abnormalities in FcRn expression or function.

The role of FcRn as an IgG homeostat suggests that the modulation of FcRn function and/or expression might be an effective approach for the treatment of IgG-mediated disease. For example, in autoimmune diseases in which pathogenic IgGs are involved, blockade of FcRn function might be an effective treatment modality (128). Indeed, the use of intravenous immunoglobulin has been shown to be efficacious in such situations through a mechanism that involves the induction of hypercatabolism of endogenous IgGs (129). The synergism that is observed between intravenous immunoglobulin therapy and methylprednisone in the treatment of Guillain-Barre syndrome (130) is most likely caused by the ability of glucocorticoids to decrease FcRn expression at the transcriptional level (131). This explanation is also consistent with the earlier report that hydrocortisone treatment results in hypogammaglobulinemia (132). An alternative way of regulating FcRn function would be to generate novel FcRn ligands that block IgG binding or affect FcRn trafficking, and our expanding knowledge of FcRn at the molecular level may facilitate this task.

Understanding the molecular basis by which IgGs persist in the serum is of relevance to the engineering of improved antibodies for use in therapy (81, 133). For example, for the passive delivery of antitumor antibodies [e.g. anti-HER-2 (134) and anti-CD20 (135)], a longer half-life of the IgG could result in improved efficacy and the need for fewer doses. Alternatively, for use in imaging, it is desirable to have a short half-life and, although this can be achieved by using Fab fragments, it is now also possible to engineer complete antibodies with single amino acid substitutions [e.g. Ile253 to Ala (31, 32)], which would be predicted to have reduced serum persistence.

An additional FcRn function that could be exploited in the clinic is the passive delivery of therapeutic antibodies in maternofetal medicine. There are many situations in which this might be useful, but one may be in the specific delivery of antipathogen IgGs. In this respect, the engineering of IgGs with higher affinities for FcRn is attractive (81), because these would be expected to be transferred more efficiently. Although it has been reported that maternally derived IgGs can adversely affect the neonatal response to immunization (136), less is known about the effects of IgGs on T-cell responses. In fact, *in vitro* analyses have indicated that some IgGs can enhance (137, 138) or suppress (139, 140) T-cell responses to specific epitopes, most likely via effects on antigen processing. It is important that a recent study in mice has demonstrated that maternal IgG does not appear to have a detrimental effect on helper T-cell responses (141). Furthermore, early prime-boosting regimens can result in normal secondary responses even in the presence of passively transferred IgG (141). This may allay concerns about interference effects of maternally derived antibodies on subsequent vaccination of the

neonate, but has yet to be tested for the panoply of pathogens for which vaccines exist.

Finally, the expression of FcRn and its possible function at other sites such as the adult intestine (113) and liver (110, 115) (Junghans, personal communication) remain to be more fully investigated and could result in yet more roles being defined for this intriguing MHC class I relative.

Note Added in Proof

Recent studies by Martin and Bjorkman (143) have demonstrated that the "lying down" FcRn dimer-Fc complex proposed earlier by Bjorkman and colleagues (42, 64, 67, 68) does not exist in solution. However, this does not exclude the possibility that these complexes exist under physiological conditions when FcRn is membrane bound.

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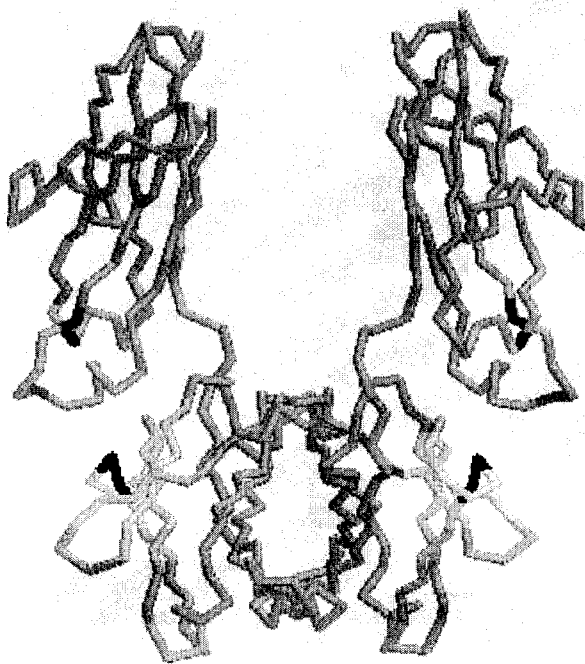


Figure 1 Alpha-carbon trace of the Fc region of human IgG1 (33). Residues shown to play a role in the FcRn:IgG interaction using both binding and in vivo assays (29-32, 39) are indicated (Ile253, green; Pro257, red; His310, blue; His435-Tyr436, black; note that the role of Tyr436 in human IgG1 has not been investigated, but His436 in mouse IgG1 is involved). Residues 307 and 309 play a less significant role (39) and are therefore not highlighted. The figure was drawn using RASMOL (Roger Sayle, Bioinformatics Research Institute, University of Edinburgh, Edinburgh, U.K.).

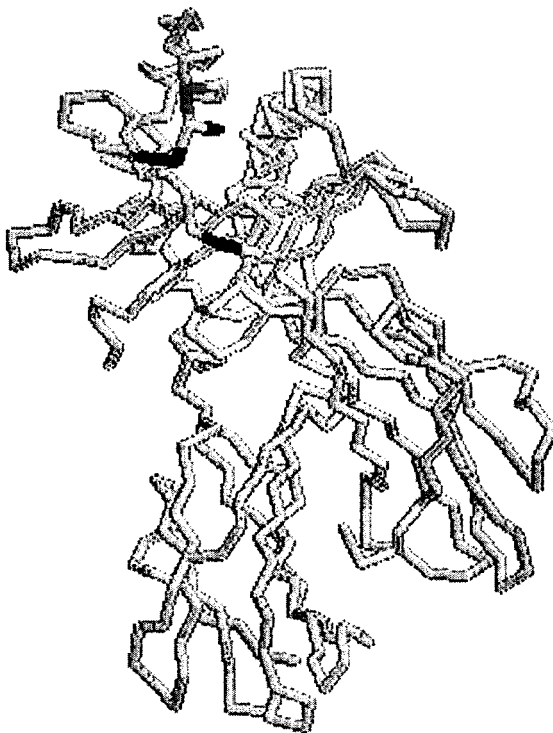


Figure 2 Alpha-carbon trace of rat FcRn with $\alpha 1$ and $\alpha 2$ domain helices perpendicular to the page (18). Indicated are the $\alpha 2$ domain residues shown by site-directed mutagenesis studies (64) to be involved in binding to rodent IgGs (Glu117, blue; Glu132-Trp133, red; Glu135, black; Asp137, green). The figure was drawn with RASMOL (Roger Sayle, Bioinformatics Research Institute, University of Edinburgh, Edinburgh, U.K.).