The structure of human CD23 and its interactions with IgE and CD21

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The low-affinity immunoglobulin E (IgE) receptor, CD23 (FcεRII), binds both IgE and CD21 and, through these interactions, regulates the synthesis of IgE, the antibody isotype that mediates the allergic response. We have determined the three-dimensional structure of the C-type lectin domain of CD23 in solution by nuclear magnetic resonance spectroscopy. An analysis of concentration-dependent chemical shift perturbations have allowed us to identify the residues engaged in self-association to the trimeric state, whereas ligand-induced changes have defined the binding sites for IgE and CD21. The results further reveal that CD23 can bind both ligands simultaneously. Despite the C-type lectin domain structure, none of the interactions require calcium. We also find that IgE and CD23 can interact to form high molecular mass multimeric complexes. The interactions that we have described provide a solution to the paradox that CD23 is involved in both up- and down-regulation of IgE and provide a structural basis for the development of inhibitors of allergic disease.

IgE binds to its effector cells through either FcεRII, the high-affinity receptor, or CD23 (FcεRII), the low-affinity receptor. The former mediates the IgE effector functions with mast cells and basophils in type I immediate hypersensitivity. CD23 has multiple functions that are controlled by a range of different ligands. These include IgE (both in its secreted form and on membranes of committed B cells), CD21 (also known as complement receptor 2), CD18/CD11b and CD18/CD11c (complement receptors 3 and 4, respectively), and the vitronectin receptor (1). The interactions with IgE and CD21 are pivotal in IgE regulation (2). Paradoxically, CD23 engages in both the up- and down-regulation of IgE synthesis, thereby constituting a two-way switch in IgE homeostasis (reviewed in reference 1).

CD23 is a 45-kD type II membrane protein expressed in various cell types, including B cells. It is unique among Fc receptors in its homology to C-type (calcium-dependent) lectins (1) and is also closely homologous, and genetically linked on human chromosome 19, to the vitronectin receptor (1). The structures of the CD23 ligands, IgE Fc (7) (as well as the Ce3-4 subfragment [8]), and the two NH2-terminal short consensus repeat domains of CD21(D1-2) (9) are known from X-ray crystallography. In contrast, that of the CD23 lectin domain has only been inferred by modelling, based on available sequence homologies (10). We have used nuclear magnetic resonance (NMR) to determine the three-dimensional structure of the lectin domain and to locate the residues involved in IgE and CD21 binding. We have also searched for the interactions of the lectin domain with calcium and a set of possible mono/disaccharide ligands to evaluate its lectin function.

Like DC-SIGN and several other C-type lectins, CD23 self-associates through its extra-cellular sequence by the formation of an α-helical coiled-coil “stalk.” In the membrane of B cells, CD23 forms trimers with the three
lectin domains held together at the end of the 15-nm stalk (11). The stalk is susceptible to proteolytic cleavage (12), generating fragments with differing trimerization propensities depending on the length of the residual stalk. The dust mite protease Der p I cleaves CD23 close to the lectin domain, and the resulting monomeric CD23 may be a factor in the high allergenicity of dust mites (13). We have determined the structure of a recombinant version of the Der p I fragment of CD23 (derCD23) by NMR spectroscopy, as well as the location of the IgE and CD21 binding sites. For comparison, we also generated a recombinant soluble CD23 fragment containing the entire extracellular sequence (exCD23).

The opposing activities of CD23 in IgE regulation are thought to be properties of the soluble and membrane forms. Soluble CD23 enhances IgE synthesis on binding to CD21 (2). When IgE binds to membrane CD23, further IgE synthesis is suppressed; in CD23-deficient mice, the level of circulating IgE is increased by orders of magnitude (14). The balance between the two forms of CD23 may accordingly be expected to regulate the level of IgE synthesis.

CD23 fragments are found in the circulation of normal human subjects. Elevated concentrations of circulating soluble fragments are commonly associated with inflammatory or lymphoproliferative diseases, such as rheumatoid arthritis, asthma, and chronic lymphoblastic leukemia, also known as CLL (15–17). It has been shown that antibodies to CD23 alleviate all three conditions, and an anti-CD23 antibody, IDEC-152, is in clinical trials for asthma (16) and CLL (17). Structural information on CD23 and its interactions is needed if the mechanisms of IgE homeostasis are to be understood and agents for intervening in this process developed.

RESULTS
derCD23 interacts with IgE and CD21

We have used surface plasmon resonance to characterize the interaction between derCD23 and the two protein ligands, IgE and CD21, involved in IgE regulation, determining equilibrium and rate constants for the Fc fragment of IgE (domains Ce2-4) and the D1-2 fragment of human CD21.

For the interaction between Ce2-4 and derCD23, we observed a marked change in affinity and off rates depending on the immobilization density of derCD23. At low density, Ce2-4 and CD21(D1-2) both show fast-on/-off kinetics with a resulting $K_D = 1.3 \pm 0.3$ and $0.87 \pm 0.09 \times 10^{-6}$ M, respectively (Fig. 1, A and B). At a higher immobilization density of derCD23 the rates of dissociation of Ce2-4 are markedly reduced (Fig. 1 D). Ce2-4 is a dimer, and the presence of two copies of the Ce3 domain may therefore explain this effect; the dimer has the potential to make a bivalent interaction and the observed affinity differences are then caused by cooperative binding. The monovalent CD21(D1-2) construct showed no change in apparent affinity at higher derCD23 densities (Fig. 1 C).

When Ce2-4 is the immobilized component, binding of derCD23 (Fig. 1 E), which is monomeric under these conditions as shown by sedimentation equilibrium (molecular mass = 18,086 ± 350 dalton [D]; unpublished data), gives similar values to Ce2-4/derCD23 (Fig. 1 B). In contrast, the binding of exCD23, with the complete extracellular sequence, shows a considerably higher affinity, with a markedly slower off rate (Fig. 1 F). In fact, these binding curves of exCD23 with Ce2-4 show two components with different affinities ($K_D = 1.1 \pm 0.2 \times 10^{-6}$ M and $3.9 \pm 0.6 \times 10^{-8}$ M) and interaction kinetics. This effect is clearly reflected in the dissociation kinetics (Fig. 1 F: one minor component with a rate constant of $4 \times 10^{-3}$ s$^{-1}$ and a major component with an off-rate constant of $5 \times 10^{-4}$ s$^{-1}$). Because exCD23 is also monomeric in solution under these conditions, as de-
The three-dimensional structure of derCD23 was solved by heteronuclear NMR spectroscopy, and its interactions with its ligands were examined. Assignment of backbone and side-chain resonances were performed by CBCA- and nuclear overhauser effect (NOE)–based assignment strategies; trosy-based pulse sequences were used to improve the efficiency of the triple resonance experiments (20). Additional data were collected to characterize derCD23 dynamics and hydrodynamics. Analysis of dynamics from \(^{15}N\) relaxation gives a direct measure of backbone flexibility. The derCD23 lectin domain is generally structurally rigid, with highly flexible NH\(^{\text{2}}\) and COOH termini and three internal loops (α2-β4, β4-β5, and β5-β6) showing some degree of flexibility. Five amino acids from a central loop (β3-β6) could not be assigned; residues flanking this loop show increased transverse relaxation rates, suggesting that this region experiences motions on the ms-μs time scale and that loss of peaks is probably caused by line broadening (NMR. relaxation data are shown in Fig. S1, available at http://www.jem.org/cgi/content/full/jem.20050811/DC1).

The structure of derCD23 was based on >2,300 NMR-derived structural constraints, including >2,100 structurally relevant NOEs, 96 dihedral angle constraints from the program TALOS (see Materials and methods) (21), and 30 hydrogen bonds, implied by hydrogen–deuterium exchange experiments and local secondary structure. A summary of restraints used is shown in Table I. The average density of structural constraints was ~25 per residue over the secondary structure elements of the protein.

The three-dimensional structure of derCD23 consists of two roughly orthogonal α helices and eight β strands forming two antiparallel β sheets. Four disulphide bonds contribute to the tertiary structure, whereas seven tryptophan residues and other conserved side chains form a hydrophobic core within the domain. The topology is that of a C-type lectin domain. It shows the greatest sequence and structural homology to the lectin domains of DC-SIGN, the H1 subunit of the asialoglycoprotein receptor, and human lung surfactant protein D, with sequence identities of 36, 35, and 26%, respectively, and root mean squared (r.m.s.) deviations of 2.7–2.8 Å over 118–126 residues. The global r.m.s. deviation for the NMR–derived ensemble of 20 structures is 0.26 Å for backbone atoms and 0.8 Å for heavy atoms in all elements of secondary structure. A bundle of the 20 lowest energy conformers and a ribbon diagram of the derCD23 structure are shown in Fig. 2, A and B, respectively. derCD23 shows a marked polarity in its electrostatic character. The
surface is highly charged, but the positive and negative charges are found on opposite faces (Fig. 2 C). The highly charged character will affect how CD23 interacts with ligands and appears to be particularly important in self-association.

We observed two distinct conformations for the derCD23 protein (conformations A and B, available from the Protein Data Bank under accession nos. 1T8D and 1T8C, respectively) in an area around the hydrophobic face of α-helix 1. Twenty residues show two sets of peaks in 1H-15N–HSQC spectra. Based on relative peak intensities, the two conformations are roughly equally populated. The relative occupancies of the conformations did not change under a large number of conditions tested, including changes in concentration, temperature, pH, and ionic strength and in several ligand-binding experiments. The two conformations are in slow exchange on the NMR timescale. Each conformer gave rise to a distinct set of NOEs; based on 220 distinct NOEs, independent ensembles of structures were calculated for each conformation. The two conformations differ in the extent of hydrophobic packing between the first β sheet (β1, β2, B3, and β8) and α-helix 1. This results in small changes in overall structure but marked changes in chemical shift for nearby residues because of the change of orientation of three aromatic side chains (Y176, W167, and W280) in this region. Because the biological importance of these two conformers is not clear at present, we will not dwell on them further here, and they will be described in detail elsewhere (unpublished data).

The CD23 calcium binding site and the lectin functions of CD23

X-ray crystallography of related C-type lectin-like domains (CTLDs) has shown one to three calcium binding sites per domain (22), but the calcium and carbohydrate binding properties of CD23 have been difficult to predict. Ca2+ site 2 in derCD23 is reasonably well conserved, but the canonical Ca2+ site 1 is poorly conserved (23). In other CTLDs, site 2 is directly involved in binding carbohydrates.

We studied the calcium-binding behavior of derCD23 by monitoring the effects of calcium titration on the 1H-15N–HSQC spectrum. derCD23 was expressed and refolded in the presence of 25 mM EDTA, and the EDTA was removed by dialysis. The calcium-free sample was well folded with only very few residues showing substantial chemical shift changes from the calcium-bound sample, in contrast to some other CTLDs that require Ca2+ for proper folding (24). Eleven datasets were collected with Ca2+ concentrations ranging from 100 μM to 50 mM. Over the course of this titration, seven residues showed large proton chemical shift changes (>0.08 parts per million [ppm]): backbone amides for I221, N225, K229, G230, E231, D270, A271, and D274 and the side-chain amide resonances of N225. Saturation binding curves for each of the eight sites were measured, and all were in good agreement, giving a Kd of 1.80 ± 0.15 mM (Fig. 3, inset). Surprisingly, the observed pattern of chemical shift changes suggests occupancy of Ca2+ site 1, but presents no evidence for the occupancy of Ca2+ site 2 (Fig. 3).

We also tested the ability of derCD23 to interact with a series of carbohydrate ligands. Individual NMR chemical shift perturbation titrations were performed with galactose, glucose, lactose, mannose, and N-acetylglucosamine to a fi-
nal carbohydrate concentration of 125 mM. Even at the highest concentrations, none of these compounds bound to derCD23. In conjunction with the apparent absence of Ca2+/H11001 site 2, CD23, if it binds sugars at all, must do so using a different mode from the canonical CTLD carbohydrate recognition mechanism.

The interaction surface of derCD23 for IgE
To investigate the nature of the CD23’s interaction with IgE, the Fc fragment of IgE (Cε2–4) was titrated with 15N-labeled derCD23. During the titration, most of the peaks in the troxy-HSQC spectrum disappeared because of line broadening. Only peaks mapping to the COOH terminus of the derCD23 fragment remained visible (unpublished data); the relaxation analysis indicated that these residues have motion independent from the overall tumbling characteristics of the protein. These observations are consistent with the formation of a high-order oligomer of the Cε2–4–derCD23 complex.

To map the ligand binding surfaces of CD23 with IgE, we instead titrated a monomeric Cε3 domain against a 15N-labeled derCD23 sample (Fig. 4 A). It has been reported that the entire CD23 binding site is contained within the Cε3 domain (25). Residues W184, R188, Y189, A190, L198, H202, I221, G222, R224, N225, L226, W234, V235, A271, C273, D274, K276, and A279 in derCD23 exhibited considerable concentration-dependent changes in chemical shifts and line broadening on addition of Cε3. The residues, when mapped onto the derCD23 surface, reveal a continuous interaction surface for Cε3 on the CD23 lectin domain (Fig. 4 C). The complete list of chemical shift changes observed during the Cε3 titration are available in the BioMagResBank database under accession no. 6734.

The interaction surface of derCD23 for CD21
We identified the interaction surface of CD21 on CD23 by titrating unlabeled CD21(D1-2) against 15N-labeled derCD23 (Fig. 4 B). This CD21 construct is identical to the one co-crystallized with C3d (9). Four residues of derCD23 show chemical shift perturbations, all of which are in the COOH-terminal “tail” (residues E294, G295, S296, and E298; Fig. 4 C). Residue S293 was not assigned, whereas the peak for residue A297 lies in a region of considerable overlap in the 15N-HSQC, making it difficult to identify its position unambiguously. Residue A292 does not show a change in chemical shift, and, hence, we infer that the CD21 interaction site comprises the COOH-terminal six residues of this CD23 construct. We note that the full-length CD23 COOH-terminal tail, with an additional 23 residues, may have a higher affinity for CD21 than the derCD23 fragment. Further studies will focus on this and the binding to other domains of CD21 (6).

Despite a high degree of conservation between the lectin head region of human and mouse CD23 (62% over 143 residues), the COOH-terminal region of derCD23 is not conserved between species (2 identities over the 10 COOH-ter-
The CD23–IgE–CD21 trimolecular complex

The two NMR titration experiments identify independent binding sites for CD21(D1–2) and IgE on CD23. We confirmed the independent nature of the interactions by forming the trimolecular complex (derCD23–Cα3–CD21(D1–2)) through sequential titrations showing additivity of the effects on the spectrum of the separate interactions (unpublished data).

derCD23 oligomerization

At a concentration of 100 μM, derCD23 has an apparent molecular mass of 16.5 kDa, but at 1.2 mM of derCD23 a monomer–oligomer equilibrium supervened, with a mass-averaged molecular mass of ~28 kDa, with both values estimated from NMR-based translational diffusion measurements (26). This self-association is accompanied by a change in the chemical shifts of some of the peaks in the HSQC spectrum. These residues (L198, K212, H213, N225, E231, V240, and Y242) map to the two distinct regions with opposite charge characteristics and suggest a possible self-association interaction surface.

On the basis of this postulated interaction surface, we generated a model for the trimer formed by full-length CD23 (Fig. 5). X-ray structures of other C-type lectin trimers have been determined, and the arrangement of the subunits are all similar in mannose-binding protein (MBP), pulmonary surfactant apoproteins D and A, and tetranectin (23). The NMR data predict a different arrangement for the CD23 trimer. MBP, pulmonary surfactant apoproteins D and A, and tetranectin all possess a similar nucleating heptad repeat sequence at the top of the coiled-coil stalk that allows the formation of a largely hydrophobic interface. Although CD23 has strong homology to these proteins in the lectin-like domain, it differs in this interface motif. Furthermore, an MBP-type arrangement for CD23 would result in an electrostatically repulsive interface. The interface predicted from the NMR chemical shifts presents an electrostatically favorable interface and results in completely solvent-exposed interaction sites for IgE and CD21 (Fig. 5).

DISCUSSION

The structure of derCD23 and its complexes with IgE and CD21

The NMR structure of derCD23 confirms that it has the topology of a C-type lectin domain, as predicted by sequence homology to other members of this family. NMR spectra revealed an equilibrium between two structures that differ in the hydrophobic packing between two of the structural elements. Structural plasticity has been suggested to confer an advantage in allowing greater diversity of ligand recognition (27). CD23’s conformational heterogeneity could potentially play a role in its interactions with ligands. However, IgE, CD21, or calcium binding do not affect the relative proportions of the two conformers, which leads us to conclude that both conformers bind to these ligands equally well. Surprisingly, occupation of only one of the putative calcium-binding sites (Ca\(^{2+}\) site 1) could be confirmed. Because Ca\(^{2+}\) site 2 is involved in carbohydrate recognition by other CTLDs, this result is in accord with the observation that glycosylation is not required for the binding to either IgE (28) or CD21(D1–2) (6). The results also demonstrate that calcium is not required to stabilize the configuration of CD23 for binding these ligands.

We have observed cooperativity and biphasicity in the binding of Ca\(^{2+}\) to derCD23 (Fig. 1 D) and of exCD23 to Ca\(^{2+}\)–4 (Fig. 1 F). The latter corresponds well with the reported biphasic kinetics of IgE binding to monomers and trimers of membrane CD23 at the cell surface (11, 29). At the concentrations of the Biacore experiments (see Materials and methods), we know from sedimentation equilibrium that both derCD23 and exCD23 are entirely monomeric, and, thus, the IgE Fc must stabilize their oligomerization, more so for exCD23 because it contains the stalk as well as the lectin domain. Ligand-induced oligomerization of exCD23 may be a further example of coupled folding and protein binding (30). In contrast to the interaction with IgE, there was no concentration dependence or evidence of cooperativity in the binding of CD21(D1–2) to derCD23 (Fig. 1, A and C), suggesting that a single lectin domain of CD23 (with a com-
Soluble CD23 is implicated in the up-regulation of IgE synthesis: its attachment to CD21 on peripheral blood B cells before differentiation into IgE-secreting plasma cells enhances IgE synthesis (2). A mechanism for the up-regulation of IgE synthesis was originally suggested by analogy to the process of up-regulation of antibody synthesis in the immune response by C3d fragments of complement component C3. C3d fragments, covalently linked to the antigen, coligate antigen receptor (IgM) and CD21 on naive B cells (31, 32), leading to cell proliferation and antibody synthesis.

We have founds that B cells express membrane IgE and CD21 before differentiation into the IgE-secreting plasma cells (unpublished data). Thus, soluble CD23 may up-regulate IgE synthesis by coligation of membrane IgE and CD21 on these transitional cells, resulting in selective proliferation and, ultimately, higher levels of IgE synthesis (Fig. 6, right). Such a mechanism is supported by our observation that coligation of membrane IgM and CD21 by anti-IgM (acting as a surrogate antigen) and CD23 stimulates B cell proliferation (33). Our discoveries that the binding sites for IgE and CD21 are distinct and that both ligands can bind simultaneously support the co-cross-linking of membrane IgE and CD21 by soluble CD23. If correct, then the inhibition of membrane CD23 cleavage or soluble CD23 binding to either IgE or CD21 offers potential targets for therapy, and the data presented here will provide a structural basis for designing inhibitors.

Feedback regulation of IgE synthesis
Membrane CD23 is associated with the down-regulation of IgE synthesis (Fig. 6, left). CD23-deficient mice exhibit abnormally high serum IgE levels, whereas CD23-overexpressing mice show decreased IgE synthesis and reduced susceptibility to systemic anaphylaxis (34). Cross-linking of membrane CD23 on human B cells by IgE or IgE–antigen complexes or by anti-CD23 antibodies inhibits B cell proliferation and IgE production (35, 36). An anti-CD23 monoclonal antibody has accordingly shown promise for lowering serum IgE levels in clinical trials (16). Moreover, co-cross-linking of CD23 with surface immunoglobulin induces the apoptosis of B cells (37), and, thus, antigen–IgE complexes may regulate the population of the specific IgE antibody–producing B cells.

Our study sheds light on possible mechanisms of feedback regulation of IgE by membrane CD23. The binding of IgE to membrane CD23 prevents cleavage and release of the soluble CD23 fragments that stimulate IgE synthesis. Our finding that IgE Fc cooperatively binds two lectin domains of CD23 and appears to promote oligomerization of exCD23 explains how IgE might stabilize the trimer of membrane CD23 on the cell surface, rendering it less susceptible to proteolysis. The observation of high molecular mass complex formation between IgE Fc and derCD23 indicates how exogenous IgE could be endocytosed and degraded. Furthermore, the co-cross-linking of membrane CD23 and specific antibodies by IgE–antigen complexes may steal the endogenous membrane IgE from CD21, thus antagonizing the positive feedback pathway (Fig. 6).

Pivotal role of CD23 in IgE homeostasis
The main effector function of IgE is thought to be sensitization of mast cells for allergen triggering of an allergic response. This serves as protection against parasite infections, but confers the risk of allergic disease in susceptible individuals. The lower affinity of IgE for CD23 (KD = \(10^{-7}\)–\(10^{-8}\) M) than for FceRI (KD = \(10^{-10}\)–\(10^{-11}\) M), collectively with feedback regulation of IgE synthesis by IgE, ensures that the mast cells remain sensitized once excess IgE has been removed. According to the scheme in Fig. 6, soluble CD23, released by B cells on stimulation in the immune response, would initially up-regulate IgE synthesis by coligating membrane IgE and CD21. As IgE concentrations enter the range in which binding to membrane CD23 becomes important, IgE synthesis would be abruptly terminated. This would preclude the accumulation of dangerous levels of IgE. The isotype specificity of this mechanism is explained by the fact the switch between up- and down-regulation pivots around IgE itself (Fig. 6). The structure of CD23 and the trimer model, the location of its binding sites for IgE and
CD21, and the clustering of CD23 caused by IgE Fc lend support to this mechanism and suggest strategies for down-regulation of IgE levels to treat allergic disease.

MATERIALS AND METHODS

Protein expression and purification. derCD23 (P06734) comprises the amino acids Ser156 to Gin298. The human derCD23 construct was subcloned from CD23 cDNA (38) by PCR. Recombinant derCD23 was expressed in the Escherichia coli host strain BL21(DE3), extracted from the cell pellets, and refolded by Taylor’s procedure (39). Unlabeled and 15N- and 13C-labeled derCD23 were prepared on minimal media or with the addition of 13C-glucose/15N-HCl to the media. Proteins were purified by hydrophobic interaction chromatography on a phenyl sepharose column (GE Healthcare). Mass spectrometry of these materials was performed on a mass spectrometer (MicroMass Platform-II ESI; Waters). Reverse-phase HPLC-purified unlabeled, 15N-labeled, and 13C, 15N-labeled material had masses of 16,143 ± 4, 16,334 ± 3, and 16,995 ± 5 Da, respectively, confirming the identity of the material and indicating that isotope incorporation was highly efficient. ExCD23, comprising Asp48 to Ser321, was subcloned from CD23 cDNA, expressed in E. coli, extracted, and refolded as described above for derCD23. Recombinant human CD21(D1–2), Cε2–4 (provided by A. Beavil, Kings College London, London, UK), and Cε3 (provided by N. Price, University of Oxford, Oxford, UK) constructs were prepared as described previously (9, 11, 40, 41).

Surface plasmon resonance. All experiments were performed at 25°C on an automated instrument (Biacore 2000; Biacore AB). A specific binding surface was prepared by coupling derCD23 to a CMS sensor chip through the amine coupling procedure. Coupling densities of 3,000 (high density) or COOH termini (residues 156–157 and 293) and five residues (residues 252–256) in a central loop were not assigned, as well as five other residues in loops and turns (residues 181, 215–216, 249, 263). Several approaches were used to try to help in the assignment of these residues, including changes in temperature, concentration, pH, ionic strength, and CaCl2 concentration, without success. NOE correlations were measured using 15N- and 13C-edited 3D-NOESY experiments and a 2D-NOESY in D2O (all mixing times of 125 ms). The backbone torsion angles φ and ψ were derived for the well-defined secondary structure elements using TALOS (21). Structure calculations were performed using the program CNS (version 1.1) (44) in an ab initio–simulated annealing protocol with a two-stage torsion angle dynamics and a Cartesian dynamics protocol. From 100 calculations, the 20 structures with the lowest energies were selected and subjected to a four-step refinement stage, adjusting for uncertainties in NOE restraints length because of overlap or spectral artifacts. Statistics for the resulting family of structures are listed in Table I.

Backbone 13N relaxation parameters, measuring the rates of 13N longitudinal (R1) and transverse (R2) relaxation and the H1–13N steady-state NOE, were collected using previously described methods (45). The “model-free” characteristics of the local motions (46) were derived from these parameters using the program DYNAMICS, and hydrodynamic characteristics were calculated using the program ROTDIF (47). Fitting the relaxation rate for all structured residues (S2 > 0.8), the following values for overall rotation were calculated: τr = 9.32 ± 0.22 ms and D∥/D⊥ = 1.40 ± 0.06.

For chemical shift perturbation experiments, unlabeled ligands were titrated in small aliquots to samples of 15N-labeled derCD23. Chemical shift changes (∆δ) in 1H–15N–HSQC spectra were followed until saturation, typically collecting 6–8 spectra per titration. Where possible, ligand samples were lyophilized and added as a powder to minimize volume changes during the experiment. For the calcium titration, the dissociation constant (KD) was estimated from the titration curves of all residues that showed considerable chemical shift changes by plotting the relative magnitude of ∆δ as a function of calcium concentration. A complete table of chemical shifts for derCD23 at low and high concentrations, chemical shifts for derCD23 bound to CD21, and the chemical shifts during the IgE Cε3 and calcium titrations are available from the BioMagResBank database under accession nos. 6732, 6733, 6734, and 6735.

Fast-exchanging amide protons were determined using a two-dimensional heteronuclear water exchange filter sequence (WEX II-FHSQC) (48). Mixing times of 100 and 500 ms for the water magnetization transfer were set. In the analysis of these data the intensities of the observed peaks were normalized against a native HSQC and plotted against residue number.

Measurements of translational diffusion coefficients were performed using pulsed field gradient methods. 16 1-D spectra, with gradient strengths varying from 6.5 to 65 G cm−1, were acquired. Intensities of NMR signals were fitted to standard equations to derive diffusion coefficients (26).

Online supplemental material. Fig. S1 shows a summary of the derCD23 secondary structure and dynamics analysis. Online supplemental material is available at http://www.jem.org/cgi/content/full/jem.20050811/DC1.

We thank Dr. Andrew Beavil for the gift of Cε2–4 and Naomi Price for Cε3.

J.M. McDonnell, B.J. Sutton, and H.J. Gould acknowledge grant support from the Wellcome Trust, the Medical Research Council (UK), and Ashima UK R.G. Hibbert was supported by a Wellcome Prize Studentship. The authors have no conflicting financial interests.

Submitted: 22 April 2005
Accepted: 1 August 2005

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J.M. McDonnell, B.J. Sutton, and H.J. Gould acknowledge grant support from the Wellcome Trust, the Medical Research Council (UK), and Ashima UK. R.G. Hibbert was supported by a Wellcome Prize Studentship.

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Submitted: 22 April 2005
Accepted: 1 August 2005

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