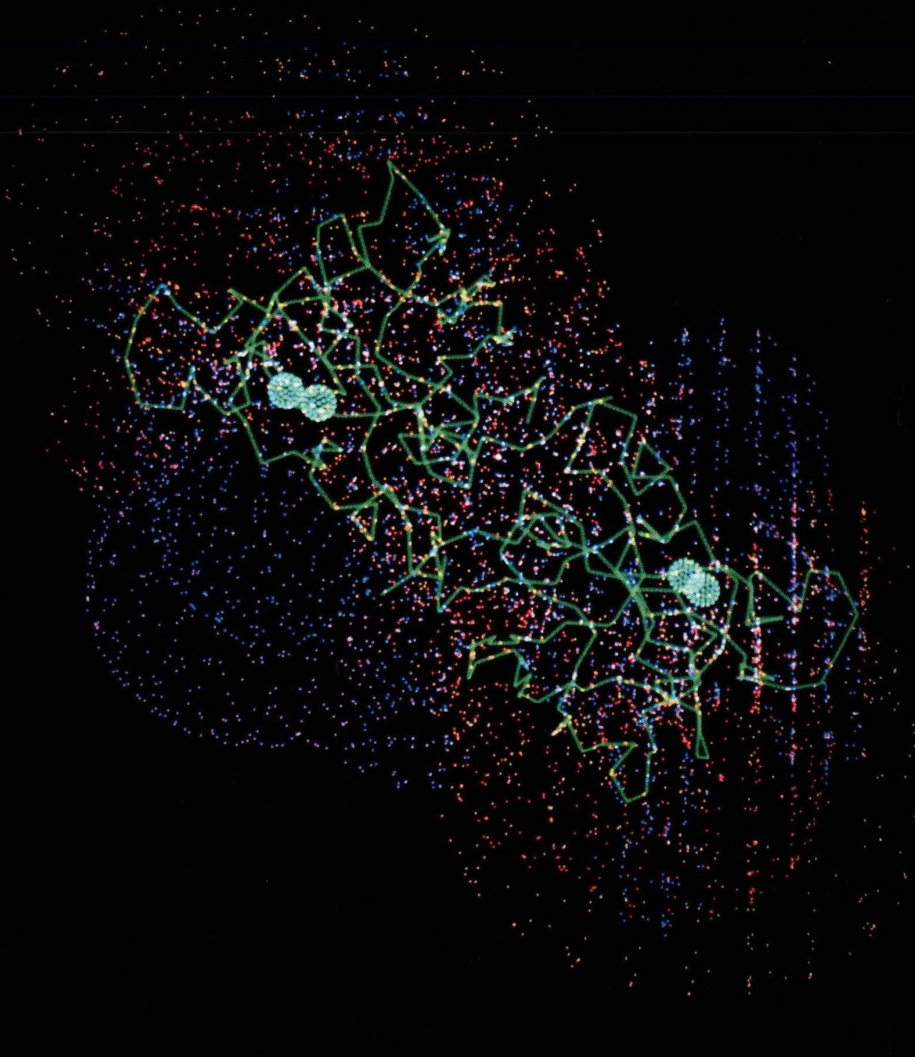


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# PROTEINS

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## The Galactan-Binding Immunoglobulin Fab J539: An X-Ray Diffraction Study at 2.6-Å Resolution

Se Won Suh,<sup>1</sup> T.N. Bhat,<sup>1</sup> Manuel A. Navia,<sup>1</sup> Gerson H. Cohen,<sup>1</sup> D.N. Rao,<sup>2</sup> Stuart Rudikoff,<sup>2</sup> and David R. Davies<sup>1</sup>

<sup>1</sup>Laboratory of Molecular Biology, National Institute of Diabetes, Digestive and Kidney Diseases and <sup>2</sup>Laboratory of Genetics, National Cancer Institute, Bethesda, Maryland 20892

**ABSTRACT** The crystal structure of the Fab of the galactan-binding immunoglobulin J539 (a mouse IgA, $\kappa$ ) has been determined at a resolution of approximately 2.6 Å by X-ray diffraction. The starting model was that obtained from the real space search described previously (Navia, M.A., Segal, D.M., Padlan, E.A., Davies, D.R., Rao, D.N., Rudikoff, S. and Potter, M. "Crystal structure of galactan-binding mouse immunoglobulin J539 Fab at 4.5 Å resolution." *Proc. Nat. Acad. Sci. USA*, 76:4071-4074, 1979). This Fab structure has now been refined by restrained least-squares procedures to an R-value of 19% for the 11,690 unique reflections between 8.0 Å and 2.6 Å. The rms deviation from ideal bond lengths is 0.025 Å. The overall structure differs from McPC603 Fab, another mouse IgA, $\kappa$  antibody, in that the elbow bend, relating the variable and constant parts of the molecule, is 145° vs. 133° for McPC603. The region of the molecule expected to be the antigen binding site contains a large cavity with two clefts leading away from it. This has been fitted with a model of an oligo-galactan.

**Key words:** antibody, crystal structure, anti-galactan, J539

### INTRODUCTION

Current knowledge of the three-dimensional structure of antibodies is based mostly on the X-ray diffraction investigations of fragments.<sup>1,2</sup> The structures of three Fabs have been determined: Kol<sup>3</sup> and New,<sup>4</sup> two human myeloma proteins, and McPC603,<sup>5,6</sup> a mouse IgA, $\kappa$  protein. Of these, New and McPC603 have known binding specificities, while the specificity of Kol is not known. There is therefore only limited information available concerning the interaction of antibodies with their antigenic determinants. In this paper we describe the crystal structure determination of J539, a mouse immunoglobulin Fab with binding specificity for  $\beta$ (1-6)-D-galactan. J539 is a member of a group of several antigalactans whose binding properties have been extensively studied. It is the only carbohydrate-binding antibody to have been so far studied by X-ray diffraction.

Previously the structure of J539 Fab had been analyzed at low resolution.<sup>7</sup> There, a poorly defined 4.5-Å electron density map was examined by using a

search procedure based on the known structure of McPC603 Fab. This analysis confirmed the overall similarity of these two Fab structures and provided a basis for the higher-resolution analysis reported here.

### MATERIALS AND METHODS

#### Crystallization and Data Collection

J539 Fab was prepared as described previously,<sup>8</sup> except that the purified material was further subjected to preparative isoelectric focusing in order to produce material that would ultimately yield large crystals suitable for the production of high-resolution X-ray diffraction data.<sup>9</sup> The crystallizations were carried out by the hanging drop method at room temperature by using the vapor diffusion technique to equilibrate the protein droplet with a solution containing approximately 35% saturated ammonium sulfate, 0.07 M imidazole, 0.03 M zinc sulfate, pH 6.8. The crystals were orthorhombic, space group P2<sub>1</sub>2<sub>1</sub>2<sub>1</sub>, with a = 54.1 Å, b = 74.2 Å, c = 130.8 Å.<sup>7</sup>

Intensity data were collected by rotation photography<sup>10</sup> on Kodak No-Screen Medical X-ray films by using an Elliott GX-6 rotating anode X-ray generator operating at 40 kV and 40 mA. A Franks double-bent mirror system<sup>11</sup> purchased from Brandeis University was used to focus the X-ray beam. Data were collected on an Enraf-Nonius Arndt-Wonacott rotation camera with a nominal 80-mm crystal-to-film distance. The c-axis of the crystal was parallel to the rotation axis of the camera and the rotation range for each film pack was 2.3° with 0.3° overlap between film packs. This range permitted us to discard the partially recorded reflections. A total rotation of 91° was sufficient to record all the independent reflections, except for those in the cusp along the c-axis. Precession camera data for the layers 0kl, 1kl, h0l, h1l, h2l, hk0, hk1, and hhl were also collected to assist in interfilm scaling and to supply some of the remaining unobserved reflections.

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S.W. Suh is now at the Department of Chemistry, College of Natural Sciences, Seoul National University, Seoul, Korea.

M.A. Navia is now at the Merck Sharpe and Dohme Research Laboratories, Rahway, NJ 07065.

Address reprint requests to D.R. Davies, Laboratory of Molecular Biology, National Institute of Diabetes, Digestive and Kidney Diseases, Bethesda, MD 20892.



The films were scanned at 100- $\mu$ m raster steps on an Optronics P-1000 film scanner. The resulting digital data were processed on a VAX 11/780 computer with a rotation film program written by G. Cornick and M.A. Navia (unpublished work), which incorporated the dynamic mask procedure of Sjolín and Wlodawer<sup>12</sup> to extract the integrated intensities of reflections. The program was modified to allow the use of roughly measured coordinates of eight strong, fully recorded reflections as supplementary fiducial marks in obtaining the initial [Q] matrix.<sup>13</sup> This provided a starting transformation for a more accurate determination of the [Q] matrix by a least-squares procedure based on all fully recorded reflections which met certain criteria.

Intensities from the three films in each pack were first scaled, corrected for Lorentz and polarization factors, and symmetry averaged. Data from individual packs were merged and scaled together with those from the set of zero- and upper-level precession films by using a program of Y. Satow (unpublished work). The current data set to 2.6- $\text{\AA}$  resolution contains 81% of the possible reflections: 90% to 3.0- $\text{\AA}$  resolution and 64% between 3.0- $\text{\AA}$  and 2.6- $\text{\AA}$  resolution. Approximately 77% of the independent reflections were measured more than once. The statistics of the data processing are given in Table I.

#### Generation and Refinement of the Model

The location and orientation of the starting model<sup>7</sup> were confirmed using the rotation method<sup>14</sup> and an R-value search.<sup>15,16</sup> Initial refinement of the model was carried out by using CORELS.<sup>17</sup> Six parameters defining the orientation and position of the molecule were refined by using 10- $\text{\AA}$  to 7- $\text{\AA}$  data. Then constant and variable domains were refined as separate rigid groups by using 10- $\text{\AA}$  to 5.4- $\text{\AA}$  data. No noticeable improvement in the R-value was obtained when light and heavy chains were also treated as separate rigid groups.

This model was then refined with 3.5- $\text{\AA}$  data by using PROLSQ.<sup>18,19</sup> Residues of Fv were "mutated" from the McPC603 original model to those appropriate for J539 during the course of refinement. As the phases improved higher-resolution data were incorporated to the limit of 2.6  $\text{\AA}$  and the J539 sequence was substituted for the McPC603 residues. The sequence used was that of Rudikoff et al.<sup>20</sup> for VL, Rao et al.<sup>21</sup> for VH, Svasti and Milstein<sup>22</sup> and Hamlyn et al.<sup>23</sup> for CL and Auffray et al.<sup>24</sup> for CH1.

Initial model building was done by using the interactive graphics program BILDER<sup>25</sup> to fit the model to 2Fo-Fc and  $\Delta$ F maps. With the availability of the OMITMAP procedure<sup>26</sup> the graphics program FRODO<sup>27</sup> was used to fit the model to an OMITMAP. This improved the location of a number of residues and the overall contrast in the maps increased along with the improvement in the phases. During the final

TABLE I. Statistics from Processing of the Film Data

Total number of reflections measured	37,222
No. of independent reflections	12,670
Interfilm scaling R-value*	0.077

$$*R = \frac{\sum_{h_i} |I_{h_i} - \bar{I}_h|}{\sum_{h_i} I_{h_i}}, \text{ where } \bar{I}_h \text{ is the average intensity}$$

for a given reflection and  $I_{h_i}$  is one of the measurements which were averaged to yield  $\bar{I}_h$ .

passes of model building, 304 water molecules were added.

The result of the final refinement cycle is summarized in Table II. The rms error in positional parameters was estimated to be 0.3  $\text{\AA}$  by the method of Luzzati.<sup>28</sup> The coordinates and other relevant data have been deposited in the Brookhaven Protein Data Bank.<sup>29</sup> Table III shows the relationship of the serial numbering system which we have used in this work to the system used by Kabat.<sup>30</sup>

#### RESULTS

In Figure 1 is drawn the carbon alpha skeleton of the J539 Fab. In overall appearance it resembles the structure of other Fabs, in particular McPC603. The pairs of domains, CH1 and CL, are quite similar, having 88 carbon alphas match to give an rms difference of 1.8  $\text{\AA}$ . The relation between CH1 and CL is that of a screw axis with a rotation of 174 $^\circ$  and a translation of 1.9  $\text{\AA}$ . Similarly, with VH and VL, 99 pairs of carbon alphas match with an rms deviation of 1.6  $\text{\AA}$  to give a rotation of 169.4 $^\circ$  and 0.04- $\text{\AA}$  translation.

As expected from their sequence identity, the constant domains of J539 resemble quite closely the two corresponding domains of McPC603. The rms deviation of the backbone atoms is 1.6  $\text{\AA}$  (2.1  $\text{\AA}$  for all atoms). The relative disposition of CL and CH1 in J539 and McPC603 is not, however, exactly the same. For McPC603 the screw relation between CL and CH1 corresponds to a 169 $^\circ$  rotation with a 2.6- $\text{\AA}$  translation. In the region of residues 131-139 (J539 numbering) there appears to be a major difference in the folding of the two CH1 domains. This region includes a proline residue that has been interpreted to be a cis-proline in McPC603 but trans- in J539. We do not know whether these differences are the result of an inadequate analysis of weak electron density or represent real differences in structure. We are undertaking a higher resolution study of J539 in order to attempt to clarify this situation.

The angle between the constant and variable pairs of domains differs between J539 (145 $^\circ$ ) and McPC603 (133 $^\circ$ ). This angle, the "elbow bend" of the Fab,<sup>31,32</sup> has been found to be quite variable in different Fabs, going from about 133 $^\circ$  in New and McPC603 to as much as 170 $^\circ$  in the Fab Kol,<sup>3</sup> probably signify-



TABLE II. Refinement Data

	Actual rms deviation†	Target $\sigma$
Average $\Delta F$	92.6	‡
R-factor*	0.19	
No. of structure factors	11,690	
rms deviations from ideal distance (Å)		
Bond distance	0.025	0.030
Angle distance	0.052	0.040
Planar 1-4 distance	0.029	0.030
rms deviation from planarity (Å)	0.016	0.025
rms deviation from ideal chirality (Å <sup>3</sup> )	0.199	0.150
rms deviation from permitted contact distances (Å)		
Single torsion contacts	0.219	0.500
Multiple torsion contacts	0.289	0.500
Possible hydrogen bond	0.269	0.500
rms deviation from ideal torsion angles (°)		
For planar group (0 or 180)	2.5	3.0
For staggered group ( $\pm 60$ or 180)	26.0	15.0
For orthonormal group ( $\pm 90$ )	22.3	15.0

$$*R = \frac{\sum_h ||F_o| - |F_c||}{\sum_h |F_o|}$$

†rms = root mean square.

‡The weight chosen for the structure factor refinement, the "target  $\sigma$ " of  $\Delta F$ , was modeled by the function  $w = (1/\sigma)^2$  with  $\sigma = 47 - 230 \times (\sin(\theta)/\lambda - 1/6)$ .

ing flexibility in the polypeptide chains between V and C.

The interdomain contacts are summarized in Tables IV and V. These tables show, for each residue, the number of atom pairs in contact with residues of the other chain. A contact is defined as a distance which is less than the sum of the atomic van der Waals radii<sup>33</sup> plus 1.0 Å. Similar tables have been published for the McPC603 Fab<sup>6</sup> and we note that while the contacts between CL and CH1 are relatively preserved, the contacts between VL and VH

contain significant differences, perhaps because of differences in the hypervariable regions. In J539 some 32 out of 86 interactions (37%) involve hypervariable residues only, compared with 46 out of 105 (44%) in McPC603. However, many of the same conserved residues found by Novotny and Haber<sup>34</sup> are also found here, making contacts across the interface. These include Y35, Q37, Y86, and F97 of the light chain and Q39, L45, W47, Y95, and W108 of the heavy chain.

### The Galactan Binding Site

The binding of galactan in J539 has been extensively studied in solution by Glaudemans and his co-workers. The antibody combining site was shown to accommodate four sequential  $\beta(1-6)$ -galactopyranosyl residues.<sup>35-37</sup> Recently, Glaudemans et al.<sup>38</sup> have concluded from a binding study of a number of deoxy-fluorogalactosides that the binding involves both of the two solvent-exposed tryptophans in the combining site (residues W92L and W33H). They also proposed a rather specific model for the orientation of the galactan on the surface of the antibody molecule.

In this crystal form of J539 the presumed binding site for galactan is in close proximity to the constant region of a neighboring molecule (Table VI). Probably because of this close contact our attempts to diffuse galactan into these crystals were unsuccessful. Thus we have no direct crystallographic evidence to define the binding pocket of the Fab. Nevertheless, the three-dimensional structure of the variable module does provide some clues. Figure 2 is a skeletal model of J539 showing just the complementarity determining

TABLE III. Correspondence Between the Numbering Scheme Used Here and That of Kabat et al.<sup>30</sup>

Light chain		Heavy chain	
This paper	Kabat et al.	This paper	Kabat et al.
1-27	1-27	1-52	1-52
28-213	29-214	53	52a
		54-83	53-82
		84-86	82a-82c
		87-104	83-100
		105	100a
		106-135	101-130
		136-138	133-135
		139-159	137-157
		160-167	162-169
		168-180	171-183
		181-196	185-200
		197-201	202-206
		202-212	208-218
		213-218	220-225

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