The Plasminogen Binding Site of the C-Type Lectin Tetranectin Is Located in the Carbohydrate Recognition Domain, and Binding Is Sensitive to Both Calcium and Lysine*

(Received for publication, June 26, 1998, and in revised form, August 13, 1998)

Jonas Heilskov Graversen‡, Rikke Høegh Lorentsen§, Christian Jacobsen§, Søren K. Moestrup§, Bent W. Sigurskjold‡, Hans Christian Thegersen‡, and Michael Etzerodt‡‡

From the ‡Laboratory of Gene Expression, Department of Molecular and Structural Biology and §Department of Medical Biochemistry, University of Aarhus, DK-8000 Aarhus C, Denmark and ¶August Krogh Institute, University of Copenhagen, DK-2100, Copenhagen, Denmark

Tetranectin (TN)1 is a 68-kDa plasminogen-binding protein occurring in plasma at an approximate concentration of 10 mg/liter (1) and is also found to be deposited extracellularly in various tissues. In particular, TN is deposited in the tumor-surrounding stroma of breast (2), colon (3), and ovarian (4) tumors and is found co-localized with plasmin/plasminogen at the invasive front of cutaneous melanoma lesions (5). TN has also been inferred to play a role in the pathophysiology of rheumatoid arthritis (6) and in bone mineralization during osteogenesis (7, 8). It is not known whether TN deposited in tumor stroma is recruited from plasma or is expressed locally.

TN appears to be expressed by a variety of cells, including fibroblasts (9), monocytes (10), neutrophils (11), and osteoblasts (7). TN mRNA has been detected in the placenta, heart, spleen, and lung and, in low amounts, also in the liver and kidney (12).

TN is a trimeric protein (13) assembled from three identical polypeptide chains of 181 amino acid residues (14). The molecular architecture of TN reflects the genomic organization (12) in that the three exons correspond to three functional domains: (i) an NH2-terminal domain of about 20 amino acid residues; (ii) a triple α-helix coiled coil-forming domain of approximately 30 amino acid residues; and (iii) a long-form carbohydrate recognition domain (CRD) characteristic of the C-type lectin protein superfamily of approximately 130 amino acid residues.

TN binds to plasminogen (Plg) by a specific and lysine-sensitive interaction with the kringle 4 domain (Plg K4), and binding facilitates the proteolytic activation of Plg to plasmin by the tissue-type plasminogen activator (1). In addition to Plg, TN has been reported to bind apolipoprotein(a) and fibrin (15, 16).

TN is also known to bind calcium as well as a number of complex sulfated polysaccharides including heparin/heparan sulfate, chondroitin, and fucoidan (17).

The three-dimensional structure of tetranectin has been determined by x-ray crystallographic analysis of crystals of full-length recombinant tetranectin, rTN (18), and the long-form CRD, rTN3 (19). The structural analyses revealed a highly conserved fold shared between TN and the neck region and CRD of the human and rat mannos-binding proteins (MBPs) of the collectin protein family. Many secondary structural elements as well as the number and location of calcium ion binding sites are conserved among all three proteins.

Calcium binding site 1 is highly conserved. Although two of the five coordinating residues in rat MBP are substituted in TN (i.e. Asp-188 to Gly-147 and Asp-194 to Asn-151, respectively), both the coordination geometry and position of calcium ion 1 are very similar.

Coordination geometry at calcium binding site 2 in TN differs from those of the MBPs because three of the five calcium-coordinating residues in MBP, i.e. Glu-185, Asn-187, and Asn-205, are replaced with TN residues Gln-143, Asp-145, and Phe-164, respectively. TN residues Gln-143 and Asp-145 coordinate calcium directly, whereas the side chain of Phe-164 is rotated away from the calcium ion, thereby allowing the accommodation of a fixed water molecule, which serves as a role as calcium coordinator in place of the Asn-205 side chain of the MBPs (19).

Calcium binding site 2 is involved in carbohydrate binding in all C-type lectins known to exhibit calcium-dependent interaction with terminal sugar residues (reviewed in Ref. 20).

At the present stage, no carbohydrate ligand to the TN CRD has been identified. However, the presence of the calcium-coordinating residues Gln-143 and Asp-145 and the Pro-164, which is structurally conserved in the cis conformation, in addition to the presence of a surface-exposed aromatic residue (Phe-164) adjacent to the calcium binding site, may be taken as
suggestive of a galactose-type specificity of the TN CRD.

Apart from calcium-dependent carbohydrate binding, CRDs of other C-type lectins have been reported to bind noncarbohydrate ligands, including proteins, lipids (21), and ice (22). Examples of protein ligands include the coagulation factors IX–X, binding protein (23), the low-affinity IgE-Fc receptor (CD23; Ref. 24), and lecticans (25).

In the present work, the Plg K4 binding site of TN is reported to be sensitive to calcium ions, to involve at least two of the calcium-coordinating residues in the CRD, and to be located at a site overlapping the putative carbohydrate binding site. EXPERIMENTAL PROCEDURES

Site-directed Mutagenesis, Expression, Refolding, and Processing of Recombinant Proteins—All single-residue mutations were performed using the Quickchange kit (Stratagene, La Jolla, CA). rTN was expressed in Escherichia coli, refolded, and purified using a two-step method as described previously (27). The purity of the protein was assessed by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and mass spectrometry. The affinity binding analysis was performed using the COINJECT option, injecting 25 pmol of the protein sample at a concentration of 0.25 mg/ml (13). Calcium sensitivity of rTN binding was analyzed by equilibrating the rTN column with Buffer A containing either 1 mM CaCl2 or 1 mM calcium lactate before loading rTN, or by the application of rTN in Buffer A, without calcium, and applying a gradient from 0 to 1 mM of calcium lactate before loading rTN, or by the application of rTN in Buffer A, without calcium, and applying a gradient from 0 to 1 mM of calcium lactate or calcium lactate over 10 column volumes.

Surface Plasmon Resonance (SPR) Assay—The SPR binding assays were performed on a BIAcore 2000 instrument (BIAcore). rPlg K4 or Plg (human Glu-plasminogen) was immobilized using the Amine Coupling Kit as described by the manufacturer (BIAcore). After chip activation, rTN or rTN3 was injected at a concentration of 0.25 mg/ml (i.e. rTN, rTN single-residue mutants, or rTN3) was applied, and the column was washed with 3–4 column volumes of Buffer A before the elution of bound protein with Buffer B. Aliquots of the run-through, wash, and elution fractions were analyzed by nonreducing SDS-PAGE.

Calcium sensitivity of rTN binding was analyzed by equilibrating the rTN column with Buffer A containing either 1 mM CaCl2 or 1 mM calcium lactate before loading rTN, or by the application of rTN in Buffer A, without calcium, and applying a gradient from 0 to 1 mM of either CaCl2 or calcium lactate over 10 column volumes. RESULTS

Initial mapping of the Plg K4 binding site on TN was carried out using the rPlg K4 affinity column for the detection of lysine-sensitive binding of rTN deletion variants. Results from these experiments showed that rTN deletion constructs containing the α-helical trimerization region as well as the CRD bound to immobilized rPlg K4, whereas free CRD (rTN3) exhibited no apparent binding (data not shown). However, the observation that bound rTN could be eluted from the rPlg K4 column by either CaCl2 or calcium lactate (at approximately 0.2 mM calcium) prompted us to focus the single-residue mutational analysis on the CRD domain. The calcium sensitivity of the interaction was further analyzed in a series of SPR experiments in which the binding of rTN to either immobilized rPlg K4 or immobilized Plg was analyzed with various concentrations of calcium in the buffer (Fig. 1). The shapes and positions of the two binding curves are virtually identical, substantiating that TN binds exclusively to the Plg K4 domain in Plg. Half-maximal binding was found to occur at approximately 0.2 mM calcium.

Binding affinities of rTN and rTN3 to rPlg K4 in solution were determined by ITC. The data fitted well to a one-binding site model for rTN3 and a one-binding site/subunit model for rTN (Fig. 2), yielding dissociation constants of 53 and 52 μM, respectively, for this strongly enthalpy-driven association (Table I).

To determine the location of the Plg K4 binding site on the CRD in greater detail, a series of single-residue substitutions in rTN was generated on the basis of inspection of the pub-
Calcium-sensitive Plasminogen Binding of Tetranectin CRD

TABLE I

<table>
<thead>
<tr>
<th>Stoichiometry</th>
<th>( K_d, \mu M )</th>
<th>( \Delta G, kJ/mol )</th>
<th>( \Delta H, kJ/mol )</th>
<th>( -\Delta S, kJ/mol )</th>
</tr>
</thead>
<tbody>
<tr>
<td>rTN3</td>
<td>0.95 ± 0.08</td>
<td>51.8 ± 5.6</td>
<td>-24.5 ± 0.3</td>
<td>113 ± 14</td>
</tr>
<tr>
<td>rTN</td>
<td>3.2 ± 0.1</td>
<td>52.9 ± 3.1</td>
<td>-24.4 ± 0.1</td>
<td>89 ± 4</td>
</tr>
</tbody>
</table>

Table 1: Binding parameters obtained from the microcalorimetric titration of rTN and rTN3 with rPlg K4.

A

B

FIG. 2. Thermograms and binding isotherms from the isothermal calorimetric titration of rTN and rTN3 with rPlg K4. A, titration of rTN with rPlg K4 at 25 °C. B, titration of rTN3 with rPlg K4 at 25 °C. The thermodynamic parameters from the binding analysis are given in Table I.

The calcium-sensitive Plasminogen Binding of Tetranectin CRD

Expression levels of the single-residue mutants of rTN were similar to the wild-type level. However, refolding efficiency differed by up to 50% relative to that of the wild type. One mutant, rTN F164A, failed to refold (data not shown). Purified protein preparations appeared to be homogeneous, correctly refolded, and free from contaminating disulfide-linked oligomer species as judged by nonreducing SDS-PAGE (Fig. 3). On the basis of the light absorption at 280 nm and amino acid analysis, A(1%)280 values for rTN and rTN3 were determined to be 2.0 and 2.8 gL \(^{-1}\), respectively. SDS-PAGE staining intensities for rTN and rTN3 were determined to be 1126A, E140A, K166A, and R167A; and (iii) mutants that appeared not to bind to immobilized rPlg K4 at all and hence eluted in the flow-through fractions (K148A, E150A, and D165A).

SPR Binding Analysis—Representative sensorgrams from the SPR analysis of rPlg K4 and Plg binding corresponding to the same concentration of each TN derivative are shown in Fig. 4, A and B, respectively. All experiments consistently showed the occurrence of a fast association and a biphasic dissociation phase with a fast and a slow component, an observation reminiscent of observations for similar protein systems (30, 31). For the group of poorly binding mutants, the binding component with slow dissociation was found to be especially pronounced relative to the fast component of dissociation. Both components of the dissociation phase reflect specific interactions, because they can be efficiently competed by 5 mM 6-AHA (data not shown).

rTN and each of the rTN mutants are all homotrimeric proteins with three potential binding sites. Therefore, a simple kinetic analysis may not be applied within this system. We have therefore chosen to evaluate the SPR binding data using a semiquantitative analytical method similar to that of MacKenzie et al. (30). In this approach, binding is assumed to be described by a simple Langmuir relationship described by the following equation.

\[
R_{pl} = R_{\text{max}} \frac{[L]}{[L] + K_D} \quad (\text{Eq. 1})
\]

\( R_{pl} \) denotes the measured response at the plateau, \( R_{\text{max}} \) is the maximum response at binding site saturation, \( [L] \) is the ligand concentration, and \( K_D \) is the dissociation constant.

Firstly, estimates of \( R_{\text{max}} \) and the apparent dissociation constant \( K_D \) were determined by measuring the \( R_{pl} \) at different concentrations of rTN ligand. The data from both the rPlg K4 chip and the Plg chip were then plotted versus ligand concentration according to the rearranged equation, which is as follows.

\[
\frac{R_{\text{max}}}{R_{pl}} = 1 + \frac{K_D}{[L]} \quad (\text{Eq. 2})
\]

\( R_{\text{max}} \) and \( K_D \) were estimated by linear regression analysis (Fig. 5). \( R_{\text{max}} \) for the rPlg K4 chip was found to be 598 ± 52 RU, and \( K_D \) was 0.50 ± 0.05 μM. For the Plg chip, \( R_{\text{max}} \) was found to be 1159 ± 34 RU, and \( K_D \) was 0.17 ± 0.01 μM (Table III).

Secondly, the binding of each single-residue mutant was analyzed in a series of experiments in which ligand (rTN) was injected over the rPlg K4 and Plg chips at equal conditions (i.e., concentration, flow, and buffer), and the \( K_D \) was estimated from the \( R_{pl} \) level (Table II).

Three mutants (rTN K148A, rTN E150A, and rTN D165A) showed very low binding to both rPlg K4 and Plg. Each of these mutants was also identified as a nonbinder on rPlg K4-Sepharose. Both rTN E150A and rTN D165A represent mutations of calcium-coordinating residues at calcium site 2. The rest of the single-residue mutations only exhibited little effect on binding. Three single-residue substitutions, rTN K166A, rTN R167A, and I140A, all showed a lower affinity for rPlg K4 and Plg. These three mutants were also retarded on the rPlg K4 column.

The calcium sensitivity of binding was further studied by characterization of mutants rTN D116A, rTN E120A, rTN Q143A, rTN D145A, and rTN N151A, which are all known calcium-coordinating residues. The SPR responses at the plateau levels were measured using both the rPlg K4 chip (Fig. 6) and the Plg chip (data not shown) at different calcium concentrations. Not only did these mutations affect the calcium sensitivity of rPlg K4 and Plg binding, but the transition from binding to nonbinding was found to be less sharp for this
Calcium-sensitive Plasminogen Binding of Tetranectin CRD

The mutational analysis maps the Plg K4 binding site to a localized region defined by two of the calcium-coordinating residues in CRD calcium site 2 (Glu-150 and Asp-165) and to a surface-exposed lysine residue located close to (Lys-148). Other surface-exposed residues in the region appear to contribute little to the affinity. The observation that Plg K4 binding can be titrated by calcium and the decreased sensitivity exhibited by the calcium-coordinating mutants indicate that binding of Plg K4 only occurs when calcium site 2 is not occupied by a calcium ion. The calcium level corresponding to half-maximal binding, the dissociation constant of the CRD-Plg K4 complex is approximately 50 \(\mu M\). 

![Image](http://www.jbc.org/)

**TABLE II**

<table>
<thead>
<tr>
<th>rTN type</th>
<th>Binding to K4-Sepharose</th>
<th>rPlg K4</th>
<th>Plg</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wild type</td>
<td>+</td>
<td>286 ± 13</td>
<td>0.55 ± 0.10</td>
</tr>
<tr>
<td>rTN3</td>
<td>-</td>
<td>NA</td>
<td>NA</td>
</tr>
<tr>
<td>D116A</td>
<td>(+)</td>
<td>251 ± 7</td>
<td>0.69 ± 0.11</td>
</tr>
<tr>
<td>E120A</td>
<td>+</td>
<td>334 ± 3</td>
<td>0.40 ± 0.08</td>
</tr>
<tr>
<td>K134A</td>
<td>+</td>
<td>292 ± 13</td>
<td>0.53 ± 0.09</td>
</tr>
<tr>
<td>I146A</td>
<td>(+)</td>
<td>221 ± 3</td>
<td>0.85 ± 0.12</td>
</tr>
<tr>
<td>Q143A</td>
<td>+</td>
<td>305 ± 27</td>
<td>0.48 ± 0.11</td>
</tr>
<tr>
<td>D145A</td>
<td>+</td>
<td>372 ± 4</td>
<td>0.31 ± 0.07</td>
</tr>
<tr>
<td>K148A</td>
<td>-</td>
<td>71 ± 7</td>
<td>3.7 ± 0.5</td>
</tr>
<tr>
<td>K150A</td>
<td>-</td>
<td>119 ± 12</td>
<td>2.0 ± 0.3</td>
</tr>
<tr>
<td>N151A</td>
<td>+</td>
<td>323 ± 4</td>
<td>0.40 ± 0.08</td>
</tr>
<tr>
<td>K162A</td>
<td>+</td>
<td>319 ± 10</td>
<td>0.44 ± 0.08</td>
</tr>
<tr>
<td>F164L</td>
<td>+</td>
<td>283 ± 5</td>
<td>0.56 ± 0.09</td>
</tr>
<tr>
<td>D165A</td>
<td>-</td>
<td>94 ± 10</td>
<td>2.7 ± 0.4</td>
</tr>
<tr>
<td>K166A</td>
<td>(+)</td>
<td>206 ± 6</td>
<td>1.0 ± 0.1</td>
</tr>
<tr>
<td>R167A</td>
<td>(+)</td>
<td>166 ± 21</td>
<td>1.3 ± 0.2</td>
</tr>
<tr>
<td>R193A</td>
<td>+</td>
<td>296 ± 9</td>
<td>0.51 ± 0.09</td>
</tr>
</tbody>
</table>

| a | +, ligand binds to K4-Sepharose; (+), ligand elutes during washing; and –, no binding. |
| b | NA (not applicable), the ligand binding is weak and out of range. |

**DISCUSSION**

The present study demonstrates that Plg K4 binds to TN by interacting with the CRDs. ITC analysis showed that the interaction between the kringle domain and the CRD is identical whether the CRD is free and monomeric or is an integral part of the TN trimer. Hence, there is no cooperative contribution to binding among the three CRDs in the TN trimer structure. The dissociation constant of the CRD-Plg K4 complex is approximately 50 \(\mu M\), as measured in solution, which probably explains why binding of the free monomeric CRD (rTN3) to Plg K4 was only detectable by ITC. As would be anticipated (30, 31), from the presence of three independent K4 binding sites in each TN homotrimer, the interaction between TN and Plg K4 was found to be significantly stronger and allowed the demonstration of binding to immobilized Plg K4 or Plg and the estimation of binding constants by SPR (\(K_D\) of 0.5 and 0.2 \(\mu M\), respectively). Thus, our detailed understanding of the interaction warrants the use of SPR analysis for characterization of mutant TN homotrimers as representative of the interaction between the mutant CRDs and Plg K4.

The mutational analysis maps the Plg K4 binding site to a localized region defined by two of the calcium-coordinating residues in CRD calcium site 2 (Glu-150 and Asp-165) and to a surface-exposed lysine residue located close to (Lys-148). Other surface-exposed residues in the region appear to contribute little to the affinity. The observation that Plg K4 binding can be titrated by calcium and the decreased sensitivity exhibited by the calcium-coordinating mutants indicate that binding of Plg K4 only occurs when calcium site 2 is not occupied by a calcium ion. The calcium level corresponding to half-maximal binding, the dissociation constant of the CRD-Plg K4 complex is approximately 50 \(\mu M\), as measured in solution, which probably explains why binding of the free monomeric CRD (rTN3) to Plg K4 was only detectable by ITC. As would be anticipated (30, 31), from the presence of three independent K4 binding sites in each TN homotrimer, the interaction between TN and Plg K4 was found to be significantly stronger and allowed the demonstration of binding to immobilized Plg K4 or Plg and the estimation of binding constants by SPR (\(K_D\) of 0.5 and 0.2 \(\mu M\), respectively). Thus, our detailed understanding of the interaction warrants the use of SPR analysis for characterization of mutant TN homotrimers as representative of the interaction between the mutant CRDs and Plg K4.

The present study demonstrates that Plg K4 binds to TN by interacting with the CRDs. ITC analysis showed that the interaction between the kringle domain and the CRD is identical whether the CRD is free and monomeric or is an integral part of the TN trimer. Hence, there is no cooperative contribution to binding among the three CRDs in the TN trimer structure. The dissociation constant of the CRD-Plg K4 complex is approximately 50 \(\mu M\), as measured in solution, which probably explains why binding of the free monomeric CRD (rTN3) to Plg K4 was only detectable by ITC. As would be anticipated (30, 31), from the presence of three independent K4 binding sites in each TN homotrimer, the interaction between TN and Plg K4 was found to be significantly stronger and allowed the demonstration of binding to immobilized Plg K4 or Plg and the estimation of binding constants by SPR (\(K_D\) of 0.5 and 0.2 \(\mu M\), respectively). Thus, our detailed understanding of the interaction warrants the use of SPR analysis for characterization of mutant TN homotrimers as representative of the interaction between the mutant CRDs and Plg K4.

The present study demonstrates that Plg K4 binds to TN by interacting with the CRDs. ITC analysis showed that the interaction between the kringle domain and the CRD is identical whether the CRD is free and monomeric or is an integral part of the TN trimer. Hence, there is no cooperative contribution to binding among the three CRDs in the TN trimer structure. The dissociation constant of the CRD-Plg K4 complex is approximately 50 \(\mu M\), as measured in solution, which probably explains why binding of the free monomeric CRD (rTN3) to Plg K4 was only detectable by ITC. As would be anticipated (30, 31), from the presence of three independent K4 binding sites in each TN homotrimer, the interaction between TN and Plg K4 was found to be significantly stronger and allowed the demonstration of binding to immobilized Plg K4 or Plg and the estimation of binding constants by SPR (\(K_D\) of 0.5 and 0.2 \(\mu M\), respectively). Thus, our detailed understanding of the interaction warrants the use of SPR analysis for characterization of mutant TN homotrimers as representative of the interaction between the mutant CRDs and Plg K4.

The present study demonstrates that Plg K4 binds to TN by interacting with the CRDs. ITC analysis showed that the interaction between the kringle domain and the CRD is identical whether the CRD is free and monomeric or is an integral part of the TN trimer. Hence, there is no cooperative contribution to binding among the three CRDs in the TN trimer structure. The dissociation constant of the CRD-Plg K4 complex is approximately 50 \(\mu M\), as measured in solution, which probably explains why binding of the free monomeric CRD (rTN3) to Plg K4 was only detectable by ITC. As would be anticipated (30, 31), from the presence of three independent K4 binding sites in each TN homotrimer, the interaction between TN and Plg K4 was found to be significantly stronger and allowed the demonstration of binding to immobilized Plg K4 or Plg and the estimation of binding constants by SPR (\(K_D\) of 0.5 and 0.2 \(\mu M\), respectively). Thus, our detailed understanding of the interaction warrants the use of SPR analysis for characterization of mutant TN homotrimers as representative of the interaction between the mutant CRDs and Plg K4.

![Image](http://www.jbc.org/)


The calcium-sensitive Plasminogen Binding of Tetranectin CRD
Calcium-sensitive Plasminogen Binding of Tetranectin CRD

1. Interpretation of the results of the mutational analysis is limited by the fact that structural information is only available for the TN CRD with bound calcium ions, and that crystals of the CRD and Plg K4 in complex have not yet been obtained. However, we predict that the interacting areas in TN and Plg K4 are essentially restricted to the characterized binding site on the CRD and the lysine binding pocket on Plg K4, because the dissociation constant for the interaction between TN and immobilized rPlg K4 of around 50 μM at 0–0.5 μM NaCl, respectively (26). Substantial additional interactions between the Plg K4 and the CRD would be expected to contribute to a significantly lower dissociation constant.

2. Calcium-dependent binding of the TN CRD to ligands other than Plg K4 has not been demonstrated. The binding of complex sulfated oligosaccharides (i.e., fucoidan and heparin) to TN is calcium-independent, does not involve the CRD, and has recently been shown to involve residues within the NH2-terminal domain of approximately 30 amino acid residues of TN. The present finding may guide more specific and clarifying biological investigations of the physiological role of TN. In particular, the sensitivity to calcium ions of the weak interaction between TN and Plg may provide a means for a tissue to recruit Plg from plasma, thus requiring only the initiation of a process, which may provide its own regulation by calcium-modulated binding and release of Plg or Plg-derived products at TN-rich regions in the tissue.

3. To our knowledge, the interaction between TN and Plg represents the first example of a calcium-sensitive protein-protein interaction directly involving the putative carbohydrate binding site of a C-type lectin CRD. Other C-type lectin CRDs have been reported to bind proteins (23–25). These interactions all appear to be calcium dependent and to involve residues located outside the calcium binding site(s).

4. The number of proteins containing C-type lectin CRDs is large and is still growing. C-type CRDs have been reported to bind such diverse compounds as carbohydrates, proteins, lipids, and even ice. We anticipate that the Plg K4 binding site on TN, together with the mannos-binding site of MBP and possibly the ice-binding site of herring antifreeze protein, offers unique protein engineering-based opportunities to study the requirements of surface topology and chemistry for grafting new binding sites for very diverse compounds on an essentially conserved single-chain structural unit.

REFERENCES


4 J. H. Graversen and R. H. Lorentsen, unpublished observations.
29246

Calcium-sensitive Plasminogen Binding of Tetranectin CRD

The Plasminogen Binding Site of the C-Type Lectin Tetranectin Is Located in the Carbohydrate Recognition Domain, and Binding Is Sensitive to Both Calcium and Lysine


doi: 10.1074/jbc.273.44.29241

Access the most updated version of this article at http://www.jbc.org/content/273/44/29241

Alerts:
- When this article is cited
- When a correction for this article is posted

Click here to choose from all of JBC's e-mail alerts

This article cites 29 references, 6 of which can be accessed free at http://www.jbc.org/content/273/44/29241.full.html#ref-list-1