

Erratum

Structural basis of heparin binding to camel peptidoglycan recognition protein-S: Int J Biochem Mol Biol. 2012; 3(1): 86-94

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Abstract: Short peptidoglycan recognition protein (PGRP-S) is a member of the innate immunity system in mammals. PGRP-S from *Camelus dromedarius* (CPGRP-S) is found to be highly potent against bacterial infections. It is capable of binding to a wide range of pathogen-associated molecular patterns (PAMPs) including lipopolysaccharide (LPS), lipoteichoic acid (LTA) and peptidoglycan (PGN). The heparin-like polysaccharides have also been observed in some bacteria such as the capsule of K5 *Escherichia coli* thus making them relevant for determining the nature of their interactions with CPGRP-S. The binding studies of CPGRP-S with heparin disaccharide in solution using surface plasmon resonance gave a value 3.3×10^{-7} M for the dissociation constant (Kd). The structure of the heparin bound CPGRP-S determined at 2.8Å resolution revealed the presence of a bound heparin molecule in the binding pocket of CPGRP-S. It was found anchored tightly to the protein with the help of several ionic and hydrogen bonded interactions. Three sulphate groups of heparin S1, S2 and S3 have been found to interact with residues, Arg-31, Lys-90, Thr-97, Asn-99, Asn-140, Gln-150 and Arg-170 of CPGRP-S. The binding site includes two subsites, S-I and S-II with cleftlike structures. Heparin disaccharide is bound in subsite S-I. Previously determined structures of the complexes of CPGRP-S with LPS, LTA and PGN also showed that their glycan moieties were also held in subsite S-I indicating that heparin disaccharide also represents an important element for the recognition by CPGRP-S.

Keywords: PGRP-S, PAMPs, heparin, crystal structure, LPS, LTA, PGN

In the article by Sharma et al Int J Biochem Mol Biol 2012; 3: 86-94, **Figure 2A** is mistakenly included and the legends of **Figures 2** and **4** got interchanged by an oversight.

Figure 2A should be deleted and **Figure 2B** should be called **Figure 2**. The legends of **Figures 2** and **4** should be interchanged. On page 90 in the text instead of **Figure 2A** and **2B**, it should be read as **Figure 2**. The figures with correct legends are given below.

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Heparin recognition by CPGRP-S

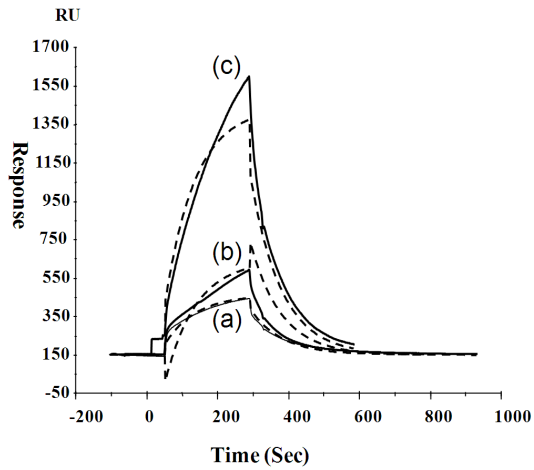


Figure 2. SPR sensograms showing the association and dissociation curves for the binding of heparin disaccharide. CPGRP-S was immobilized on CM-5 chip and three concentrations (1.4 mM, 2.5 mM and 5.0 mM) of analyte heparin disaccharide were used in the mobile phase. The corresponding curves are indicated by a, b and c respectively. The fitted curves are shown by dashed lines.

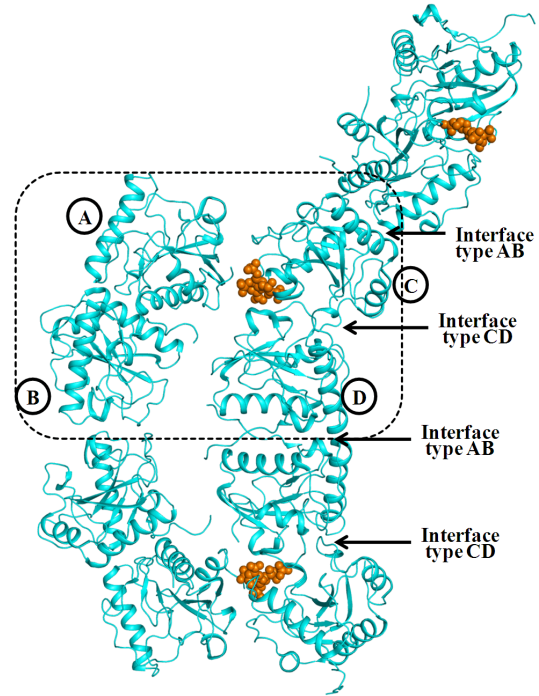


Figure 4. The columns of linear polymers of CPGRP-S with alternating contacts A-B and C-D. Heparin disaccharide molecules are bound to molecule C at C-D contact site.