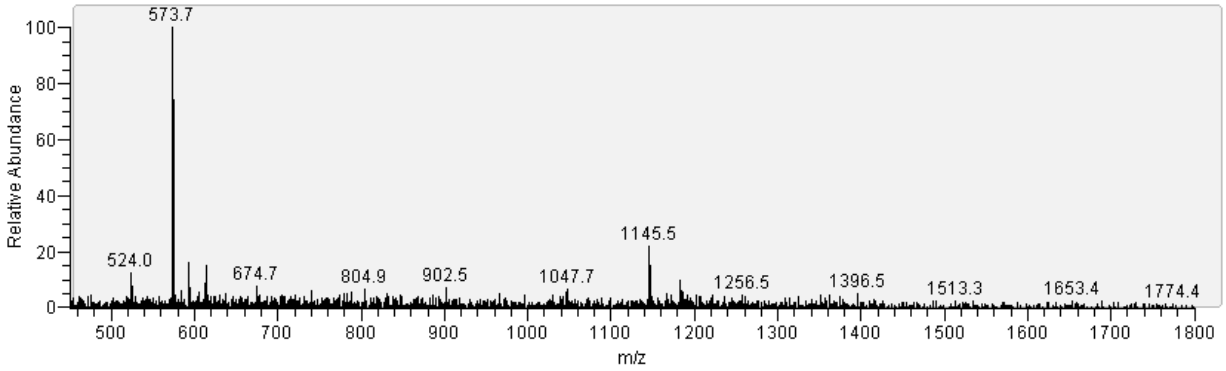
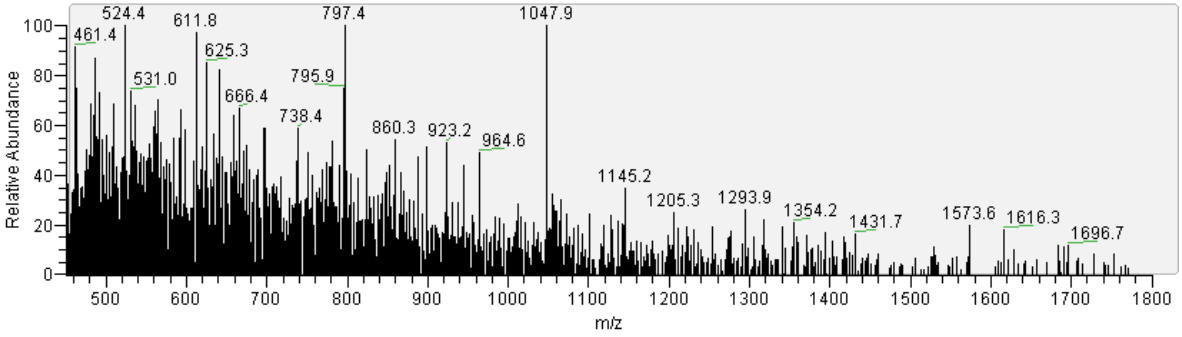
Supplemental Figure 1

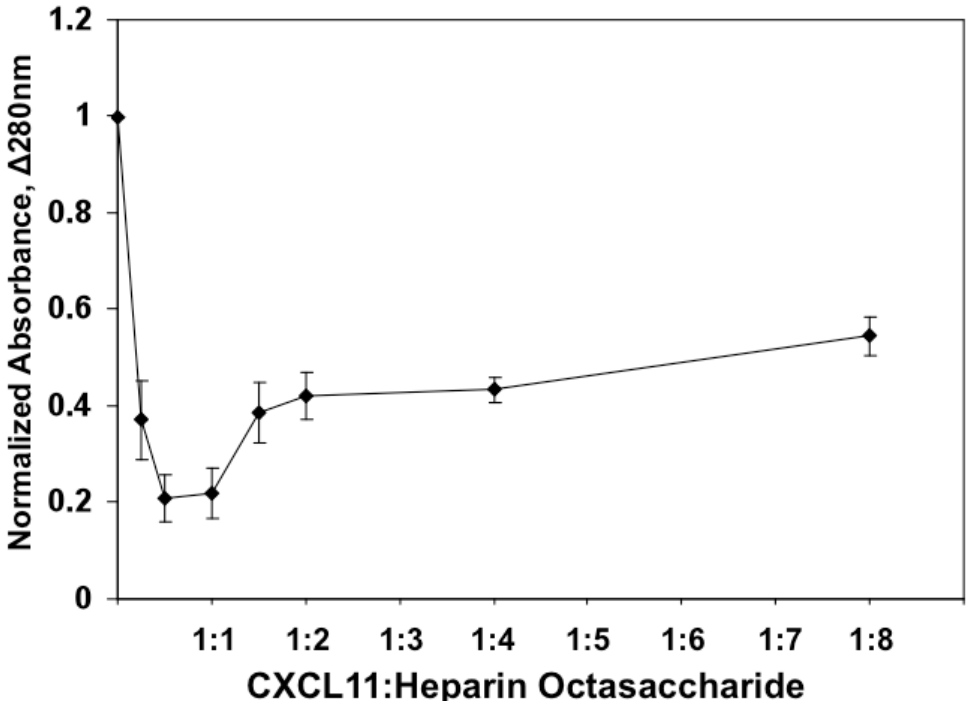
A



B



Supplemental Figure 2



Supplemental Figure 3

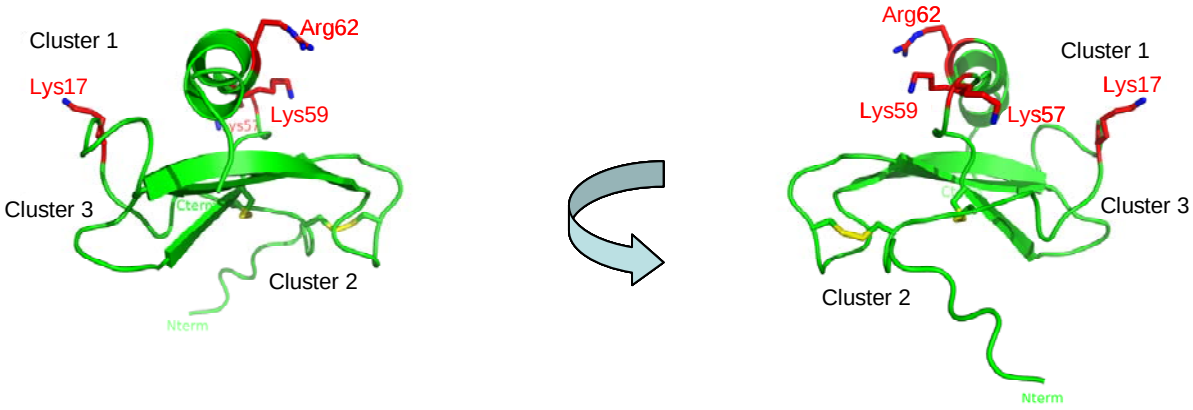


FIGURE LEGENDS

Suppl. Fig. 1. (A) Mass spectrum of the non-digested peptide ^{53}CLNPKSKQAR^{62} with missed (protected) cleavage sites at K57 and K59, respectively. The m/z value at 1145.5 represents the singly charged peptide with a measured MW of 1144.5. The m/z value at 573.7 represents the doubly charged peptide with a measured MW of 1145.4. (B) Mass spectrum of trypsin-digested CXCL11 in the absence of heparin.

Suppl. Fig. 2. Solubility analysis of 0.1 mM CXCL11 in the presence of increasing amounts of heparin octasaccharide. Samples were prepared in 50 mM acetate buffer at pH 5.6. The protein absorbance values were measured at 280 nm using a NanoDrop 2000c spectrophotometer (*Thermo Scientific*). The data was normalized to the absorbance values measured in the absence of heparin octasaccharide. Although less dramatic, precipitation was observed even at 20 μM CXCL11.

Suppl. Fig. 3. Localization of the four amino acids that were determined to significantly contribute to the GAG binding site in CXCL11, shown in a ribbon structure. The binding site we found coincides with the general GAG binding site for CXC chemokines described by Lortat-Jacob et al. (44;45).