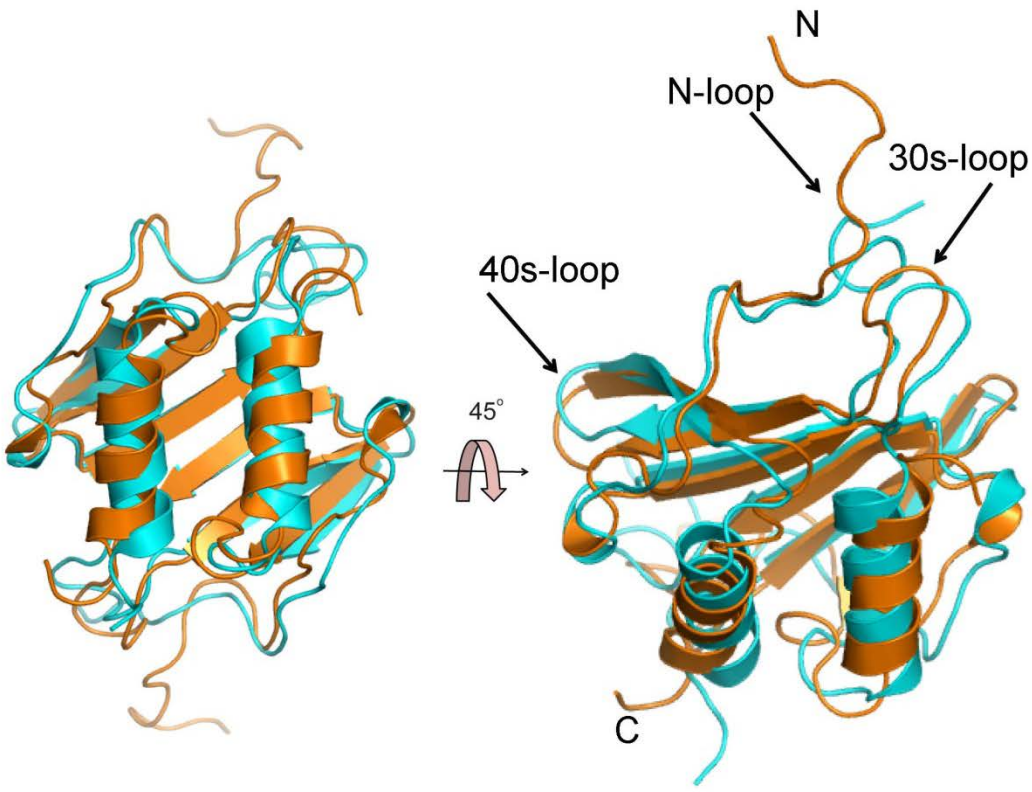
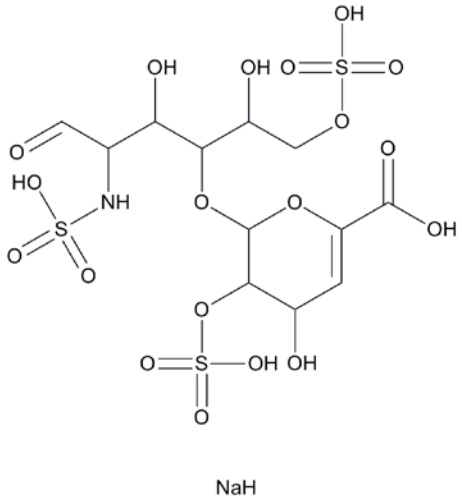
Supporting Figure 1



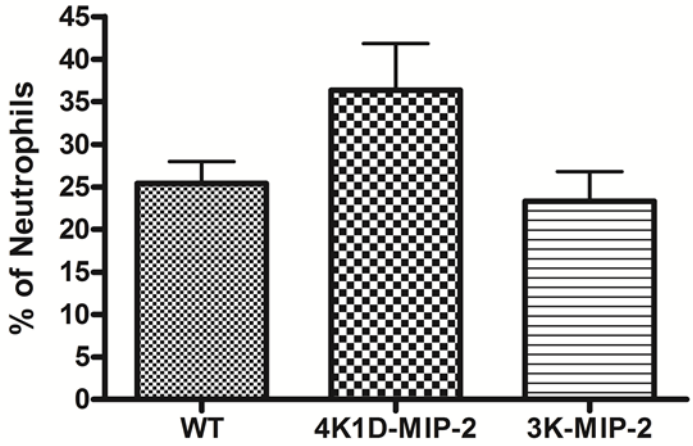
Dimeric MIP-2 derived from X-ray diffraction (Gold) and NMR (Cyan) was superposed with RMSD of 2.3Å. The sheets superpose better than the helices (left panel). Major deviations are seen in the N-terminal loop, the 30s and 40s loop regions.

Supporting Figure 2

Chemical structure of Heparin disaccharide I-S sodium salt

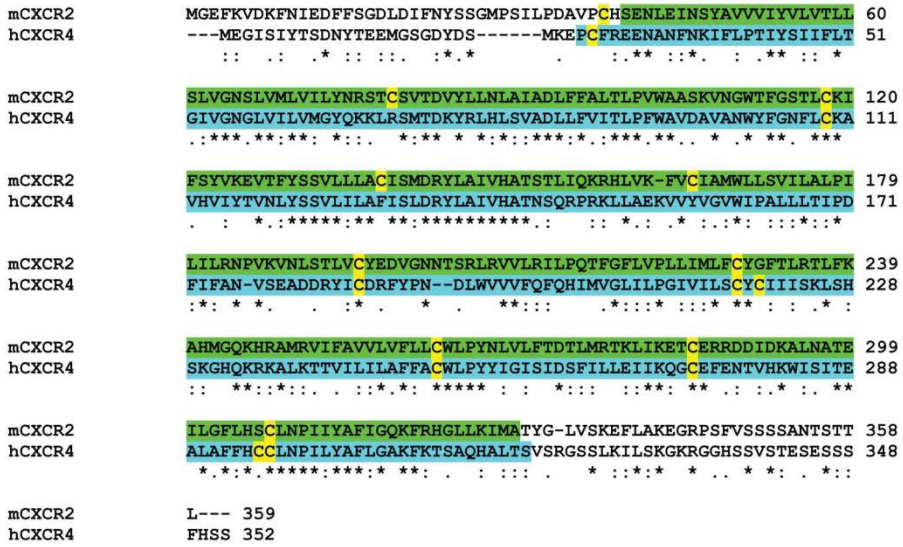


Supporting Figure 3



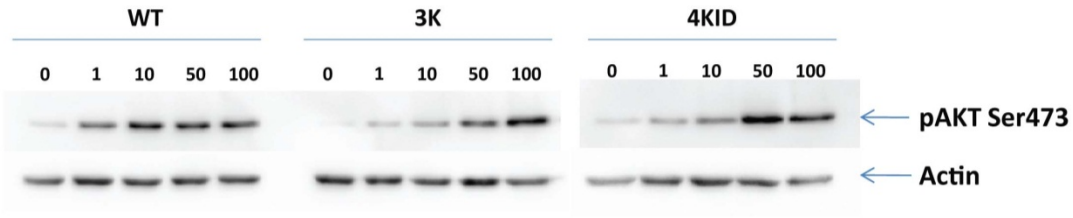
Effects of GAG-deficient mutations of MIP-2 *in vivo*. Percentage of neutrophils recruited to the peritoneum in response to 100ng IP injection of WT, 3K-MIP-2, and 4K1D-MIP-2. The percentage of neutrophils was calculated by FACS and the data represent the mean number of neutrophils from six female BALB/c mice of 8-10 weeks of age.

Supporting Figure 4



Sequence alignment of murine CXCR2 and human CXCR4. mCXCR2 and hCXCR4 share a sequence identity of 31%. The residues of hCXCR4 (27-319) for which the three dimensional position were reported in the PDB (3ODU) is highlighted in cyan. The CXCR2 residues which were modeled using CXCR4 structure as template is shown in green and has 36% sequence identity. The cysteines are colored yellow.

Supporting Figure 5



Akt activation by wild-type and MIP-2 GAG-deficient mutants. Neutrophils were isolated from C57BL/6 mice, aged 8-12 weeks obtained from Taconic (Germantown, NY) bone marrow by using discontinuous percoll gradient. Neutrophils were then stimulated with MIP-2 WT and mutants at the concentrations described for 1 minute at 37˚C prior to lysis with SDS-PAGE sample buffer. Proteins were separated by SDS-PAGE and the proteins phospho Akt and actin were detected by Western blotting performed using anti-pSer473-Akt (Cell Signaling Technology, Beverly, MA) and anti-actin (Santa Cruz Biotechnology, Santa Cruz, CA) antibodies. The proteins were detected by using the SuperSignal West Pico chemiluminescence substrate (Thermo Fisher Scientific, Rockford, IL).