

Supplementary data: Lineshape simulations of the effect of CXCR3 peptide binding on IP-10 resonances (A+B \leftrightarrow AB). Simulations are shown for three different values of Δ (chemical shift difference between the IP-10 peak in the bound and unbound states). An off rate of 20 s⁻¹ was used for all the simulations. The peak in the bound state was assumed to be 1.3 times broader than the unbound peak.