Figure S1. Kringle 3 NMR sequential connectivities and dihedral constraints, versus amino acid sequence. Thickness of the horizontal bars reflects relative intensities (weak, medium, strong) of the sequential (**i, i+1**) NOEs $\mathbf{d_{NN}}$, $\mathbf{d_{\alpha N}}$ and $\mathbf{d_{\beta N}}$. $^3J_{HNH\alpha}$ couplings are represented by variously patterned circles: $^3J_{HNH\alpha} < 6$ Hz, ○; 6 Hz $\leq {}^3J_{HNH\alpha} \leq 8$ Hz, ◑; $^3J_{HNH\alpha} > 8$ Hz, ●. Pro and Gly residues are labeled **P** and **G**, respectively. Dihedral angle constraints are indicated; for backbone: $\varphi = -120 \pm 20°$, ▲; $\varphi = -120 \pm 30°$, ►; $\varphi = -120 \pm 40°$, ▼; $\varphi = -70 \pm 20°$, Δ; $\varphi = -45 \pm 20°$, ∇; $\omega \approx 0°$ (*cis* Pro, **c**); $\omega \approx 180°$ (*trans* Pro, **t**) (backbone); and side chains: $\chi_1 = +60° \pm 30°$ (*gauche* +), $\chi_1 = -60° \pm 30°$ (*gauche* −), $\chi_1 = 180° \pm 30°$ (*trans* ¦).

Figure S2. Zwitterionic ligands docked to the wild type kringle 3 binding site. (A) Chemical structure of the ligands. (B) and (C) Protein surface electrostatics (calculated and and colored as in Figure 6C) were modeled for the NMR structure of K3 and the X-ray structure of the angiostatin K3, respectively. Selected residues are labeled; residue Glu34 is indicated in parentheses, it was mutated from Asn to prevent glycosylation (*22*). Docking was *via* AutoDock 4.0 on a rigid protein structure; the lowest energy conformations of the ligands are shown only if docking was observed at the canonical binding site. Ligand atoms are in stick representation and superposed with Van der Waals surfaces (dotted); carbon, nitrogen, oxygen and sulfur atoms are denoted in magenta, blue, red and yellow, respectively; only polar hydrogen atoms are shown.

Figure S3. Lysine-binding site of K57D kringle 3: sampling of docked AMCHA poses. The animation results from sequential displays of individual AutoDock simulation snapshots. Details are as given for Figure 8.