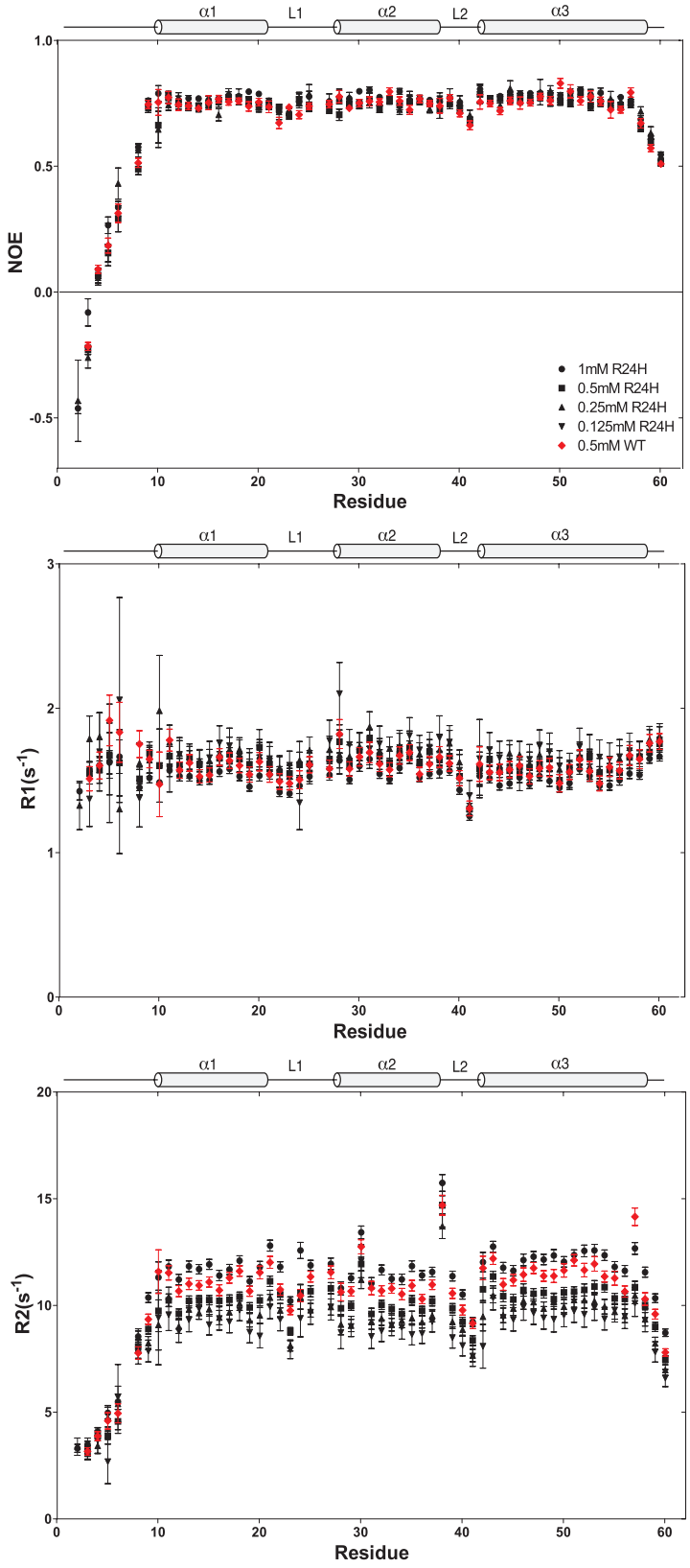
Supporting Information

Structural and Biophysical Insights into the Ligand-Free Pitx2 Homeodomain and a Ring Dermoid of the Cornea Inducing Homeodomain Mutant

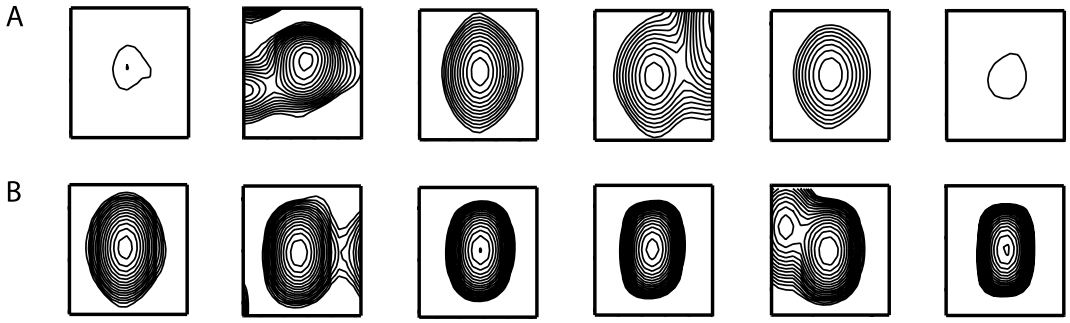
*Thomas Doerdelmann[†], Douglas J. Kojetin[†,‡], Jamie M. Baird-Titus[§], Laura A. Solt[‡], Thomas P. Burris[‡] and Mark Rance[†]**

Supplementary Figure 1

^{15}N-relaxation rates for the Pitx2 wild-type homeodomain (red) and R24H mutant (black). The concentration series for the mutant protein establishes the concentration dependence of the R_1 and R_2 measurements, but clearly demonstrates the increased flexibility of the N-terminal arm and the L1 and L2 loop regions independent of protein concentration. Cylinders indicate the positions of the α-helices.



Supplementary Figure 2
Amide backbone chemical shift resonances in a standard ^{1}H-^{15}N HSQC experiment. **A.** N-terminal resonances 1-7 (left to right) with the second box to the left including overlapped residues 2 and 3. **B.** C-terminal tail of the expression system resonances 61-66 (left to right)



Supplementary Figure 3
2D ^{1}H-^{15}N HSQC spectra of the wild-type (top), R24H mutant (middle) and V45L (bottom) Pitx2 homeodomains. Data was recorded at 600 MHz and a temperature of 295K.