

# Protein environment affects the water-tryptophan binding mode. MD, QM/MM, and NMR studies of Engrailed homeodomain mutants<sup>†</sup>

Nad'a Špačková,<sup>a</sup> Zuzana Trošanová,<sup>a,b</sup> Filip Šebesta,<sup>c</sup> Séverine Jansen,<sup>a,d</sup>  
Jaroslav V. Burda,<sup>c</sup> Pavel Srb,<sup>b,‡</sup> Milan Zachrdla,<sup>b,||</sup> Lukáš Žídek,<sup>b,d</sup>  
and Jiří Kozelka<sup>\*a,d,f</sup>

<sup>a</sup> Department of Condensed Matter Physics, Faculty of Science, Masaryk University, Kotlářská 2, CZ-6137 Brno, Czech Republic

<sup>b</sup> National Centre for Biomolecular Research, Faculty of Science, Masaryk University, Kamenice 5/A4, CZ-62500 Brno, Czech Republic

<sup>c</sup> Department of Chemical Physics and Optics, Faculty of Mathematics and Physics, Charles University, Ke Karlovu 3, 12116 Praha, Czech Republic

<sup>d</sup> CEITEC – Central European Institute of Technology, Masaryk University, Kamenice 5/A4, CZ-62500 Brno, Czech Republic

<sup>e</sup> Biologie Intégrée du Globule Rouge UMR\_S1134, Inserm, Univ. Paris Diderot, Sorbonne Paris Cité, Univ. de la Réunion, Univ. des Antilles, 75739 Paris, France

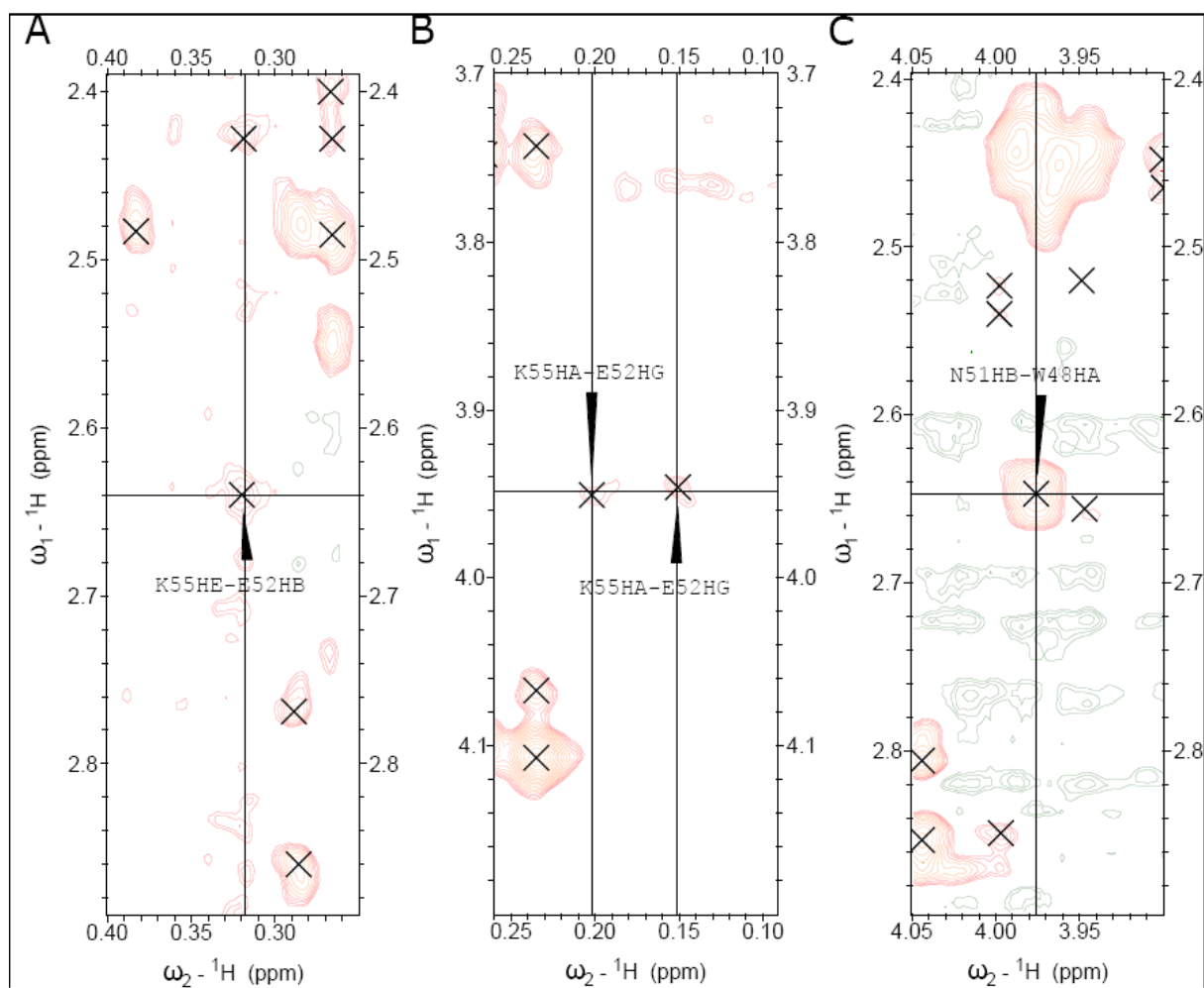
<sup>f</sup> Institut National de la Transfusion Sanguine (INTS), 75739 Paris, France

<sup>g</sup> Laboratoire d'Excellence GR-Ex, 75739 Paris, France. E-mail : [kozelka.jiri@gmail.com](mailto:kozelka.jiri@gmail.com)

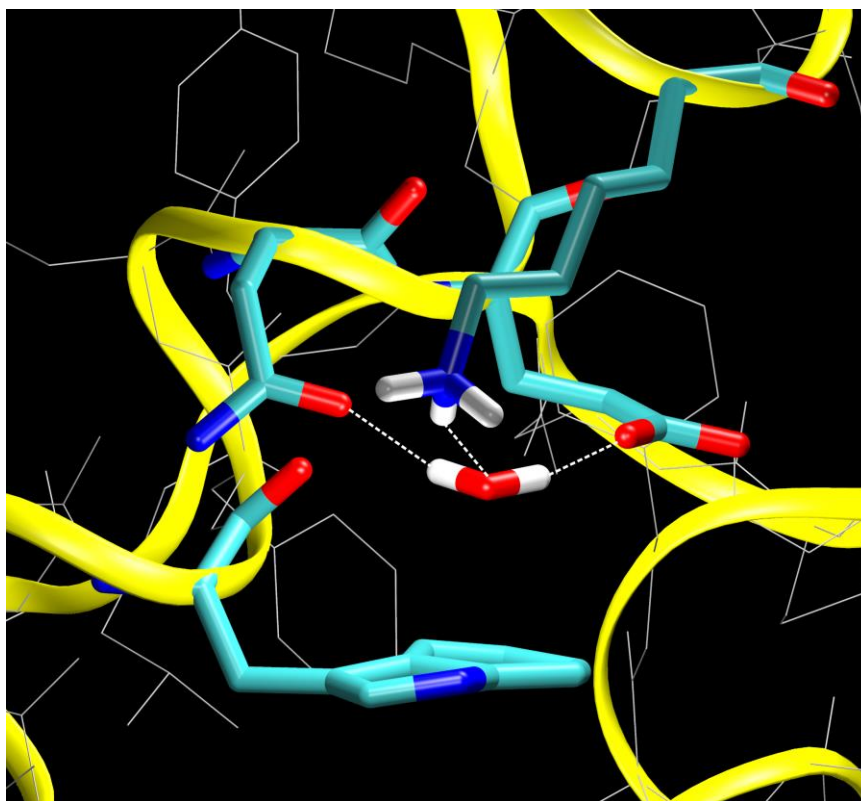
<sup>‡</sup> Present address: Institute of Organic Chemistry and Biochemistry, Academy of Sciences of the Czech Republic, v.v.i., Flemingovo nám 2, 16000 Praha, Czech Republic

<sup>||</sup> Present address: Département de chimie, École normale supérieure, 24 rue Lhomond, 75005 Paris, France

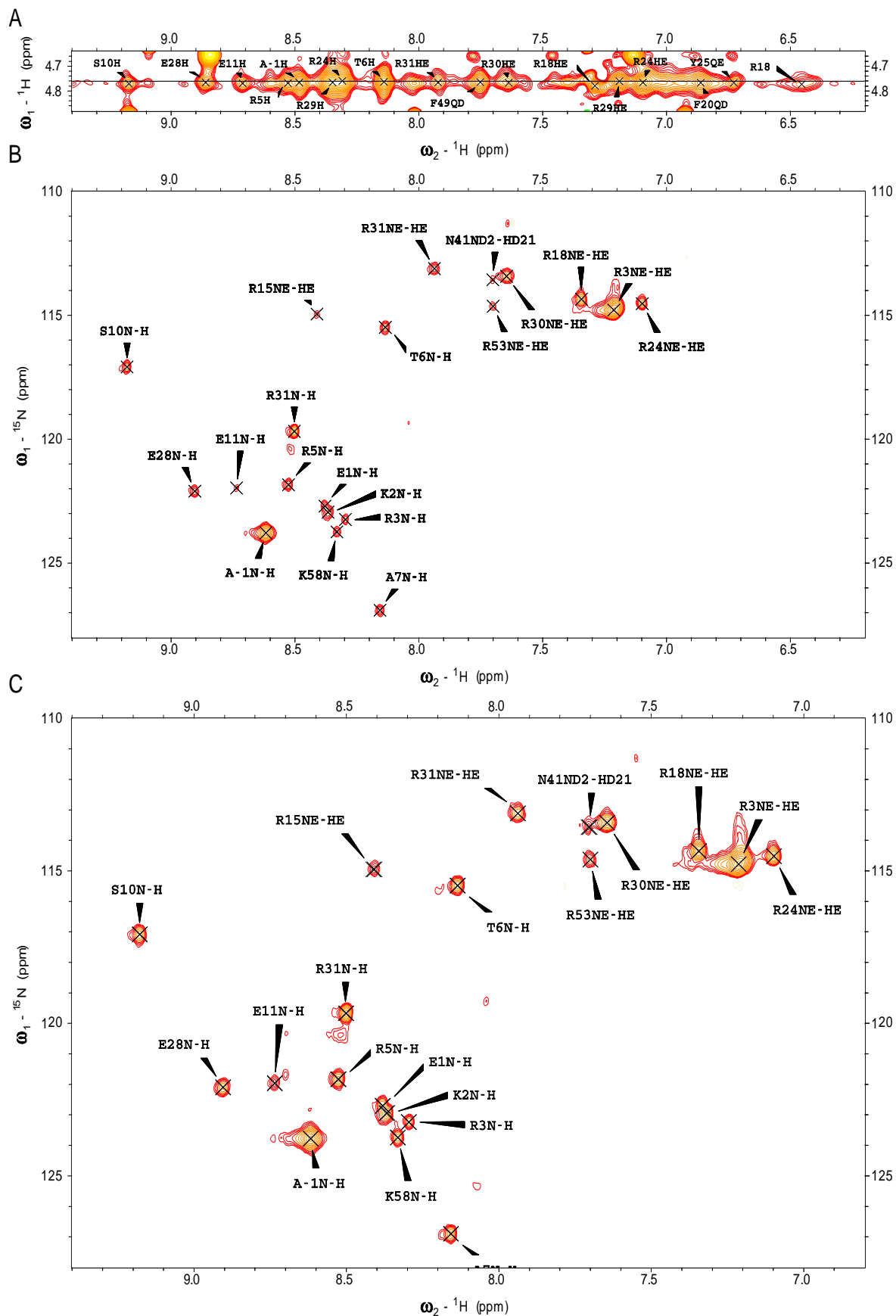
## ELECTRONIC SUPPLEMENTARY INFORMATION



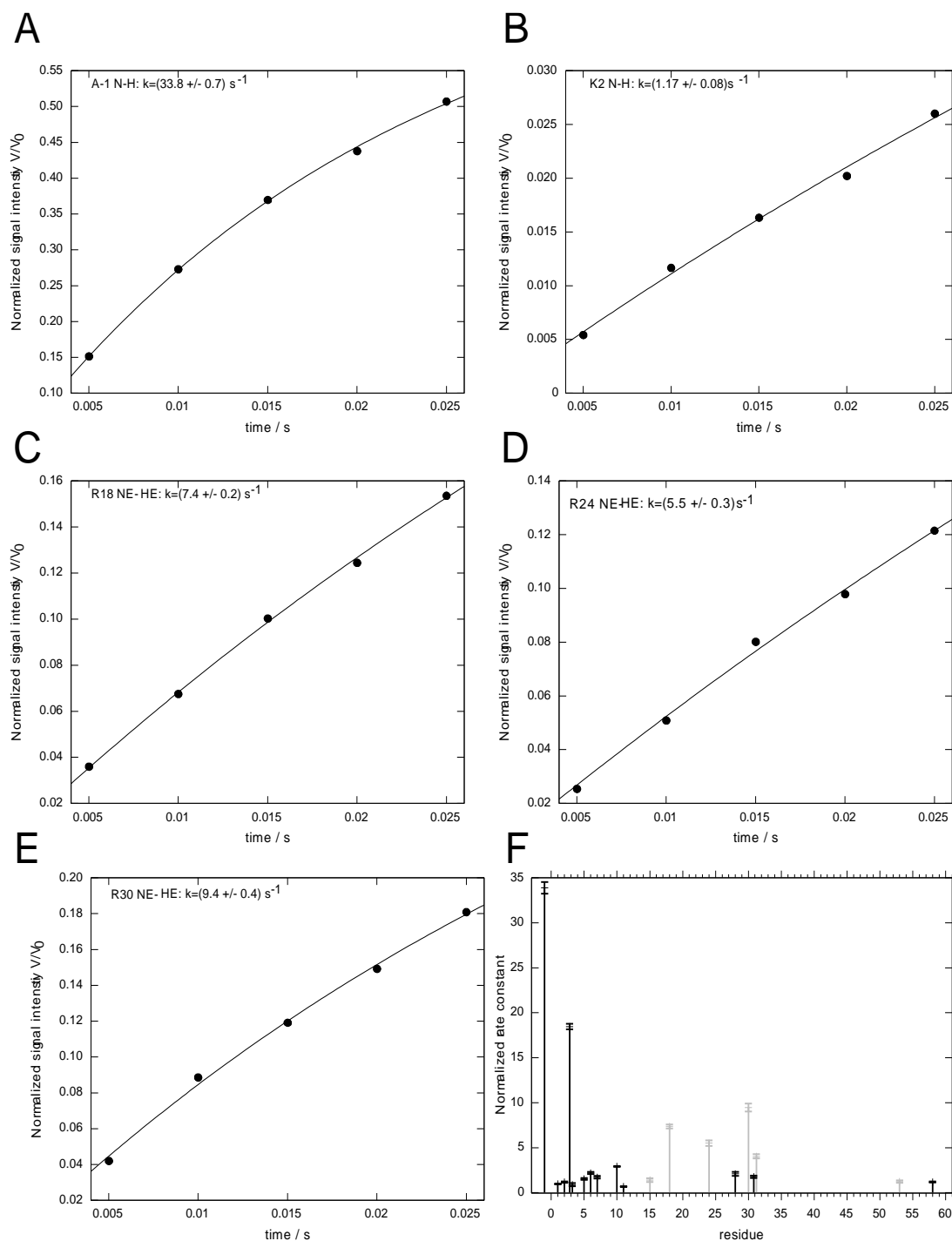
**Fig. S1.** Regions of NOESY spectra with cross-peaks providing NOEs restraining asparagine N51 in the NMR structure. A: correlation of K55 HE and E52 HB; B: correlation of K55 HA and E52 HG; C: correlation of W48 HA and N51 HB.



**Fig. S2.** Typical snapshot from the restrained MD simulation of the K52E mutant of the *Drosophila* EnHD in the  $g^+$  conformation along the torsion angle N-CA-CB-CG of asparagine N51. Close-up view depicting the interaction between the cavity water and the amino acids W48 (below), N51 (left), E52 (right), and K55 (above).

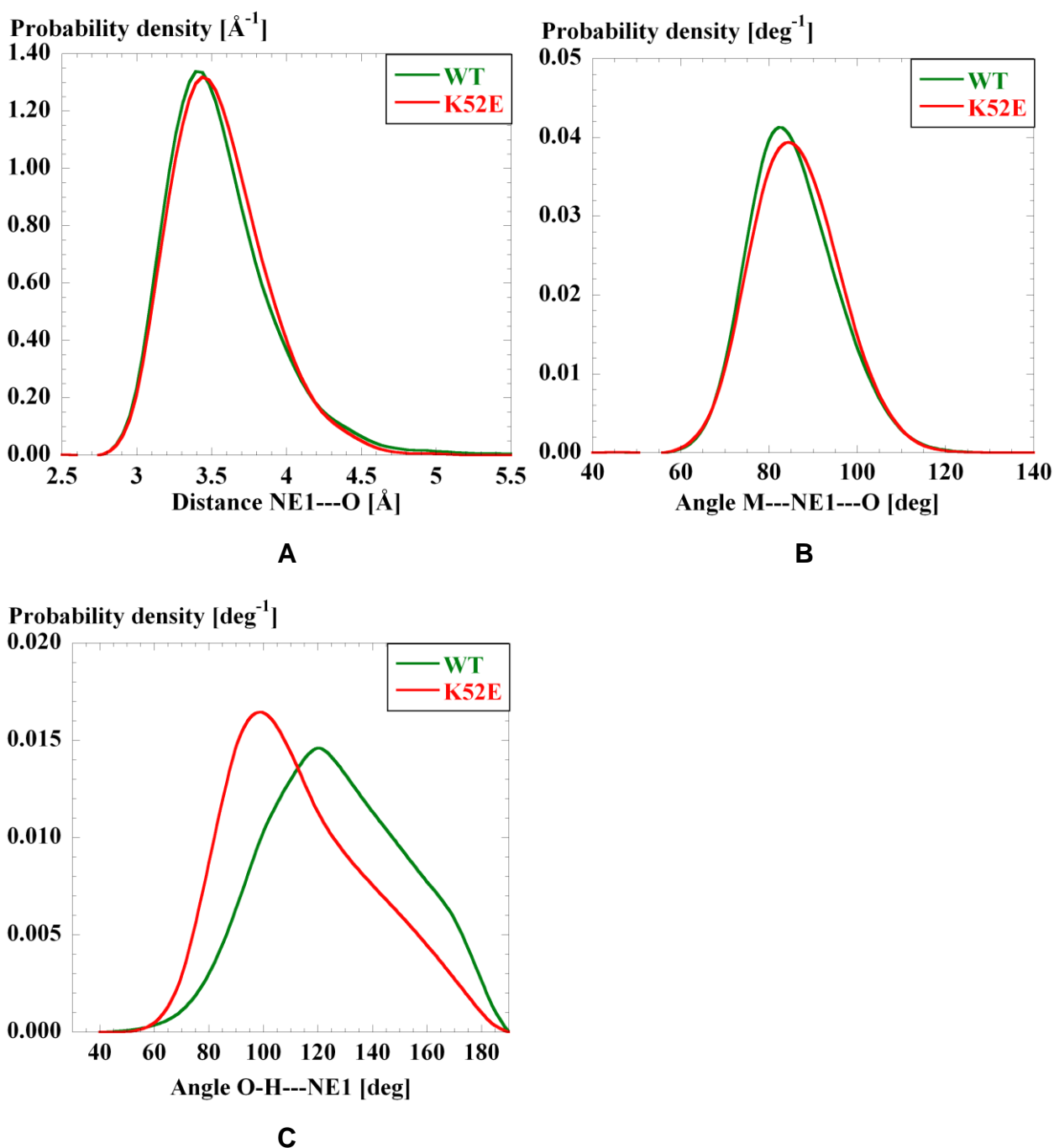


**Fig. S3.** Strip from 2D NOESY spectrum recorded at 293 K (A);  $[{}^{15}\text{N}-{}^1\text{H}]$  CLEANEX-PM-FHSQC spectrum recorded with the mixing time of 5 ms (B) and 25 ms (C).



**Fig. S4.** Examples of initial slope analysis<sup>1</sup> of CLEANEX-PM-FHSQC peaks (A-E) and plot of all evaluated exchange rates (F). Values for backbone and side-chain protons are plotted in black and gray, respectively, in Panel F. The residue labeled “A-1” is alanine of the GlyAlaMet tripeptide preceding E1 of the Engrailed homeodomain sequence in the constructs of the K52E mutant used in this study.

<sup>1</sup> T.-L. Hwang, P. C. M. Van Zijl, and S. Mori, *J. Biomol. NMR*, 1998, **11**, 221.



**Fig. S5.** Position and orientation with respect to W48 indole of the cavity water during unrestrained MD simulations of *Drosophila* EnHD (WT, green; K52E, red). Only trajectories with the N-CA-CB-CG torsion angle of N51 in the *trans* domain were taken into account. A: Probability distribution of the NE1(W48)-O(wat) distance. B: Probability distribution of the M(W48)-NE1(W48)---O(wat) angle (M=center of the five-membered ring of indole). C: Probability distribution of the O(wat)-H(wat)---NE1(W48) angle (H is the H-atom closer to NE1).