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ARTICLE

Mats A.L. Eriksson · Lennart Nilsson

Structural and dynamic differences of the estrogen receptor DNA-binding domain, binding as a dimer and as a monomer to DNA: molecular dynamics simulation studies

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Figures 2 and 4 in Eriksson & Nilsson (1999) European Biophysics Journal 28, 102–111, have been swapped. The diagram in figure 2 should replace that in figure 4, and vice versa.

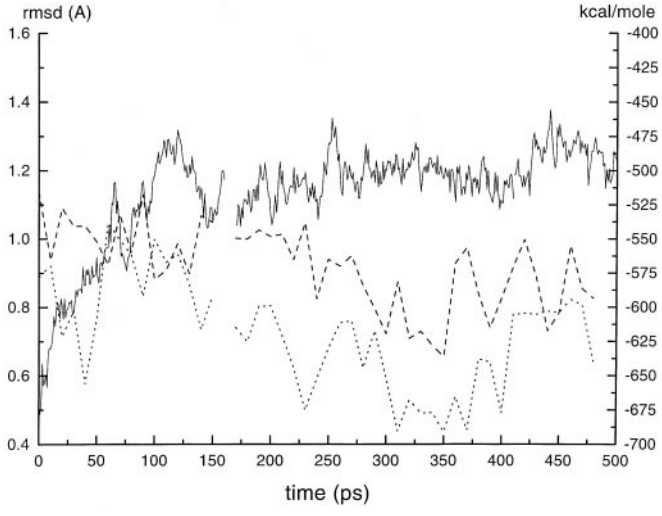

Fig. 2 *Solid line*, time evolution of the root mean square deviation (rmsd, Å) of the non-hydrogen atoms in ERE-$(ERDBD)_2$ from the energy minimized crystal structure; *dashed line*, total interaction energy (kcal/mol) between $ERDBD_{A1}$ and ERE; *dotted line*, total interaction energy (kcal/mol) between $ERDBD_{A2}$ and ERE. There is gap in the curves at around 175 ps, owing to an accidental loss of a piece of trajectory during the equilibration

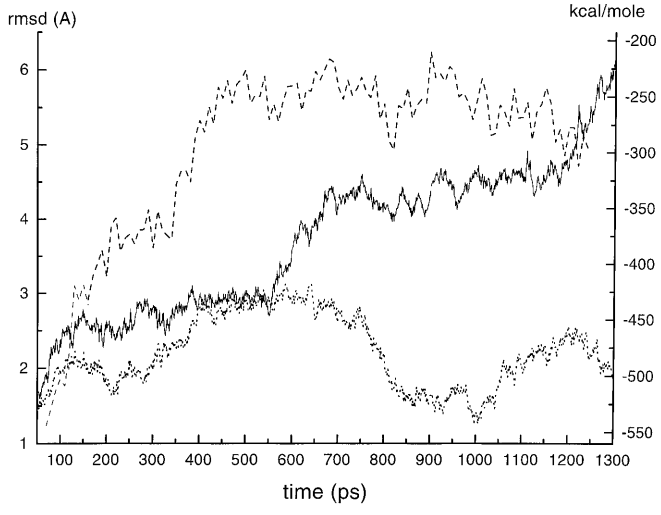

Fig. 4 Time-evolution of the EREH-$ERDBD_{A1}$ simulation. *Solid line*, rmsd (Å) of the non-hydrogen atoms in $ERDBD_{A1}$ from the energy minimized crystal structure; *dotted line*, rmsd (Å) of non-hydrogen atoms in EREH; *dashed line*, total interaction energy (kcal/mol) between $ERDBD_{A1}$ and EREH