MD simulation of the WW-loop

This paper summarizes some results of the investigation of energy flow in the WW-loop using MD simulations. The target system is the modified WW loop with 34 residues, where residuum 19 was substituted with azulenylalanine (AZU) and residue 8 was substitued with azidohomoalanine (AHA). AZU can in experiment be excited at a typical wavelength of 600 nm and decays on the sub-picosecond timescale due to internal conversion. Because of this it is well suited to pump energy into the system. AHA has a typical vibrational band at 2100 cm^{-1} which is separable in the IR spectrum. The AHA-AZU pair is thus well suited for pump-probe-spectroscopy of vibrational energy transport in the WW-loop [1].

The goal of the herein evaluated simulations was to model the heating of AHA and observe the vibrational energy transport through the protein. The simulation flow is the following: All simulations are performed with the GROMACS program suite [2]. and the AMBER99sb*-ildn force field is used to model the WW-loop and the TIP3P water.
To couple the system to the heat bath, we use the velocity-rescale algorithm [3], and for pressure coupling the Berendsen algorithm[4]. In the beginning the protein was inserted in a dodecahedron box. For the simulation in solvent we add about 1600 water molecules. For the hydrated system we use the Particle-Mesh Ewald method[5] for the electrostatic interactions beyond a miniamal cut-off of 1.4 nm and for the van der Waals interaction a plain cut off at 1.4 nm. After energy minimization, the system is equilibrated for 100 ns at a pressure of 1 atm and a temperature of 100 K. From the second half of this simulation we obtained the average box size for the followed NVT simulation.
We then take 200 statistically independent conformations from a 100 ns 100 K NVT simulation as starting structures for the non-equilibrium simulations. All the starting structures were cooled down to 10 K using a NPT ensemble to improve the signal to noise ratio of the following nonequilibrium simulation.

For the excitation with T-jump method we first freeze out all degrees of freedom of the system except for the chromophore of residue AZU 19. The chromophore is then coupled to a 910 K bath and heated for 1 ps. Following the heating step the velocities of the frozen atoms are set back to the velocities of the corresponding equilibrium step.

Finally the non-equilibrium simulations of all 200 structures were run in a NVE ensemble for 100 ps each, using a timestep of 0.2 fs. The time evolution of the kinetic energy of all residues was averaged over all 200 trajectories and is shown in the plots below.

0.1 Results in total kinetic energiy

0.2 Results in kinetic energy per dof

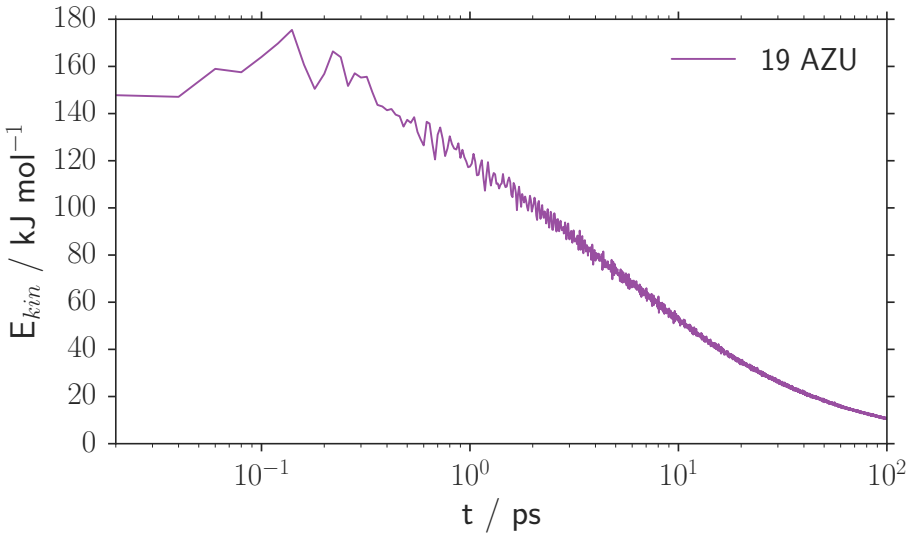

Figure 1: Kinetic energy of the heated residuum AZU 19. The characteristic time of decay between 0.2 ps and 40 ps obtained from fitting is $\tau_{AZU} \approx 10$ ps.

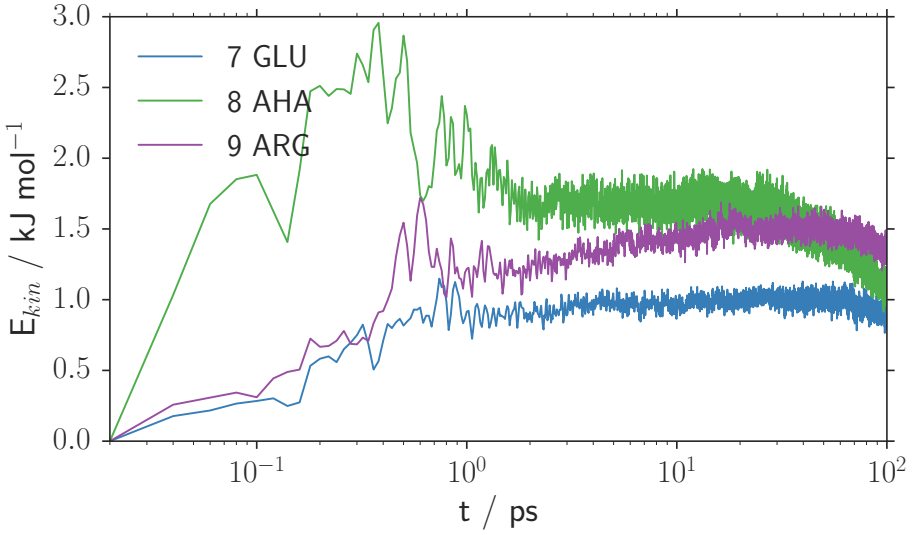

Figure 2: Kinetic energy of residues 7 GLU, 9 ARG and the possible thermometer 8 AHA. The maximum rise in the kinetic energy of 8 AHA is around three times smaller than that of the direct neighbour of AZU 18 TYR. The energies are normalized to the value at $t = 0$.

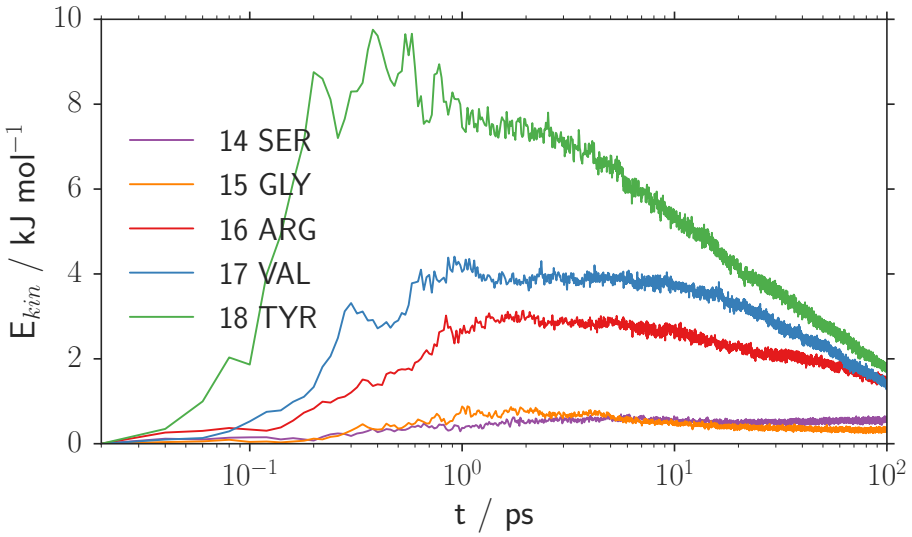

Figure 3: Kinetic energy of downstream residues 14 to 18. The energies are normalized to the value at $t = 0$.

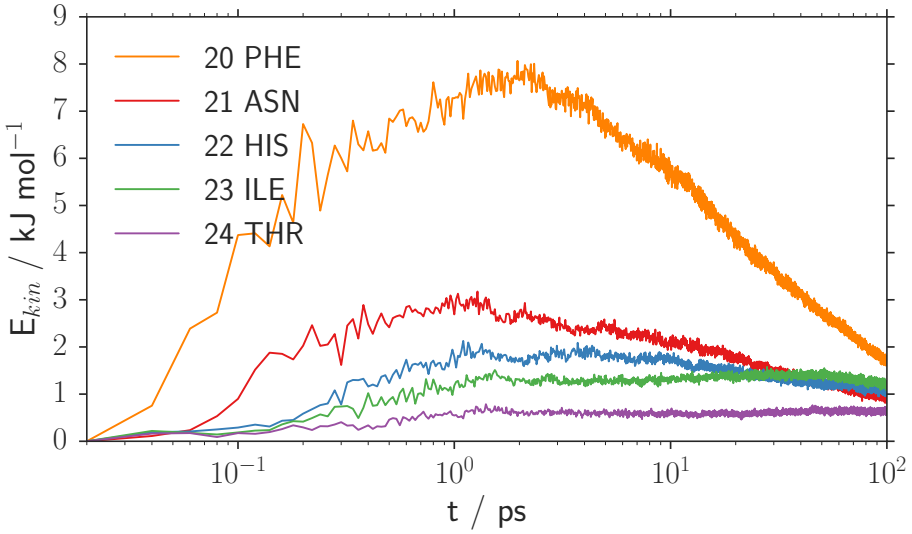

Figure 4: Kinetic energy of upstream residues 20 to 24.The energies are normalized to the value at $t = 0$.

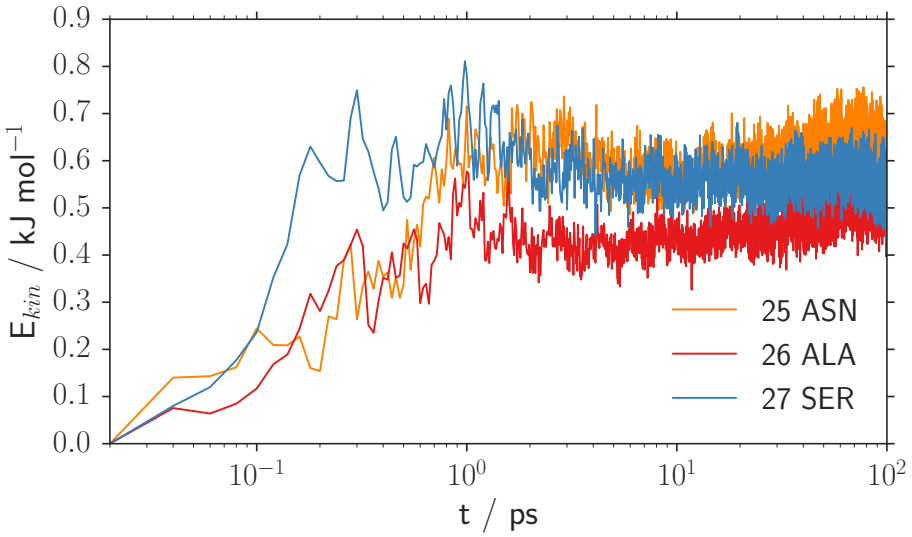

Figure 5: Kinetic energy of residues 25 ASN, 26 ALA and 27 SER. The energy dose for 26 ALA, which is a possible thermometer position, is one order of magnitude smaller than the energy rise of 8 AHA. The energies are normalized to the value at $t = 0$.

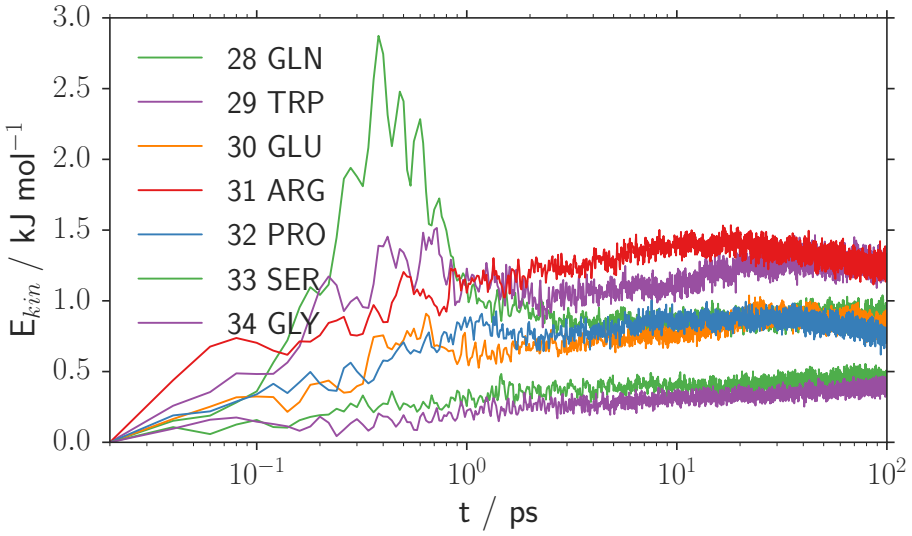

Figure 6: Kinetic energy of residues 28 till end, of which 28 is in polar contact with 19 AZU. The energies are normalized to the value at $t = 0$.

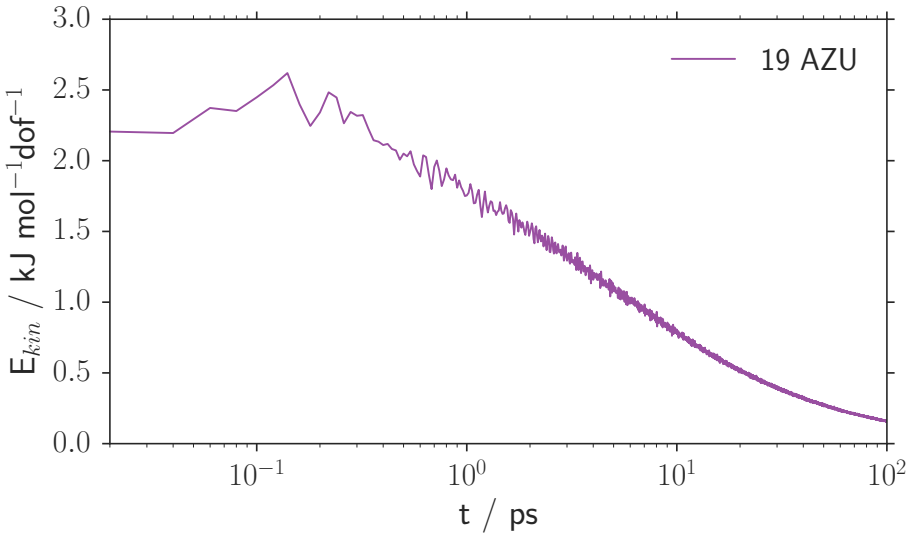

Figure 7: Kinetic energy per dof of the heated residuum AZU 19. The characteristic time of decay between 0.2 ps and 40 ps obtained from fitting is $\tau_{AZU} \approx 10$ ps.

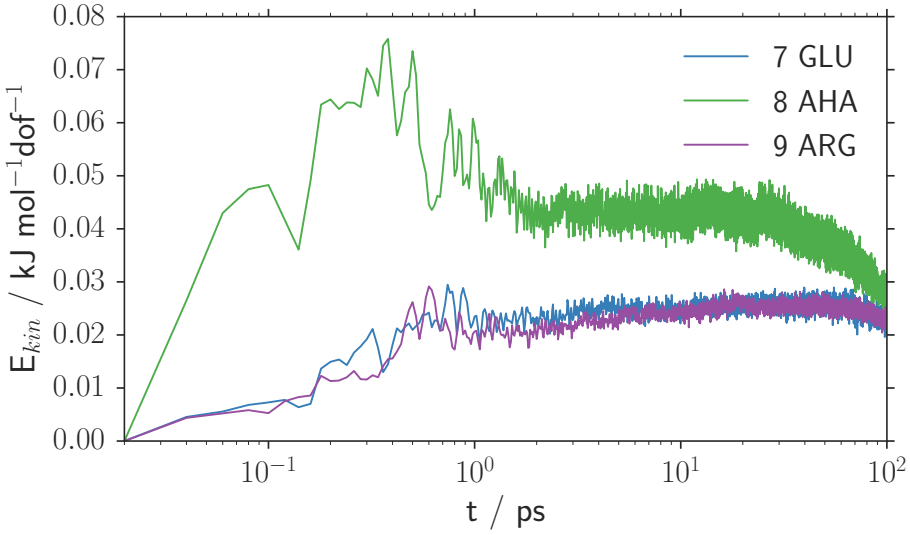

Figure 8: Kinetic energy per dof of residues 7 GLU, 9 ARG and the possible thermometer 8 AHA. The maximum rise in the kinetic energy of 8 AHA is around three times smaller than that of the direct neighbour of AZU 18 TYR. The energies are normalized to the value at $t = 0$.

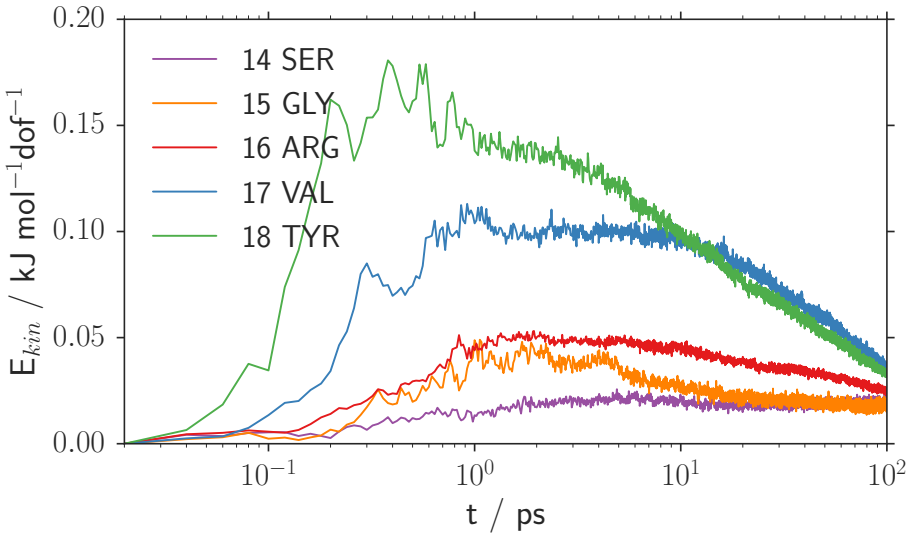

Figure 9: Kinetic energy per dof of downstream residues 14 to 18. The energies are normalized to the value at $t = 0$.

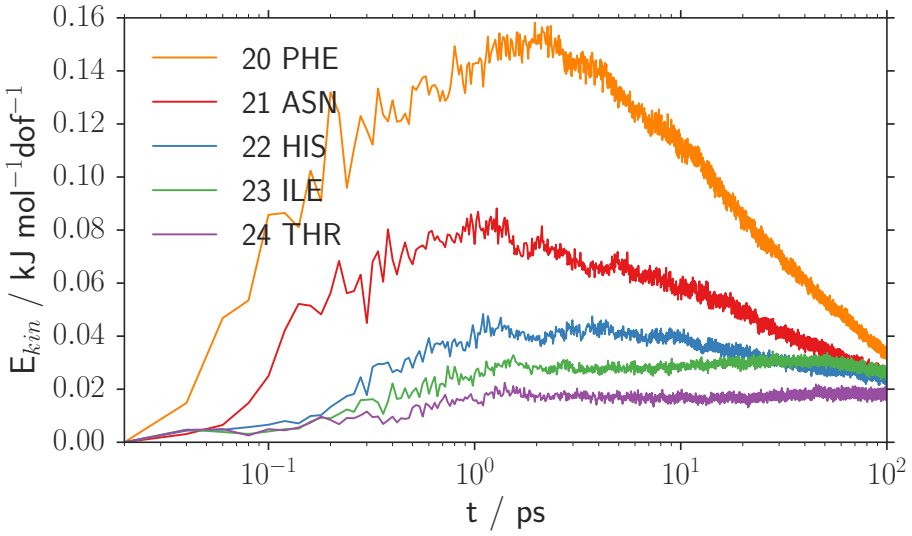

Figure 10: Kinetic energy per dof of upstream residues 20 to 24.The energies are normalized to the value at $t = 0$.

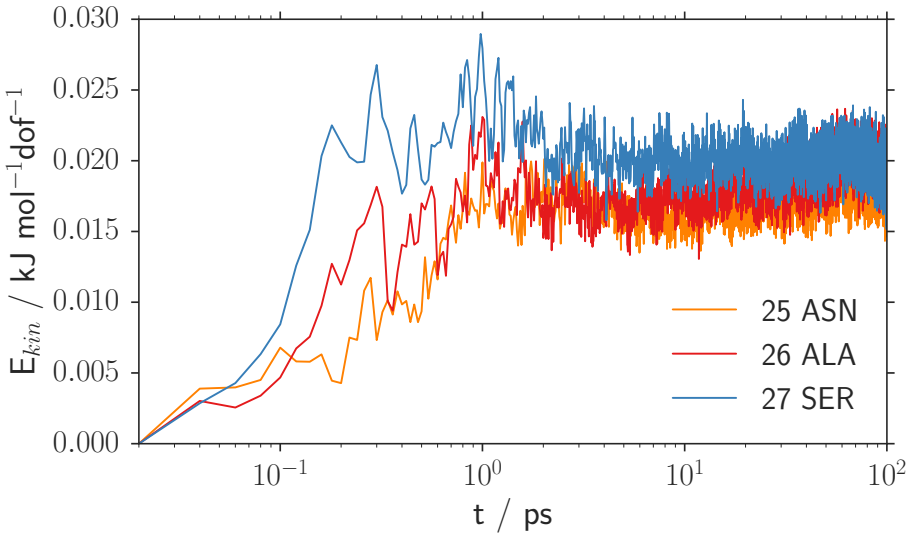

Figure 11: Kinetic energy per dof of residues 25 ASN, 26 ALA and 27 SER. The energy dose for 26 ALA, which is a possible thermometer position, is one order of magnitude smaller than the energy rise of 8 AHA. The energies are normalized to the value at $t = 0$.

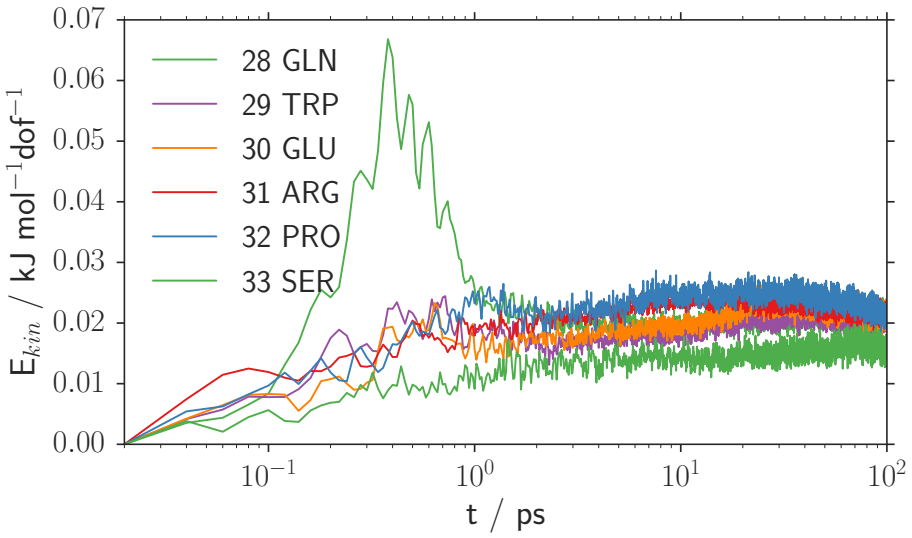

Figure 12: Kinetic energy per dof of residues 28 till end, of which 28 is in polar contact with 19 AZU. The energies are normalized to the value at $t = 0$.

Bibliography

[1] H. M. Muller-Werkmeister and J. Bredenbeck, A donor-acceptor pair for the real time study of vibrational energy transfer in proteins, Phys. Chem. Chem. Phys. **16**, 3261 (2014).

[2] S. Pronk et al., GROMACS 4.5: a high-throughput and highly parallel open source molecular simulation toolkit, Bioinformatics **29**, 845 (2013).

[3] G. Bussi, D. Donadio, and M. Parrinello, Canonical sampling through velocity rescaling, J. Chem. Phys. **126**, 0141011 (2007).

[4] H. J. C. Berendsen, J. P. M. Postma, W. F. van Gunsteren, A. Dinola, and J. R. Haak, Molecular dynamics with coupling to an external bath, J. Chem. Phys. **81**, 3684 (1984).

[5] T. Darden, D. York, and L. Petersen, Particle mesh Ewald: An N log(N) method for Ewald sums in large systems, J. Chem. Phys. **98**, 10089 (1993).