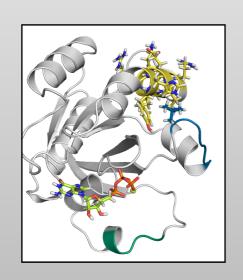
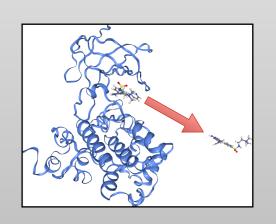
Questions



Are there fundamental differences in the dynamics of wild type and oncogenic mutant proteins?



How does a drug bind/unbind from its target site? What role do non-target short-lived binding poses play?

Simulation philosophy

- Unbiased dynamics: Make as few assumptions as possible about what degrees of freedom are important
- Full atomistic: High resolution in space and time
- Calculate rates, observe mechanisms:
 Compare with experiment and provide new insight