

Erik Nordquist¹, Charles English², Woody Sherman³, Eugenia Clerico², Lila Gierasch^{1,2}, Jianhan Chen^{1,2}

¹Chemistry Dept., ²Biology & Molecular Biology Dept., ³Silicon Therapeutics

Introduction

Molecular chaperone **DnaK** aids cellular **Quality Control** by binding to misfolded proteins.

Big Question:

What is the physical nature of DnaK's selective preferences?

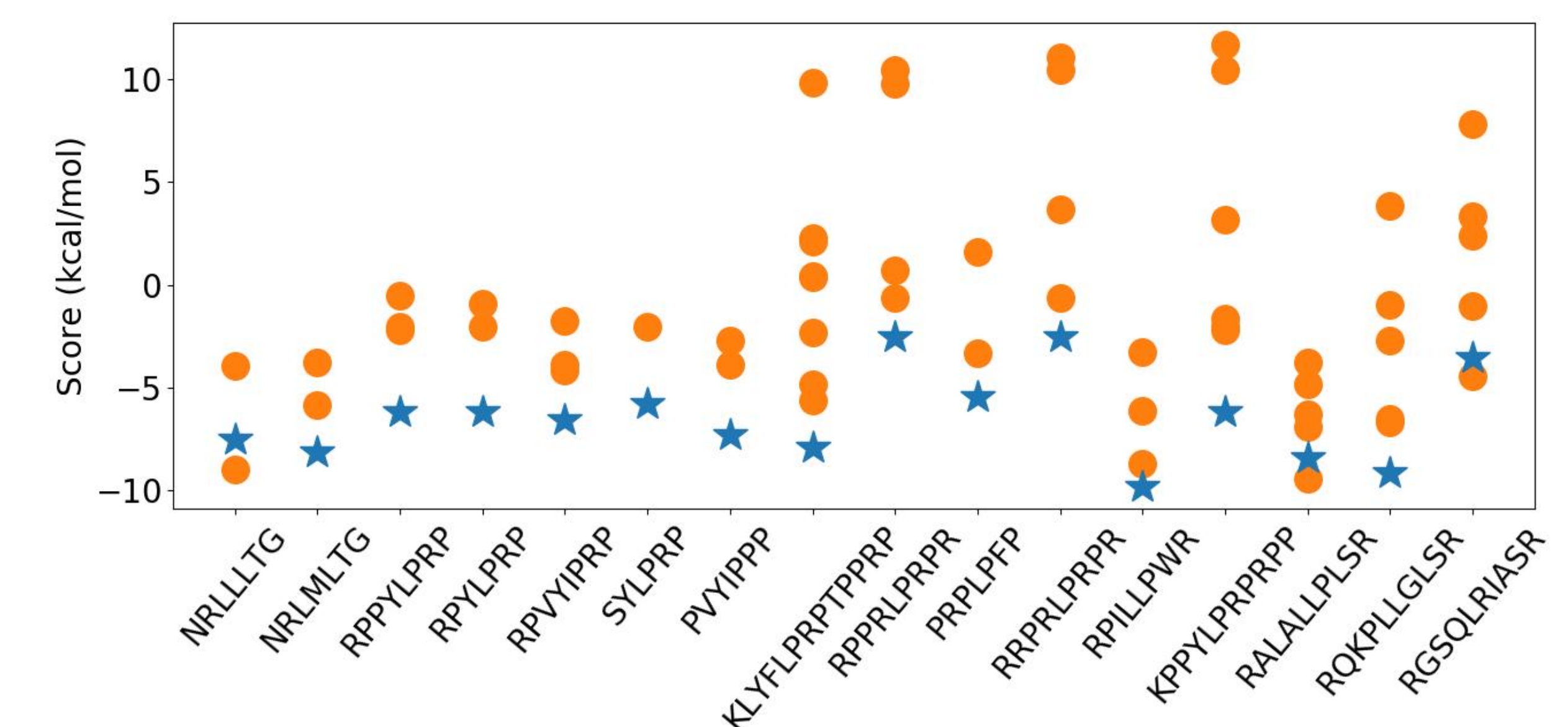
PALADIN: Physics-based model of DnaK-substrate binding

PALADIN is highly extensible and can distinguish peptides in both orientations.

PALADIN model form:

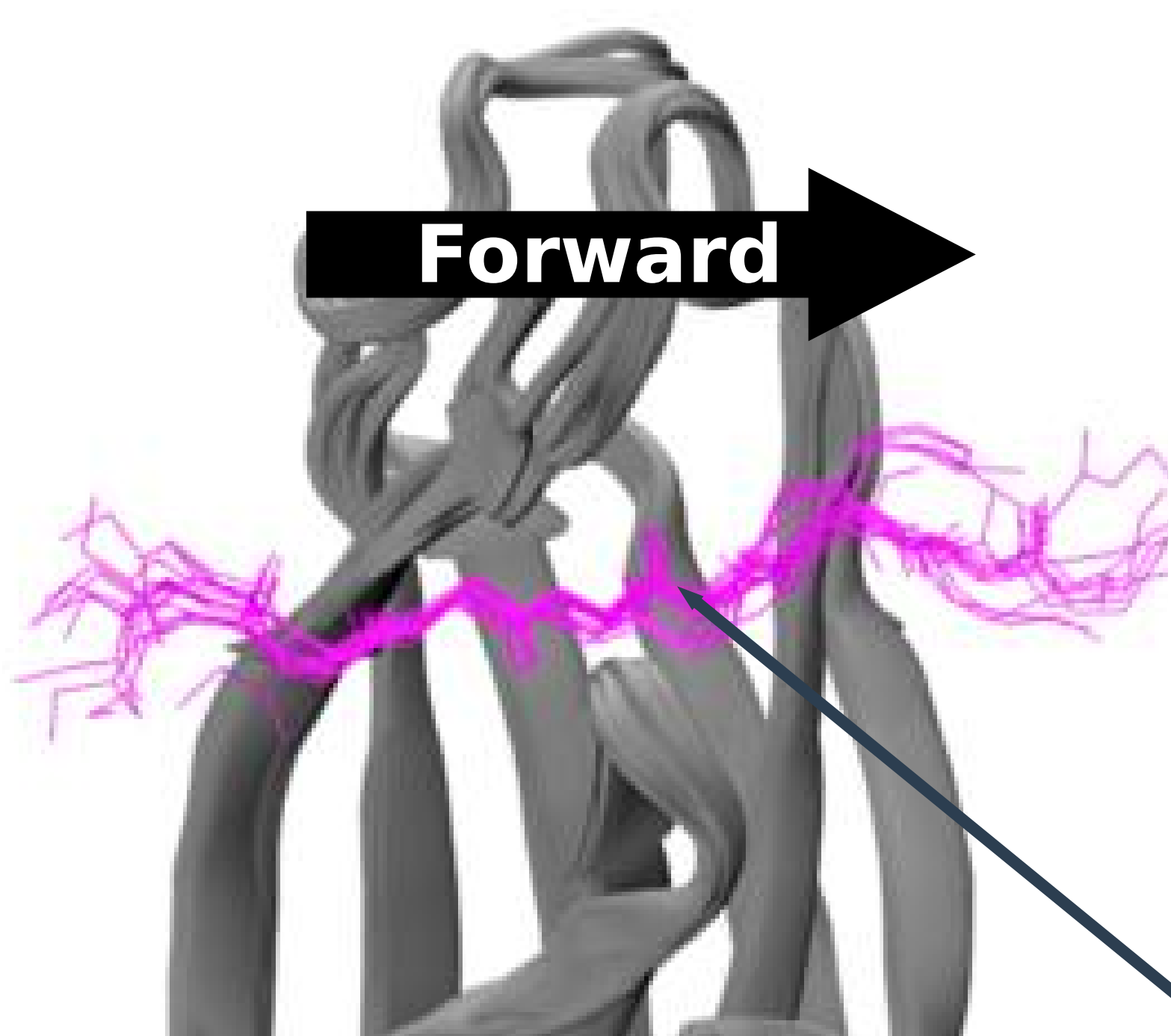
$$\Delta E(5\text{-mer}) = \sum_{\text{sites}} w_{\text{site}} \sum_{\text{terms}} w_{\text{term}} E_{\text{site,term}}^{\text{res}}$$

PALADIN has high resolution



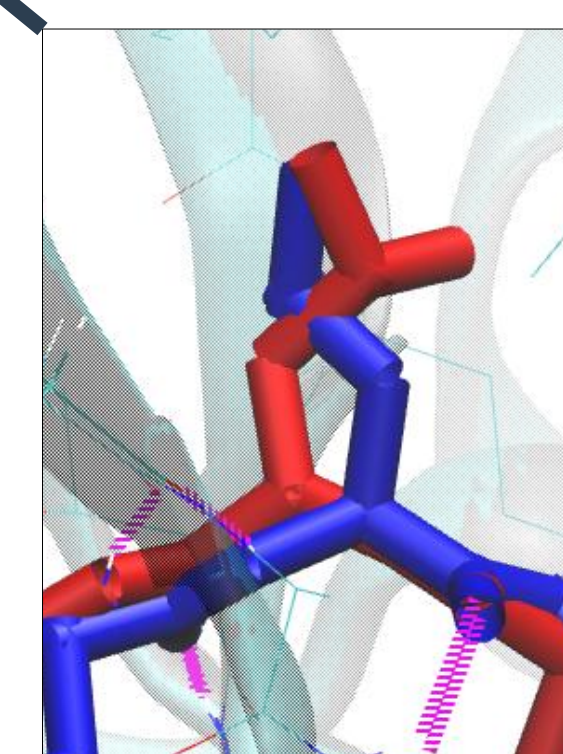
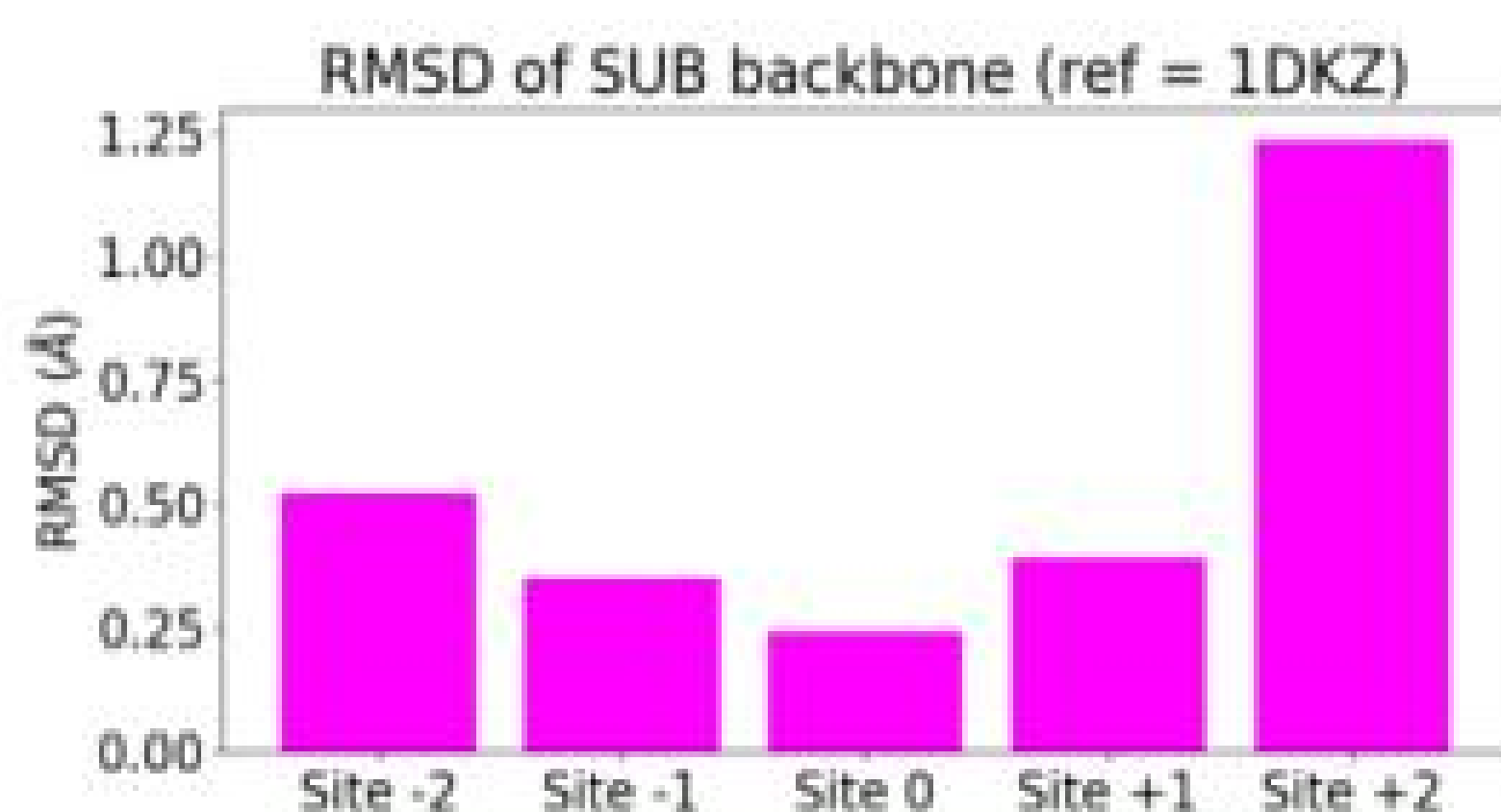
Where **blue star** is lowest in energy = correct prediction

Consistent Binding Pose



Overlay of many **Substrates** and **DnaK** binding domains. Pose is invariant of:

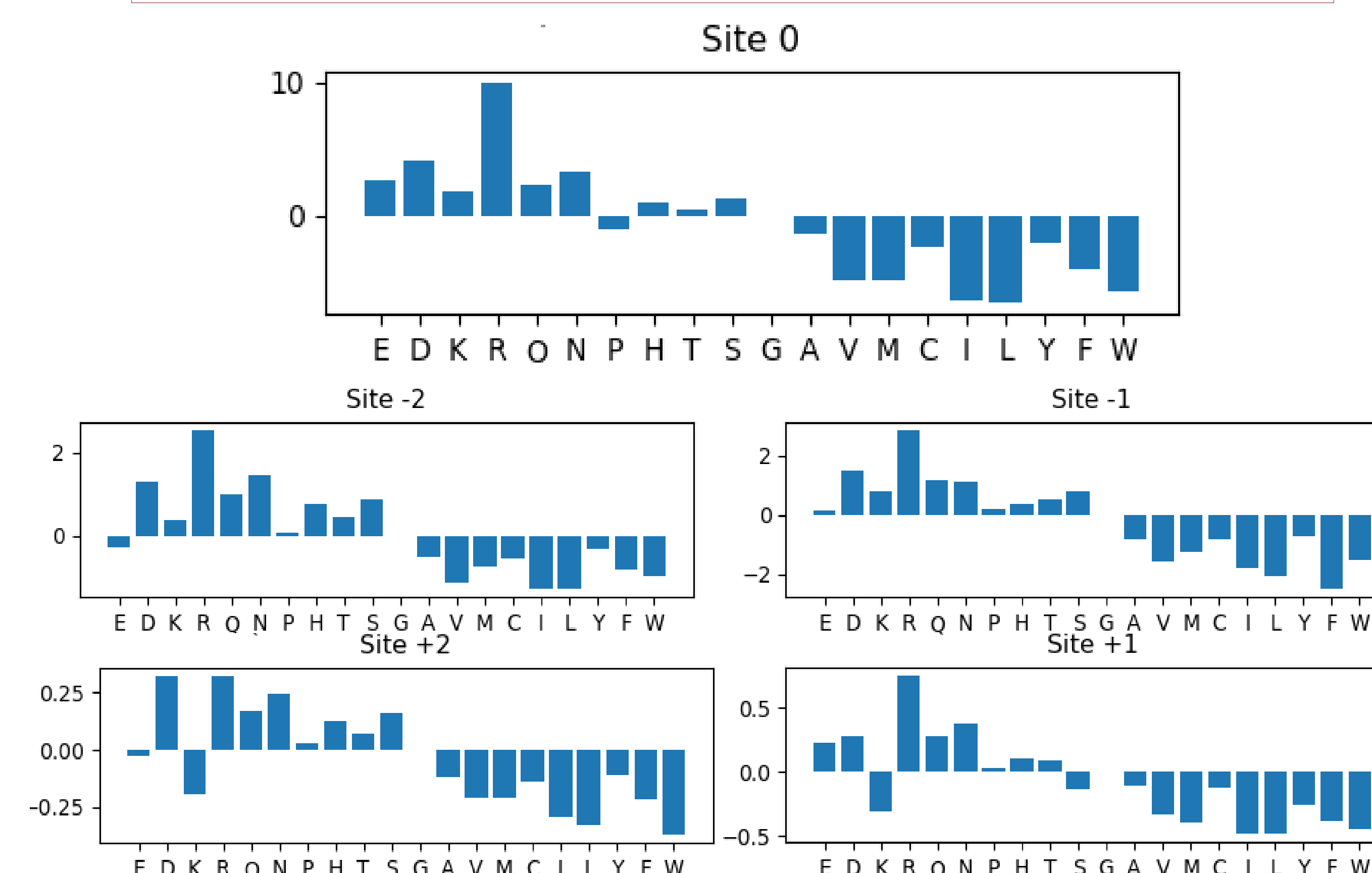
- Sidechain
- Orientation



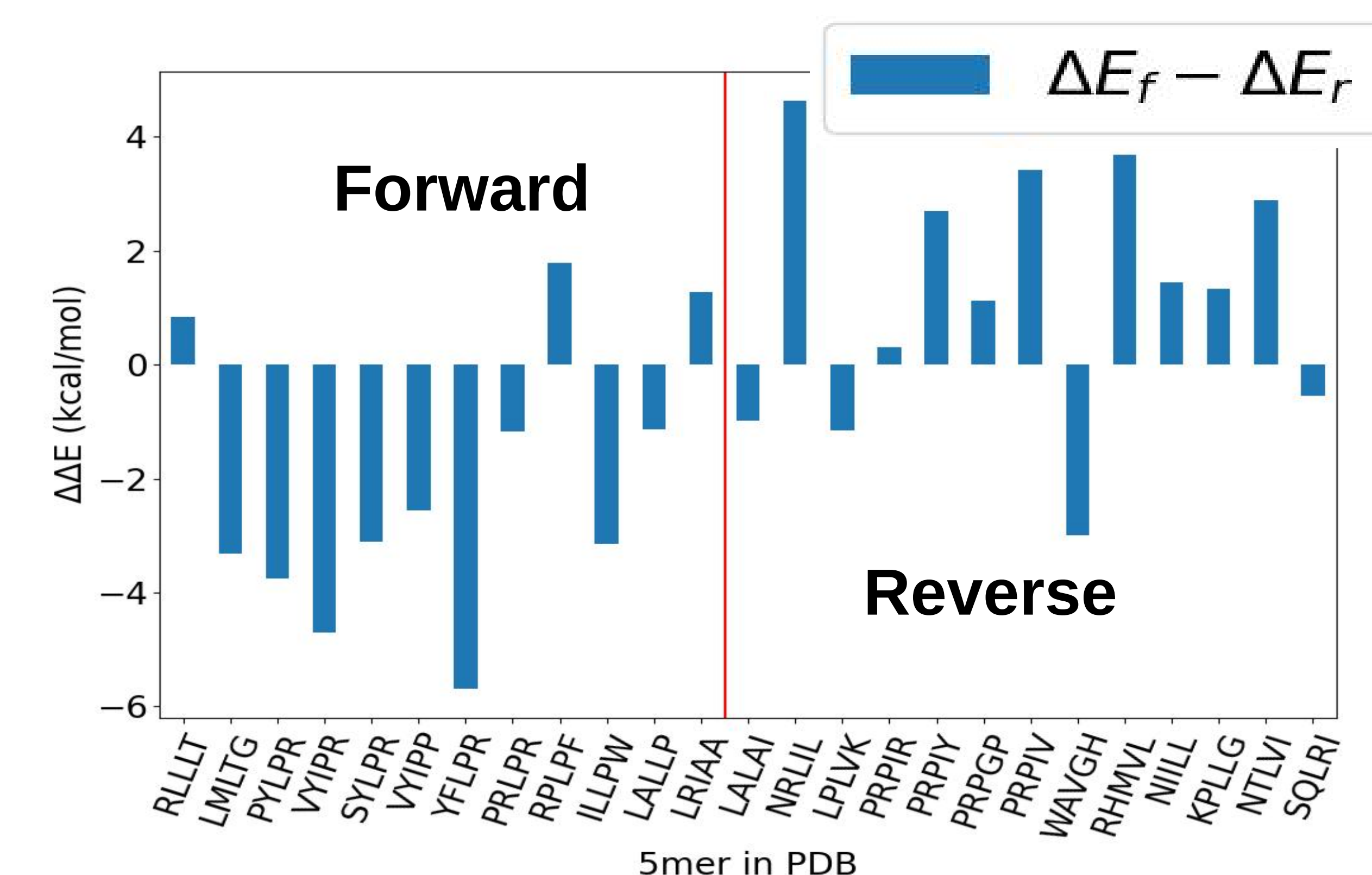
Forward
Reverse
Leu @ Site 0

Physical Interaction Terms

Basis-set **MD simulations** to sample interactions between DnaK and substrates in **binding pose** yield terms that combine effects of: **sterics, electrostatics and solvation.**



PALADIN distinguishes orientations!



Applications

- Extend to other Hsp70 homologs
- Iteratively design new binding motifs with desired affinity

References:

1. Rüdiger, et al. (1997) EMBO J. 16, 1501-1507
2. Clerico, et al. (2019) Biochem J., 476(11):1653-1677
3. Zahn, et al. (2013) J. Mol. Biol. 425, 2463-2479
4. Clerico, et al. (in prep.)

Funded thanks to:

