

## Abstract

The ubiquitin-like, containing PHD and ring finger domains 1 (UHRF1) reader protein has been characterized as a “universal biomarker” of cancer, as its overexpression has been associated with DNA hypermethylation and tumorigenesis.<sup>1,2</sup> The dual-domain reader protein consists of a tandem tudor domain (TTD) and a plant homeodomain (PHD) connected by a short linker.<sup>2</sup> On the histone 3 tail, the PHD domain binds to unmodified arginine at position 2, and the TTD domain binds to trimethylated lysine (Kme3) at position 9 (H3K9me3) through an aromatic cage configuration that is highly conserved among reader proteins.<sup>3,4</sup> Binding in aromatic cages is typically driven by cation- $\pi$  interactions, but recent reports unexpectedly show that the dual-domain UHRF1 protein binds to *tert*-butyl norleucine (tBuNle), a neutral isostere of Kme3, with equal affinity.<sup>4,5,6,7</sup> To investigate the driving forces of binding in this system, electrostatic tunability studies were conducted using Genetic Code Expansion (GCE) to mutate one of the residues forming the aromatic cage with para-substituted phenylalanine derivatives varying in electrostatic potential.<sup>9,10</sup> Isothermal titration calorimetry (ITC) was then used to measure changes in binding affinity and enthalpies of binding between each of the dual-domain UHRF1 variants and the two H3 tail peptides containing Kme3 or tBuNle at position 9 of histone 3. Our results show no correlation between free energy of binding and electrostatic potential, hydrophobicity, or polarizability of the aromatic portion of the phenylalanine derivatives, indicating that interactions within the aromatic cage of the TTD domain do not drive binding. To conclusively determine whether the PHD domain is responsible for binding, future experiments mutating residues within the PHD domain to disrupt acidic contacts with arginine 2 on histone 3 must be performed.

## References

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