

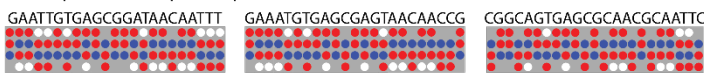
## UNLOCKING THE HIDDEN CODE: PRECISION PROTEIN-DNA BINDING THROUGH HYDROGEN BOND MAPPING

This innovative algorithm revolutionizes the analysis of protein-DNA binding by focusing on hydrogen bond interactions in the major groove of DNA. Traditional methods can overlook the minimal hydrogen bonding patterns that proteins maintain across different DNA sequences. By aligning these bond arrays, Mason researchers are able to uncover shared information that enhances the understanding of DNA recognition and specificity, even when base pairs differ.

### Key Features

- **Precision Protein-DNA Binding Analysis:** Identifies conserved hydrogen bond interactions, providing deeper insights into protein-DNA specificity
- **Novel Alignment Algorithm:** Converts DNA sequences into hydrogen bond and methyl group arrays for a focused analysis
- **Supports Protein Design:** Enables the creation of proteins that bind multiple DNA sequences, fostering advancements in therapeutic and gene therapy applications
- **Evolutionary Insights:** Reveals hidden evolutionary relationships through conserved bonding patterns, independent of base pair identity
- **Open-Source Tool:** The algorithm is available for free on GitHub, supporting community-driven research and development

Step 1 and 2: Input Sequences Are Converted Into Bond/Contacts' Pattern

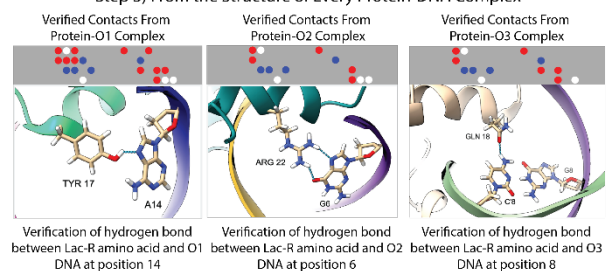


Step 3: The Alignment of the Three Sites' Patterns To Get One Consensus Pattern



The consensus pattern has all of the bonds and contacts shared among the three binding sites and represents the predicted bonds and contacts that the Lac-R protein can make with each of them.

Step 4: Verifying the Predicted Contacts of the Consensus Pattern (Obtained in Step 3) From the Structure of Every Protein-DNA Complex



Step 5: Alignment of the Three Refined Consensus Patterns (From Step 4) To Get the Distinct Pattern Shared Between the Three Refined Patterns



The distinct pattern represents the minimal amount of direct readout information needed for Lac-R to specifically recognize its binding sites.

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