

## Keynote Lectures

### KN-1

#### The vocabulary of protein-DNA interactions: Symmetry, degeneracy, modifications

Matthias Bochtler<sup>1</sup>

1. International Institute of Molecular and Cell Biology & Institute of Biochemistry and Biophysics, Warsaw, Poland

**email:** [mbochtler@iimcb.gov.pl](mailto:mbochtler@iimcb.gov.pl)

The basics of protein nucleic acid interactions have been worked out a long time ago, but new themes are still emerging. The vocabulary for the non-degenerate recognition of DNA bases is well understood, but this is not the case for semi-degenerate recognition, which may occur “accidentally”, or be imposed by symmetry. In the first part of my talk, I will focus on principles of semi-degenerate readout of DNA sequence, by minor groove readout, base unstacking, and nucleotide flipping (1). In the second part of my talk, I will concentrate on modification specific DNA binding. How nucleic acid modifications such as methylation inhibit DNA binding by steric exclusion is readily understandable. Whether a predicted clash is biologically relevant depends on whether protein and nucleic acid are sufficiently flexible to avoid the steric conflict (2). How nucleic acid conformations become a prerequisite for binding is harder to understand, especially when the dependence on the modification is stringent and when a modifier group (such as a methyl group) offers little opportunity for strong attractive interactions. In my talk, I will focus on several published and unpublished structures from our own work which illustrate the modification selective binding of nucleic acids containing 6-methyladenine, 5-methylcytosine (5mC), 5-hydroxymethylcytosine (5hmC), and glucosyl-5-hydroxymethylcytosine (g5hmC) (3).

References:

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### KN-2

#### The Joy of Seeing - in honour of Dorothy Hodgkin

Eleanor Dodson<sup>1</sup>

1. University of York, York, United Kingdom

**email:** [eleanor.dodson@york.ac.uk](mailto:eleanor.dodson@york.ac.uk)

To quote Dorothy Hodgkin: The great advantage of X-ray analysis as a method of chemical structure analysis is its power to show some totally unexpected and surprising structure and to do so with absolute certainty.

I will show examples of how Fourier analysis using X-ray observations from a crystal, combined with imperfect phases, can allow us to boot-strap our way to a satisfactory structure. Combining these basic principals with the great computing power, and excellent data acquisition facilities now available has extended our power to “see” to new levels.

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