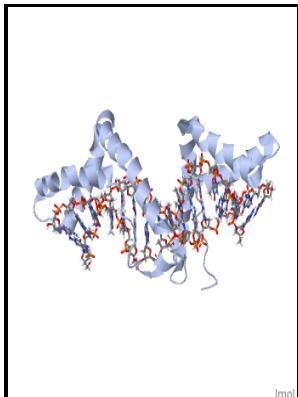


# Structure and DNA binding of HMG boxes

Universityof Portsmouth, School of Biological Sciences - The crystal structure of the Sox4 HMG domain



Description: -

-Structure and DNA binding of HMG boxes

-Structure and DNA binding of HMG boxes

Notes: Thesis (Ph.D.) - University of Portsmouth, 1996.

This edition was published in 1996



Filesize: 58.1010 MB

Tags: #DNA #Bend #Angle #and #Binding #Affinity #of #an #HMG #Box #Increased #by #the #Presence #of #Short #Terminal #Arms

## Structural analysis and DNA binding of the HMG domains of the human mitochondrial transcription factor A

All reactions contained 100 nM DNA. We are grateful to the other members of the laboratory Parinaz Aliahmad, Olivia Goularte, Peggy Han and Jian-Ming Yang for valuable discussion during the preparation of this manuscript and to Olivia Goularte for technical assistance.

### A critical role in structure

However, the structure of an HMG box bound to DNA is not presently available.

## Structural analysis and DNA binding of the HMG domains of the human mitochondrial transcription factor A

Although there is similarity between the two structures, negative charged electrostatic surface potential in the concave face of the molecule of box 5 exhibits great difference compared to that of box 1 and other HMG boxes with known structures. D Calculated sedimentation coefficient distributions for the full-length h-mtTFA.

### HMG

An N-terminal GST fusion with box B mtTFA 110—179 was tested for its ability to interact with the various deletion constructs of h-mtTFA mtTFA 1—109, mtTFA 1—79, mtTFA 1—80—204, mtTFA 110—204, mtTFA 110—179, mtTFA 80—179, mtTFA 1—95 and mtTFA 96—179 in 50 mM HEPES—Na pH 7. HMGB1 and UBF-1 contain multiple HMG-box motifs, although only one is shown indicated by decimal in Fig. One group of HMG-box proteins recognizes structural features of DNA with low or absent sequence specificity.

## DNA binding by single HMG box model proteins — NYU Scholars

The heterogeneous subunit assay introduced by Hope and Struhl was used to determine the stoichiometry of h-mtTFA bound to the LSP promoter DNA. A tyrosine located eight residues C-terminal to this proline in mLEF-1 residue 372 in , binds in the minor groove and serves, in part, to fix this change in direction of the polypeptide chain.

## **DNA binding by single HMG box model proteins**

As well as being the first structure of an HMG-box di-domain bound to DNA, this provides the first structure of the B domain of HMGB1 bound to DNA. Human homologues of the three additional murine genes have also been identified Fig.

### **Solution structure of a DNA**

Each of the HMG boxes and the C-terminal tail were evaluated for their ability to bind to the LSP DNA. Isolation and characterization of human cDNA clones encoding a high mobility group box protein that recognizes structural distortions to DNA caused by binding of the anticancer agent cisplatin. Here we clearly showed that in the absence of DNA, h-mtTFA exists as a monomer , and that it assembles as a dimer on a short segment of the mitochondrial promoter.

### **WDHD1**

However, if the N-terminal extension alone is added to the parent box,  $K_d$  rises slightly, i.

## Related Books

- [Turning pages - reflections in info-times](#)
- [Legacy of service](#)
- [Sublieme vormen met zicht vanat 5M.](#)
- [Potential combat officer - a medicopsychological study of officer candidates for the United States M](#)
- [Senate of Canada.](#)