

# SMART Teams 2014-2015

## Research and Design Phase

### Cedarburg High School SMART Team

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### The T Protein: *Vertebrae Fit to a T*

**PDB:** 1XBR.pdb

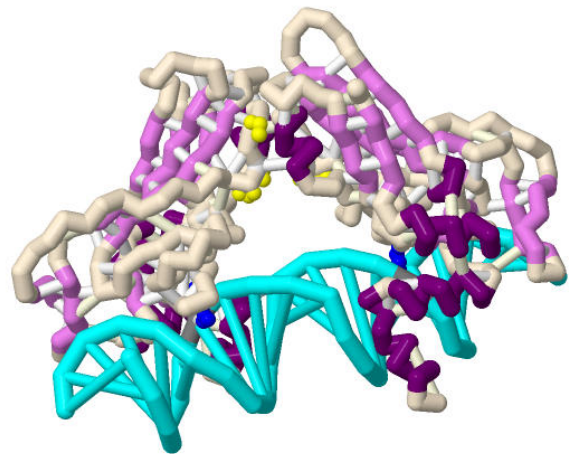
**Primary Citation:** Muller, C. and Herrmann, B. (1997). Crystallographic structure of the T domain–DNA complex of the Brachyury transcription factor. *Nature* 389: 884-888.

**Format:** Alpha carbon backbone

**RP:** Zcorp with plaster

#### Description:

Congenital vertebral malformations (CVMs) comprise a group of spinal abnormalities that include alterations in vertebral shape or number. Evidence suggests CVMs have a genetic link, possibly resulting from mutations in multiple genes. One candidate gene is T. T protein, a transcription factor found in a variety of animals including humans, is essential for correct embryonic development and guides the development of bone and cartilage from embryonic mesodermal tissue. T protein accumulates in the nuclei of notochord cells, interacts with DNA at specific genes, and acts as a genetic switch to activate the genes. T protein binds to the major and minor grooves of DNA as a dimer. Mutations in T (turning “off” the T protein switch) are hypothesized to result in defects in spinal development. The Cedarburg SMART (Students Modeling A Research Topic) Team has designed a partial model of T protein using 3D printing technology to investigate its structure-function relationship, focusing primarily on the residues important for dimerization of T (Pro125, Asp126, and Pro128) and for binding DNA (Arg67). A 3D model could indicate how the location of the mutations may impact the function of T. T could consequently be a potential target for the development of treatment or prevention options. Program supported by a grant from NIH-CTSA.



### Specific Model Information:

- The carbon backbone of T protein is colored papaya whip.
- The alpha helices are colored purple.
- The beta sheets are colored lavender.
- The amino acids involved in dimer formation of T protein (Pro125, Pro128, and Asp126) are colored yellow.
- The amino acid (Arg67) that interacts with Guanine157 of DNA is colored blue.
- The DNA double helix is colored cyan.
- Guanine517 is colored grey. (Arg67 of T protein interacts with this guanine in DNA)
- Hydrogen bonds and structural supports (struts) are colored white.

<http://cbm.msoe.edu/smartTeams/>

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