



Hartford Union High School SMART Team

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Serine Rich Splicing Factor 2 (SRSF2) Flips for RNA Binding

PDB: 2LEB

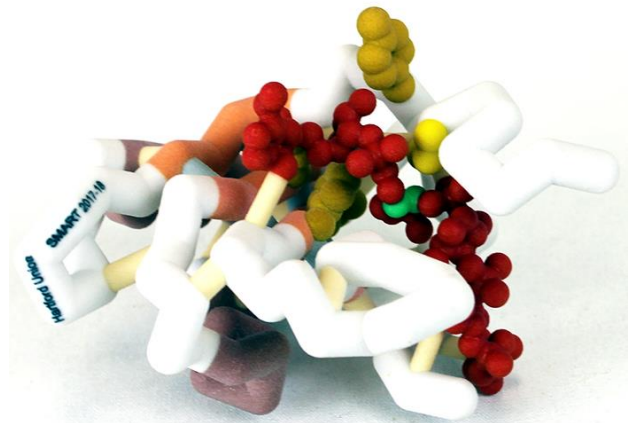
Primary Citation: Daubner GM, Cléry A, Jayne S, Stevenin J, Allain F H-T (2012). A syn-anti conformational difference allows SRSF2 to recognize guanines and cytosines equally well. *EMBO J.* 31:162-74

Format: Alpha carbon backbone

RP: Zcorp with plaster

Description:

Mistakes in alternative splicing of RNA cause diseases such as acute myeloid leukemia. Serine Rich Splicing Factor 2 (SRSF2) is a splicing factor that controls alternative splicing by promoting exon inclusion, so it is not surprising that mutations to SRSF2 are linked to cancers. SR proteins harbor an RNA recognition motif (RRM) at the N-terminus that binds to mRNA. SRSF2 has the unusual ability to bind to both pyrimidine and purine rich RNA sequences by flipping two C or G nucleotides in the mRNA into anti or syn orientations. The RRM specifically recognizes only C2, C3, and G5. Arg61 forms a hydrogen bond to C3, Phe59 hydrogen bonds to C2, and Lys17 is involved in flipping C2 or G2 into syn or anti conformations. Tyr92 binds with C2 and forms a hydrogen bond with C3. The mutation Pro95His binds better to UCCAGU and has been linked to cancer. The Hartford Union High School SMART (Students Modeling A Research Topic) Team modeled SRSF2 using 3D printing technology to highlight structural characteristics involved in RNA binding. Additional research on SRSF2 mutations and sequence binding has the potential to find both causes of and treatments for diseases like cancer.



Specific Model Information:

Amino acid side chains involved:

- tyr92-golden rod
- lys17-golden rod
- phe59-golden rod
- arg61-golden rod
- pro95-yellow

The amino acids displayed in this model of SRSF2 are tyr92, lys17, phe59, pro95 and arg61.

They are believed to play a role in binding the RNA to the protein by allowing the protein to recognize two different sequences, anti and syn. Specifically, pro95 is the location of the change seen in the configurations, so it is separately highlighted. The ability to switch the amino acid orientation gives this protein that unique ability to recognize the different sequences on the RNA.

Highlighted protein structures:

- Alpha helix structures are colored rosy brown
- Beta sheet structures are colored light salmon
- Hydrogen bonds are colored silver
- Backbone is colored white smoke
- RNA is colored fire brick
- C3 and C4 of the RNA is colored medium spring green

Supporting Features:

- Struts are colored papaya whip

CBM SMART Teams Website:

<http://cbm.msos.edu/smartTeams/smartTeamsLocal.php>