TRANSFAC®s Matrix Library

Offering unparalleled advantages for binding site prediction

BIOBASE
BIOLOGICAL DATABASES

Transcription factors are recognized as important components of signaling cascades controlling all types of normal cellular processes as well as response to external stimulus, conditions of disease, drug treatment and more. While functional studies of transcription factors can provide indirect clues to the genes regulated by a single transcription factor under a specific set of experimental conditions, it's only through transcription factor binding site analysis that we can understand the mechanism of regulation, including coordinate regulation by multiple transcription factors acting together, and effectively identify and characterize mutations disrupting the regulatory mechanism. As there are comparatively few experimentally characterized binding sites known relative to the total number expected, the ability to reliably predict as yet uncharacterized binding sites is a critical and unparalleled tool in the quest to understand normal as well as disease processes. Binding site predictions, however, are only as reliable as the data upon which they are based.

TRANSFAC® has been built by manually curating transcription factor – target gene relationships from the peer-reviewed scientific literature, with a focus on directly targeted transcription factor DNA binding experiments supplemented with data from high-throughput methods such as ChIP-chip and ChIP-seq, SELEX and protein-binding microarrays. These published, experimentally verified binding sites are then aligned and used to create a consensus binding sequence or motif for a transcription factor. TRANSFAC®s extensive library of binding matrices can be used by the included MATCH™ analysis tool, or downloaded independently, to predict the most probable transcription factor binding sites within the promoter of any gene.

TRANSFAC®s matrix library offers:

- The broadest transcription factor coverage available
- Full transparency regarding how each matrix was constructed including, when relevant, the binding sites used and supporting experimental details from the literature
- More than one matrix for many transcription factors, providing independent confirmation of binding site preferences through complementary experimental methods
- Quarterly updates incorporating information from the most recently published literature
- A commitment to advancing research into the latest matrix generation techniques, most recently leading to development of a novel algorithm to calculate matrices from 3 dimensional protein-DNA structures

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