The Bejerano Lab at Stanford University developed the Predicting Regulatory Interactions from Single Motifs (PRISM) and Complexes tool and hosts the PRISM/Complex web server at \( \text{http://bejerano.stanford.edu/prism} \) and \( \text{http://bejerano.stanford.edu/complex} \), respectively.

Understanding vertebrate development requires unraveling the cis-regulatory architecture of gene regulation. PRISM provides accurate genome-wide computational predictions of transcription factor binding sites for the human and mouse genomes, and integrates the predictions with GREAT to provide functional biological context. Together, accurate computational binding site prediction and GREAT produce for each transcription factor:

1. putative binding sites
2. putative target genes
3. putative biological roles of the transcription factor
4. putative cis-regulatory elements through which the factor regulates each target in each functional role.

PRISM/Complex Help

General

- Citation - How do I cite PRISM/Complex?
- Publications & Reprints
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Output

- Transcription Factors - Which transcription factors are assayed in PRISM?
- Output - What output does PRISM provide?
- Table Filters - How can I filter the table of enrichments for entries that satisfy particular criteria?