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cis-regulatory modules

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Deciphering the regulatory codes that dictate developmental and tissue-specific patterns of transcriptional control is a formidable challenge. In the January 22 [Proceedings of the National Academy of Sciences](#), Berman *et al.* describe a computational approach to explore the grammar of cis-regulatory modules (*Proc Natl Acad Sci USA* 2002, **99**:757-762). They focused on the *Drosophila* genome and searched for high, local densities of binding sites for multiple transcription factors (Bicoid, Caudal, Hunchback, Kruppel and Knirps) using position weight matrices. They identified clusters of binding sites that defined cis-regulatory modules implicated in developmental expression patterns. These clusters were located adjacent to genes exhibiting localized anterior-posterior expression. An accompanying paper by Markstein *et al.* describes a similar study using clusters of binding sites to identify novel target genes for the Dorsal transcription factor (*Proc Natl Acad Sci USA* 2002, **99**:763-768). Both reports highlight the value of combining *in silico* predictions of cis-regulatory modules with experimental confirmation of target gene networks.

References

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2. Cis-analyst, [<http://www.fruitfly.org/cis-analyst>]
3. A cascade of transcriptional control leading to axis determination in *Drosophila*.