

## IN BRIEF

**RESOURCE****A comprehensive catalogue of human RNA-binding protein reagents**

A new resource of validated antibodies and short hairpin RNA (shRNA) constructs that recognize and target human RNA-binding proteins (RBPs) promises to help foster our understanding of RBP function. Sundararaman *et al.* tested the efficiency and specificity of 700 commercially available antibodies for 535 target RBPs. Using immunoprecipitation followed by western blot assays, the authors generated a validated catalogue of 438 commercially available antibodies that interrogate 365 RBPs. Antibody specificity was confirmed using 362 shRNA constructs against 276 unique RBPs. Subcellular RBP localization can be determined using these antibodies, as verified by immunofluorescence assays. These resources should prove valuable for mapping of functional RNA elements in the human transcriptome. Information about these resources is available at <https://www.encodeproject.org>.

**ORIGINAL ARTICLE** Sundararaman, B. *et al.* Resources for the comprehensive discovery of functional RNA elements. *Mol. Cell* <http://dx.doi.org/10.1016/j.molcel.2016.02.012> (2016)

**GENETIC VARIATION****New tool to map genetic modifiers of transcription factor–gene target connections**

Fazlollahi *et al.* have developed a computational approach to determine genetic variants that affect the functional interactions of gene regulatory networks. Using this algorithm, the team were able to map so-called connectivity quantitative trait loci (cQTLs). These cQTLs are natural genetic variants that influence the regulatory interactions of specific transcription factors and their target genes (for example, a polymorphism that occurs in the coding or promoter sequence of a required cofactor). Application of the algorithm to yeast genotype and gene expression data revealed a non-synonymous polymorphism in the *DIG2* gene that acts as a cQTL for the transcription factor Ste12p. That is, the variant modulates the strength of the Ste12p-mediated transcriptional response to mating pheromone, as validated experimentally, through its alteration of the encoded amino acid sequence.

**ORIGINAL ARTICLE** Fazlollahi, M. *et al.* Identifying genetic modulators of the connectivity between transcription factors and their transcriptional targets. *Proc. Natl Acad. Sci. USA* <http://dx.doi.org/10.1073/pnas.1517140113> (2016)

**BIOINFORMATICS****Taking the epigenome to another dimension**

A new algorithm called EpiTensor can infer 3D genomic contacts from 1D maps of epigenomic data. The team analysed 16 histone modifications, DNase I sequencing and RNA sequencing data in five cell types to identify spatial patterns within topologically associating domains (TADs) at a resolution of 200 bp. Associations between promoters and enhancers, promoters and promoters, and between enhancers and enhancers that were identified by EpiTensor mirrored those determined using alternative approaches, such as Hi-C, ChIA-PET (chromatin interaction analysis by paired-end tag sequencing) or expression quantitative trait loci analyses. EpiTensor also detected interaction hotspots, which exhibited increased chromatin and transcriptional activity and were enriched for transcription factor and long non-coding RNA binding across cell types.

**ORIGINAL ARTICLE** Zhu, Y. *et al.* Constructing 3D interaction maps from 1D epigenomes. *Nat. Commun.* <http://dx.doi.org/10.1038/ncomms10812> (2016)