

TRANSFAC® release 2018.3

The TRANSFAC® database on transcription factors, their genomic binding sites and DNA-binding motifs (PWMs), contains these new data features:

- **HOCOMOCO v11 core collection added to matrix library**

311 human and 250 mouse matrices from [HOCOMOCO's v11](#) core collection of transcription factor binding models have been imported.

- **Integration of new human ChIP-Seq experiments from ENCODE**

38 new human transcription factor binding site ChIP-Seq experiments released by the between February 2018 and May 2018 have been integrated. The data sets comprise 690,754 fragments bound by 29 distinct transcription factors, of which 12 factors were not yet covered by ChIP-Seq data.

For 14 of the sets, an existing positional weight matrix for the respective transcription factor was used together with the MATCH tool to predict altogether 436,024 best binding sites inside the fragments.

Predicted best binding sites as well as complete fragments are available in FASTA and BED format via the ChIP Experiment Reports, as are lists of genes in a distance range to the fragments as specified by the user.

- **Interactions between transcription factors**

1,529 new and 114 updated human and mouse interactions between transcription factors have been added based on data published in "Ravasi T. et al, An atlas of combinatorial transcriptional regulation in mouse and man. Cell. 2010 Mar 5;140(5):744-52, PubMed PMID: [20211142](#)".

- **Enhanced human SNP content**

The new 2018 dbSNP Build 151 data for human has been integrated and increases the number of SNPs mapped to human promoter sequences from 73,423,232 in the last release to 142,487,394.

- **Ensembl version update**

Genomic information for genes, promoters, and ChIP fragments for the species human, mouse, rat, macaque, and Arabidopsis is now based on Ensembl release 93.