

TRANSFAC® release 2022.2

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

- **Increase in enhancer-target genes relations**

57,038 additional enhancer – target gene relations have been imported from the FOCS (<http://acgt.cs.tau.ac.il/focs>) web site.

- **Additional interactions between human transcription factors**

7,949 human transcription factor interactions have been included from a recent publication (<https://pubmed.ncbi.nlm.nih.gov/35140242>).

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

70 new human transcription factor binding site ChIP-Seq experiments released by the ENCODE phase 4 project and further publications have been integrated. The data sets comprise 603,016 fragments bound by 66 distinct transcription factors, of which 19 factors were not yet covered by ChIP-Seq data in TRANSFAC.

For 54 of the sets, an existing positional weight matrix for the respective transcription factor was used together with the MATCH tool to predict altogether 436,596 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.