

TRANSFAC® release 2023.2

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

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

91 new human transcription factor binding site ChIP-Seq experiments released by the ENCODE phase 4 project have been integrated. The data sets comprise 1,029,262 fragments bound by 85 distinct transcription factors, of which 33 factors were not yet covered by ChIP-Seq data in TRANSFAC.

For 58 of the sets, an existing positional weight matrix for the respective transcription factor was used together with the MATCH tool to predict altogether 615,813 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.

- **New matrices derived from ENCODE ChIP-Seq data**

24 new positional weight matrices for yet uncovered human transcription factors have been generated from new ENCODE phase 4 ChIP-Seq data and integrated into the TRANSFAC matrix library.