TRANSFAC® release 2023.1

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

- **JASPAR 2022 matrix library integration**

  New position frequency matrices from the JASPAR 2022 release either added as matrix entries (375 cases) or hyperlinked to existing counterparts in the TRANSFAC matrix library.

- **Additional interactions between human transcription factors**

  13,100 new human transcription factor interactions have been included from BIOGRID.

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

  162 new human transcription factor binding site ChIP-Seq experiments released by the ENCODE phase 4 project have been integrated. The data sets comprise 1,700,273 fragments bound by 143 distinct transcription factors, of which 39 factors were not yet covered by ChIP-Seq data in TRANSFAC.
  For 134 of the sets, an existing positional weight matrix for the respective transcription factor was used together with the MATCH tool to predict altogether 1,316,751 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**

  12 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