

The TRANSFAC® Database

Dating back as early as 1988, when the first data collection of transcription factors (TFs) and their binding sites was published [Wingender, Nucleic Acids Res. 16:1879-1902, 1988], TRANSFAC® has been the first and is the most comprehensive database on eukaryotic transcription regulation. It has been merged with TRANSCompel (a database on composite elements) and TRANSpro (a comprehensive collection of promoters of human and eight other genomes).

TRANSFAC® is now also available under the geneXplain platform, providing the most comprehensive collection of TF DNA-binding profiles available for the state-of-the-art sequence analysis implemented in the platform.

GeneXplain offers a one-stop shopping solution for the platform together with the TRANSFAC® database as well as stand-alone solutions.

Applications

The most popular application of TRANSFAC contents is the prediction of potential transcription factor binding sites (TFBSs). Its contents can also be used to train own pattern finding algorithms, or to mine the wealth of information about transcription factors.

Further reading

Wingender, E. (2008) The TRANSFAC project as an example of framework technology that supports the analysis of genomic regulation. *Brief. Bioinform.* 9:326-332.

About geneXplain

GeneXplain's mission is to provide a comprehensive platform for bioinformatic, systems biological and cheminformatic tools. The raison d'être of this platform is to assist translational research in the life sciences, mainly in the context of personalized medicine and pharmacogenomics. We intend to make our expertise available to academic and commercial partners in collaborative research projects.

To achieve this, geneXplain offers:

- The geneXplain platform providing a large number of bioinformatic and systems biological data analysis workflows. Unique is geneXplain's Upstream Analysis for causal interpretation of expression data.
- TRANSPATH®, one of the largest pathway/network databases presently available, particularly well suited for geneXplain's proprietary *Upstream Analysis*.
- HumanPSD, a rich information resource connecting pathways with targets, drugs and clinical trials.
- PASS and PharmaExpert for predicting biological activities of compounds qualitatively
- GUSAR for QSAR model building and quantitative activity prediction

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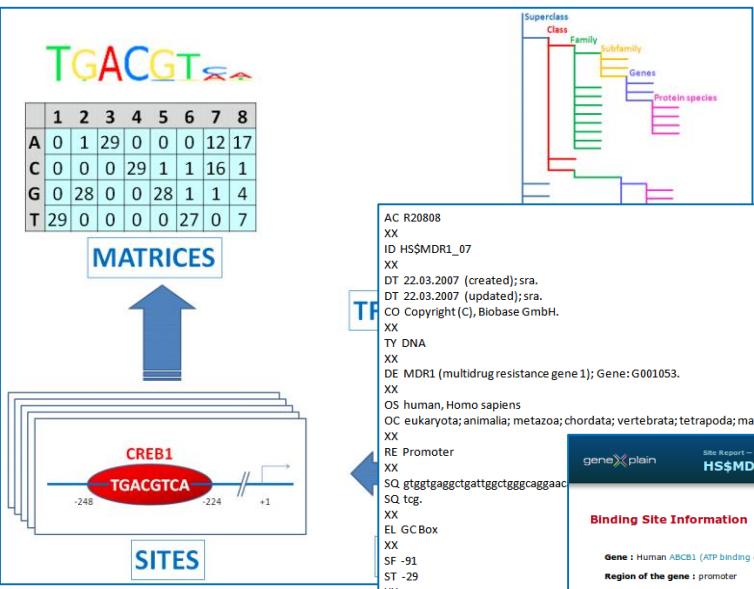


*The database of
transcription factors,
their genomic binding
sites, and DNA-binding
profiles*

TRANSFAC®

geneXplain

TRANSFAC®: the database on eukaryotic transcription



Key features

- 71,000+ transcription factor binding site reports containing details from the primary literature for more than 300 species, with a focus on human, mouse, rat, yeast, and plants
- 48,000+ transcription factor and miRNA reports, a subset of which provide GO functional assignments, disease associations and expression pattern assignments
- 99,000,000+ ChIP fragment reports that include the best scoring site prediction for the respective factor as well as downloadable sequences and gene lists
- 355,000+ promoter reports including ChIP-chip/Seq based histone modification locations, transcription start sites, and single nucleotide polymorphisms (SNPs)
- A pathway visualization tool for building custom regulatory networks out of experimentally demonstrated factor-DNA and factor-factor interactions

Site & promoter analysis

Using the rich library of 6500+ positional weight matrices of the TRANSFAC® database, DNA sequences can be scanned for potential transcription factor binding sites. One option for this is the proven tool Match™, which comes along with a standard TRANSFAC® license, or to use one of the new sophisticated tools that are additionally provided by the geneXplain platform.

Availability

The most up-to-date version of TRANSFAC® can be obtained either

- for downloading as textual flat files, to have the full content locally at your disposal;
- for online access through the geneXplain platform, making full use of the rich functionality of this unique toolbox, or
- for online use of the familiar look-and-feel provided by a dedicated server, or
- any combination of these options.

The structure

The core of TRANSFAC® comprises contents of two domains: Eukaryotic transcription factors (TFs) and TF binding sites (TFBSs).

Binding sites referring to the same TF are merged into **positional weight matrices (PWM)**. A PWM reflects the frequency with which each nucleotide is found in each position of the known and aligned TFBSs and, thus, the base preference in each position.

Transcription factors are classified based on the general properties of their DNA-binding domains. The most up-to-date and comprehensive **TF classification** available has been included in the geneXplain platform.

Encyclopedic use

TRANSFAC® is the most comprehensive encyclopedia about eukaryotic transcription factors. The structural and functional properties of each factor are documented by extensive manual annotation from the scientific literature by the BIOBASE team.

Individual TFBSs are documented including experimental details and a corresponding quality assessment.

Overview of high-throughput data

TRANSFAC® also documents HTP data on TF binding sites in eukaryotic genomes, usually from ChIP-chip or ChIP-seq experiments. These data are carefully selected and interpreted w.r.t. the binding regions and motifs found in the corresponding data sets.

AC R20808
 XX
 ID H5\$MDR1_07
 DT 22.03.2007 (created);sra.
 DT 22.03.2007 (updated);sra.
 CO Copyright (C), Biobase GmbH.
 XX
 TY DNA
 XX
 DE MDR1 (multidrug resistance gene 1); Gene: G001053.
 XX
 OS human, Homo sapiens
 OC eukaryota; animalia; metazoa; chordata; vertebrata; tetrapoda; mammalia; eutheria; primates
 XX
 RE Promoter
 XX
 SQ gtggtgaggctgattggctggcgaggaaac
 SQ tgc-
 XX
 EL GCBox
 XX
 SF -91
 ST -29
 XX
 BF T00759; Sp1; Quality: 3; Species
 XX
 SO 0130; KB-3-1.
 SO 3658; KB-3-1+UV.
 XX
 MM direct gel shift
 MM functional analysis
 MM supershift (antibody binding)
 XX
 CC This site is required for UV irradi
 XX
 DR TRANSPRO:HSA_12513_1.
 XX
 RN [1]; RE0049631.
 RX PUBMED:10644769.
 RA Hu Z, Jin S, Scotto K. W.
 RT Transcriptional activation of the
 RL J. Biol. Chem. 275:2979-2985 (2
 XX
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geneXplain
 Site Report - ABCB1 (ATP binding cassette, sub-family B (MRK/TAP), member 1)
 H5\$MDR1_07
 Table of Contents

Binding Site Information what is this?

Gene: Human ABCB1 (ATP binding cassette subfamily B member 1)
 Region of the gene: promoter
 Sequence: gtggtgaggctgattggctggcgaggaaac
 Sequence type: DNA
 Position (relative to TSS unless stated): from -91 to -29
 Genomic coordinates: Build hg38: Chr7:87600913-87600975 -
 Description: GC Box
 Promoters that the element is mapped to:
 ABCB1 (Promoter: 87601072) - Build hg38: Chr7:87600913-87600975

Binding factors (with assigned measure of interaction)

Sp1(h) Quality:3

Experimental source of the factors:

KB-3-1; Human; epidermoid carcinoma cell line;
 KB-3-1 + UV; Human; epidermoid carcinoma cell line

Method which measured binding: Functional analysis

Identifiers what is this?

BIOBASE accession: R20808
 External accessions:
 Genbank: M29423.1; (348-410)

Annotations what is this?

• This site is required for UV irradiation-dependent pro

References (1)

Show 5 entries

SLNo	PMID	Citation
1	10644769	Hu, Z., Jin, S., Scotto, K. W., 2979-85. (2000). Show abstract

Showing 1 to 1 of 1 entries

ENS0000022926

VSGR_Q6_01	8	GR
VSGSC_01	17	Gsc
VSGSH2_01	16	GSH2
VSGTF2IRB1_01	9	GTF2IRD1-isoform
VSGZF1_01	12	
VSHAND1E47_01	16	
VSHB24_01	15	
VSHBB_01	16	
VSHBP1_Q2	9	
VSHDX_01	17	Hdx
VSHIB_Q6	8	HEB
VSHILOSA_01	11	Helos A
VSHILOSA_Q2	11	Helos A

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Showing 1 to 50 of 1815 entries

ID	Symbol	Site view	Total count
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ENS0000022778	XXyc:YX598.2		8
ENS0000022926	RP11-146L1		8
ENS00000174796	THAP8		6
ENS00000182293	SVNM		6
ENS00000196507	TCEAL3		6
ENS0000022778	AMY1A		6
ENS00000249338	AMY2B		6
ENS00000001961	FNFR1		6

ExtendedGeneTrack
 VSDMRT3_01.V59F_Q6
 VSNXC_01 VSNX_02 VSNX_Q3 V59F_Q6
 VSNXVNT1_01 VSNX_01 VSNX22_01
 VSNXC_01
 Score: 0.9691939949989319
 Model: VSNXC_01
 Properties: