

Resource Summary Report

Generated by [ASWG](#) on Aug 23, 2026

ABS: A Database of Annotated Regulatory Binding Sites From Orthologous Promoters

RRID:SCR_002276

Type: Tool

Proper Citation

ABS: A Database of Annotated Regulatory Binding Sites From Orthologous Promoters (RRID:SCR_002276)

Resource Information

URL: <http://genome.imim.es/datasets/abs2005/index.html>

Proper Citation: ABS: A Database of Annotated Regulatory Binding Sites From Orthologous Promoters (RRID:SCR_002276)

Description: Public database of known binding sites identified in promoters of orthologous vertebrate genes that have been manually curated from bibliography. We have annotated 650 experimental binding sites from 68 transcription factors and 100 orthologous target genes in human, mouse, rat or chicken genome sequences. Computational predictions and promoter alignment information are also provided for each entry. For each gene, TFBSs conserved in orthologous sequences from at least two different species must be available. Promoter sequences as well as the original GenBank or RefSeq entries are additionally supplied in case of future identification conflicts. The final TSS annotation has been refined using the database dbTSS. Up to this release, 500 bps upstream the annotated transcription start site (TSS) according to REFSEQ annotations have been always extracted to form the collection of promoter sequences from human, mouse, rat and chicken. For each regulatory site, the position, the motif and the sequence in which the site is present are available in a simple format. Cross-references to EntrezGene, PubMed and RefSeq are also provided for each annotation. Apart from the experimental promoter annotations, predictions by popular collections of weight matrices are also provided for each promoter sequence. In addition, global and local alignments and graphical dotplots are also available.

Abbreviations: ABS

Synonyms: A database of Annotated regulatory Binding Sites from orthologous promoters

Resource Type: data or information resource, database

Defining Citation: [PMID:16381947](https://pubmed.ncbi.nlm.nih.gov/16381947/)

Keywords: gene, alignment, annotation, binding, computational, genome, nucleotide, ortholog, prediction, promoter, sequence, target, transcription, transcriptional factor, binding site, promoter sequence, protein motif, benchmark, transcription factor binding site, bio.tools

Funding: European Union FP6 contract LSHG-CT-2003-503265

Availability: Acknowledgement requested, GNU General Public License, v2

Resource Name: ABS: A Database of Annotated Regulatory Binding Sites From Orthologous Promoters

Resource ID: SCR_002276

Alternate IDs: biotools:alggen, nif-0000-21006

Alternate URLs: <https://bio.tools/alggen>

Record Creation Time: 20220129T080212+0000

Record Last Update: 20260821T193640+0000

Ratings and Alerts

No rating or validation information has been found for ABS: A Database of Annotated Regulatory Binding Sites From Orthologous Promoters.

No alerts have been found for ABS: A Database of Annotated Regulatory Binding Sites From Orthologous Promoters.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at [ASWG](#) .

Marini MG, et al. (2026) Reduced cyclin D3 expression in erythroid cells protects against malaria. Nature, 651(8106), 698.

Pavlovic D, et al. (2025) Transcript PHF19-207 May Be a Long Non-Coding RNA with Tumor-Promoting Role in Colon Cancer. Biomolecules, 15(7).

Blanco E, et al. (2006) ABS: a database of Annotated regulatory Binding Sites from orthologous promoters. Nucleic acids research, 34(Database issue), D63.