

# Resource Summary Report

Generated by [kravitz2](#) on Jul 29, 2026

## SELEX DB

RRID:SCR\_007921

Type: Tool

### Proper Citation

SELEX DB (RRID:SCR\_007921)

### Resource Information

**URL:** <http://wwwmgs.bionet.nsc.ru/mgs/systems/selex/>

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**Description:** A database for the accumulation of experimental data on selected affinity-enriched sequences from different combinatorial libraries. During the last ten years, the novel technologies have been designed for identification of high affinity DNA and RNA sequences (ligands) to a wide variety of different targets, including nucleic acid binding proteins, peptides, and small organic molecules. Among these technologies are the following: SELEX (Systematic Evolution of Ligands by Exponential enrichment), SAAB (Selected And Amplified Binding site imprint assay), REPSA (Restriction Endonuclease Protection Selection and Amplification), CASTing (Cyclical Amplification and Selection of Targets) and other binding site selection procedures. In general, genetic analysis in vitro of the structural and functional properties of many nucleic acids was enhanced by the availability of methods for the amplification of nucleic acid sequences. Given current advance in sequencing whole genomes, combinatorial methods will be important in the next generation of studies, thus making the bridge between raw sequence data and actual biological processes. At present, enormous starting libraries are used in different SELEX processes and contain up to  $10^{14}$ – $10^{15}$  sequences. Naturally, this information needs to be collected into public databases available via the Internet. The site sequences listed within the SELEX\_DB may be used as independent control data in developing both novel methods for functional site recognition within gene sequences and recognition under concrete experimental conditions documented in the database. Additionally, information on functional site sequences and experimental conditions for their determination is useful for planning novel experiments applying SELEX technology.

**Abbreviations:** SELEX\_DB

**Resource Type:** data or information resource, database

**Resource Name:** SELEX DB

**Resource ID:** SCR\_007921

**Record Creation Time:** 20220129T080244+0000

**Record Last Update:** 20260729T044214+0000

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## Ratings and Alerts

No rating or validation information has been found for SELEX DB.

No alerts have been found for SELEX DB.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. Nucleic acids research, 33(Database issue), D5.

Ladd AN, et al. (2002) Finding signals that regulate alternative splicing in the post-genomic era. Genome biology, 3(11), reviews0008.