

## Mouse OligoLibrary™

The Mouse OligoLibrary™ by Compugen and Sigma-Genosys combines Compugen's superior computational platform and oligo design tools with Sigma's high-quality oligo synthesis.

### The difference is design

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#### Accurate and comprehensive transcriptome data

Compugen's proprietary LEADS™ platform for transcriptome prediction performs accurate clustering and assembly of EST and mRNA sequences. LEADS clustering algorithms take into account novel and known repetitive elements, low complexity regions, chimeric sequences, vector contamination, and correct sequence orientation. LEADS assembly algorithms correct for sequencing errors, predict antisense genes, and use expressed and genomic data to model alternative splicing and predict transcripts for each gene. Selecting oligos from the fully assembled LEADS clusters instead of representative sequences increases sensitivity and specificity.

#### Optimal probe selection

- **Alternative splicing structure** is incorporated by selecting probes from regions that are common to a maximal number of predicted splice variants.
- **Cross-homology** is minimized for the highest specificity.
- **Sequence quality** is maintained by avoiding sequencing errors and polymorphic sites.
- **GC content / melting temperature** is normalized across the collection to ensure identical hybridization conditions for all of the probes.
- **Distance from the 3' end** is minimized to enable hybridization to the cDNA produced by oligo (dT) reverse transcription of RNA.
- **Secondary structures**, such as hairpins and palindromes, are avoided for minimal self-hybridization.

### The Mouse OligoLibrary at a glance

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The Mouse OligoLibrary is comprised of the original library and an extension. In the original library, one oligo per gene was designed for each mouse gene identified in GenBank 121. The annotations for these oligos are periodically updated to accurately reflect the available data. The extension is designed to reflect the rapid accumulation of data in the public domain since the release of the original library and contains oligos representing all of the mouse genes associated with public mRNA sequences found in GenBank 126 and not represented in the original library.

Mouse Library	Catalog number	Number of oligos	Unique genes (LEADS clusters) represented	Quantity per oligo	Oligo length / modification	Number of 96-well plates*
Complete	MOULIB96T	21,997	21,587	1 nmole (500 pmole also available)	65 bp / 5'-C6 amino modifier	231
Extension	MOULIB96B	14,473	14,321	Same	Same	152
Evaluation	MOULIBTST	96	95	1 nmole	Same	1

\*The OligoLibrary is also available in custom 384-well plates. The evaluation plate is available only in 96-well format.

### Quality control

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The OligoLibrary is manufactured using Sigma-Genosys' patented Abacus oligo synthesis platform and is subject to stringent analysis, which ensures the highest oligo quality:

- Statistical MALDI-TOF mass spectrometry is performed on every batch of synthesized oligos to confirm molecular weight and to ensure correct well location and oligo sequence.
- Sigma-Genosys' proprietary closed loop synthesis technology provides coupling efficiency of 99% to ensure more pure full-length product. PAGE analysis is used to verify oligo lengths.
- OD measurements on every oligo provide a high quality control standard.

*Over, please...*

For more information and pricing, please contact us:  
Tel.: (800) 234-5362 (US toll-free number)  
(1) (609) 655-5105 (outside US)

[support@labonweb.com](mailto:support@labonweb.com)  
<http://www.labonweb.com/oligo>



## Plate selection by Gene Ontology assignment

You can purchase the complete Mouse OligoLibrary, the Mouse OligoLibrary Extension, or subsets of four 96-well plates. Oligos are arranged on the plates according to standard Gene Ontology (GO) assignments for easy selection of oligos derived from genes with similar function. GO annotation was developed by Compugen using nomenclature obtained from the Gene Ontology Consortium ([www.geneontology.org](http://www.geneontology.org)).

Catalog number	Plates	Description based on GO assignments
MOU96-1, 7, 31, 32	1–4, 25–28, 120–127	Metabolism
MOU96-2, 34	5–8, 132–135	Nucleobase, nucleoside, nucleotide, and nucleic acid metabolism
MOU96-3, 4, 35	9–16, 136–139	Transcription regulation
MOU96-5	17–20	Protein metabolism and modification
MOU96-6, 33	21–24, 128–131	Proteolysis and peptidolysis
MOU96-8, 37	29–32, 144–147	Transport
MOU96-9	33–36	Intracellular protein traffic
MOU96-10	37–40	Response to biotic stimulus
MOU96-11	41–44	Cytoplasm organization and biogenesis
MOU96-12	45–48	Oncogenesis
MOU96-13, 30	49–52, 116–119	Cell cycle
MOU96-14	53–56	Cell adhesion
MOU96-15, 29	57–60, 112–115	Signal transduction
MOU96-16	61–64	Cell surface receptor linked signal transduction
MOU96-17	65–68	Developmental processes
MOU96-18, 39	69–72, 152–155	Histogenesis and organogenesis
MOU96-19, 20, 40–58	73–79, 156–231	GO unknown
MOU96-21	80–83	Cell communication
MOU96-22 to 28	84–111	Immune response
MOU96-36	140–143	Protein amino acid phosphorylation
MOU96-38	148–151	Embryogenesis and morphogenesis

## Gene lists and oligo information

With each order of a complete library or library subset, you will receive a product-specific code. The code will give you access to Compugen's LabOnWeb.com, where you will find detailed information about the oligos and genes, including accession numbers, sequence information, gene annotation, GO assignments, and more.

## Product specifications

- **Quantity:** 1 nmole per well (lyophilized) or 20 µl per well, conc. 50 µM (hydrated).
- **Modification:** 5'-C6 amino modifier.
- **Oligo synthesis efficiency:** >99%.
- **Positive control oligo:** One oligo per 96-well plate or four oligos per 384-well plate from GAPDH.
- **Distance from the 3' end:** Average distance from the 3' end is 379 bases.
- **Cross-homology:** Less than 81.5% for 90% of the oligos. Average cross-homology is 37.7%.
- **GC content:** Average GC content is 49.9%.

For more information and pricing, please contact us at (800) 234-5362, (609) 655-5105, or [support@labonweb.com](mailto:support@labonweb.com).

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