



Cat # MOULIB384T Product Profile

Mouse OligoLibrary™ Release 2.0: 384 well format, 58 plates

- Lyophilized, size: 1 nmole/well, store at 4°C (long term at –20 °C)
- Hydrated, size: 20 µl/well, conc.: 50 µM, store at –20 °C

Important: Plates 22-29, 45, 47, 51, and 58 contain empty wells. For the exact location of empty wells, please refer to gene lists available at www.labonweb.com/oligo.

Important note for recipients of the hydrated product: Upon receipt, thaw and quick spin so that the liquid is consolidated at the bottom of each well.

Description

The Mouse OligoLibrary™ Release 2.0 is comprised of the original library (Mouse OligoLibrary™ Release 1.0) and an extension. In the original library, one oligo was designed for each mouse gene identified in GenBank release 121 (December 2000). The annotations of 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 release 126 (October 2001) and not represented in the original library.

The OligoLibrary can be used for various molecular biology experiments, such as expression profiling, specific hybridization, Northern blotting, and more. The oligos in this OligoLibrary are 65-mers with a 5'-C6 amino modification for flexible and universal covalent binding of the oligo to special substrates. The OligoLibrary consists of 21,997 oligonucleotides, which represent 21,587 LEADS™ clusters plus 231 controls.

Oligos in the OligoLibrary are arranged on the plates according to Gene Ontology (GO) assignments. GO annotation is developed by Compugen using nomenclature obtained from Gene Ontology Consortium¹.

The oligo sequences in this product are designed and optimized using the following criteria:

- **Alternative splicing structure.** The oligo sequence is selected from a sequence segment of the gene that is common to a maximal number of predicted splice variants for this gene and that is predicted to be conserved following alternative splicing.
- **Cross-homology.** To minimize cross-hybridization and for the highest specificity, cross-homology of the oligo sequences against all the available sequence information of all the mouse genes is minimized.
- **Sequence quality.** For best hybridization results, the oligos are selected from sequence segments with the best, low error-rate, coverage of mRNA sequences and /or EST sequences, while avoiding sequence segments that include suspected polymorphic sites.
- **GC content.** The GC content of the designed oligos is restricted to a narrow range to guarantee a strict common melting temperature and thus ensure identical hybridization conditions for all the oligos in the OligoLibrary.
- **Distance from the 3' end.** The distance from the 3' end is minimized in order to enable hybridization to the cDNA produced by oligo (dT) reverse transcription of RNA.
- **Secondary structure.** Each oligo sequence is optimized for minimal secondary structure, such as hairpins and palindromes, and for minimal self-hybridization.

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Contact us: tel. (888) 482-9800 (US toll free number)
(1) (609) 655-5105 (outside US)

support@labonweb.com
<http://www.labonweb.com/oligo>



Product specifications

- *Hydrated product*: volume: 20 µl per well, concentration: 50 µM (in H₂O).
- *Lyophilized product*: 1 nmole of oligo lyophilized from water per well.
- Plates: custom 384-well plates.
- Oligo length: 65 bases.
- Modification: 5'-C6 amino modifier.
- Oligo synthesis efficiency (per step): 99%.
- Number of oligos: 21,997.
- Number of genes: 21,587 (excluding controls).
- Positive controls: four oligos per plate from glyceraldehyde-3-phosphate dehydrogenase (GAPDH).
- Distance from the 3' end: 95% of the oligos are within the range of 65–1,072 bases from the 3' end. Average distance from the 3' end is 379 bases.
- Cross-homology: 90% of the oligos contain a predicted cross-homology of less than 81.5%. Average cross-homology is 37.7%.
- Longest full match stretch: in addition to cross-homology percentage, oligos are also selected with a minimal length of sequence identity in the cross-homology alignment.
- GC content: 95% of the oligos contain a GC content within the range of 40%–60%. Average GC content is 49.9%.

Gene list and detailed oligo information

You can access oligo information relating to this product at www.labonweb.com/oligo by entering the product code supplied with the product and **accepting the terms of the LabOnWeb Oligo Sequence Terms of Use Agreement** (found at www.labonweb.com/oligo). Type the product code into the text field to access detailed information including accession numbers, UniGene IDs, sequence information, links to NCBI, gene descriptions, GO assignments, and more.

IMPORTANT INFORMATION

General Terms and Conditions

Any purchase and use of the product shall be subject to the General Terms and Conditions, which are included with the product. Access to and use of the oligo information shall be subject to the terms of LabOnWeb Oligo Sequence Terms of Use Agreement appearing on www.labonweb.com/oligo.

If the purchaser is not willing to accept the General Terms and Conditions or the terms of LabOnWeb Oligo Sequence Terms of Use Agreement, Compugen, Inc. and Sigma-Genosys, Inc. are willing to accept return of unopened product, provided it is returned within 15 days of delivery by Sigma-Genosys to purchaser, for a full refund.

Commercial use licenses

For information on obtaining commercial use licenses, contact support@labonweb.com or call (888) 482-9800 (US toll free number) or (1) (609) 655-5105 (outside US) and ask for customer support.

¹Gene Ontology is a trademark of Gene Ontology Consortium (<http://www.geneontology.org>).

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