

# Resource Summary Report

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## Sequencing of Idd regions in the NOD mouse genome

RRID:SCR\_001483

Type: Tool

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### Proper Citation

Sequencing of Idd regions in the NOD mouse genome (RRID:SCR\_001483)

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### Resource Information

**URL:** <https://www.sanger.ac.uk/collaboration/sequencing-idd-regions-nod-mouse-genome/>

**Proper Citation:** Sequencing of Idd regions in the NOD mouse genome (RRID:SCR\_001483)

**Description:** Genetic variations associated with type 1 diabetes identified by sequencing regions of the non-obese diabetic (NOD) mouse genome and comparing them with the same areas of a diabetes-resistant C57BL/6J reference mouse allowing identification of single nucleotide polymorphisms (SNPs) or other genomic variations putatively associated with diabetes in mice. Finished clones from the targeted insulin-dependent diabetes (Idd) candidate regions are displayed in the NOD clone sequence section of the website, where they can be downloaded either as individual clone sequences or larger contigs that make up the accession golden path (AGP). All sequences are publicly available via the International Nucleotide Sequence Database Collaboration. Two NOD mouse BAC libraries were constructed and the BAC ends sequenced. Clones from the DIL NOD BAC library constructed by RIKEN Genomic Sciences Centre (Japan) in conjunction with the Diabetes and Inflammation Laboratory (DIL) (University of Cambridge) from the NOD/MrkTac mouse strain are designated DIL. Clones from the CHORI-29 NOD BAC library constructed by Pieter de Jong (Children's Hospital, Oakland, California, USA) from the NOD/ShiLtJ mouse strain are designated CHORI-29. All NOD mouse BAC end-sequences have been submitted to the International Nucleotide Sequence Database Consortium (INSDC), deposited in the NCBI trace archive. They have generated a clone map from these two libraries by mapping the BAC end-sequences to the latest assembly of the C57BL/6J mouse reference genome sequence. These BAC end-sequence alignments can then be visualized in the Ensembl mouse genome browser where the alignments of both NOD BAC libraries can be accessed through the Distributed Annotation System (DAS). The Mouse Genomes Project has used the Illumina platform to sequence the entire NOD/ShiLtJ genome and this should help to position unaligned BAC end-sequences to novel non-reference regions of the NOD genome. Further information about the BAC end-sequences, such as their alignment, variation data and Ensembl gene

coverage, can be obtained from the NOD mouse ftp site.

**Abbreviations:** Sequencing of Idd regions in the NOD mouse genome

**Synonyms:** Sequencing of Insulin-dependent diabetes regions in the NOD mouse genome

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

**Defining Citation:** [PMID:23729657](#)

**Keywords:** genome, sequencing, genome sequencing, insulin-dependent diabetes, c57bl/6j, single nucleotide polymorphism, genetic variation, bacterial artificial chromosome, sequence, gene, animal model, clone, annotation, contig

**Related Condition:** Type 1 diabetes, Diabetes

**Funding:** NIAID AI 15416;  
NIDDK ;  
JDRF

**Availability:** Free, Freely available

**Resource Name:** Sequencing of Idd regions in the NOD mouse genome

**Resource ID:** SCR\_001483

**Alternate IDs:** nlx\_152738

**Old URLs:** <http://www.sanger.ac.uk/resources/mouse/nod/>

**Record Creation Time:** 20220129T080207+0000

**Record Last Update:** 20260905T133036+0000

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## Ratings and Alerts

No rating or validation information has been found for Sequencing of Idd regions in the NOD mouse genome .

No alerts have been found for Sequencing of Idd regions in the NOD mouse genome .

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Steward CA, et al. (2013) The non-obese diabetic mouse sequence, annotation and variation resource: an aid for investigating type 1 diabetes. Database : the journal of biological databases and curation, 2013, bat032.